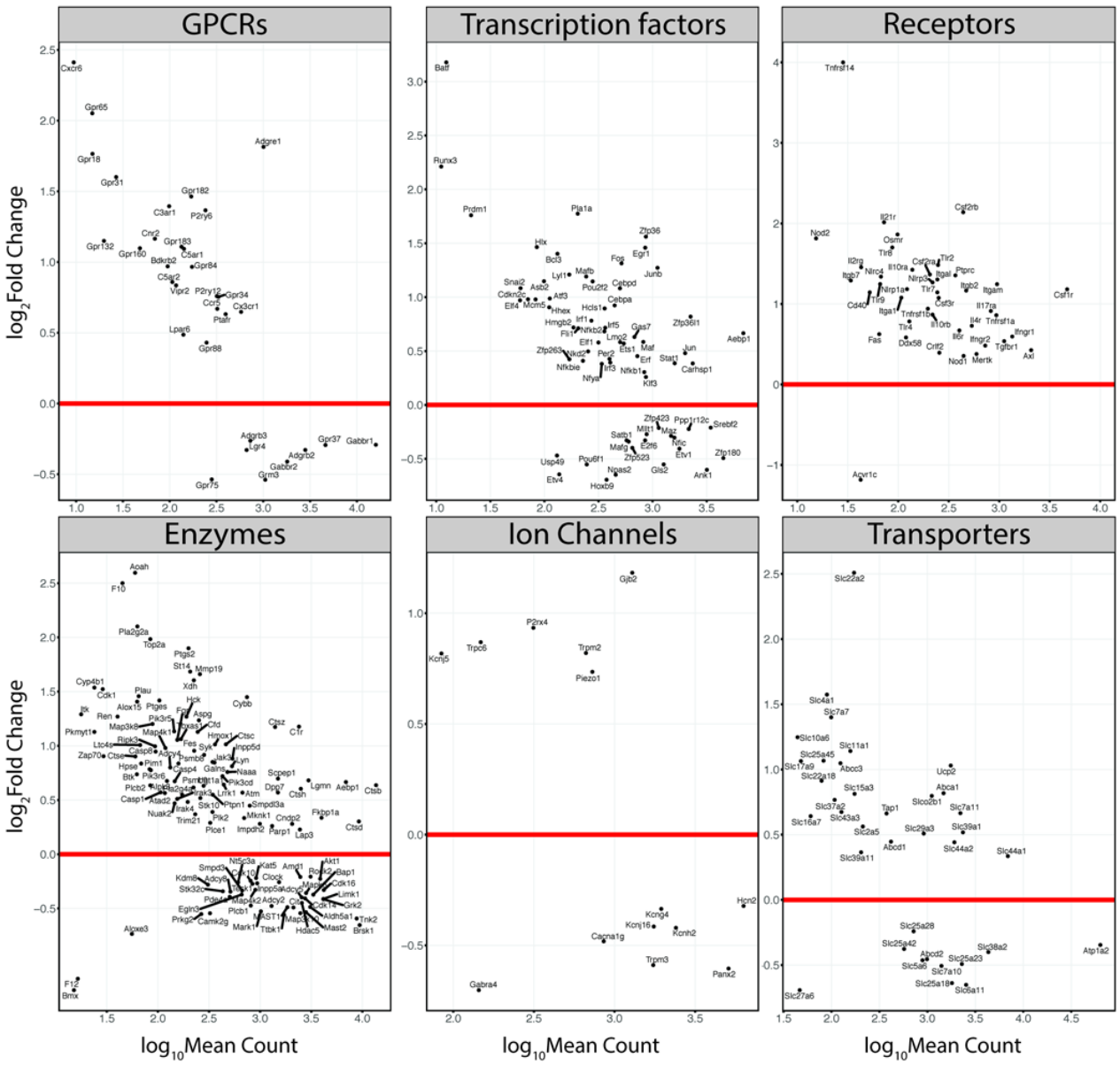
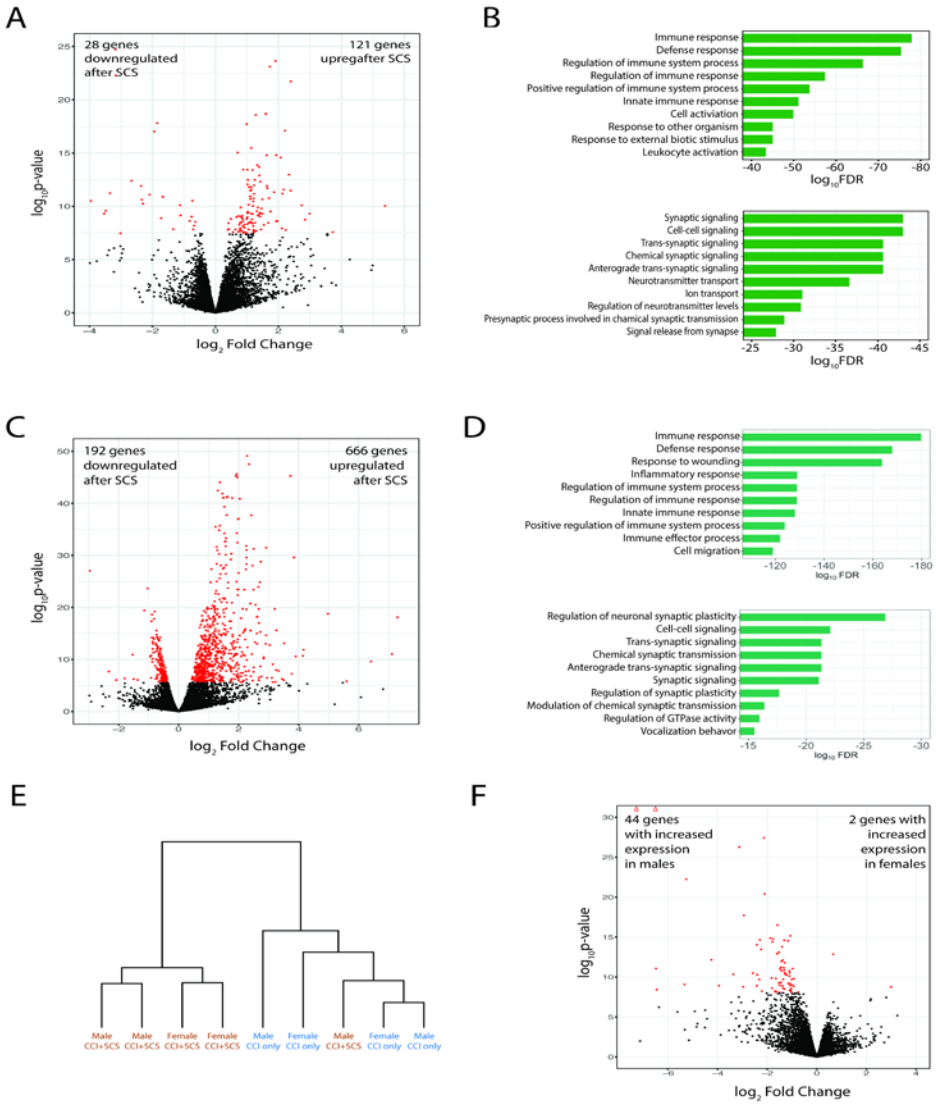
Supplemental Table 1. Genes significantly increased in the ipsilateral spinal cord of males versus females after SCS

Ensembl ID	Gene symbol	Full gene name	log2 Fold Change	Standard error	FDR
ENSRNOG00000057231	Ddx3	DEAD-box helicase 31	-8.30	0.46	3.33E-68
ENSRNOG00000060048	Eif2s3y	Eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked	-8.64	0.61	3.41E-41
ENSRNOG00000025670	Shisa3	Shisa family member 3	-3.13	0.47	1.76E-07
ENSRNOG00000006096	Slc26a7	Solute carrier family 26 member 7	-5.26	0.89	9.23E-06
ENSRNOG00000022101	Crabp2	Cellular retinoic acid binding protein 2	-2.10	0.38	8.49E-05
ENSRNOG00000015567	Slc9a2	Solute carrier family 9 member A2	-2.93	0.54	1.08E-04
ENSRNOG00000012660	Postn	Periostin	-2.42	0.47	4.18E-04
ENSRNOG00000045829	Thbs1	Thrombospondin 1	-4.25	0.85	8.18E-04
ENSRNOG00000005781	Wnt16	Wingless-type MMTV integration site family, member 16	-2.30	0.47	1.21E-03
ENSRNOG00000013954	Alpl	Alkaline phosphatase, liver/bone/kidney	-1.87	0.38	1.21E-03
ENSRNOG00000039668	Col8a1	Collagen type VIII alpha 1 chain	-1.59	0.33	1.21E-03
ENSRNOG00000004516	Itgbl1	Integrin subunit beta like 1	-1.77	0.37	1.63E-03
ENSRNOG00000018748	Slc16a11	Solute carrier family 16, member 11	-1.31	0.28	1.87E-03
ENSRNOG00000029047	Cubn	Cubilin	-2.25	0.49	3.18E-03
ENSRNOG00000009204	Il17re	Interleukin 17 receptor E	-2.58	0.58	7.04E-03
ENSRNOG00000036827	Ppp1r1a	Protein phosphatase 1, regulatory (inhibitor) subunit 1A	-1.37	0.31	1.04E-02
ENSRNOG00000016299	Klf4	Kruppel like factor 4	-1.10	0.25	1.07E-02
ENSRNOG00000029911	Cilp	Cartilage intermediate layer protein	-1.49	0.35	1.19E-02
ENSRNOG00000002385	Prg4	Proteoglycan 4	-6.48	1.52	1.21E-02
ENSRNOG00000012876	Slc6a13	Solute carrier family 6 member 13	-1.40	0.33	1.24E-02
ENSRNOG00000051854	Enpep	Glutamyl aminopeptidase	-1.42	0.34	1.25E-02
ENSRNOG00000025001	Pcolce	Procollagen C-endopeptidase enhancer 2	-1.53	0.36	1.41E-02
ENSRNOG00000010832	Pdgfrl	Platelet-derived growth factor receptor-like	-2.40	0.58	1.64E-02
ENSRNOG00000033734	Tnnt2	Troponin T2, Cardiac Type	-2.94	0.71	1.73E-02
ENSRNOG00000010840	Adamtsl3	ADAMTS-like 3	-1.60	0.39	1.73E-02
ENSRNOG00000016366	Colec12	Collectin sub-family member 12	-1.30	0.31	1.73E-02
ENSRNOG00000060949	Anxa8	Annexin A8	-3.37	0.83	2.18E-02
ENSRNOG00000003172	Serpinf1	Serpin family F member 1	-1.79	0.44	2.27E-02
ENSRNOG00000016085	Mpzl2	Myelin protein zero-like 2	-1.43	0.35	2.27E-02

ENSRNOG00000004610	Lum	Lumican	-1.31	0.33	2.69E-02
ENSRNOG00000021155	Ctsk	Cathepsin K	-1.29	0.33	2.81E-02
ENSRNOG00000059890	Clec2d2	C-type lectin domain family 2 member D2	-5.34	1.38	4.00E-02
ENSRNOG00000015902	Cpxm2	Carboxypeptidase X (M14 family), member 2	-2.13	0.55	4.12E-02
ENSRNOG00000009694	Bmp4	Bone morphogenetic protein 4	-1.15	0.30	4.12E-02
ENSRNOG00000006526	Sema3c	Semaphorin 3C	-1.09	0.28	4.26E-02
ENSRNOG00000010265	Ada	Adenosine deaminase	-1.63	0.43	4.55E-02
ENSRNOG00000010666	Wisp2	WNT1 inducible signaling pathway protein 2	-2.56	0.67	4.58E-02
ENSRNOG00000006553	Bnc2	Basonuclin 2	-1.80	0.47	4.58E-02
ENSRNOG00000014426	Lox	Lysyl oxidase	-1.33	0.35	4.69E-02
ENSRNOG00000039744	RT1-CE4	RT1 class I, locus CE4	-0.92	0.24	4.69E-02
ENSRNOG00000014443	Pde5a	Phosphodiesterase 5A	-1.65	0.44	4.69E-02
ENSRNOG00000010947	Mmp14	Matrix metallopeptidase 14	-0.98	0.26	4.69E-02
ENSRNOG00000043332	Foxd1	Forkhead box D1	-1.82	0.48	4.71E-02
ENSRNOG00000009437	Ewsr1	EWS RNA-binding protein 1	-1.05	0.28	4.85E-02



Supplemental figure 1. Differentially expressed genes by gene class. A total of 343 of the 1113 differentially expressed genes (FDR < 0.05) were assigned gene classes (i.e., transporters, enzymes, G protein coupled receptors, ion channels, catalytic receptors, transcription factors) as defined by IUPHAR. Figure 2C of the main text shows a bar chart (top) and heatmap (bottom) of the relative difference in expression of genes within each class between CCI only rats and CCI+SCS. Plotted here are a series of scatterplots that identify the mean normalized expression level of each gene and its fold change after SCS (i.e., positive log2 fold change values indicate increased expression after SCS) for genes assigned to each gene class (i.e., receptors, GPCRs, enzymes, transporters, ion channels, transcription factors). Red line indicates no change between groups.



Supplemental figure 2. Sex differences in differential gene expression after SCS in CCI rats. (A) Volcano plot showing RNA-seq data of the ipsilateral spinal cord from CCI only and CCI+SCS male rats. DEGs are designated in red and are defined as differentially expressed genes with a FDR < 0.05. Triangles represent genes with extremely high log10FDR or log2fold change values. (B) Barplot showing the top GO biological processes associated with genes upregulated (FDR<0.05; top) and downregulated (unadjusted p-value<0.05; bottom) in male CCI+SCS versus CCI only rats. (C) Volcano plot showing RNA-seq data of the ipsilateral spinal cord from CCI only and CCI+SCS female rats. DEGs are designated in red and are defined as differentially expressed genes with a FDR < 0.05. Triangles represent genes with extremely high log10FDR or log2fold change values. (D) Barplot showing the top 10 GO biological processes associated with genes upregulated (top) and downregulated (bottom) in female CCI+SCS versus CCI only rats (FDR<0.05). (E) Dendrogram showing hierarchical clustering of samples by treatment group and sex of rat. (F) Volcano plot showing differentially expressed genes from the ipsilateral spinal cord of males versus female rats. Positive log2 fold change indicates increased gene expression in female rats versus males. DEGs are designated in red and are defined as differentially expressed genes with a FDR < 0.05. Triangles represent genes with extremely high log10FDR or log2fold change values.