

## Supplemental Figure S1

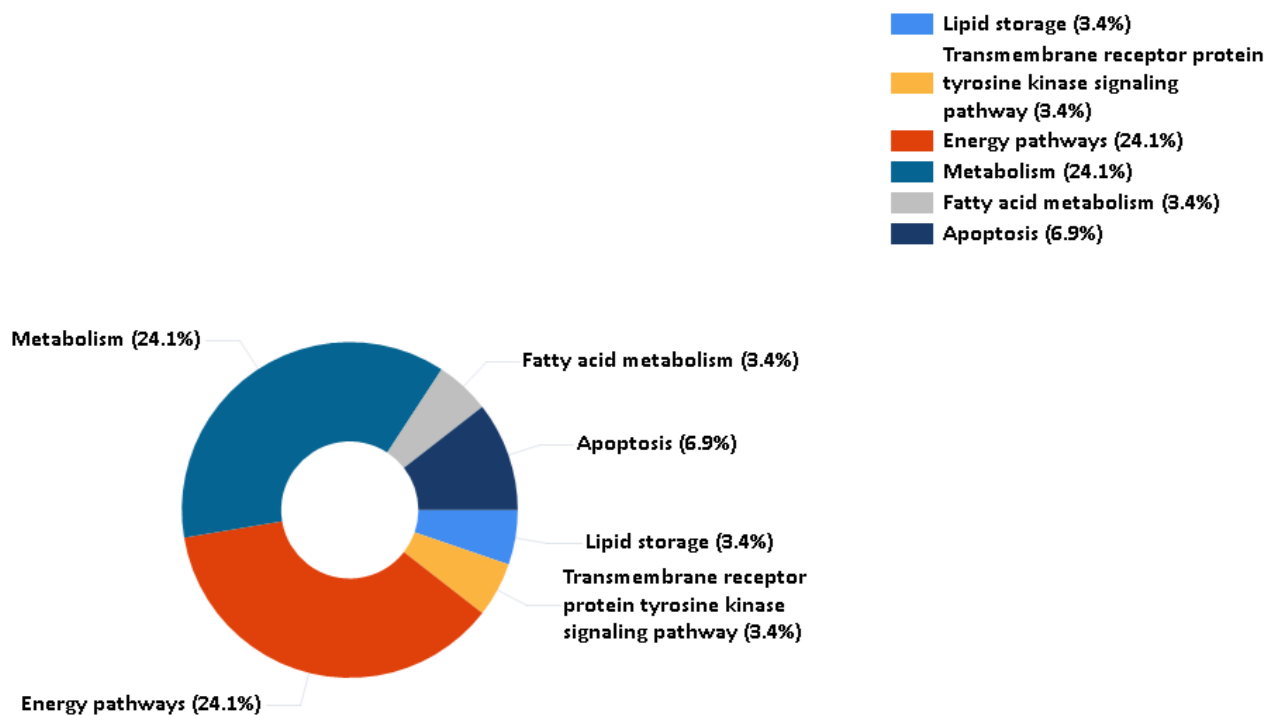
### Supplementary Code 1 & 2.ijm

```
1 //These are the variables to change for the threshold cell counts.
2 //These are the variables used for the NeuN cell count.
3 //They real values must be empirically determined by user.
4
5
6 lowT = 0;
7 upperT = 70;
8 lowerS= 25;
9 upperS= 2000;
10
11
12
13 dir = getDirectory("choose a Directory")
14 list = getFileList(dir);
15
16 Dialog.create("threshold");
17 Dialog.addNumber("Lower", lowT);
18 Dialog.addNumber("Upper", upperT);
19 Dialog.show();
20 //setThreshold(lowT, upperT);
21
22 for (i = 0; i < list.length; i++){
23     if(File.isDirectory(dir+list[i])){}
24     else {
25         open(dir+list[i]);
26         //run("Split Channels");
27         //close();
28         //close("\\Others");
29
30         getDimensions(width, height, channels, slices, frames);
31         title = File.nameWithoutExtension;
32         if (slices > 1){
33             run("Z Project..."); //error add code max int
34         }
35         setThreshold(lowT, upperT);
36         run("Threshold");
37         run("Invert");
38         run("Analyze Particles...", "size="+ lowerS + "-" + upperS + " show=Overlay summarize in_situ include_holes");
39         run("Close All");
40     }
41 }
42
43
```

```
1 //These are the variables used to measure GFAP fluorescence intensity.
2 //They real values must be empirically determined by user
3
4 makeRectangle(12, 18, 2736, 2562);
5 waitForUser;
6 run("Crop");
7 setThreshold(0, 80);
8 run("Create Selection");
9 run("Measure"); // Make sure you have area integrated intensity and mean grey value selected
10
```

Supplemental code for Fiji Image analysis used for immunofluorescence quantification.

Supplemental Figure S2



Functional analysis of genes that are significantly upregulated in GFAP-Cre<sup>+</sup>/TG2fl/fl mice three days post injury using FunRich (<http://www.funrich.org>).

**Supplemental Table S1**

<b>ANTIBODY</b>	<b>SOURCE</b>	<b>CATALOGUE NUMBER</b>
rabbit anti-GFAP	Dako	Z033401-2
goat anti-GFAP	Novus	NB100-53809
rabbit anti-SOX9	Millipore-Sigma	AB5535
chicken anti-NeuN	Millipore-Sigma	ABN91
Anti-NG2, Alexa Fluor 488 conjugate	Millipore-Sigma	AB5320A4
donkey anti-goat Alexa Fluor 488	Invitrogen	A-11055
goat anti-chicken Alexa Fluor 488	Invitrogen	A32931
goat anti-rabbit Alexa Fluor 647	Invitrogen	A32733
donkey anti-goat Alexa Fluor 647	Invitrogen	A32849
donkey anti-rabbit Alexa Fluor 647	Invitrogen	A48258

**Supplemental Table S2**

<b>Target</b>	<b>Forward primer</b>	<b>Reverse primer</b>
Lipoprotein lipase	5'GGGAGTTTGGCTCCAGAGTT T3'	5'TGTGTCTTCAGGGGTCCTTA G3'
Fatty acid binding protein 4	5'AAGGTGAAGAGCATCATAAC CCT3'	5'TCACGCCTTTCATAACACAT TCC3'
Perilipin	5'GGGACCTGTGAGTGCTTCC3 '	5'GTATTGAAGAGCCGGGATC TTTT3'
Glyceraldehyde-3-Phosphate Dehydrogenase	5'ATGGGACGATGCTGGTACTA G3'	5'TGCTGACAACCTTGAGTGAA AT3'

Supplemental Table S3

**Genes that are significantly different in spinal cords of  
GFAP-Cre+/-TG2fl/fl mice compared to TG2fl/fl mice 3 days postinjury**

<b>Gene</b>	<b>BaseMean</b>	<b>log2FoldChange</b>	<b>stat</b>	<b>pvalue</b>	<b>padj</b>
Ucp1	1839.018	3.204	7.039	1.94E-12	5.16E-08
Pck1	544.603	3.23	6.864	6.69E-12	8.91E-08
Cidec	379.985	3.29	6.378	1.80E-10	1.60E-06
Plin1	229.471	3.241	6.119	9.43E-10	6.29E-06
Adipoq	165.857	3.359	6.066	1.31E-09	7.01E-06
Tmem79	76.832	2.268	5.739	9.53E-09	4.23E-05
Trarg1	313.398	2.7	5.27	1.37E-07	0.00052
Tmem45b	47.06	2.373	5.203	1.97E-07	0.000655
Hp	2084.877	3.129	5.149	2.62E-07	0.000777
Ces1d	49.255	2.407	5.07	3.98E-07	0.001062
Cidea	585.054	2.679	4.897	9.72E-07	0.002355
Retn	23.804	2.775	4.865	1.14E-06	0.002539
Fabp4	4711.471	2.878	4.843	1.28E-06	0.002621
Cd300lg	111.464	2.537	4.777	1.78E-06	0.003165
Adtrp	82.11	2.817	4.789	1.67E-06	0.003165
Lpl	2917.602	2.565	4.753	2.00E-06	0.003334
Btnl9	31.183	2.496	4.611	4.01E-06	0.006283
Aqp7	47.057	2.51	4.584	4.57E-06	0.006761
Elovl3	157.437	2.352	4.495	6.94E-06	0.009743
Th	109.153	1.704	4.433	9.29E-06	0.012381
Ctcflos	55.689	2.004	4.417	1.00E-05	0.012714
Cyp2e1	67.719	2.278	4.288	1.81E-05	0.021228
Cfd	219.85	2.35	4.285	1.83E-05	0.021228
Adig	27.797	2.314	4.244	2.20E-05	0.024394
Ntrk1	62.048	1.941	4.216	2.49E-05	0.02455
Otop1	58.498	2.495	4.224	2.40E-05	0.02455
Pirt	238.056	2.063	4.218	2.47E-05	0.02455
Acaa1b	104.13	2.317	4.154	3.27E-05	0.031167
Alkal2	19.039	1.863	4.141	3.46E-05	0.031789
Slc6a2	25.009	2.4	4.072	4.66E-05	0.041444
Slc18a2	18.511	2.269	4.063	4.85E-05	0.041741
Cyp2f2	10.428	2.267	4.032	5.54E-05	0.045051
C7	19.398	2.371	4.03	5.58E-05	0.045051
Chad	48.389	1.949	4.012	6.01E-05	0.047116
Acot2	246.088	1.395	3.989	6.64E-05	0.049205
2010003K1	17.845	2.458	3.989	6.63E-05	0.049205
Ccdc80	318.311	1.054	3.98	6.89E-05	0.049669

## Supplemental Table S4

Biological Process	Adjusted P-v	Odds Ratio	Combined Score	Genes
brown fat cell differentiation (GO:0050873)	1.52E-04	352.2	5262.453429	ADIPOQ;UCP1;ADIG
long-chain fatty acid metabolic process (GO:0001676)	0.00268941	30.50863061	336.1408856	ELOVL3;ACOT2;ADTRP;CYP2E1
response to insulin (GO:0032868)	0.00268941	30.12575758	330.4923304	TRARG1;ADIPOQ;OTOP1;PCK1
positive regulation of cold-induced thermogenesis (GO:0120162)	0.00356049	25.89768654	269.3920495	FABP4;ADIPOQ;ELOVL3;UCP1
cellular response to peptide hormone stimulus (GO:0071375)	0.00403567	23.60190137	237.2875724	TRARG1;ADIPOQ;OTOP1;PCK1
positive regulation of metabolic process (GO:0009893)	0.00431888	22.07839867	216.4478246	FABP4;ADIPOQ;ELOVL3;UCP1
synaptic transmission, dopaminergic (GO:0001963)	0.00465807	228.0914286	2183.712167	TH;SLC6A2
cellular response to insulin stimulus (GO:0032869)	0.00474921	19.23684848	178.6773171	TRARG1;ADIPOQ;OTOP1;PCK1
monoamine transport (GO:0015844)	0.00474921	190.0666667	1765.211478	SLC6A2;SLC18A2
response to glucose (GO:0009749)	0.00474921	38.20396419	351.3922501	ADIPOQ;LPL;PCK1
positive regulation of sequestering of triglyceride (GO:0010890)	0.00506972	162.9061224	1472.211648	CIDEA;LPL
fat cell differentiation (GO:0045444)	0.00653855	31.93796791	277.6550177	ADIPOQ;UCP1;ADIG
regulation of biosynthetic process (GO:0009889)	0.00653855	126.6920635	1091.539997	UCP1;PCK1
fatty acid biosynthetic process (GO:0006633)	0.0102331	25.81531142	208.9406809	ELOVL3;LPL;CYP2E1
regulation of sequestering of triglyceride (GO:0010889)	0.01076804	87.69230769	699.2344145	CIDEA;LPL
regulation of fat cell differentiation (GO:0045598)	0.01227769	22.78762414	176.4266626	ADIPOQ;LPL;ADIG
cellular response to fatty acid (GO:0071398)	0.01227769	75.99238095	586.4606264	UCP1;LPL
response to fatty acid (GO:0070542)	0.01454584	67.04537815	502.2155781	UCP1;LPL
positive regulation of lipid storage (GO:0010884)	0.01688376	59.98195489	437.1224949	CIDEA;LPL
lipid droplet organization (GO:0034389)	0.017623	56.98	409.8811226	CIDEA;CIDEA
triglyceride catabolic process (GO:0019433)	0.01836088	54.26394558	385.4700929	FABP4;LPL
response to hexose (GO:0009746)	0.02073383	49.54037267	343.5896724	ADIPOQ;LPL
negative regulation of protein transport (GO:0051224)	0.02146006	47.47380952	325.5122514	ADIPOQ;ADTRP
regulation of reactive oxygen species biosynthetic process (GO:0000000)	0.0238641	43.81758242	293.9252254	UCP1;SLC18A2
regulation of macrophage derived foam cell differentiation (GO:0000000)	0.02691638	39.27881773	255.4802892	ADIPOQ;LPL
fatty acid metabolic process (GO:0006631)	0.02691638	14.4691298	93.61217318	ADIPOQ;ACOT2;LPL
regulation of tumor necrosis factor production (GO:0032680)	0.02691638	14.4691298	93.61217318	ADIPOQ;CIDEA;LPL
very long-chain fatty acid metabolic process (GO:0000038)	0.02840625	36.74101382	234.3909225	ELOVL3;ACOT2
acylglycerol catabolic process (GO:0046464)	0.02980736	34.51082251	216.1207577	FABP4;LPL
regulation of lipid biosynthetic process (GO:0046890)	0.02980736	34.51082251	216.1207577	ADIPOQ;PCK1
proton transmembrane transport (GO:1902600)	0.03221294	32.5355102	200.1585487	UCP1;OTOP1
negative regulation of cell-cell adhesion (GO:0022408)	0.03708499	29.19267399	173.6566538	ADIPOQ;ADTRP
hexose metabolic process (GO:0019318)	0.03708499	29.19267399	173.6566538	ADIPOQ;PCK1
negative regulation of tumor necrosis factor production (GO:0032680)	0.04516859	25.86883117	148.0109909	ADIPOQ;CIDEA
negative regulation of cold-induced thermogenesis (GO:0120163)	0.04577499	25.29269841	143.6441165	ADIPOQ;CIDEA
negative regulation of tumor necrosis factor superfamily cytokine production (GO:0000000)	0.04638449	24.74161491	139.4901066	ADIPOQ;CIDEA
positive regulation of multicellular organismal process (GO:0051224)	0.04649415	6.974851151	39.11575762	FABP4;ADIPOQ;ELOVL3;UCP1
positive regulation of fat cell differentiation (GO:0045600)	0.04822795	23.22332362	128.1662168	LPL;ADIG
inositol lipid-mediated signaling (GO:0048017)	0.04822795	23.22332362	128.1662168	NTRK1;PIRT

**Gene ontology pathway analysis identifies a preponderance of lipid biosynthetic pathways among differentially expressed genes in mice lacking astrocytic TG2.** 22 out of 39 GO terms with an adjusted p-value of less than 0.05 are involved with lipid biosynthetic pathways and storage (highlighted in yellow). Enrichr, GO Biological Process 2021.