### Reporting Checklist for Nature Neuroscience

This checklist is used to ensure good reporting standards and to improve the reproducibility of published results. For more information, please read [Reporting Life Sciences Research](#).

Please note that in the event of publication, it is mandatory that authors include all relevant methodological and statistical information in the manuscript.

#### Statistics reporting, by figure

- Please specify the following information for each panel reporting quantitative data, and where each item is reported (section, e.g. Results, & paragraph number).
- Each figure legend should ideally contain an exact sample size (n) for each experimental group/condition, where n is an exact number and not a range, a clear definition of how n is defined (for example x cells from x slices from x animals from x litters, collected over x days), a description of the statistical test used, the results of the tests, any descriptive statistics and clearly defined error bars if applicable.
- For any experiments using custom statistics, please indicate the test used and stats obtained for each experiment.
- Each figure legend should include a statement of how many times the experiment shown was replicated in the lab; the details of sample collection should be sufficiently clear so that the replicability of the experiment is obvious to the reader.
- For experiments reported in the text but not in the figures, please use the paragraph number instead of the figure number.

**Note:** Mean and standard deviation are not appropriate on small samples, and plotting independent data points is usually more informative. When technical replicates are reported, error and significance measures reflect the experimental variability and not the variability of the biological process; it is misleading not to state this clearly.

<table>
<thead>
<tr>
<th>TEST USED</th>
<th>n</th>
<th>DESCRIPTIVE STATS (AVERAGE, VARIANCE)</th>
<th>P VALUE</th>
<th>DEGREES OF FREEDOM &amp; F/T/Z/R/ETC VALUE</th>
</tr>
</thead>
<tbody>
<tr>
<td>FIGURE NUMBER</td>
<td>WHICH TEST?</td>
<td>SECTION &amp; PARAGRAPH #</td>
<td>Exact Value</td>
<td>Defined?</td>
</tr>
<tr>
<td>1a</td>
<td>one-way ANOVA</td>
<td>Fig. legend</td>
<td>9, 9, 10, 15</td>
<td>mice from at least 3 litters/group</td>
</tr>
<tr>
<td>results para 6</td>
<td>unpaired t-test</td>
<td>Results para 6</td>
<td>15</td>
<td>slices from 10 mice</td>
</tr>
</tbody>
</table>

Nature Neuroscience: doi:10.1038/nn.3857
<table>
<thead>
<tr>
<th>FIGURE NUMBER</th>
<th>WHICH TEST?</th>
<th>SECTION &amp; PARAGRAPH</th>
<th>n</th>
<th>EXACT VALUE</th>
<th>DEFINED?</th>
<th>SECTION &amp; PARAGRAPH</th>
<th>REPORTED?</th>
<th>EXACT VALUE</th>
<th>SECTION &amp; PARAGRAPH</th>
<th>P VALUE</th>
<th>DEGREES OF FREEDOM &amp; F/T/Z/R/ETC VALUE</th>
</tr>
</thead>
<tbody>
<tr>
<td>2a</td>
<td>Limma moderated t-test</td>
<td>Fig. Legend and Methods</td>
<td>4</td>
<td>different biological replicates in each experimental conditions</td>
<td>fold change</td>
<td>Fig. Legend and Methods</td>
<td>P&lt;0.01, PTGDS (P= 0.00015)</td>
<td>Fig. Legend and Methods</td>
<td>df=6</td>
<td>t(PTGDS)=5.25</td>
<td>Fig. Legend</td>
</tr>
<tr>
<td>2b</td>
<td>one-way ANOVA Dunnett's multiple comparison test</td>
<td>Fig. Legend and Methods</td>
<td>3</td>
<td>different mRNA preparations</td>
<td>error bars are mean +/- SEM</td>
<td>Fig. Legend</td>
<td>P&lt;0.0001</td>
<td>Fig. Legend</td>
<td>F=706.0 R squared= 0.9958</td>
<td>Fig. Legend</td>
<td></td>
</tr>
<tr>
<td>2c</td>
<td>Two tailed unpaired t test</td>
<td>Fig. Legend and Methods</td>
<td>3</td>
<td>different mRNA preparations</td>
<td>error bars are mean +/- SD</td>
<td>Fig. Legend</td>
<td>P= 0.0004</td>
<td>Fig. Legend</td>
<td>t=10.80 df=4</td>
<td>Fig. Legend</td>
<td></td>
</tr>
<tr>
<td>2d</td>
<td>one-way ANOVA Dunnett's multiple comparison test</td>
<td>Fig. Legend and Methods</td>
<td>3</td>
<td>different mRNA preparations</td>
<td>error bars are mean +/- SD</td>
<td>Fig. Legend</td>
<td>Sod3: P= 0.0007 Nfatc4: P= 0.0003</td>
<td>Fig. Legend</td>
<td>F=30.95 R squared= 0.9116 F=40.42 R squared= 0.9309</td>
<td>Fig. Legend</td>
<td></td>
</tr>
<tr>
<td>4b</td>
<td>Two tailed unpaired t test and Linear regression</td>
<td>Fig. Legend and Methods</td>
<td>413 and 371 fibers from 1m wt and ko mice, respectively</td>
<td>The graph represent linear regression analyses slope wt: 0.00236 ± 0.02743 slope ko: -0.004818 ± 0.002799</td>
<td>P= 0.3949 (wt) P=0.0860 (ko)</td>
<td>g ratio: P&lt;0.0001</td>
<td>Fig. Legend</td>
<td>t=13.19 df=782</td>
<td>Fig. Legend</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4c</td>
<td>Two sided Fisher's exact test</td>
<td>Fig. Legend and Methods</td>
<td>Total fibers wt: 413; total fibers ko: 371: 1-2 um wt: 147; 1-2 um ko: 112: 2-3 um wt: 179; 2-3 um ko: 154: 3-4 um wt: 63: 3-4 um ko: 70: 4-5 um wt: 19: 4-5 um ko: 25: 5-6 um wt: 5: 5-6 um ko: 10. Total fibers versus 1-2 um; Total fibers versus 2-3 um; Total fibers versus 3-4 um; Total fibers versus 4-5 um; Total fibers versus 5-6 um</td>
<td>P=0.2811 (total vs 1-2 um) P= 0.7437 (total vs 2-3 um) P= 0.2618 (total vs 3-4) P= 0.2776 (total vs 4-5) P= 0.1917 (total vs 5-6)</td>
<td>Fig. Legend</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>#</td>
<td>4e</td>
<td>Two tailed unpaired t test and Linear regression</td>
<td>Fig. Legend and Methods</td>
<td>155 and 139 fibers from 6m wt and ko mice, respectively</td>
<td>The graph represent linear regression analyses slope wt: 0.009932 ± 0.002540 slope ko: 0.01530 ± 0.002913</td>
<td>P=0.0001 (wt) P &lt;0.0001 (ko) g ratio: P&lt;0.0001</td>
<td>t=9.983 df=292</td>
<td>Fig. Legend</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>----</td>
<td>----</td>
<td>-----------------------------------------------</td>
<td>------------------------</td>
<td>-----------------------------------------------------</td>
<td>-------------------------------------------------</td>
<td>-----------------------------------------------</td>
<td>----------------</td>
<td>-------------</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Total fibers wt: 155; total fibers ko: 139. 1-2 um wt: 42; 1-2 um ko: 17, 2-3 um wt: 52; 2-3 um ko: 53, 3-4 um wt: 34; 3-4 um ko: 36, 4-5 um wt: 12; 4-5 um ko: 22, 5-6 um wt: 8; 5-6 um ko: 8, 6-7 um wt: 3; 6-7 um ko: 2, 7-8 um wt: 4; 7-8 um ko: 1. Total fibers versus 1-2 um; Total fibers versus 2-3 um; Total fibers versus 3-4 um; Total fibers versus 4-5 um; Total fibers versus 5-6 um; Total fibers versus 6-7 um; Total fibers versus 7-8 um</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>4f</td>
<td>Two sided Fisher’s exact test</td>
<td>Fig. Legend and Methods</td>
<td>Total fibers wt: 337; total fibers ko: 378. 1-2 um wt: 215; 1-2 um ko: 264, 2-3 um wt: 105; 2-3 um ko: 106, 3-4 um wt: 15; 3-4 um ko: 7, 4-5 um wt: 0; 4-5 um ko: 1. Total fibers versus 1-2um; Total fibers versus 2-3 um; Total fibers versus 3-4 um; Total fibers versus 4-5um.</td>
<td>The graph represent linear regression analyses slope wt: 0.02408 ± 0.006460 slope ko: 0.01114 ± 0.006805</td>
<td>P= 0.0002 (wt) P=0.1024 (ko) g ratio: P&lt;0.0001</td>
<td>t=6.308 df=713</td>
<td>Fig. Legend</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Total fibers versus 1-2 um; Total fibers versus 2-3 um; Total fibers versus 3-4 um; Total fibers versus 4-5 um; Total fibers versus 5-6 um; Total fibers versus 6-7 um; Total fibers versus 7-8 um</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>5b</td>
<td>Two tailed unpaired t test and Linear regression</td>
<td>Fig. Legend and Methods</td>
<td>337 and 378 fibers from P7 wt and ko mice, respectively</td>
<td>The graph represent linear regression analyses slope wt: 0.02048 ± 0.006460 slope ko: 0.01114 ± 0.006805</td>
<td>P= 0.0002 (wt) P=0.1024 (ko) g ratio: P&lt;0.0001</td>
<td>t=6.308 df=713</td>
<td>Fig. Legend</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>5c</td>
<td>Two sided Fisher’s exact test</td>
<td>Fig. Legend and Methods</td>
<td>Total fibers wt: 337; total fibers ko: 378. 1-2 um wt: 215; 1-2 um ko: 264, 2-3 um wt: 105; 2-3 um ko: 106, 3-4 um wt: 15; 3-4 um ko: 7, 4-5 um wt: 0; 4-5 um ko: 1. Total fibers versus 1-2um; Total fibers versus 2-3 um; Total fibers versus 3-4 um; Total fibers versus 4-5um.</td>
<td>The graph represent linear regression analyses slope wt: 0.02408 ± 0.006460 slope ko: 0.01114 ± 0.006805</td>
<td>P= 0.0002 (wt) P=0.1024 (ko) g ratio: P&lt;0.0001</td>
<td>t=6.308 df=713</td>
<td>Fig. Legend</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Total fibers versus 1-2 um; Total fibers versus 2-3 um; Total fibers versus 3-4 um; Total fibers versus 4-5 um; Total fibers versus 5-6 um; Total fibers versus 6-7 um; Total fibers versus 7-8 um</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Nature Neuroscience: doi:10.1038/nn.3857
<p>| 5e | Two tailed unpaired t test and Linear regression | Fig. Legend and Methods | 148 and 126 fibers from 1m wt and ko mice, respectively | The graph represent linear regression analyses slope wt: -0.01206 ± 0.004728 slope ko: -0.0004691 ± 0.006287 | P = 0.0118 (wt) P = 0.9406 (ko) g ratio: P &lt; 0.0001 | Fig. Legend | t = 6.104 df = 272 | Fig. Legend |
| 5f | Two sided Fisher's exact test | Fig. Legend and Methods | Total fibers wt: 148; total fibers ko: 126; 1-2 um wt: 67; 1-2 um ko: 58; 2-3 um wt: 63; 2-3 um ko: 55; 3-4 um wt: 13; 3-4 um ko: 9; 4-5 um wt: 3; 4-5 um ko: 4. Total fibers versus 1-2 um; Total fibers versus 2-3 um; Total fibers versus 3-4 um; Total fibers versus 4-5 um. | Fig. Legend and Methods | P = 0.9143 (total vs 1-2 um) P = 0.9124 (total vs 2-3 um) P = 0.8245 (total vs 3-4) P = 0.7071 (total vs 4-5) | Fig. Legend |
| 5h | Two tailed unpaired t test and Linear regression | Fig. Legend and Methods | 347 and 349 fibers from 9m wt and ko mice, respectively | The graph represent linear regression analyses slope wt: 0.005172 ± 0.002701 slope ko: 0.007232 ± 0.001948 | P = 0.0563 (wt) P = 0.0002 (ko) g ratio: P &lt; 0.0001 | Fig. Legend | t = 6.386 df = 694 | Fig. Legend |
| 5i | Two sided Fisher's exact test | Fig. Legend and Methods | Total fibers wt: 347; total fibers ko: 349; 1-2 um wt: 90; 1-2 um ko: 83; 2-3 um wt: 140; 2-3 um ko: 128; 3-4 um wt: 80; 3-4 um ko: 71; 4-5 um wt: 26; 4-5 um ko: 42; 5-6 um wt: 9; 5-6 um ko: 17; 6-7 um wt: 1; 6-7 um ko: 5; 7-8 um wt: 1; 7-8 um ko: 2; &gt;8 um wt: 0; &gt;8 um ko: 1. Total fibers versus 1-2 um; Total fibers versus 2-3 um; Total fibers versus 3-4 um; Total fibers versus 4-5 um; Total fibers versus 5-6 um; Total fibers versus 6-7 um; Total fibers versus 7-8 um; Total fibers versus &gt;8 um | Fig. Legend and Methods | P = 0.6116 (total vs 1-2 um) P = 0.5183 (total vs 2-3 um) P = 0.5299 (total vs 3-4) P = 0.0754 (total vs 4-5) P = 0.162 (total vs 5-6) P = 0.2168 (total vs 6-7) P = 1 (total vs 7-8) P = 1 (total vs &gt;8) | Fig. Legend |</p>
<table>
<thead>
<tr>
<th>#</th>
<th>Test Type</th>
<th>Description</th>
<th>n</th>
<th>Unit</th>
<th>Parameter</th>
<th>Error Bars</th>
<th>P-value</th>
<th>t-value</th>
<th>df</th>
<th>P-value</th>
<th>t-value</th>
<th>df</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>5k</td>
<td>Two tailed unpaired t test</td>
<td>% altered fibers/mouse/genotype</td>
<td>3</td>
<td></td>
<td></td>
<td></td>
<td>P &lt; 0.0001</td>
<td>24.17</td>
<td>4</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>6c</td>
<td>Two tailed unpaired t test</td>
<td>number of coverslips</td>
<td>39</td>
<td></td>
<td></td>
<td></td>
<td>P &lt; 0.0001</td>
<td>13.66</td>
<td>76</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>6d</td>
<td>Two tailed unpaired t test</td>
<td>number of MBP+ segments measured</td>
<td>216</td>
<td></td>
<td></td>
<td></td>
<td>P = 0.1772</td>
<td>1.352</td>
<td>430</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>7a</td>
<td>One-way ANOVA Dunnett's multiple comparison test</td>
<td>different mRNA preparations</td>
<td>3</td>
<td></td>
<td>error bars</td>
<td>mean +/- SD</td>
<td>P = 0.6408 wt-shscr</td>
<td>98.33</td>
<td>0.9752</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>7b</td>
<td>One-way ANOVA Dunnett's multiple comparison test</td>
<td>different mRNA preparations</td>
<td>3</td>
<td></td>
<td>error bars</td>
<td>mean +/- SEM</td>
<td>P = 0.0418 (wt)</td>
<td>0.0081 (ko)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>7f</td>
<td>Two tailed unpaired t test and Linear regression</td>
<td>fibers from 2m wt and ko mice, respectively</td>
<td>170 and 233</td>
<td></td>
<td></td>
<td></td>
<td>P = 0.5733 (total vs 1-2 um)</td>
<td>0.3816 (total vs 2-3 um)</td>
<td>0.8086 (total vs 3-4)</td>
<td>0.182 (total vs 4-5)</td>
<td>0.2889 (total vs 5-6)</td>
<td>0.3219 (total vs 6-7)</td>
<td></td>
</tr>
<tr>
<td>7g</td>
<td>Two sided Fisher's exact test</td>
<td>Total fibers wt: 170; total fibers ko: 223. 1-2 um wt: 40; 1-2 um ko: 60. 2-3 um wt: 58; 2-3 um ko: 92. 3-4 um wt: 38; 3-4 um ko: 46. 4-5 um wt: 22; 4-5 um ko: 18. 5-6 um wt: 9; 5-6 um ko: 6. 6-7 um wt: 5; 6-7 um ko: 1.</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Supp</td>
<td>Section</td>
<td>Method</td>
<td>Legend and Methods</td>
<td>Number</td>
<td>Fibers from</td>
<td>The graph represents linear regression analyses: slope wt:</td>
<td>P=</td>
<td>P=</td>
<td>t=</td>
<td>df=</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>------</td>
<td>---------</td>
<td>--------</td>
<td>-------------------</td>
<td>--------</td>
<td>-------------</td>
<td>------------------------------------------------------------</td>
<td>-----</td>
<td>-----</td>
<td>-----</td>
<td>------</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3c</td>
<td></td>
<td>Two tailed unpaired t test and Linear regression</td>
<td>413 and 251</td>
<td>1m wt and ko mice, respectively</td>
<td></td>
<td>0.002336 ± 0.002743 slope ko: 0.008401 ± 0.009872</td>
<td>0.3949 (wt)</td>
<td>0.031 (ko)</td>
<td>0.7964</td>
<td>662</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3d</td>
<td></td>
<td>Two sided Fisher's exact test</td>
<td>Total fibers wt: 413; total fibers ko: 251. 1-2 um wt: 147; 1-2 um ko: 101. 2-3 um wt: 179; 2-3 um ko: 99. 3-4 um wt: 63; 3-4 um ko: 29. 4-5 um wt: 19; 4-5 um ko: 19. 5-6 um wt: 5; 5-6 um ko: 3.</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3f</td>
<td></td>
<td>Two tailed unpaired t test and Linear regression</td>
<td>155 and 235</td>
<td>6m wt and ko mice, respectively</td>
<td></td>
<td>0.009932 ± 0.002540 slope ko: 0.01199 ± 0.002627</td>
<td>0.0001 (wt)</td>
<td>&lt;0.001 (ko)</td>
<td>0.5725</td>
<td>3</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Supp 3g
Two sided Fisher’s exact test
Fig. Legend and Methods
Total fibers wt: 155; total fibers ko: 236. 1-2 um wt: 42; 1-2 um ko: 47. 2-3 um wt: 52; 2-3 um ko: 84. 3-4 um wt: 34; 3-4 um ko: 56. 4-5 um wt: 12; 4-5 um ko: 33. 5-6 um wt: 8; 5-6 um ko: 8. 6-7 um; wt: 3; 6-7 um ko: 4. 7-8 um wt: 4; 7-8 um ko: 2. >8 um wt: 0; >8 um ko: 1. Total fibers versus 1-2 um; Total fibers versus 2-3 um; Total fibers versus 3-4 um; Total fibers versus 4-5 um; Total fibers versus 5-6 um; Total fibers versus 6-7 um; Total fibers versus >8 um.

Supp 5c
Two tailed unpaired t test and Linear regression
Fig. Legend and Methods
338 and 326 fibers from 8m wt and ko mice, respectively
The graph represent linear regression analyses slope wt: 0.02317 ± 0.002665 slope ko: 0.01920 ± 0.002171
P= <0.0001 (wt)
P= <0.0001 (ko)
g ratio P= <0.0001

t=8.448 df=662

Supp 5d
Two sided Fisher’s exact test
Fig. Legend and Methods
Total fibers wt: 338; total fibers ko: 326. 1-2 um wt: 113; 1-2 um ko: 110. 2-3 um wt: 124; 2-3 um ko: 126. 3-4 um wt: 57; 3-4 um ko: 53. 4-5 um wt: 33; 4-5 um ko: 28, 5-6 um wt: 11; 5-6 um ko: 8. 6-7 um; wt: 0; 6-7 um ko: 1. Total fibers versus 1-2 um; Total fibers versus 2-3 um; Total fibers versus 3-4 um; Total fibers versus 4-5 um; Total fibers versus 5-6 um; Total fibers versus 6-7 um.

Supp 6a
Two tailed unpaired t test
Fig. Legend and Methods
3 motor roots from different mice, 1 month
error bars are mean +/- SEM
P= 0.0517

t=2.744 df=4
<table>
<thead>
<tr>
<th>Supp</th>
<th>Test Type</th>
<th>Fig. Legend and Methods</th>
<th>Group 1</th>
<th>Group 2</th>
<th>Error Bars</th>
<th>P-value</th>
<th>t-value</th>
<th>df</th>
<th>Fig. Legend</th>
</tr>
</thead>
<tbody>
<tr>
<td>6b</td>
<td>Two tailed unpaired t test</td>
<td>Fig. Legend and Methods</td>
<td>sensory roots from different mice, 1 month</td>
<td>error bars are mean +/- SEM</td>
<td>t=2.756 df=4</td>
<td>0.051</td>
<td>Fig. Legend</td>
<td></td>
<td></td>
</tr>
<tr>
<td>6c</td>
<td>Two tailed unpaired t test</td>
<td>Fig. Legend and Methods</td>
<td>motor roots from different mice, 8 month</td>
<td>error bars are mean +/- SEM</td>
<td>t=0.04154 df=4</td>
<td>0.9689</td>
<td>Fig. Legend</td>
<td></td>
<td></td>
</tr>
<tr>
<td>6d</td>
<td>Two tailed unpaired t test</td>
<td>Fig. Legend and Methods</td>
<td>sensory roots from different mice, 8 month</td>
<td>error bars are mean +/- SEM</td>
<td>t=1.739 df=4</td>
<td>0.1571</td>
<td>Fig. Legend</td>
<td></td>
<td></td>
</tr>
<tr>
<td>6e</td>
<td>Two sided Fisher's exact test</td>
<td>Fig. Legend and Methods</td>
<td>sciatic nerves from different mice, 9 month</td>
<td>error bars are mean +/- SEM</td>
<td>t=0.5566 df=4</td>
<td>0.6075</td>
<td>Fig. Legend</td>
<td></td>
<td></td>
</tr>
<tr>
<td>6f</td>
<td>Two sided Fisher's exact test</td>
<td>Fig. Legend and Methods</td>
<td>Total fibers versus different binning classes</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Supp 6g</td>
<td>Two sided Fisher's exact test</td>
<td>Fig. Legend and Methods</td>
<td>Total fibers wt: 181; total fibers ko: 165. 1-5 wt: 56; 1-5 ko: 46. 6-10 wt: 51; 6-10 ko: 34. 11-15 wt: 25; 11-15 ko: 31. 16-20 wt: 21; 16-20 ko: 20. 21-25 wt: 10; 21-25 ko: 13. 26-30 wt: 7; 26-30 ko: 3; 31-35 wt: 7; 31-35 ko: 3; 36-40 wt: 1; 36-40 ko: 3; 41-45 wt: 2; 41-45 ko: 5; 45-50 wt: 0; 41-45 ko: 0; &gt;50 wt: 1; &gt;50 ko: 3.</td>
<td>Total fibers versus different binning classes</td>
<td>Fig. Legend and Methods</td>
<td>P= 0.6537 (total vs 1-5) P= 0.2255 (total vs 6-10) P= 0.3149 (total vs 11-15) P= 1 (total vs 16-20) P= 0.5191 (total vs 21-25) P=0.3447 (total vs 26-30) P=1 (total vs 31-35) P= 0.3539 (total vs 36-40) P= 0.2685 (total vs 41-45) P= 0.359 (total vs &gt;50)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Supp 7a</td>
<td>Two tailed unpaired t test</td>
<td>Fig. Legend and Methods</td>
<td>% Caspase 3+ cells in 3-6 coverslip/ experiment (3 different experiments)</td>
<td>Fig. Legend</td>
<td>error bars are mean +/- SEM</td>
<td>Fig. Legend</td>
<td>Untreated-20 uM: P= 0.1138 Untreated-50 uM: P= &lt;0.0001</td>
<td>Fig. Legend</td>
<td>Untreated-20uM: t=1.807 df=7 Untreated-50uM: t=7.028 df=7</td>
</tr>
<tr>
<td>Supp 7b</td>
<td>Two tailed unpaired t test</td>
<td>Fig. Legend and Methods</td>
<td>number of MBP+ segments measured in at least 3 coverslip/ experiment (3 different experiments)</td>
<td>Fig. Legend</td>
<td>error bars are mean +/- SEM</td>
<td>Fig. Legend</td>
<td>Untreated-1uM: P= 0.3866 Untreated-10 uM: P= &lt;0.0001 Untreated-25 uM: P= &lt;0.0001</td>
<td>Fig. Legend</td>
<td>Untreated-1uM: t=0.8806 df=26 Untreated-10uM: t=5.651 df=31 Untreated-25uM: t=6.736 df=22</td>
</tr>
<tr>
<td>Supp 7c</td>
<td>Two tailed unpaired t test</td>
<td>Fig. Legend and Methods</td>
<td>% Caspase 3+ cells in 3 coverslip/ experiment (3 different experiments)</td>
<td>Fig. Legend</td>
<td>error bars are mean +/- SEM</td>
<td>Fig. Legend</td>
<td>Untreated-25 uM: P= 0.3874</td>
<td>Fig. Legend</td>
<td>Untreated-25uM: t=0.9318 df=6</td>
</tr>
<tr>
<td>Supp 8a</td>
<td>One-way ANOVA Dunnett's multiple comparison test</td>
<td>Fig. Legend and Methods</td>
<td>different mRNA preparations</td>
<td>Fig. Legend</td>
<td>error bars are mean +/- SD</td>
<td>Fig. Legend</td>
<td>P= 0.0648 SC- Not Inf P= 0.2853 SC-ICD P= 0.04 Not Inf-ICD</td>
<td>Fig. Legend</td>
<td>F=10.77 R squared=0.8015</td>
</tr>
<tr>
<td>Supp Table 2</td>
<td>Two tailed unpaired t test</td>
<td>Fig. Legend and Methods</td>
<td>% aberrant myelin in sciatic nerves from different mice</td>
<td>Fig. Legend</td>
<td>exact values</td>
<td>Fig. Legend</td>
<td>1 month double knock out P= 0.07 1 month L-PGDS single knock out P= 0.065</td>
<td>Fig. Legend</td>
<td>1 month double knock out t=2.458 df=4 1 month L-PGDS single knock out t=3.733 df=2</td>
</tr>
</tbody>
</table>
### Representative figures

1. Are any representative images shown (including Western blots and immunohistochemistry/staining) in the paper?
   - Yes, Main Figures (1, 3-8) and Supplementary Figs (1-5, 7-8)

2. For each representative image, is there a clear statement of how many times this experiment was successfully repeated and a discussion of any limitations in repeatability?
   - All analyses (immunohistochemistry and western blot) were repeated at least 3 times with different biological preparations (i.e. different cell cultures preparation and different transgenic mice). Detailed sample size are provided in each figure legend.

### Statistics and general methods

1. Is there a justification of the sample size?
   - We did not predetermine the sample size. Our study used similar numbers of animals for individual experiments, with the same genetic background and sex (at least N=3).

2. Are statistical tests justified as appropriate for every figure?
   - Detailed statistical analyses are described in each Figure legends and in Methods. Statistical significance was considered if P < 0.05.

   a. If there is a section summarizing the statistical methods in the methods, is the statistical test for each experiment clearly defined?

   b. Do the data meet the assumptions of the specific statistical test you chose (e.g. normality for a parametric test)?

   c. Is there any estimate of variance within each group of data?

   d. Are tests specified as one- or two-sided?

   e. Are there adjustments for multiple comparisons?

   - Yes, Methods and Figure legends
   - Yes
   - No
3. Are criteria for excluding data points reported?
   Was this criterion established prior to data collection?
   Where is this described (section, paragraph #)?
   We did not exclude any point from the analyses.

4. Define the method of randomization used to assign subjects (or samples) to the experimental groups and to collect and process data.
   If no randomization was used, state so.
   Where does this appear (section, paragraph #)?
   We did not use any randomization.

5. Is a statement of the extent to which investigator knew the group allocation during the experiment and in assessing outcome included?
   If no blinding was done, state so.
   Where (section, paragraph #)?
   All g ratio analyses were performed blindly. The operator was not aware of the genotype of the animals. Animals were numbered during the genotype (AT) and a different number was assigned to each sample (sciatic nerve/saphenous nerve) at the time of processing for morphological analyses (AQ and GD). The operator measuring g ratio (CT) was not aware of any of them. Details are provided in Methods.

6. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included?
   Where (section, paragraph #)?
   Yes, stated in Methods

7. Is the species of the animals used reported?
   Where (section, paragraph #)?
   Yes, stated in Methods

8. Is the strain of the animals (including background strains of KO/transgenic animals used) reported?
   Where (section, paragraph #)?
   Yes, stated in Methods

9. Is the sex of the animals/subjects used reported?
   Where (section, paragraph #)?
   Yes, stated in Methods

10. Is the age of the animals/subjects reported?
    Where (section, paragraph #)?
    Yes, stated in Figure legends, Methods and Result sections.

11. For animals housed in a vivarium, is the light/dark cycle reported?
    Where (section, paragraph #)?
    N/A

12. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported?
    Where (section, paragraph #)?
    N/A

13. For behavioral experiments, is the time of day reported (e.g. light or dark cycle)?
    Where (section, paragraph #)?
    N/A
14. Is the previous history of the animals/subjects (e.g. prior drug administration, surgery, behavioral testing) reported?
Where (section, paragraph #)?
N/A

a. If multiple behavioral tests were conducted in the same group of animals, is this reported?
Where (section, paragraph #)?
N/A

15. If any animals/subjects were excluded from analysis, is this reported?
Where (section, paragraph #)?
N/A

a. How were the criteria for exclusion defined?
Where is this described (section, paragraph #)?
N/A

b. Specify reasons for any discrepancy between the number of animals at the beginning and end of the study.
Where is this described (section, paragraph #)?
N/A

Reagents

1. Have antibodies been validated for use in the system under study (assay and species)?
Yes, we and other groups have already used the majority of the antibody described in this study. In this study we validated L-PGDS and H-PGDS antibodies.
We validated the L-PGDS in lysates and conditioned media of DRG neurons infected with a lentivirus expressing L-PGDS cDNA. Expected MW: 25-27 KDa, as per antibody's developer (Supplementary Fig. 2).
We validated the H-PGDS in immunofluorescence against H-PGDS null sciatic nerves (Supplementary Fig. 3).

a. Is antibody catalog number given?
Yes, stated in Methods

Where does this appear (section, paragraph #)?

b. Where were the validation data reported (citation, supplementary information, Antibodypedia)?
L-PGDS validation: Supplementary Figure 2.
H-PGDS validation: Supplementary Figure 3.
All other antibodies previous publications: citations

Where does this appear (section, paragraph #)?

2. If cell lines were used to reflect the properties of a particular tissue or disease state, is their source identified?
Where (section, paragraph #)?
N/A

a. Were they recently authenticated?
Where is this information reported (section, paragraph #)?
N/A
**Data deposition**

Data deposition in a public repository is mandatory for:

- Protein, DNA and RNA sequences
- Macromolecular structures
- Crystallographic data for small molecules
- Microarray data

Deposition is strongly recommended for many other datasets for which structured public repositories exist; more details on our data policy are available [here](#). We encourage the provision of other source data in supplementary information or in unstructured repositories such as [Figshare](#) and [Dryad](#).

1. Are accession codes for deposit dates provided?
   - Where (section, paragraph #)?
     - Yes, stated in Methods.

**Computer code/software**

Any custom algorithm/software that is central to the methods must be supplied by the authors in a usable and readable form for readers at the time of publication. However, referees may ask for this information at any time during the review process.

1. Identify all custom software or scripts that were required to conduct the study and where in the procedures each was used.
   - N/A

2. Is computer source code/software provided with the paper or deposited in a public repository? Indicate in what form this is provided or how it can be obtained.
   - N/A

**Human subjects**

1. Which IRB approved the protocol?
   - Where is this stated (section, paragraph #)?
     - N/A

2. Is demographic information on all subjects provided?
   - Where (section, paragraph #)?
     - N/A

3. Is the number of human subjects, their age and sex clearly defined?
   - Where (section, paragraph #)?
     - N/A

4. Are the inclusion and exclusion criteria (if any) clearly specified?
   - Where (section, paragraph #)?
     - N/A

5. How well were the groups matched?
   - Where is this information described (section, paragraph #)?
     - N/A
6. Is a statement included confirming that informed consent was obtained from all subjects?
   Where (section, paragraph #)? N/A

7. For publication of patient photos, is a statement included confirming that consent to publish was obtained?
   Where (section, paragraph #)? N/A

**fMRI studies**

For papers reporting functional imaging (fMRI) results please ensure that these minimal reporting guidelines are met and that all this information is clearly provided in the methods:

1. Were any subjects scanned but then rejected for the analysis after the data was collected?
   N/A

   a. If yes, is the number rejected and reasons for rejection described?
      Where (section, paragraph #)? N/A

2. Is the number of blocks, trials or experimental units per session and/or subjects specified?
   Where (section, paragraph #)? N/A

3. Is the length of each trial and interval between trials specified?
   N/A

4. Is a blocked, event-related, or mixed design being used? If applicable, please specify the block length or how the event-related or mixed design was optimized.
   N/A

5. Is the task design clearly described?
   Where (section, paragraph #)? N/A

6. How was behavioral performance measured?
   N/A

7. Is an ANOVA or factorial design being used?
   N/A

8. For data acquisition, is a whole brain scan used?
   If not, state area of acquisition.
   N/A

   a. How was this region determined?
      N/A
9. Is the field strength (in Tesla) of the MRI system stated?
   a. Is the pulse sequence type (gradient/spin echo, EPI/spiral) stated?
      N/A
   b. Are the field-of-view, matrix size, slice thickness, and TE/TR/flip angle clearly stated?
      N/A

10. Are the software and specific parameters (model/functions, smoothing kernel size if applicable, etc.) used for data processing and pre-processing clearly stated?
    N/A

11. Is the coordinate space for the anatomical/functional imaging data clearly defined as subject/native space or standardized stereotaxic space, e.g., original Talairach, MNI305, ICBM152, etc? Where (section, paragraph #)?
    N/A

12. If there was data normalization/standardization to a specific space template, are the type of transformation (linear vs. nonlinear) used and image types being transformed clearly described? Where (section, paragraph #)?
    N/A

13. How were anatomical locations determined, e.g., via an automated labeling algorithm (AAL), standardized coordinate database (Talairach daemon), probabilistic atlases, etc.?
    N/A

14. Were any additional regressors (behavioral covariates, motion etc) used?
    N/A

15. Is the contrast construction clearly defined?
    N/A

16. Is a mixed/random effects or fixed inference used?
   a. If fixed effects inference used, is this justified?
      N/A

17. Were repeated measures used (multiple measurements per subject)?
   a. If so, are the method to account for within subject correlation and the assumptions made about variance clearly stated?
      N/A

18. If the threshold used for inference and visualization in figures varies, is this clearly stated?
    N/A

19. Are statistical inferences corrected for multiple comparisons?
   a. If not, is this labeled as uncorrected?
      N/A
20. Are the results based on an ROI (region of interest) analysis?
   a. If so, is the rationale clearly described? N/A
   b. How were the ROI's defined (functional vs anatomical localization)? N/A

21. Is there correction for multiple comparisons within each voxel? N/A

22. For cluster-wise significance, is the cluster-defining threshold and the corrected significance level defined? N/A

▶ Additional comments

Additional Comments