

**Pro-EMT genes  
upregulated  
in reactive astrocytes  
14-days post-SCI**

Gene	log2-fold change
ANPEP	8.10
CXCL1	7.81
TIMP1	7.71
CRLF1	7.27
ECM1	6.43
SERPINE1	6.15
FN1	5.43
COL3A1	5.02
COL6A2	4.97
TGFB1	4.71
FSP1	4.43
SDC1	4.23
ELN	4.10
SPP1	4.07
ITGA5	4.03
MGP	4.03
POSTN	3.73
CAPG	3.64
COL16A1	3.63
COL1A1	3.47
FGF2	3.38
COL5A1	3.34
COL11A1	3.25
ITGB3	3.25
VIM	3.18
PLAUR	3.08
MYLK	3.04
TGM2	3.04
GPC1	2.96
TAGLN	2.96
TGFB1	2.96
NID2	2.90
TPM4	2.64
ITGB5	2.47
BGN	2.22
FLNA	2.15
IGFBP3	2.11
MSX1	2.02
PCOLCE	1.91
TNFRSF12A	1.89
PVR	1.78
PLOD3	1.76
WIPF1	1.65
QSOX1	1.63
EMP3	1.58
LOXL2	1.58
JUN	1.56
MMP2	1.54
CXCL12	1.45
LRP1	1.37
VCAN	1.35
COL1A2	1.22
PMEP1	1.11
TPM1	0.94
ZEB2	0.94
CALU	0.70
ITGB1	0.70

**Pro-EMT genes  
unchanged  
in reactive astrocytes  
14-days post-SCI**

Gene	log2-fold change
GADD45B	NS
GEM	NS
GLIPR1	NS
CD44	NS
CD59	NS
CDH6	NS
EDIL3	NS
FAP	NS
ITGA2	NS
LRRC15	NS
THBS1	NS
THBS2	NS
THY1	NS
TNFRSF11B	NS
ETS1	NS
FOXC2	NS
LEF1	NS
SNAI1	NS
SNAI2	NS
SNAI3	NS
TWI1	NS
TWI2	NS
ZEB1	NS
ADAM12	NS
CCN1	NS
CCN2	NS
COL12A1	NS
COL5A2	NS
COL5A3	NS
COL6A3	NS
COL8A2	NS
COMP	NS
CTHRC1	NS
FBLN2	NS
FBLN5	NS
FBN1	NS
FBN2	NS
LGALS1	NS
LOX	NS
MFAP5	NS
MMP14	NS
MMP3	NS
PCOLCE2	NS
PLOD1	NS
PLOD2	NS
SERPINE2	NS
SERPINH1	NS
SPOCK1	NS
TNC	NS
NNMT	NS
NT5E	NS
SCG2	NS
BMP1	NS
FAS	NS
FSTL1	NS
FZD8	NS
GREM1	NS
IGFBP2	NS
IL6	NS
INHBA	NS
RHOB	NS
WNT5A	NS
ACTA2	NS
CALD1	NS
MYL9	NS
SDC4	NS
TPM2	NS
MAGEE1	NS
MCM7	NS
MEST	NS

**Pro-EMT genes  
down-regulated  
in reactive astrocytes  
14-days post-SCI**

Gene	log2-fold change
TIMP3	-0.7
CDH2	-0.86
ENO2	-0.94
ITGAV	-1.15
CTNNA1	-1.16
FERMT2	-1.16
IGFBP4	-1.26
PDGFRB	-1.39
CDH11	-1.84
LOXL1	-2.61
BDNF	-3.56
PTHLH	-6.82

**Gene function related to:**

- Intra-cellular signaling
- Cell-surface and adhesion
- Transcription
- Extracellular matrix
- Metabolism/protein synthesis
- Intercellular signaling
- Cytoskeleton

**Figure S1.** Changes in pro-EMT gene expression levels in an RNA-seq database (Anderson et al., 2016) for reactive astrocytes 14 days post-SCI. Related to Figure 1. Genes with expression levels that either significantly increased, remain unchanged, or significantly decreased in reactive astrocytes relative to uninjured astrocytes are listed on the left, center, and right, respectively. For genes with significant changes, the corresponding log<sub>2</sub>-fold change in expression levels are listed, whereas genes with non-significant changes are indicated by “NS.” Measures of significance are provided by the database (Anderson et al., 2016).

**Anti-EMT genes  
upregulated  
in reactive astrocytes  
14-days post-SCI**

Gene	log2-fold change
DSP	4.48
LAMC2	3.84
TNFAIP3	2.97
DCN	2.40
COL4A1	2.00
DPYSL3	1.64
LAMC1	1.53
EFEMP2	1.46

**Anti-EMT genes  
unchanged  
in reactive astrocytes  
14-days post-SCI**

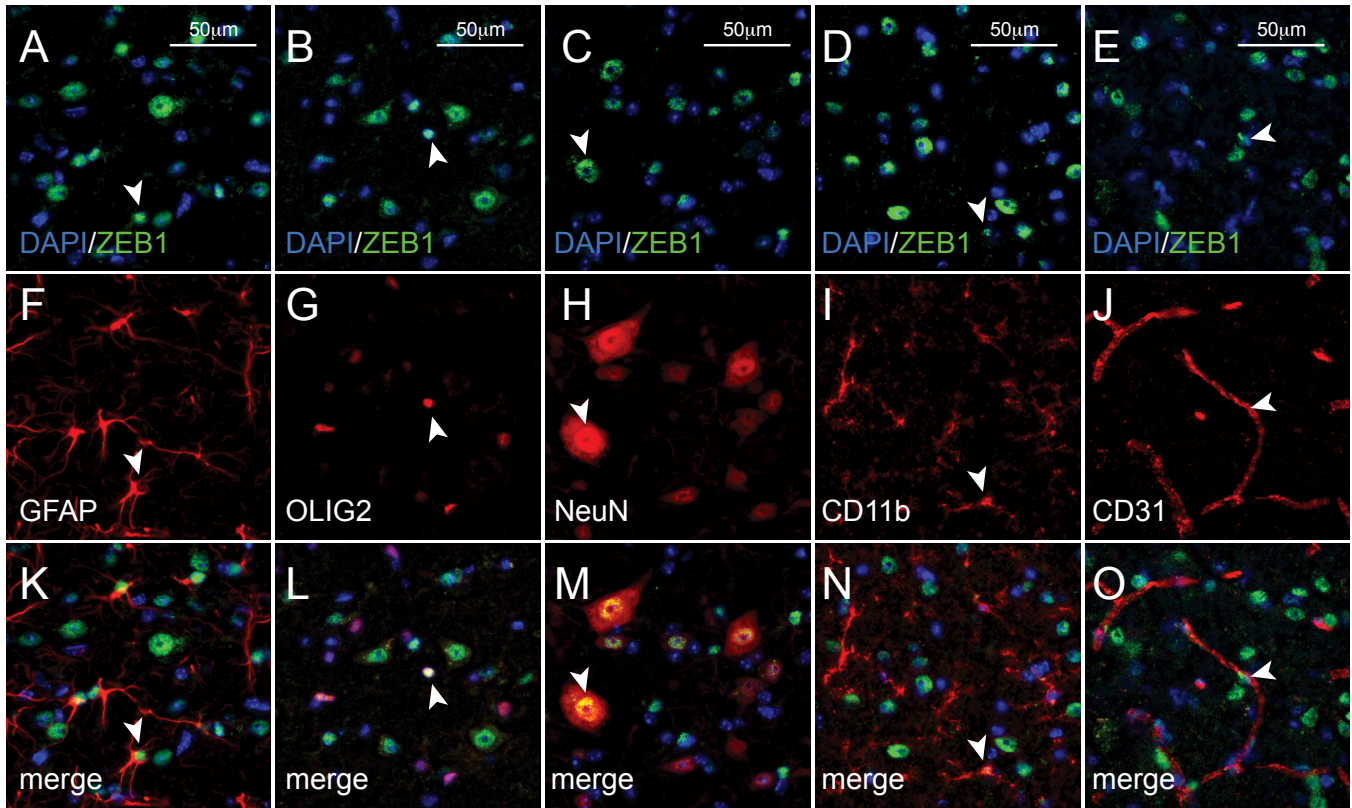
Gene	log2-fold change
AREG	NS
CADM1	NS
CDH1	NS
BASP1	NS
GSC	NS
PRRX1	NS
COL4A2	NS
COL7A1	NS
FBLN1	NS
LAMA1	NS
LAMA2	NS
LAMA3	NS
LUM	NS
TFPI2	NS
SAT1	NS
DKK1	NS
GADD45A	NS
NOTCH2	NS
SFRP1	NS
SFRP4	NS
SLIT2	NS
SLIT3	NS
TGFBR3	NS
KRT1	NS
PDLIM4	NS
PFN2	NS

**Anti-EMT genes  
down-regulated  
in reactive astrocytes  
14-days post-SCI**

Gene	log2-fold change
TJP1	-0.69
RGS4	-1.41
GAS1	-1.67
HTRA1	-1.89
GJA1	-2.01
ABI3BP	-2.22
OXTR	-2.46
ID2	-3.30

Gene function related to:	
<span style="color: red;">■</span>	Intra-cellular signaling
<span style="color: orange;">■</span>	Cell-surface and adhesion
<span style="color: yellow;">■</span>	Transcription
<span style="color: green;">■</span>	Extracellular matrix
<span style="color: cyan;">■</span>	Metabolism/protein synthesis
<span style="color: blue;">■</span>	Intercellular signaling
<span style="color: magenta;">■</span>	Cytoskeleton

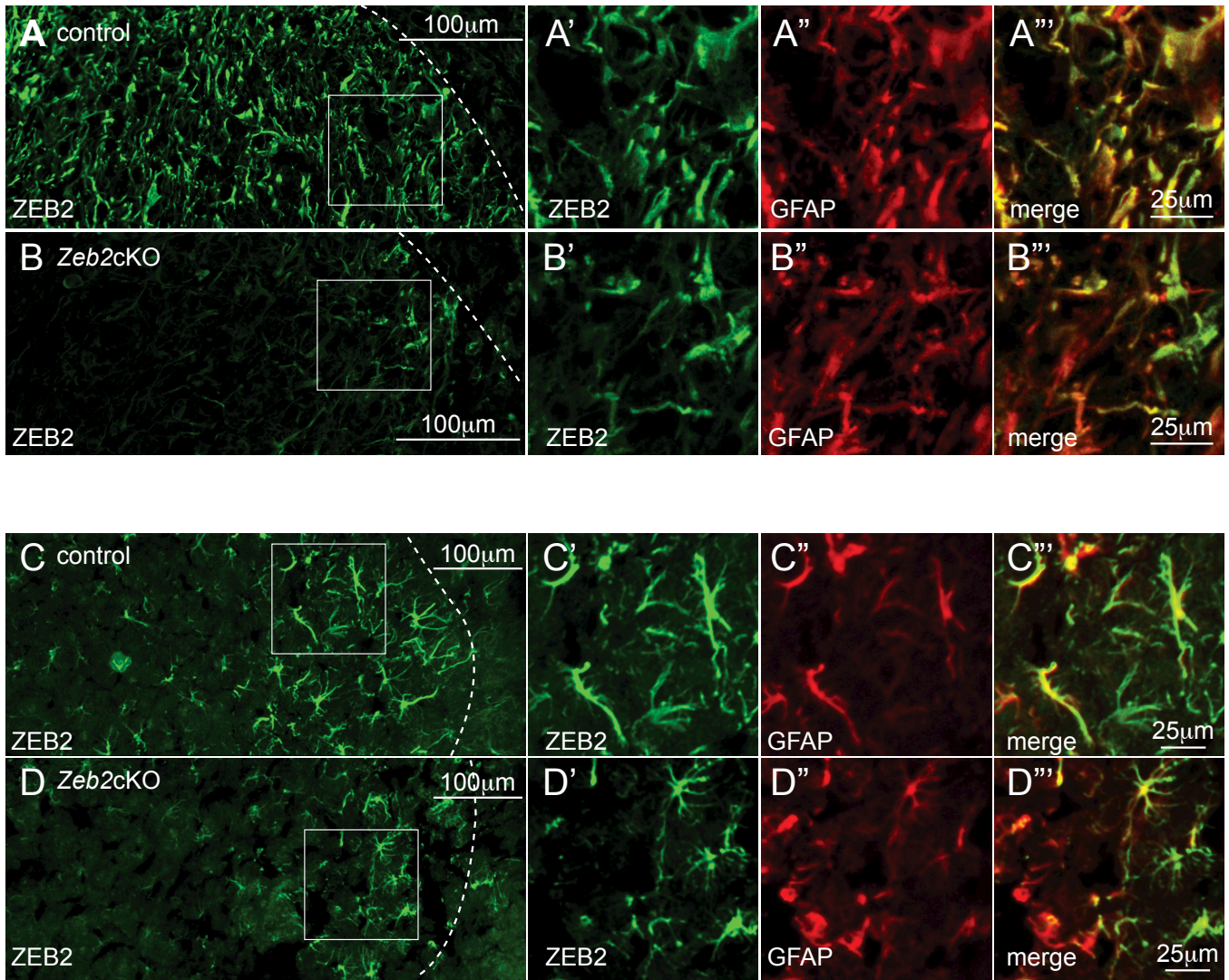
**Figure S2.** Changes in EMT gene expression levels in an RNA-seq database (Anderson et al., 2016) for reactive astrocytes 14 days post-SCI. Related to Figure 1. Genes with expression levels that either significantly increase, remain unchanged, or significantly decrease in reactive astrocytes relative to uninjured astrocytes are listed on the left, center, and right, respectively. For genes with significant changes, the corresponding log2-fold change in expression levels are listed, whereas genes with non-significant changes are indicated by “NS.” Measures of significance are provided by the database (Anderson et al., 2016).



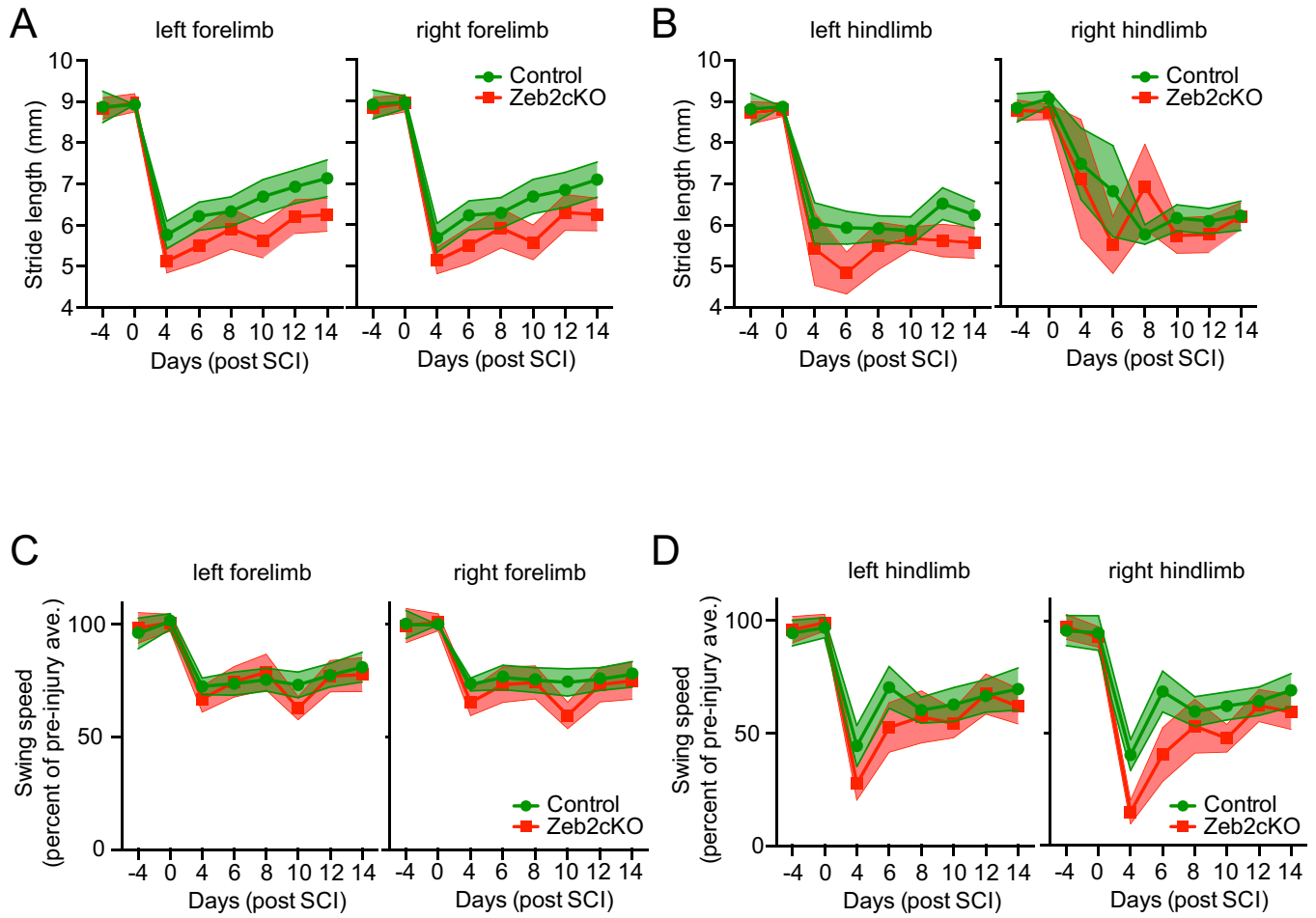
**Figure S3.** ZEB1 expression in spinal cord cell types following SCI. Related to Figure 1. **A-O**, immunofluorescence analysis in the spinal cord 14 days after injury at  $\sim 1500\mu\text{m}$  from the lesion shows ZEB1 was expressed in a subset of astrocytes (GFAP; panels A,F,K), oligodendrocytes (OLIG2; panels B,G,L), neurons (NeuN; panels C,H,M), microglia/macrophages (CD11b; panels D,I,N), and endothelial cells (CD31; panels E,J,O).

<b>lncRNA</b>	<i>log2 fold change</i>		
	<b>WT</b>	<b>Stat3<sup>-/-</sup></b>	
<i>H19</i>	6.74	3.90	<b><i>lncRNA without detectable expression</i></b>
<i>Rpph1</i>	5.53	3.68	
<i>Halr1</i>	4.92	5.42	
<i>RMPR</i>	4.70	2.47	
<i>Kncq1ot1</i>	2.91	NS	
<i>Airn</i>	2.18	NS	
<i>Zeb2os</i>	2.18	NS	
<i>Syne3</i>	1.94	2.52	
<i>Malat1</i>	1.92	1.24	
<i>Firre</i>	1.79	NS	
<i>Pvt1</i>	1.66	NS	
<i>Gas5</i>	1.35	NS	
<i>Neat1</i>	1.29	NS	
<i>Plscr4</i>	-2.00	NS	
<i>Dancr</i>	-3.06	NS	
<i>Paupar</i>	-7.23	NS	
<i>Lhx1os</i>	-8.44	NS	
<i>LncOL1</i>	NS	1.92	
<i>Pantr1</i>	NS	-1.69	
<i>Snhg3</i>	NS	-4.12	
<i>Abcc2</i>	NS	NS	<b><i>lncRNA not contained within database</i></b>
<i>Crnde</i>	NS	NS	
<i>Evx2</i>	NS	NS	
<i>Fendrr</i>	NS	NS	
<i>Itga2</i>	NS	NS	
<i>Meg3</i>	NS	NS	
<i>Miat</i>	NS	NS	
<i>Moxi</i>	NS	NS	
<i>Snhg1</i>	NS	NS	
<i>Snhg5</i>	NS	NS	
<i>Snhg14</i>	NS	NS	
<i>Tsix</i>	NS	NS	
<i>Tug1</i>	NS	NS	
<i>Tunar</i>	NS	NS	
<i>Xist</i>	NS	NS	

**Figure S4.** Changes in gene expression levels for lncRNAs in an RNA-seq database (Anderson et al., 2016) of reactive astrocytes 14 days post-SCI. Related to Figure 3. lncRNAs with expressed levels that either significantly increase, remain unchanged, or significantly decrease in reactive astrocytes relative to uninjured astrocytes are listed with either their corresponding log<sub>2</sub>-fold change in expression levels or “NS” to indicate a non-significant change. Measures of significance are provided by the database (Anderson et al., 2016). Established lncRNAs that either did not have detectable expression levels or were not included the database are also listed.



**Figure S5.** Residual ZEB2 expression at lesion borders in *Zeb2cKO* mice. Related to Figures 4 and 5. **A-B** and **C-D**, ZEB2 expression in 14 days post-SCI and 3 days post-stroke, respectively, show a knockout, but not complete elimination, of ZEB2 in GFAP<sup>+</sup> astrocytes near the lesion borders.



**Figure S6.** Analysis of motor function recovery following SCI. Related to Figure 6. **A-B** and **C-D**, quantitative analysis of gait (CatWalk) parameters following SCI show no change in the recovery of stride length and swing speed for control and *Zeb2cKO* mice. Two-way ANOVA with repeated measures,  $n=9$  for control and  $n=11$  for *Zeb2cKO* mice, power=0.97 and 0.95 (A), 0.41 and 0.69 (B), 0.65 and 0.77 (C), 0.92 and 0.98 (D).