

Supplementary data

Table S1. Real-time PCR primers used in this study.

mRNA	Acc. #	Forward primer	Reverse primer	Size
<i>MBP</i>	K00512	CACAGAGACACGGGCATCC	CTGGGTTTTTCATCTTGGGTCC	154
<i>MOBP-81A</i>	X87900	AACGCTGTGCATGTGTTAGC	AACGCTGTGCATGTGTTAGC	130
<i>PLP1</i>	NM_030990	GTGTTTCTTTGGAGTGGCAC	GGCCCCATAAAGGAAGAAGA	181
<i>MOBP-81B</i>	X89637	GGGAATGGGTCTTTTGGTTT	AGAGAGGGGAATTGGAAGGA	164
<i>CNP</i>	M18630	GTCTRGACGAGGACCTGGCT	TAGTCGCCACGCGTCTTG	161
<i>UGT8A</i>	NM_019276	CCACCTCAGATGCTTTCCTG	GTTGCCAACCATCATGTCAC	122
<i>MOG</i>	NM_022668	GCAGGTCYCTGTAGGCCTTG	GGGCACYCTCAGGAAGTGAG	115
<i>SLC44A1</i>	NM_001033852.1	CTGCTGCAGCTCCGCCTC	GTCTGTGCAGCTACGGTCCT	76
<i>CSPG4</i>	NM_031022	GACCCTCGTCACCTGCTCTA	ATTCCAGCATTCACCTCAG	126
<i>PDGFRA</i>	NM_012802	GGTCTTATGGCGTTCTGCTC	CCATCCTGTATCCGCTCTTG	111
<i>NEFL</i>	NM_031783	GCCGAAGAGTGGTTCAAGAG	TGTCTGCATTCTGCTTGTCC	150
<i>TUBB3</i>	NM_139254	CTCCCGGGTTAAAGTCCTTC	CAGGCCTGGAGCCATAATAA	127
<i>AQP4</i>	NM_012825	CGGTTTCATGGAAACCTCACT	TCAGTCCGTTTGGGAATCACA	106
<i>GFAP</i>	NM_017009	CCTGCCAGGGTRGACTTCTC	TGTAGCTAGCAAAGCGGTCA	112
<i>APOD</i>	NM_012777	CGGTGCAAGAGAATTTTCGAT	GGACGCAGCTCCTTGTTTAG	154
<i>DYNC1LI2</i>	NM_145772	CTGCTGGGTGARGATGGAG	CCTTTGTGGTAYAGATCTCC	176
<i>ENPP2</i>	NM_012848	TCCCCACCCACTACTACAGC	AAGTGGGCCAGAACTACCAC	187
<i>GSN</i>	NM_001004080	GGTCTTTGTCTGGGTTGGAA	AAAGGAAGGAGGCTCAAAGC	151
<i>KIF1A</i>	XM_343630	GAGGATGAAGTCCAATGGAC	TAGCTCCAGACTGATGGCR	150
<i>LPAR1</i>	NM_053936	ATTTTCACAGCCCCAGTTCAC	GTTGACGTARATTGCCACCA	201
<i>MAPK8IP1</i>	NM_053777	CTGAAGACAGGGGAGCAGAC	ATTCGATCTCGATGGGAGTG	208
<i>NDRG1</i>	NM_133583	ATGCCGTGGTGGAAATGTAAT	CGAGACAGGCGAGTCATACA	175
<i>PADI2</i>	NM_017226	GAACCTGGTGGAGAAAACCA	GCACTACTGGGAAGCCTTTG	131
<i>SH3GL3</i>	AF009604	GGTGAGGCCCTGAAACTCA	CCTCGGGGATCTTACCYAC	190
<i>TPPP</i>	XM_341746	CCAAGGCTGCTAAGAGGTTG	CTTGCTGAAGACGATGTCCA	417
<i>TRAK2</i>	NM_163550	GATGTCAGAGGAGGCTCACC	AGTGCACTGAGCACACACCT	151
<i>TRP53INP2</i>	XM_00106397	GCCTTTGTCTCTGAGGAGGA	ACAAACCAGCTCTCGTCCAT	149
<i>GAPDH</i>	NM_017008	TGCCACTCAGAAGACTGTGG	TTGAGCTCTGGGATGACCTT	129

Legend: Primer 3 (<https://bioinfo.ut.ee/primer3-0.4.0/>) was used to select PCR primers to each mRNA. Each primer pair was analyzed with conventional PCR with cDNA prepared from P60 rat cerebral cortex total RNA as template to ensure that single appropriately sized products were obtained. Knowing that the primers amplified the correct mRNA specific products, they were used in the RT-qPCR analyses. Color coding used throughout reference mRNAs located in oligodendrocyte processes (*MSAS/OL-P*),

oligodendrocyte soma (**OL-S**), newly-formed oligodendrocytes (**NFO**), oligodendrocyte precursor cells (**OPC**), neurons (**NE**), astrocytes (**AST**). Putative **MSAS** mRNAs are listed as is *GADPH* used to normalize results.

Table S2. Expression patterns of cell-type specific mRNAs – MBRS data.

#	Gene	OPC	NFO	MO	NE	AST	MG	EP	%MO/CT	%NFO	%OPC	%OL	MO/NFO
MO1	<i>MBP</i>	271	26708	95398	12	2	175	1	77.8	21.8	0.2	99.8	3.6
MO2	<i>MOBP</i>	8	1214	2543	0	0	3	0	67.5	32.2	0.1	99.9	2.1
MO3	<i>MAL</i>	4	761	2574	0	1	1	26	76.4	22.6	0.1	99.2	3.4
NFO1	<i>GPR17</i>	441	930	67	6	0	1	0	4.6	64.3	30.5	99.5	0.1
NFO2	<i>MYRF</i>	8	178	118	1	0	0	0	38.7	58.3	2.6	99.6	0.7
OPC1	<i>PDGFRA</i>	596	80	1	9	0	1	28	0.6	11.1	83.5	94.7	--
OPC2	<i>CSPG4</i>	117	23	0	9	1	0	4	0.2	15.0	76.0	91.1	--
NE1	<i>STMN2</i>	9	2	6	387	3	6	2	92.3*	--	--	--	--
NE2	<i>TUBB3</i>	14	6	17	339	2	5	4	87.6*	--	--	--	--
AST1	<i>AQP4</i>	11	1	11	12	318	0	2	91.9*	--	--	--	--
AST2	<i>ALDH1L1</i>	6	0	3	8	145	4	2	86.4*	--	--	--	--
MG1	<i>C1QA</i>	2	2	96	7	21	3988	0	96.9*	--	--	--	--
EP1	<i>CLDN5</i>	4	0	2	8	11	11	3437	98.9*	--	--	--	--

Represent percentage expression by NE (), AST (*), MG (*) and EP (*).

Legend: Cell-type-specific expression patterns of mRNAs highly expressed by myelinating oligodendrocytes (**MO1-MO3**), newly formed oligodendrocytes (**NFO1-NFO2**), oligodendrocyte precursor cells (**OPC1-OPC2**), neuron (**NE1-NE2**), astrocyte (**AST1-AST2**), microglia (**MG1**) and ependymal cell (**EP1**). Values in Fragments Per Kilobase of transcript per Million mapped reads (FPKM). Maximum expression values plus those falling within 10% of the maximum value are in bold and colored based on cell type. Percentages expressed by **MO/CT** (**%MO/CT**), **NFO** (**%NFO**), **OPC** (**%OPC**) and oligodendrocyte lineage (**%OL**, **%OPC+%NFO+%MO**) are given in marked columns as well as **MO/NFO** for MOs and NFOs. These mRNAs were used to identify cell-type-specific expression patterns in AMBA and AMSCA images (Figure 3).

Table S3. Links of cell-type specific mRNAs - AMBA, AMSCA and ADMBA data.

#	mRNA	Br sagittal	Br coronal	SC – P56	SC – P4	Dev Brain
MO1	<i>MBP</i>	79632288	12202838	100001620^{wm}	100001621^{wm}	++
MO2	<i>MOBP</i> ¹	69174034	--	100017643^{wm}	100017644^{wm}	++
MO3	<i>MAL</i>	386243	--	100006019^{wm}	100006018^{wm}	--
NFO1	<i>GPR17</i>	73513814	74641313	100032104^{wm}	100032105^{wm}	--
NFO2	<i>MYRF</i> ²	70295805	--	100026205^{wm}	100026206^{wm}	--
OPC1	<i>PDGFRA</i>	79354743	77280309	100003956	100003955	++
OPC2	<i>CSPG4</i>	69608160	--	100020669	100020670	--
NE1	<i>STMN2</i>	68632984	74819695	100013852	100013853	--
NE2	<i>TUBB3</i>	68196914	--	100013057	100013058	++
AST1	<i>AQP4</i> ³	109	108	100002844^{ra}	100002845^{ra}	++
AST2	<i>ALDH1L1</i>	1725	1724	100001676	100001677^{vdra}	--
MG1	<i>C1QA</i> ⁴	68191456	79591671	100015379^{lmgm}	100018950	++
EP1	<i>CLDN5</i>	79360268	79490120	100002146^{vl}	100002147^{vl}	++

¹*MOBP* mRNA – additional sagittal section: [769201510](#), ²*MYRF* mRNA – two additional sagittal sections ([71161357](#), [71764437](#)), ³*AQP4* mRNA – additional sagittal ([77454660](#)) and coronal ([79556722](#)) sections, and ⁴*C1QA* mRNA – additional sagittal section ([77923147](#)).

Legend: Links of the three MO-, two NFO-, two OPC-, two neuron-, two astrocyte-, one microglia- and one ependymal cell mRNA used to obtain AMBA and AMSCA images examined in Figure 3 are given. If images were present in the Allen Developing Mouse Brain Atlas (ADMBA), they were indicated (++). In the AMSCA data sets where an expression category is assigned, the category is included as a superscript following the accession number. Categories: **cc** – central canal, **gm** – gray matter, **ra** – white matter and radially arrayed white matter, **gw** – gray matter and white matter, **lm** – lamina 1-x and gray matter, **rv** – radial arrayed and vascular like in gray and white matter, **vd** – ventral-dorsal midline in gray matter, **vl** – vascular-like in gray and **wm** – white matter.

Table S4. Links to *MSAS* mRNAs – AMBA, AMSCA and AMDMB data.

#	mRNA	Brain - sagittal	Brain - coronal	SC – P56	SC – P4	Dev
MSAS1	<i>LPAR1</i> ¹	75749420	79556595	100037166^{wm}	100037167^{wm}	--
MSAS2	<i>TRP53INP2</i>	70192081	--	100024314	100024315	--
MSAS3	<i>TRAK2</i> ²	75990672	--	100051344	100051345	--
MSAS4	<i>TPPP</i> ³	69407355	74724775	100018955^{wm}	100018956^{wm}	--
MSAS5	<i>SH3GL3</i>	79632219	--	100002780 (ne)	100002781	--
MSAS6	<i>GSN</i>	68444642	72081395	100011054^{wm}	100011055^{wm}	--
MSAS7	<i>APOD</i>	71380893	--	100020110^{wmvl}	100020111^{wmvl}	++
MSAS8	<i>MAPK8IP1</i>	68148737	--	100022617	100022618	--
MSAS9	<i>KIF1A</i>	69735759	--	100030717	100030718	--
MSAS10	<i>ENPP2</i> ⁴	532631	70613967	100001398^{wm}	100001399^{wm}	--
MSAS11	<i>NDRG1</i>	70429303	--	100039463^{wm}	100039464^{wmlmgm}	--
MSAS12	<i>DYNC1LI2</i>	69627027	--	100022042	100022043	--
MSAS13	<i>PADI2</i>	69013438	--	--	--	--
MSAS14	<i>CAR2</i>	69014434	72103831	100016060^{wm}	100016061^{wm}	--
MSAS15	<i>CRYAB</i>	72182998	74357575	100008586^{wm}	100008585	--

¹*LPAR1* is listed as *EDG2*, an additional sagittal image series - [79360278](#), ²*TPPP* is listed in ASCA as 2900041A09Rik, ³*TRAK2* mRNA – an additional P56 spinal cord image series:

[100039894](#), ⁴*ENPP2* mRNA – an additional brain coronal image series - [77413700](#)

Legend – *MSAS* mRNAs are ordered based on enrichment in myelin vesicles and are color coded according to enrichments. **MSAS1 – MSAS5** were enriched at levels suggesting locations in *MSAS*. **MSAS6 – MSAS9** were enriched at levels suggesting locations of oligodendrocyte somata. **MSAS10 – MSAS11** were not enriched in myelin (Figure 1). *MSAS12 – MSAS13* were not present at levels sufficient to determine enrichment. *MSAS14 – MSAS15* were not examined. All *MSAS* mRNAs were obtained from the AMBA (<https://mouse.brain-map.org/>) and AMSCA (<http://mousespinal.brain-map.org/>) databases. With the exception of *APOD* mRNA, *MSAS* mRNAs are not found in the Allen Developing Mouse Brain Atlas (<http://developingmouse.brain-map.org>). Hyperlinks to available data sets are shown.

Expression categories from spinal cord image sets as indicated in Table 4S. *SH3GL3* mRNA is not expressed (ne) in P56 spinal cord.