

Article

Oligodendrocytes remodel the genomic fabrics of functional pathways in astrocytes

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Supplementary Material

Table S1. Genes whose >1.5x absolute fold-change did not meet the individual CUT criterion. Red/green background of the expression ratio indicates not significant (false) up-/down-regulation.

Gene	Description	X	CUT
<i>Acap2</i>	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2	-1.540	1.816
<i>Adamts18</i>	a disintegrin-like and metallopeptidase	-1.514	1.594
<i>Akr1c12</i>	aldo-keto reductase family 1, member C12	1.866	1.994
<i>Alx3</i>	aristaless-like homeobox 3	1.536	1.769
<i>Alyref2</i>	Aly/REF export factor 2	-1.880	2.208
<i>Ankrd33b</i>	ankyrin repeat domain 33B	1.593	1.829
<i>Ankrd45</i>	ankyrin repeat domain 45	1.514	1.984
<i>Ankrd50</i>	ankyrin repeat domain 50	1.628	1.832
<i>Ankrd61</i>	ankyrin repeat domain 61	1.645	1.802
<i>Arid1a</i>	AT rich interactive domain 1A	-1.668	2.066
<i>Artn</i>	artemin	1.524	1.732
<i>Aspm</i>	abnormal spindle microtubule assembly	-1.693	1.716
<i>Atp6v1e1</i>	ATPase, H ⁺ transporting, lysosomal V1 subunit E1	-1.679	1.777
<i>Bag4</i>	BCL2-associated athanogene 4	1.723	1.914
<i>Birc3</i>	baculoviral IAP repeat-containing 3	-1.588	1.722
<i>Ccdc104</i>	coiled-coil domain containing 104	-1.819	2.130
<i>Ccl2</i>	chemokine	-1.699	2.034
<i>Cdc20b</i>	cell division cycle 20 homolog B	1.512	1.605
<i>Cenpf</i>	centromere protein F	2.041	2.128
<i>Cep97</i>	centrosomal protein 97	-1.641	1.723
<i>COX1</i>	mitochondrially encoded cytochrome c oxidase I	-1.607	1.650
<i>Cpsf7</i>	cleavage and polyadenylation specific factor 7	-1.635	1.891
<i>Crct1</i>	cysteine-rich C-terminal 1	-1.530	1.701
<i>Cul4b</i>	cullin 4B	-1.550	1.574
<i>Cyp4a12b</i>	cytochrome P450, family 4, subfamily a, polypeptide 12B	-1.628	1.751
<i>Ddx11</i>	DEAD/H	2.057	2.228
<i>Defb1</i>	defensin beta 1	-1.581	1.629
<i>Defb45</i>	defensin beta 45	1.986	2.226
<i>Deptor</i>	DEP domain containing MTOR-interacting protein	1.839	1.899
<i>Dmtf1</i>	cyclin D binding myb-like transcription factor 1	-1.671	1.727
<i>Dnaic1</i>	dynein, axonemal, intermediate chain 1	-1.533	1.859
<i>Dnmt3b</i>	DNA methyltransferase 3B	-1.780	1.932
<i>Draxin</i>	dorsal inhibitory axon guidance protein	1.513	1.564
<i>Eda2r</i>	ectodysplasin A2 receptor	-1.525	1.682
<i>Eif4g2</i>	eukaryotic translation initiation factor 4, gamma 2	-2.150	2.324
<i>Exoc5</i>	exocyst complex component 5	-1.553	1.778
<i>Fam110c</i>	family with sequence similarity 110, member C	1.617	1.818
<i>Fam124b</i>	family with sequence similarity 124, member B	1.502	1.509
<i>Fbxo34</i>	F-box protein 34	-1.672	1.763
<i>Fech</i>	ferrochelataase	-1.624	1.908
<i>Fgf18</i>	fibroblast growth factor 18	1.716	1.729

<i>Gdap10</i>	ganglioside-induced differentiation-associated-protein 10	1.558	1.681
<i>Gdf7</i>	growth differentiation factor 7	1.501	1.560
<i>Gfi1b</i>	growth factor independent 1B	1.512	1.919
<i>Glg1</i>	golgi apparatus protein 1	-1.778	2.010
<i>Gpr3</i>	G-protein coupled receptor 3	-1.644	1.664
<i>Gpx2</i>	glutathione peroxidase 2	-1.527	1.794
<i>Gria2</i>	glutamate receptor, ionotropic, AMPA2	1.760	2.147
<i>H2-Ke2</i>	H2-K region expressed gene 2	-1.584	1.631
<i>H2-Q4</i>	histocompatibility 2, Q region locus 4	1.612	2.316
<i>Herc6</i>	hect domain and RLD 6	2.162	2.204
<i>Hirip3</i>	HIRA interacting protein 3	-1.636	1.877
<i>Hmga2</i>	high mobility group AT-hook 2	1.759	1.844
<i>Hnrnpa2b1</i>	heterogeneous nuclear ribonucleoprotein A2/B1	2.005	2.434
<i>Hoxb6</i>	homeobox B6	1.860	2.061
<i>Hsd17b4</i>	hydroxysteroid	-1.658	1.933
<i>Id2</i>	inhibitor of DNA binding 2	-1.647	1.665
<i>Igh-VJ558</i>	immunoglobulin heavy chain	-1.723	1.898
<i>Il11</i>	interleukin 11	-1.777	1.835
<i>Isoc1</i>	isochorismatase domain containing 1	-1.648	2.044
<i>Itpril2</i>	inositol 1,4,5-triphosphate receptor interacting protein-like 2	-1.523	1.812
<i>Kcna5</i>	potassium voltage-gated channel, shaker-related subfamily, member 5	1.800	1.842
<i>Kcnip1</i>	Kv channel-interacting protein 1	-1.519	1.521
<i>Klk11</i>	kallikrein related-peptidase 11	-1.982	2.027
<i>Kpna7</i>	karyopherin alpha 7	-1.547	1.627
<i>Krt6b</i>	keratin 6B	1.647	1.826
<i>Lamtor1</i>	late endosomal/lysosomal adaptor, MAPK and MTOR activator 1	-1.726	1.745
<i>Lrrc29</i>	leucine rich repeat containing 29	1.696	1.845
<i>Lrrc48</i>	leucine rich repeat containing 48	2.168	2.295
<i>Lrrc66</i>	leucine rich repeat containing 66	1.705	2.131
<i>Mad2l1bp</i>	MAD2L1 binding protein	1.523	1.530
<i>Megf10</i>	multiple EGF-like-domains 10	-1.644	1.702
<i>Mgat2</i>	mannoside acetylglucosaminyltransferase 2	1.606	1.740
<i>Mios</i>	missing oocyte, meiosis regulator, homolog	1.653	1.669
<i>Mpp5</i>	membrane protein, palmitoylated 5	-1.551	1.908
<i>Mrpl11</i>	mitochondrial ribosomal protein L11	-1.562	2.125
<i>Mrs2</i>	MRS2 magnesium homeostasis factor homolog	-1.597	1.695
<i>Mthfs</i>	5, 10-methenyltetrahydrofolate synthetase	1.680	1.793
<i>Mtss1l</i>	metastasis suppressor 1-like	-1.580	1.669
<i>Myo5b</i>	myosin VB	-1.829	2.143
<i>Nat8l</i>	N-acetyltransferase 8-like	-1.661	2.099
<i>Net1</i>	neuroepithelial cell transforming gene 1	-1.686	2.039
<i>Nfat5</i>	nuclear factor of activated T cells 5	-1.740	1.791
<i>Ngb</i>	neuroglobin	1.561	1.665
<i>Noc4l</i>	nucleolar complex associated 4 homolog	1.697	1.948
<i>Notch3</i>	notch 3	-1.634	1.798
<i>Nox4</i>	NADPH oxidase 4	1.595	2.030
<i>Olf417</i>	olfactory receptor 417	1.573	1.862
<i>Pappa</i>	pregnancy-associated plasma protein A	-1.608	2.168
<i>Pcnt</i>	pericentrin	-1.641	2.572
<i>Pdf</i>	peptide deformylase	-1.593	1.830
<i>Pdxk</i>	pyridoxal	-1.671	1.798
<i>Pebp1</i>	phosphatidylethanolamine binding protein 1	-1.517	1.852
<i>Pias1</i>	protein inhibitor of activated STAT 1	1.751	1.905
<i>Pipox</i>	pipecolic acid oxidase	-1.548	1.973
<i>Plekhb1</i>	pleckstrin homology domain containing, family B	1.514	1.566
<i>Pm20d1</i>	peptidase M20 domain containing 1	-1.538	1.665

<i>Polr1d</i>	polymerase	-1.707	1.914
<i>Prr13</i>	proline rich 13	1.908	1.915
<i>Psg19</i>	pregnancy specific glycoprotein 19	1.602	2.148
<i>Pthlh</i>	parathyroid hormone-like peptide	-1.545	1.905
<i>Ptprn</i>	protein tyrosine phosphatase, receptor type, N	1.849	1.955
<i>Ptx4</i>	pentraxin 4	1.571	1.667
<i>Rffl</i>	ring finger and FYVE like domain containing protein	1.900	1.988
<i>Rhox3h</i>	reproductive homeobox 3H	2.043	2.074
<i>Rn18s</i>	18S ribosomal RNA	1.838	1.998
<i>Rnf139</i>	ring finger protein 139	-1.728	1.754
<i>Rpl19</i>	ribosomal protein L19	-1.590	1.977
<i>Rpl5</i>	ribosomal protein L5	-1.604	2.085
<i>Rplp2</i>	ribosomal protein, large P2	-1.709	2.297
<i>Rpp21</i>	ribonuclease P 21 subunit	-1.678	1.720
<i>Rtn4rl2</i>	reticulon 4 receptor-like 2	1.614	1.816
<i>Samd8</i>	sterile alpha motif domain containing 8	1.536	1.758
<i>Sec61b</i>	Sec61 beta subunit	-1.683	1.812
<i>Senp5</i>	SUMO/sentrin specific peptidase 5	1.619	2.074
<i>Serpinc3c</i>	serine	-1.606	1.750
<i>Sfn</i>	stratifin	1.761	2.195
<i>Slc38a11</i>	solute carrier family 38, member 11	1.538	2.052
<i>Slc6a5</i>	solute carrier family 6	1.890	1.984
<i>Smim5</i>	small integral membrane protein 5	-1.850	2.290
<i>Snord116</i>	Pwcr1 mRNA, complete sequence.	2.012	2.167
<i>Snrpg</i>	small nuclear ribonucleoprotein polypeptide G	-1.554	1.926
<i>Stmn4</i>	stathmin-like 4	1.546	1.679
<i>Stpg2</i>	sperm tail PG rich repeat containing 2	1.628	2.123
<i>Syt1</i>	synaptotagmin I	1.992	2.153
<i>Syt6</i>	synaptotagmin VI	1.670	1.671
<i>Tal1</i>	T cell acute lymphocytic leukemia 1	1.660	1.763
<i>Tbccd1</i>	TBCC domain containing 1	-1.509	1.688
<i>Thoc3</i>	THO complex 3	-1.643	2.254
<i>Thoc5</i>	THO complex 5	-1.582	1.666
<i>Tinagl1</i>	tubulointerstitial nephritis antigen-like 1	-1.585	1.676
<i>Tm9sf1</i>	transmembrane 9 superfamily member 1	-1.664	2.007
<i>Tmem201</i>	transmembrane protein 201	1.732	2.208
<i>Tmem242</i>	transmembrane protein 242	-1.592	1.721
<i>Tspan32</i>	tetraspanin 32	1.562	1.833
<i>Ubl3</i>	ubiquitin-like 3	-1.521	1.786
<i>Vpreb3</i>	pre-B lymphocyte gene 3	-1.692	1.709
<i>Zbed3</i>	zinc finger, BED domain containing 3	1.615	1.643
<i>Zc3h14</i>	zinc finger CCCH type containing 14	-1.850	2.064
<i>Zfml</i>	zinc finger, matrin-like	-1.694	1.794
<i>Zfp235</i>	zinc finger protein 235	1.776	1.821
<i>Zfp354b</i>	zinc finger protein 354B	-1.883	1.901
<i>Zkscan5</i>	zinc finger with KRAB and SCAN domains 5	-1.671	1.834

Table S2. Genes considered as significantly up-regulated although their absolute fold-change was below the traditional 1.5x.

Gene	Description	X	CUT
<i>Adora2b</i>	adenosine A2b receptor	1.441	1.194
<i>Anapc2</i>	anaphase promoting complex subunit 2	1.230	1.087
<i>Arrb1</i>	arrestin, beta 1	1.167	1.138
<i>Arrb2</i>	arrestin, beta 2	1.264	1.216
<i>Atg2a</i>	autophagy related 2A	1.173	1.160
<i>Ccl5</i>	chemokine	1.488	1.371
<i>Cd37</i>	CD37 antigen	1.413	1.153
<i>Cd38</i>	CD38 antigen	1.335	1.224
<i>Chuk</i>	conserved helix-loop-helix ubiquitous kinase	1.100	1.097
<i>Col6a1</i>	collagen, type VI, alpha 1	1.258	1.217
<i>Col9a2</i>	collagen, type IX, alpha 2	1.239	1.233
<i>Ctsb</i>	cathepsin B	1.460	1.250
<i>Ednrb</i>	endothelin receptor type B	1.428	1.245
<i>Eif2s1</i>	eukaryotic translation initiation factor 2, subunit 1 alpha	1.274	1.242
<i>Fgf1</i>	fibroblast growth factor 1	1.442	1.218
<i>Fgf9</i>	fibroblast growth factor 9	1.498	1.250
<i>Fgr</i>	Gardner-Rasheed feline sarcoma viral	1.330	1.269
<i>Foxo1</i>	forkhead box O1	1.401	1.107
<i>G6pc3</i>	glucose 6 phosphatase, catalytic, 3	1.212	1.163
<i>Glul</i>	glutamate-ammonia ligase	1.433	1.260
<i>Gnal</i>	guanine nucleotide binding protein, alpha stimulating, olfactory type	1.337	1.329
<i>Gng11</i>	guanine nucleotide binding protein	1.195	1.192
<i>Gng3</i>	guanine nucleotide binding protein	1.443	1.254
<i>Gsn</i>	gelsolin	1.269	1.267
<i>Gucy1b2</i>	guanylate cyclase 1, soluble, beta 2	1.346	1.268
<i>Igfbp1</i>	immunoglobulin	1.131	1.130
<i>Igf1</i>	insulin-like growth factor 1	1.330	1.245
<i>Itga9</i>	integrin alpha 9	1.299	1.193
<i>Itgb2</i>	integrin beta 2	1.403	1.155
<i>Jak1</i>	Janus kinase 1	1.143	1.135
<i>Limk1</i>	LIM-domain containing, protein kinase	1.289	1.239
<i>Mad2l2</i>	MAD2 mitotic arrest deficient-like 2	1.443	1.335
<i>Mapk3</i>	mitogen-activated protein kinase 3	1.379	1.324
<i>Med24</i>	mediator complex subunit 24	1.260	1.242
<i>Naip2</i>	NLR family, apoptosis inhibitory protein 2	1.249	1.203
<i>Ncf1</i>	neutrophil cytosolic factor 1	1.325	1.183
<i>Nod1</i>	nucleotide-binding oligomerization domain containing 1	1.327	1.196
<i>Nos3</i>	nitric oxide synthase 3, endothelial cell	1.274	1.225
<i>Panx1</i>	pannexin 1	1.423	1.138
<i>Pde1b</i>	phosphodiesterase 1B, Ca ²⁺ -calmodulin dependent	1.402	1.145
<i>Phka2</i>	phosphorylase kinase alpha 2	1.165	1.090
<i>Pik3r5</i>	phosphoinositide-3-kinase, regulatory subunit 5, p101	1.345	1.179
<i>Pik3r6</i>	phosphoinositide-3-kinase, regulatory subunit 6	1.093	1.092
<i>Pip4k2c</i>	phosphatidylinositol-5-phosphate 4-kinase, type II, gamma	1.131	1.079
<i>Rac3</i>	RAS-related C3 botulinum substrate 3	1.262	1.170
<i>Rbck1</i>	RanBP-type and C3HC4-type zinc finger containing 1	1.228	1.122
<i>Slc2a1</i>	solute carrier family 2	1.497	1.408
<i>Sphk2</i>	sphingosine kinase 2	1.179	1.117
<i>Ssh3</i>	slingshot homolog 3	1.309	1.161
<i>Syk</i>	spleen tyrosine kinase	1.219	1.131
<i>Tab1</i>	TGF-beta activated kinase 1/MAP3K7 binding protein 1	1.249	1.056
<i>Tbc1d4</i>	TBC1 domain family, member 4	1.392	1.365

<i>Tgfb1</i>	transforming growth factor, beta 1	1.372	1.311
<i>Ticam1</i>	toll-like receptor adaptor molecule 1	1.285	1.246
<i>Tsc2</i>	tuberous sclerosis 2	1.222	1.218
<i>Txnip</i>	thioredoxin interacting protein	1.304	1.250

Table S3. Genes considered as significantly down-regulated although their absolute fold-change was below the traditional 1.5x.

Gene	Description	X	CUT
<i>Adcy2</i>	adenylate cyclase 2	-1.267	1.214
<i>Adrb3</i>	adrenergic receptor, beta 3	-1.437	1.432
<i>Antxr2</i>	anthrax toxin receptor 2	-1.340	1.232
<i>Arhgef6</i>	Rac/Cdc42 guanine nucleotide exchange factor	-1.384	1.200
<i>Atg16l2</i>	autophagy related 16-like 2	-1.485	1.242
<i>Bcar1</i>	breast cancer anti-estrogen resistance 1	-1.438	1.229
<i>Bcl2l1</i>	BCL2-like 1	-1.395	1.242
<i>Bdnf</i>	brain derived neurotrophic factor	-1.488	1.221
<i>Braf</i>	Braf transforming gene	-1.241	1.209
<i>Bub1</i>	budding uninhibited by benzimidazoles 1 homolog	-1.470	1.362
<i>Camk2d</i>	calcium/calmodulin-dependent protein kinase II, delta	-1.182	1.152
<i>Casp1</i>	caspase 1	-1.388	1.231
<i>Ccna2</i>	cyclin A2	-1.348	1.195
<i>Cdc14b</i>	CDC14 cell division cycle 14B	-1.231	1.221
<i>Cdc20</i>	cell division cycle 20	-1.311	1.166
<i>Cdc25a</i>	cell division cycle 25A	-1.227	1.226
<i>Cdk2</i>	cyclin-dependent kinase 2	-1.482	1.226
<i>Cdk6</i>	cyclin-dependent kinase 6	-1.338	1.228
<i>Cfl2</i>	cofilin 2, muscle	-1.355	1.287
<i>Col1a1</i>	collagen, type I, alpha 1	-1.497	1.455
<i>Col1a2</i>	collagen, type I, alpha 2	-1.318	1.176
<i>Col2a1</i>	collagen, type II, alpha 1	-1.281	1.128
<i>Creb3l4</i>	cAMP responsive element binding protein 3-like 4	-1.267	1.256
<i>Cry1</i>	cryptochrome 1	-1.227	1.198
<i>Ctnnb1</i>	catenin	-1.305	1.285
<i>Cxcr3</i>	chemokine	-1.375	1.134
<i>E2f1</i>	E2F transcription factor 1	-1.255	1.168
<i>Eif2ak3</i>	eukaryotic translation initiation factor 2 alpha kinase 3	-1.444	1.269
<i>Fadd</i>	Fas (TNFRSF6)-associated via death domain	-1.123	1.115
<i>Fgd3</i>	FYVE, RhoGEF and PH domain containing 3	-1.244	1.209
<i>Flt3l</i>	FMS-like tyrosine kinase 3 ligand	-1.286	1.275
<i>Gadd45a</i>	growth arrest and DNA-damage-inducible 45 alpha	-1.342	1.190
<i>Gadd45b</i>	growth arrest and DNA-damage-inducible 45 beta	-1.378	1.223
<i>Gbp5</i>	guanylate binding protein 5	-1.335	1.326
<i>Gjc1</i>	gap junction protein, gamma 1	-1.316	1.142
<i>Gnaq</i>	guanine nucleotide binding protein, alpha q polypeptide	-1.284	1.220
<i>Gng12</i>	guanine nucleotide binding protein	-1.282	1.161
<i>Gng2</i>	guanine nucleotide binding protein	-1.134	1.099
<i>Hif1a</i>	hypoxia inducible factor 1, alpha subunit	-1.361	1.235
<i>Hsp90b1</i>	heat shock protein 90, beta	-1.183	1.145
<i>Ins2</i>	insulin II	-1.334	1.194
<i>Insr</i>	insulin receptor	-1.337	1.315
<i>Iqgap1</i>	IQ motif containing GTPase activating protein 1	-1.416	1.183
<i>Iqgap2</i>	IQ motif containing GTPase activating protein 2	-1.391	1.248
<i>Iqgap3</i>	IQ motif containing GTPase activating protein 3	-1.478	1.316
<i>Itgav</i>	integrin alpha V	-1.434	1.294
<i>Itgb5</i>	integrin beta 5	-1.368	1.160

<i>Itpr1</i>	inositol 1,4,5-trisphosphate receptor 1	-1.338	1.127
<i>Lama2</i>	laminin, alpha 2	-1.438	1.255
<i>Mad2l1</i>	MAD2 mitotic arrest deficient-like 1	-1.484	1.393
<i>Mapk12</i>	mitogen-activated protein kinase 12	-1.350	1.324
<i>Mapk8</i>	mitogen-activated protein kinase 8	-1.356	1.317
<i>Mcl1</i>	myeloid cell leukemia sequence 1	-1.166	1.123
<i>Mcm2</i>	minichromosome maintenance deficient 2 mitotin	-1.399	1.304
<i>Mcm4</i>	minichromosome maintenance deficient 4 homolog	-1.398	1.185
<i>Mcm7</i>	minichromosome maintenance deficient 7	-1.320	1.229
<i>Mdm2</i>	transformed mouse 3T3 cell double minute 2	-1.301	1.270
<i>Med30</i>	mediator complex subunit 30	-1.199	1.164
<i>Msn</i>	moesin	-1.330	1.137
<i>Myl2</i>	myosin, light polypeptide 2, regulatory, cardiac, slow	-1.386	1.361
<i>Orc2</i>	origin recognition complex, subunit 2	-1.273	1.212
<i>Orc6</i>	origin recognition complex, subunit 6	-1.195	1.171
<i>P2ry1</i>	purinergic receptor P2Y, G-protein coupled 1	-1.213	1.119
<i>Pak3</i>	p21 protein	-1.350	1.189
<i>Pdgfc</i>	platelet-derived growth factor, C polypeptide	-1.328	1.114
<i>Per2</i>	period circadian clock 2	-1.372	1.232
<i>Pfn1</i>	profilin 1	-1.342	1.341
<i>Phlpp1</i>	PH domain and leucine rich repeat protein phosphatase 1	-1.144	1.111
<i>Pkn3</i>	protein kinase N3	-1.341	1.185
<i>Ppp1r12a</i>	protein phosphatase 1, regulatory	-1.292	1.288
<i>Prkaa2</i>	protein kinase, AMP-activated, alpha 2 catalytic subunit	-1.499	1.190
<i>Rad21</i>	RAD21 homolog	-1.340	1.276
<i>Rb1cc1</i>	RB1-inducible coiled-coil 1	-1.233	1.129
<i>Rbl1</i>	retinoblastoma-like 1	-1.470	1.362
<i>Rcan1</i>	regulator of calcineurin 1	-1.246	1.184
<i>Rock1</i>	Rho-associated coiled-coil containing protein kinase 1	-1.263	1.237
<i>Rock2</i>	Rho-associated coiled-coil containing protein kinase 2	-1.329	1.311
<i>Shc3</i>	src homology 2 domain-containing transforming protein C3	-1.307	1.227
<i>Slc16a10</i>	solute carrier family 16	-1.320	1.215
<i>Smad2</i>	SMAD family member 2	-1.205	1.134
<i>Smc1a</i>	structural maintenance of chromosomes 1A	-1.344	1.239
<i>Spp1</i>	secreted phosphoprotein 1	-1.448	1.406
<i>Stat2</i>	signal transducer and activator of transcription 2	-1.463	1.273
<i>Tbk1</i>	TANK-binding kinase 1	-1.332	1.225
<i>Tgfb3</i>	transforming growth factor, beta 3	-1.394	1.199
<i>Thbs3</i>	thrombospondin 3	-1.321	1.096
<i>Thrb</i>	thyroid hormone receptor beta	-1.361	1.221
<i>Trpc1</i>	transient receptor potential cation channel, subfamily C, member 1	-1.221	1.188
<i>Trpv2</i>	transient receptor potential cation channel, subfamily V, member 2	-1.215	1.101
<i>Tsc1</i>	tuberous sclerosis 1	-1.185	1.164
<i>Uvrug</i>	UV radiation resistance associated gene	-1.416	1.245
<i>Vav3</i>	vav 3 oncogene	-1.234	1.225
<i>Vegfc</i>	vascular endothelial growth factor C	-1.307	1.089
<i>Wee1</i>	WEE 1 homolog 1	-1.195	1.124
<i>Ywhah</i>	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	-1.360	1.307

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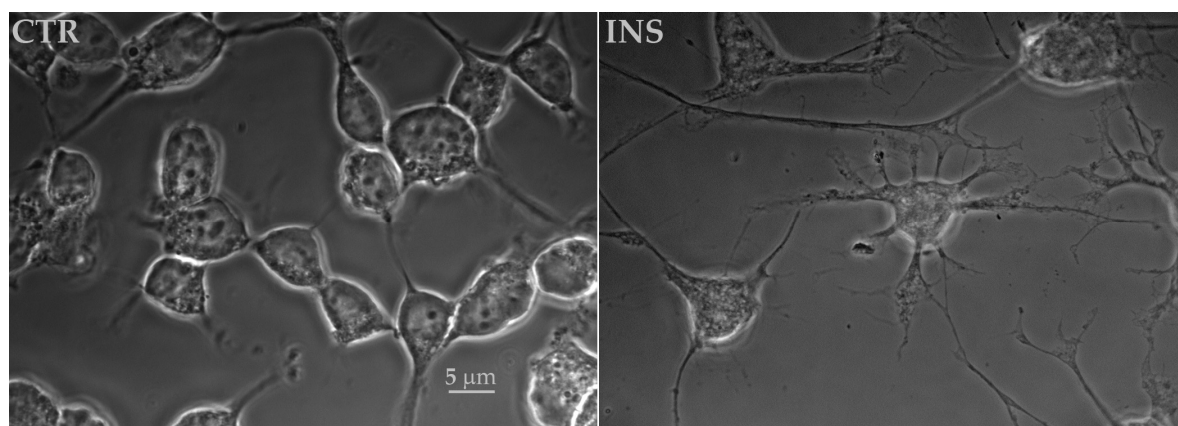


Figure S1. MAG-labeled phase contrast micrographs showing the morphological changes of Oli-neu cells cultured alone (CTR) and co-cultured with astrocytes (INS). **Note the progression from precursor oligodendrocytes to preoligodendrocytes.**

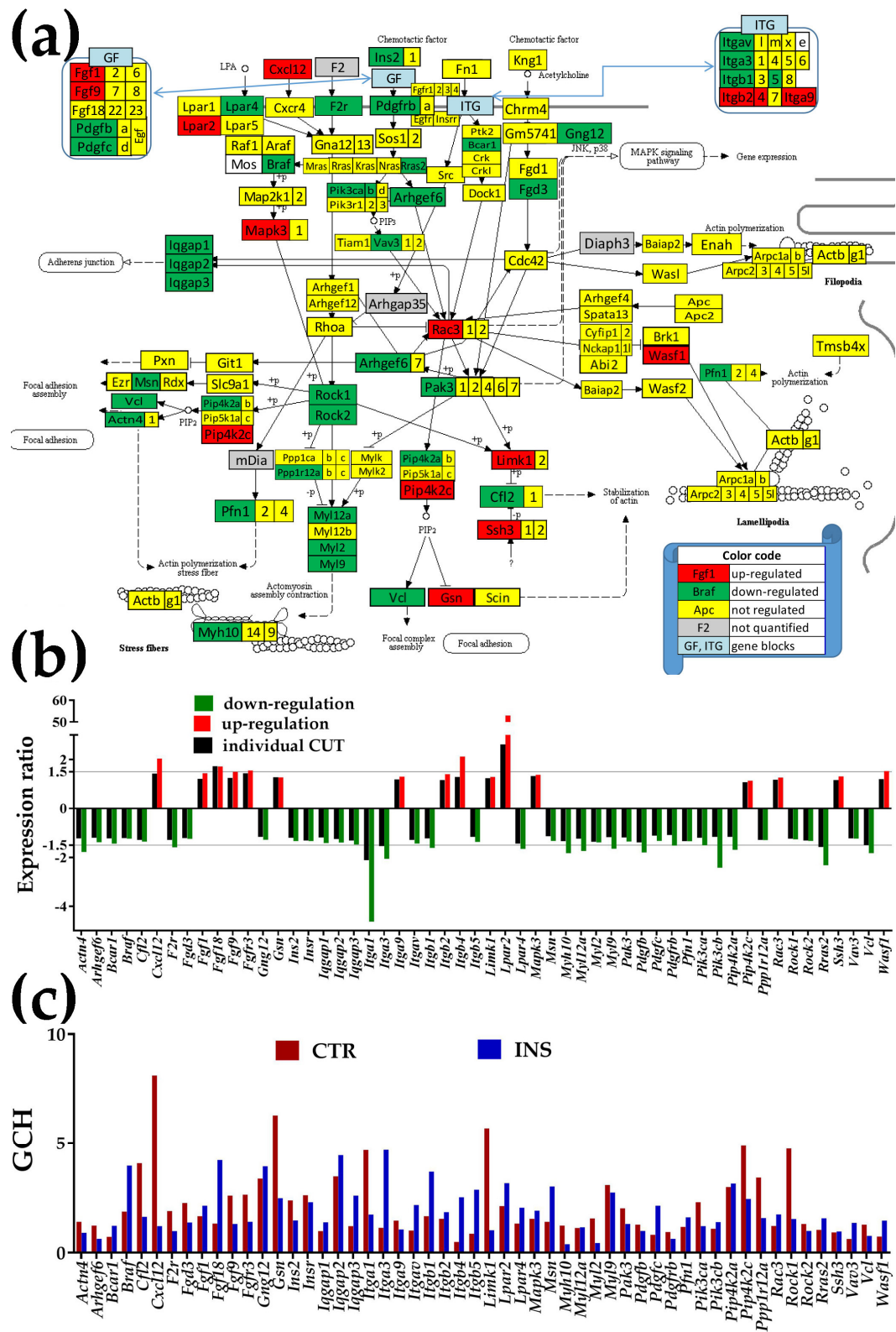


Figure S2. Presence of non-touching precursor oligodendrocytes regulate the actin cytoskeleton (AC) pathway. (a) Regulation of interconnected genes with the AC pathway. (b) Expression ratios and individual fold-change cut-offs (negative for down-regulation) of the significantly regulated genes. Note that regulation of several genes would be neglected by the traditional analysis, while for others the individual gene cut-off exceeded 1.5x. (c) Oli-neu proximity changes the gene hierarchy. The display is limited to the significantly regulated genes plus the actins: *Actb*, *Actg1* and *Actn1*. The dominant gene in this pathway is *Pip4k2c* with GCH = 15.00 in INS.

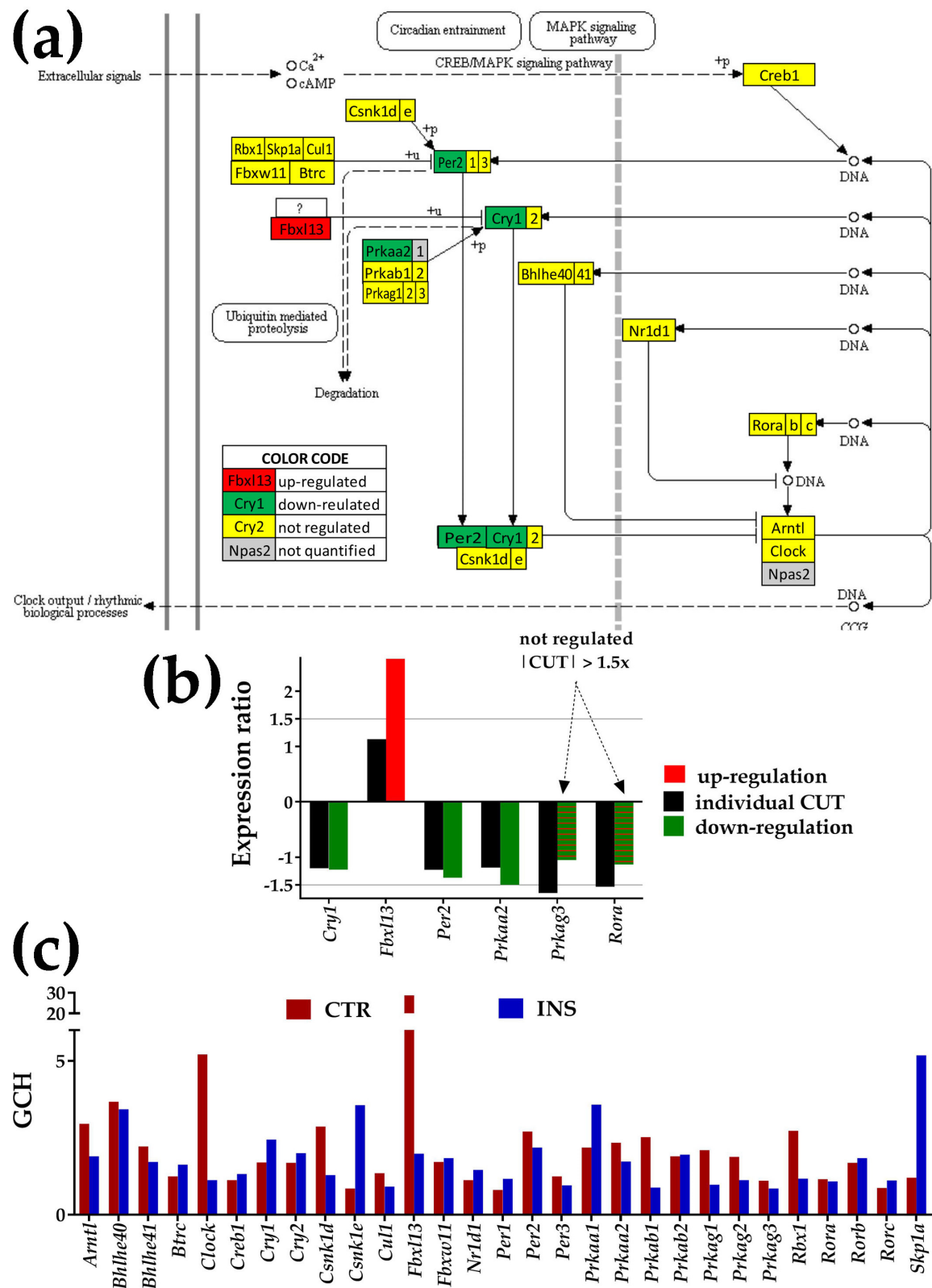


Figure S3. Presence of non-touching precursor oligodendrocytes regulates the Circadian Rhythm. (CR) pathway. **(a)** Regulation of the interconnected genes within CC pathway. **(b)** Expression ratios and individual fold-change cut-offs (negative for down-regulation) of the significantly regulated genes. Note that regulation of *Cry1* and *Per22* would be neglected by the traditional analysis and that the individual gene cut-off for *Prkag3* and *Rora* exceeded 1.5x. **(c)** Changes in the gene commanding height (GCH) scores. The most prominent gene, towering by far all other genes in the CTR astrocytes is *Fbxl13* (GCH = 28.82).