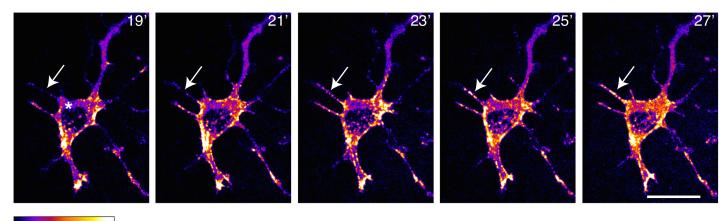


Figure S1 – Differential expression of NM2B and NM2C during *in vivo* **myelination.** Western blot from whole CNS rat brain at different time points of developmental myelination to analyze bulk protein expression levels of NM2B (down-regulation) and NM2C (up-regulation) and their correlation with MBP expression.

S2 Figure



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Figure S2 - Dynamic changes on NM2B-GFP subcellular distribution in OPC nascent protrusions. Time-lapse images of OPC cultures purified from transgenic NM2B-GFP mice. Images were acquired using a 63x oil-objective for a period of 35 min. Selected frames clearly show re-localization of NM2B signal from the cortex to the protrusions. Scale bar corresponds to 20µm.

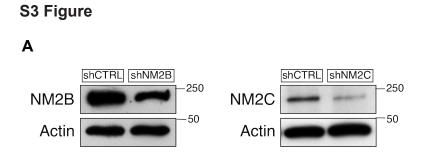


Figure S3 – Validation of knockdown efficiency. Western blots showing the decrease of NM2B and NM2C protein expression in OPC cultures transduced with lentiviral particles. Extracts were prepared 3 days after transduction. Data related to **Figure 5**.

Table S1 – Global NM2A, NM2B, NM2C and Myo18a interactomes. Raw datarelated to Figure 3A.

Click here to Download Table S1

 Table S2 - Functional enrichment heatmap analysis of pooled NM2A/NM2B vs.

 NM2C/Myo18a interactors using DAVID bioinformatics tool. Raw data related to

 Figure 3B.

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Table S3 - NM2A/NM2B Functional Annotation Table, using DAVIDbioinformatics tool. Raw data related to Figure 3B.

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Table S4 - NM2C/Myo18a Functional Annotation Table, using DAVIDbioinformatics tool. Raw data related to Figure 3B.

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Table S5 - NM2A/NM2B Functional Annotation Clustering, using DAVIDbioinformatics tool. Raw data related to Figure 3B.

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 Table S6 - NM2C/Myo18a Functional Annotation Clustering, using DAVID
 bioinformatics tool. Raw data related to Figure 3B.

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