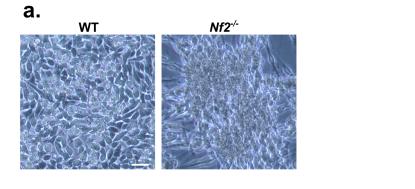
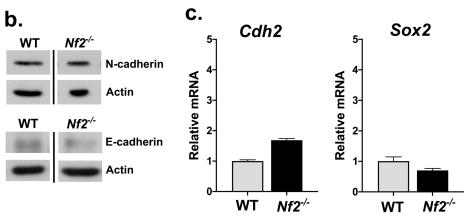


shScr shEzrin

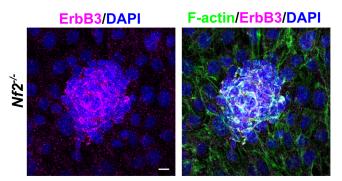
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Supplemental Figure 1. A. Representative immunoblot showing protein levels of merlin and the SC marker p75 in Nf2<sup>flox/flox</sup> (WT) and Nf2<sup>-/-</sup> SCs. B. Quantitation of polarity in WT and Nf2<sup>-/-</sup> SCs as determined by the aspect ratio (long to short axis). Bars represent mean +/- SEM in  $n \ge 50$  cells per condition. N=3 independent experiments. **C.** Confocal images depicting enhanced Nrg1-induced cortical ruffling in late confluent Nf2<sup>-/-</sup> but not control SCs. Images were generated by overlaying MIP of cortical actin (magenta) and basal actin (green) from 3D zstack images. D. Representative immunoblot showing protein levels of ErbB3 and activation of pAKT S473 and pERK1/2 in response to stimulation of WT and Nf2<sup>-/-</sup> SCs with Nrg. Total levels of AKT and ERK1/2 served as loading controls. The line between lanes 2 and 3 indicates the removal of unrelated lanes from the image of the blot. E. Representative immunoblot showing protein levels of ezrin in *Nf2<sup>-/-</sup>* SCs infected with shSCR- or shEzrin-expressing lentiviruses. Actin served as a loading control. F. Confocal images showing ezrin (magenta) and F-actin (green) localization in Nf2<sup>-/-</sup> SCs infected with shSCR or shEzr-expressing lentiviruses. G. Quantitation of cortical ruffling area in *Nf2<sup>-/-</sup>* SCs infected with shSCR or shEzr-expressing lentiviruses. Data are presented as mean +/- SEM of n≥10 cells per condition, N=2 independent experiments. P values were calculated with unpaired two-tailed Student's t-test. \*\*\*p<0.001, \*\*p<0.01. Scale bars=10 µm.

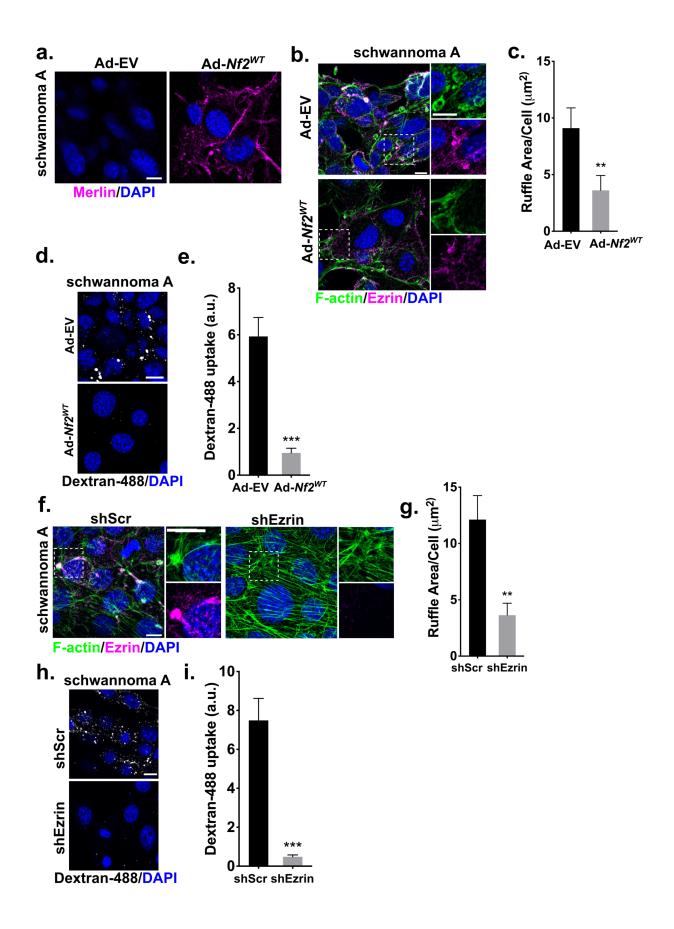




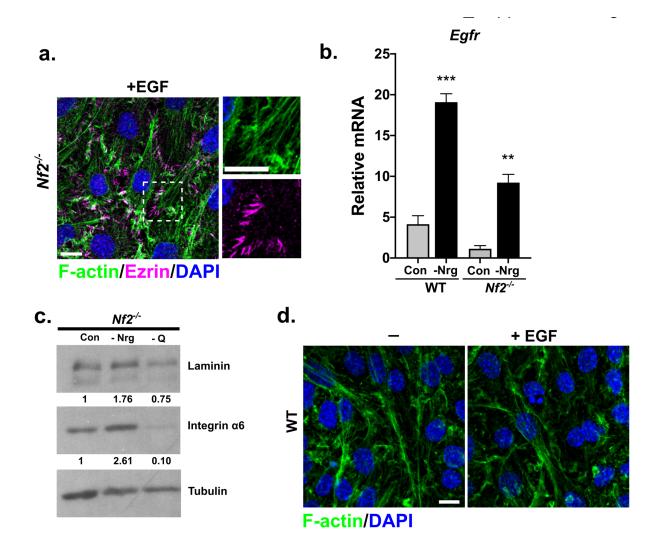




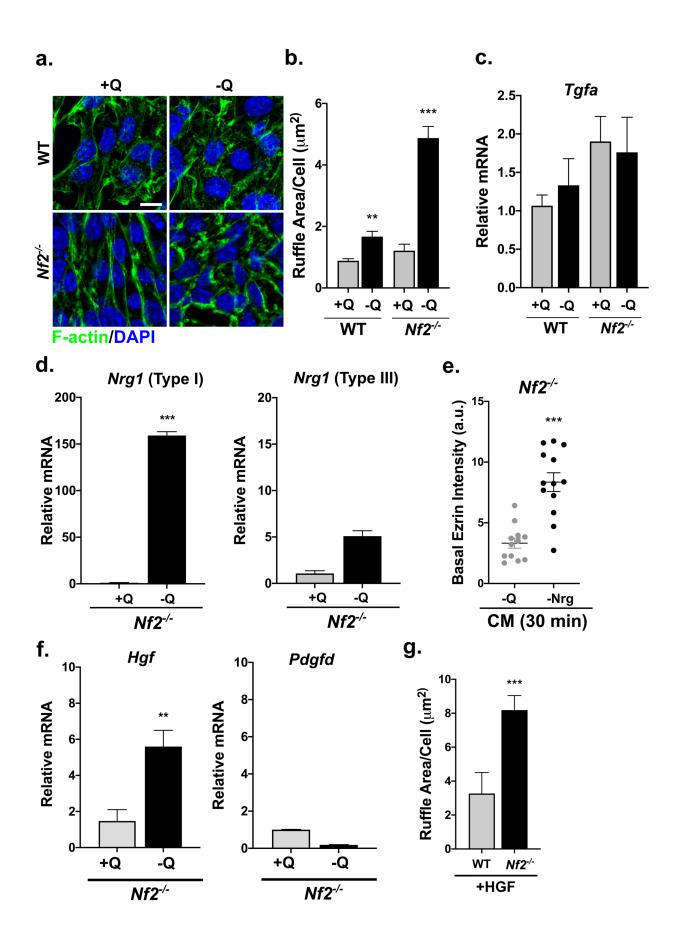
**Supplemental Figure 2**. **A.** Phase contrast images of late confluent WT and *Nf2<sup>-/-</sup>* SCs. **B**. Immunoblot showing protein levels of N-cadherin and E-cadherin in WT and *Nf2<sup>-/-</sup>* SCs. Actin served as a loading control. The line between lanes indicates the removal of unrelated lanes from the image of the blot. **C.** mRNA expression of *Sox2* and *Ncad* in WT and *Nf2<sup>-/-</sup>* SCs. Data is presented as mean +/- SEM relative to WT mRNA levels, N=3. **D**. MIP from Fig.2F showing membrane recruitment and colocalization of ErbB3 (magenta) and F-actin (green) in late confluent *Nf2<sup>-/-</sup>* SCs. Scale bars=10 μm.



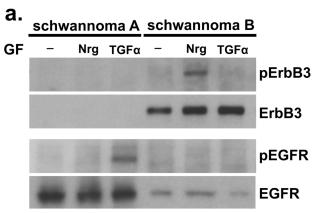
**Supplemental Figure 3. A.** Confocal images showing merlin (magenta) localization in  $Nf2^{-/-}$  schwannoma cells expressing EV or  $Nf2^{WT}$  via adenoviral infection. **B.** Confocal images of F-actin (green) and ezrin (magenta) localization in  $Nf2^{-/-}$  schwannoma cells expressing EV or  $Nf2^{WT}$  adenovirus. **C.** Quantitation of cortical ruffling in cells shown in (B). **D.** Dextran-488 uptake in  $Nf2^{-/-}$  schwannoma cells expressing EV or  $Nf2^{WT}$  adenovirus. **E.** Graph of (D). **F.** Confocal images of F-actin (green) and ezrin (magenta) localization in  $Nf2^{-/-}$  schwannoma cells infected with shSCR- or shEzrin-expressing lentivirus. **G.** Quantitation of cortical ruffling of cells in (F). **H.** Dextran-488 uptake in  $Nf2^{-/-}$  schwannoma cells expressing shSCR- or shEzrin lentivirus. **I.** Graph of (H). For all graphs, bars represent mean +/- SEM for n  $\ge$  10 cells per condition, N $\ge$ 2 independent experiments. P values were calculated with unpaired two-tailed Student's t-test. \*\*\*p<0.001, \*\*p<0.01. Scale bars=10 µm.



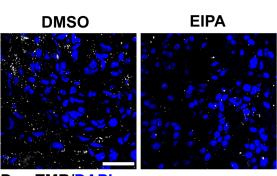
**Supplemental Figure 4. A.** Confocal images depicting the distribution of F-actin (green) and ezrin (magenta) in *Nf2<sup>-/-</sup>* SCs starved of Nrg1 overnight and stimulated with 10 ng/ml EGF. **B.** mRNA expression *EGFR* in WT and *Nf2<sup>-/-</sup>* SCs under steady state conditions or after 24 h Nrg1-deprivation. Data is presented as mean +/- SEM relative to WT mRNA levels, N=2. **C.** Immunoblot depicting the levels of the basal markers laminin and α6 integrin in *Nf2<sup>-/-</sup>* SCs under steady-state, Nrg1-deprived and glutamine-deprived (-Q) conditions. Tubulin was used as a loading control. **D.** Confocal images of F-actin (green) localization in WT SCs starved of Nrg1 overnight and stimulated with EGF. P values were calculated with unpaired two-tailed Student's t-test. \*\*\*p<0.001, \*\*p<0.01. Scale bars=10 μm.



**Supplemental Figure 5. A.** Confocal images depicting F-actin (green) localization in WT and  $Nf2^{-L}$  SCs grown in complete medium (+Q) or glutamine-deprived medium (-Q) for 24 h. **B.** Quantitation of cortical ruffling in cells shown in (A). Bars represent mean +/- SEM for n≥10 cells per condition. N=3 independent experiments. **C.** mRNA expression of *Tgfa* in WT and *Nf2^{-L}* SCs grown in complete (+Q) or glutamine-deprived (-Q) medium for 24 h. Data is presented as mean +/- SEM relative to WT, +Q mRNA levels, N=3. **D.** mRNA expression of soluble *Nrg1 Type I* and membrane-tethered *Nrg1 Type III* in *Nf2^{-L}* SCs grown in complete or glutamine-deprived medium. Data is presented as mean +/- SEM relative to +Q mRNA levels, N=2. **E.** mRNA expression of *Hgf and Pdgfd* in *Nf2^{-L}* SCs grown in complete or glutamine-deprived medium. Data is presented as mean +/- SEM relative to +Q mRNA levels, N=2. **E.** mRNA expression of *Hgf and Pdgfd* in *Nf2^{-L}* SCs grown in complete or glutamine-deprived medium. Data is presented as mean +/- SEM relative to +Q mRNA levels, N=2. **F.** Quantitation of cortical ruffles in *Nf2^{-L}* SCs with and without HGF stimulation. Bars represent mean +/- SEM for n ≥ 10 cells per condition. P values were calculated with unpaired two-tailed Student's t-test. \*\*\*\*p<0.001, \*\*p<0.01. Scale bars=10 µm.

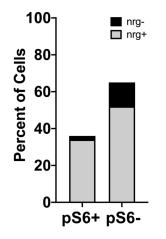






Dex-TMR/DAPI





**Supplemental Figure 6. A.** Immunoblot showing protein levels of pErbB3, total ErbB3, pEGFR, and total EGFR in schwannoma A and schwannoma B cells upon stimulation with Nrg1 or TGF $\alpha$  for 10 min. **B.** Confocal images of *ex vivo* macropinocytic uptake of dextran-TMR in schwannoma tissue with and without EIPA treatment, as shown in Fig. 6H. Scale bar=30 µm. **C.** Quantitation of percentages of cells staining positive or negative for pS6 and/or Nrg1 in tissue from early DRG lesions in *P0-Nf2*<sup>Δ2-3</sup> mice.