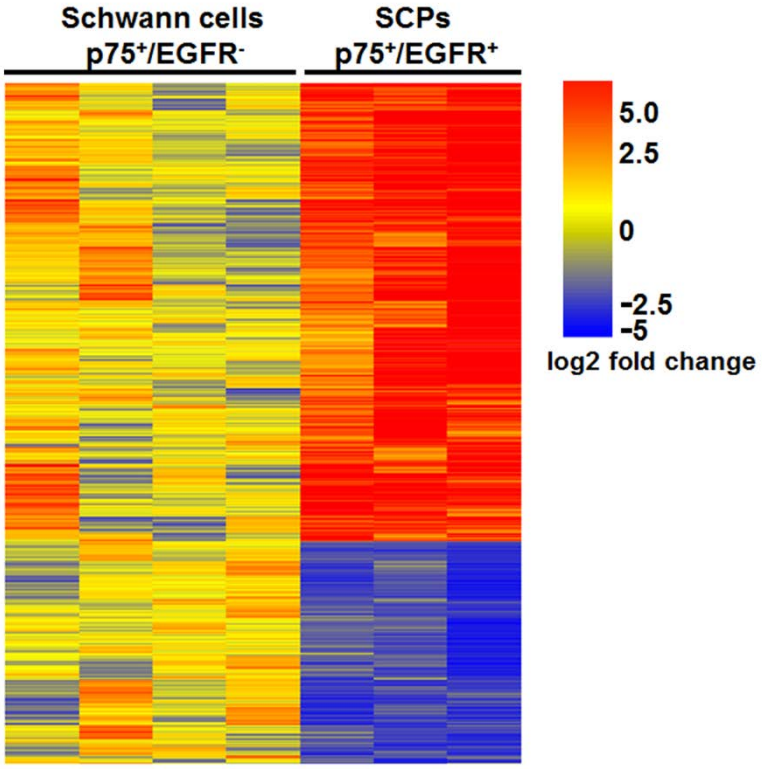
Supplemental figure 1. **Heat map of transcripts differentially expressed between FACS sorted $p75^{+}/EGFR^{-}$ Schwann cells and $p75^{+}/EGFR^{+}$ SCP like tumor initiating cells**

Two-way hierarchical clustering grouped samples as $p75^{+}/EGFR^{-}$ Schwann cells and $p75^{+}/EGFR^{+}$ SCPs. $P75^{+}/EGFR^{+}$ SCPs expression levels relative to $p75^{+}/EGFR^{-}$ Schwann cells are identified**.** Genes with increased expression are shown in red. Genes with decreased expression are shown in blue.



Supplemental figure 2 Loss of Nf1 leads to increase in Runx1^{+}/P0^{+} progenitors in E12.5 DRGs

A. Immunofluorescence staining on E12.5 DRGs. Tissues were embedded in OCT and cut into 12- μm sections. Sections were incubated overnight at 4°C with antibodies:anti-Runx1 (Abcam) and anti- P0 (Abcam) and then were incubated with FITC-anti-mouse and TRITC-anti-rabbit secondary antibody at room temperature for 1 hours. Nuclei were stained with DAPI. Top: WT, Bottom: *Nf1*$^{-/-}$, Red: P0, Green: Runx1, Blue: nuclei. White arrow: Runx1^{+}/Blbp^{+} progenitors. Arrow head: Runx1^{-}/Blbp^{+} progenitors. B. Quantification on percentage of Runx1^{+}/P0^{+} progenitors in E12.5 WT (black bar) and E12.5 *Nf1*$^{-/-}$ DRGs (white bar). Statistical analyses were performed by unpaired, two-tailed student *t* test. ***=p<0.001.