Supplemental Data

Supplementary Figure S1. Egr2 immunoblot analysis.

The two Egr2 antibodies were tested for their ability to detect Egr2 in the rat S16 Schwann cell line, which was treated with either control or Egr2 siRNA.

Supplementary Figure S2. Validation of Egr2 at selected lipid biosynthetic genes

Supplemental Table S1. Complete list of genes on custom microarray

Specified coordinates indicate tiled windows on custom microarray based on Rn4 genome build at the UCSC genome browser.

Supplemental Table S2. Analysis of Egr2 and Sox10 binding sites in ChIP-chip peaks.

Lists of peaks common to both replicates for each antibody (Table S3) were used to identify overlapping peaks that were present in all ChIP-chip assays. The overlap peaks are defined by coordinates encompassing the combined width of the overlapping peaks. The sequences within these coordinates were analyzed by scanning for Egr2 and Sox10 binding sites by comparison to previously constructed position weight matrices as described in the Methods section. Searches for inverted, dimeric Sox10 binding sites (consensus AACAANGNNNNCNTTGTT) were performed allowing for a central spacer length of 3-6 bp, which were labeled consecutively as matrices 1-4. The start and end positions are in negative coordinates relative to the end of the peak (the last nucleotide has value -1).

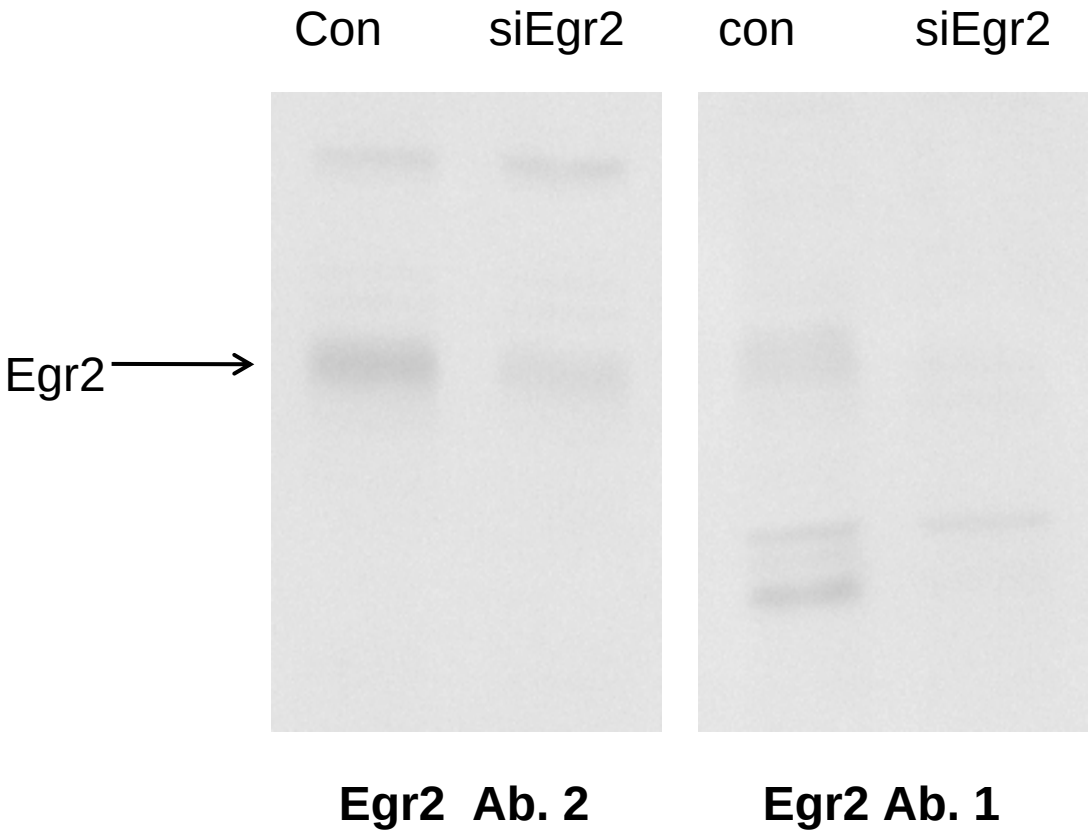

Figure S1. S16 rat schwann cells cultured in DMEM with 5% BGS, were transfected with either control siRNA or siRNA directed against rat Egr2 (Invitrogen RSS331864), using the rat nucleofector kit (Lonza). After 48 h, cell lysates were immunoblotted with either Covance (Ab2) or Abcam Egr2 (Ab1) antibody as indicated.

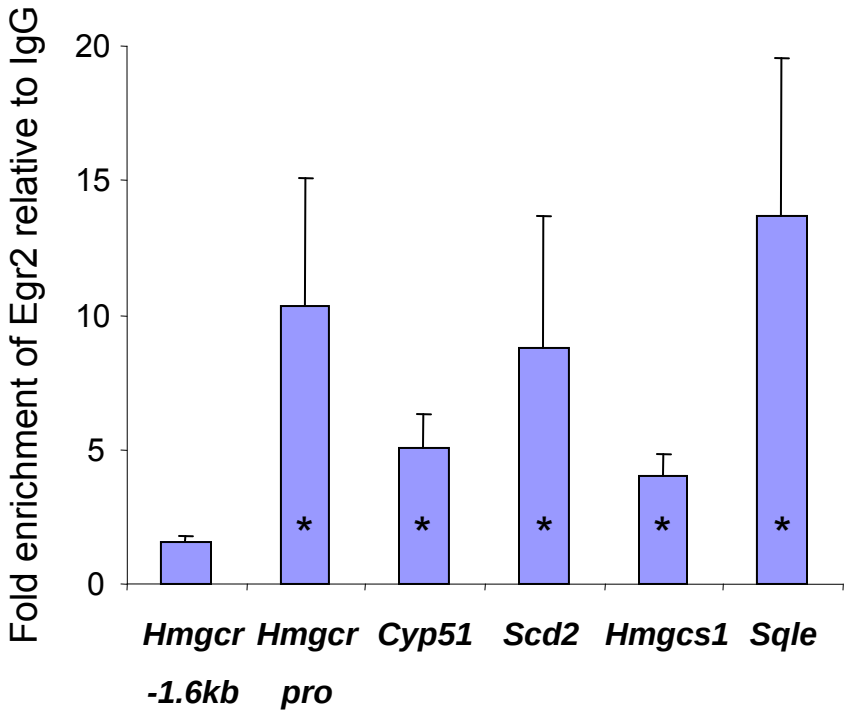

Figure S2. Egr2 binds to promoters of lipid biosynthesis genes.
ChIP-chip analysis had identified peaks of Egr2 binding in several promoter regions of lipid biosynthetic genes. Binding of Egr2 was independently validated by quantitative PCR analysis of ChIP samples in the *Hmgcr*, *Hmgcs1, Cyp51*, *Sqle*, and *Scd2* genes using Egr2 Ab. 2, and fold enrichment relative to the IgG negative control ChIP assay is shown. Average fold enrichment from three independent litters of P15 rat pups is shown, and error bars indicate the standard deviation. Asterisks indicate primer sets for which Egr2 is enriched ≥2-fold relative to the negative IgG control, with p values ≤0.05 (Student's t-test). As a negative control, a primer set positioned at -1.6kb upstream of *Hmgcr.*