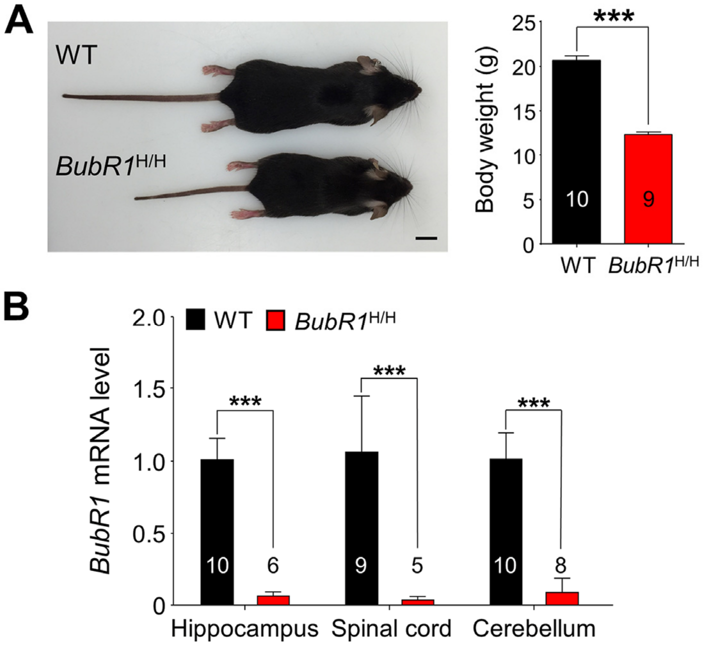
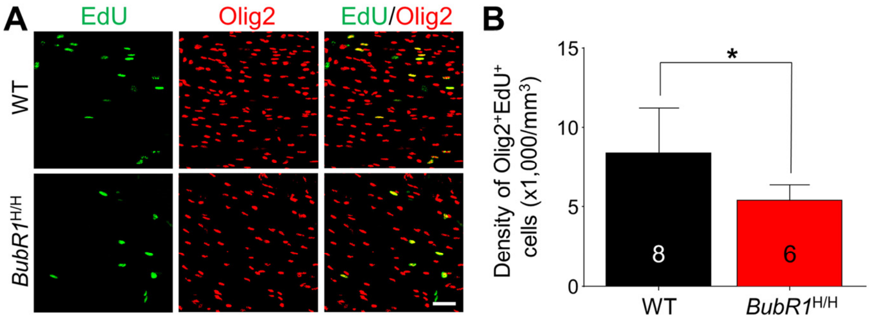
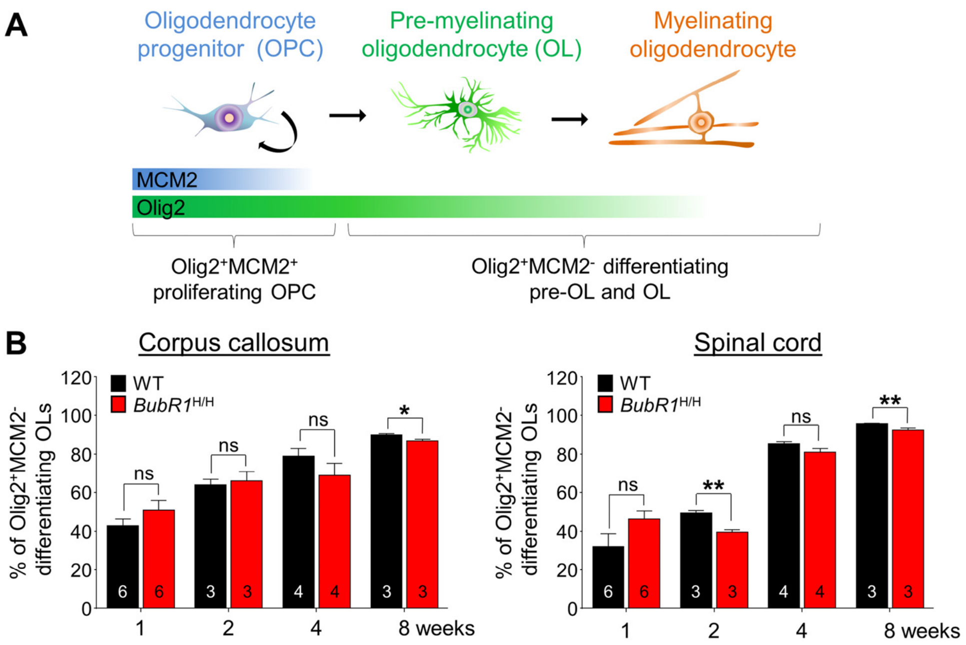
SUPPLEMENTARY MATERIAL



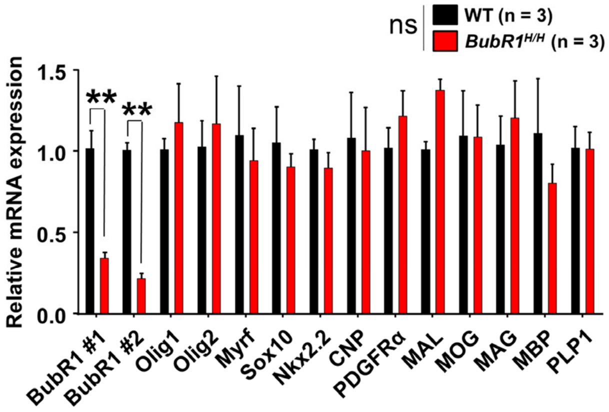
Supplementary Figure 1. Body size and BubR1 expression level in 8 weeks old BubR1 insufficient mice. (**A**) *BubR1*$^{H/H}$ mice are significantly smaller than WT mice. Left: Representative image of WT and *BubR1*$^{H/H}$ mice at 8 weeks of age. Right: Reduced body weight and length in *BubR1*$^{H/H}$ mice. Scale bar = 1 cm. (**B**) qRT-PCR experiments indicate reduced *BubR1* mRNA in isolated adult mouse hippocampi, spinal cord, and cerebellum. All values represent mean ± SEM (***P < 0.001, student's t-test). Number associated with bar graphs indicates number of animals examined.



Supplementary Figure 2. Reductions in proliferating OPCs in the corpus callosum of 1-week-old BubR1 insufficient mice. (**A**) Representative images of EdU (green) and Olig2 (red) staining of 1 week-old WT and *BubR1*$^{H/H}$ mice corpus callosum. WT and *BubR1*$^{H/H}$ mice were injected with a single dose of EdU (41.2 mg/kg body weight, i.p.) and sacrificed after 2 hours. Scale bars: 100 µm. (**B**) Quantification of EdU$^+$Olig2$^+$ cell density in the corpus callosum. All values represent mean ± SEM (*P < 0.05, student's t-test). Number associated with bar graphs indicates number of animals examined.



Supplementary Figure 3. The proportion of proliferating OPCs among total Olig2$^+$ cells in BubR1 insufficient mice at different ages. (**A**) Schematic representation of the proportion of proliferating oligodendrocyte progenitor cells (OPCs) vs. differentiating oligodendrocytes (OLs) among total Olig2$^+$ cells. (**B**) Quantification of differentiating pre-OLs and OLs (Olig2$^+$MCM2$^-$) in the corpus callosum (left) and white matter of spinal cord (right). All values represent mean ± SEM (ns: non-significant, *$P < 0.05$, **$P < 0.01$, student's t-test). Number associated with bar graphs indicates number of animals examined.



Supplementary Figure 4. No changes in selected genes related to oligodendrocyte development and myelination in 1-week-old BubR1 insufficient mice. Quantification of mRNA expression of oligodendrocyte development and myelination-related genes were significantly reduced in *BubR1*$^{H/H}$ mice at 1 week by qRT-PCR. All values represent mean ± SEM (ns: non-significant, **$p < 0.01$, student's t-test).

Supplementary Table 1. Summary list of enriched genes in BubR1 insufficient mice by RNA-sequencing analysis. Please browse the Full text version to see the data of Supplementary Table 1.

Supplementary Table 2. Summary of significantly enriched genes in BubR1 insufficient mice by RNA-sequencing analysis.

	Gene	*p*-value	F.C.(log$_2$)
Oligodenrocyte lineage cells	Mog	0.01582	-2.29
	Mal	0.01367	-2.22
	Mag	0.00024	-2.14
	Enpp6	0.00091	-2.13
	Pdlim2	0.02058	-2.12
	Plekhh1	0.00644	-2.04
	Opalin	0.01285	-1.99
	Insc	0.04700	-1.91
	Bcas1	0.00032	-1.86
	Plxnb3	0.02214	-1.79
	Cnp	0.00059	-1.78
	Mobp	0.00670	-1.75
	Aspa	0.00071	-1.69
	Gpr17	0.00048	-1.68
	Ninj2	0.00780	-1.65
	Cldn11	0.00296	-1.65
	Erbb3	0.00709	-1.62
	Tmem88b	0.00151	-1.60
	Lpar1	0.00189	-1.60
	Bmp4	0.00236	-1.56
	Mbp	0.00098	-1.55
	Fa2h	0.00118	-1.55
	Pllp	0.01043	-1.47
	Tspan2	0.00225	-1.43
	Plp1	0.00255	-1.41
	Sox10	0.00914	-1.37
	Tprn	0.03378	-1.35
	Gamt	0.00530	-1.34
	Gltp	0.02723	-1.33
	Galnt6	0.03866	-1.30
	Dock5	0.00360	-1.29
	Gm98	0.02498	-1.27
	Prr18	0.02808	-1.22
	Cpm	0.04832	-1.20
	Qdpr	0.00424	-1.20
	Adamts4	0.00337	-1.18
	Efhd1	0.02822	-1.10
	Gsn	0.00434	-1.07
	Arhgef10	0.00276	-1.02
	9630013A20Rik	0.01037	-1.02
	Tmem141	0.04560	1.04
	Rbpjl	0.03948	1.61

	Gene	*p*-value	F.C.(log$_2$)
Neurons	Lhx5	0.02313	-1.27
	Bmp5	0.04600	-1.17
	C030023E24Rik	0.00924	1.07
	Mia1	0.00903	1.43
	Pla2g4e	0.01884	1.83
	Pth2r	0.01704	2.14

	Gene	*p*-value	F.C.(log$_2$)
Astrocytes	Nmb	0.01456	-1.23
	Scara3	0.00411	-1.13
	Mamdc2	0.00772	1.08
	Sp6	0.04233	1.22
	Exd1	0.02362	2.09

	Gene	*p*-value	F.C.(log$_2$)
Microglia	Cd80	0.01424	-1.26
	Tgfb1	0.04308	1.02
	H2-Eb1	0.00344	1.05
	Cst7	0.03294	1.08
	Nfam1	0.00884	1.37
	Il4ra	0.04537	1.43
	Clec4a1	0.04750	1.49
	Card9	0.01122	1.55

	Gene	*p*-value	F.C.(log$_2$)
Endothelial cells	Rasip1	0.03193	-1.62
	Clec14a	0.03186	1.06
	Ifi47	0.01498	1.11
	Hspa12b	0.04922	1.11
	Fam129a	0.02479	1.57
	Mmrn1	0.02199	1.95
	Aplnr	0.03804	2.00
	Fam124b	0.00127	2.32

Expanded list of significantly enriched genes as visualized in Figure 2. Blue text indicates down-regulated genes and red indicates up-regulated genes. F.C.; fold change. N=3 mice per group.

Supplementary Table 3. Summary of qRT-PCR primers used for validation.

Target	Sequence	Product (bp)
mBubR1 #1-F	ACCAGGCCCTCATCATAAAG	87
mBubR1 #1-R	AAGAAGACCTGGAGAAGCCA	
mBubR1 #2-F	AGCTGAAAGAACGAAGGGAA	93
mBubR1 #2-R	TCAGCCTCCTCTCCATCTCT	
mOilg1-F	CCACCACAACTCACCCACTG	65
mOilg1-R	ACGGATACGAGAATAGCCCG	
mOlig2-F	CGCAGCGAGCACCTCAAATCTAA	81
mOlig2-R	CCCAGGGATGATCTAAGCTCTCGAA	
mMyrf-F	TGGCAACTTCACCTACCACA	160
mMyrf-R	GTGGAACCTCTGCAAAAAGC	
mSox10-F	AGCCCAGGTGAAGACAGAGA	146
mSox10-R	AGTCAAACTGGGGTCGTGAG	
mNkx2.2-F	CCTCCCCGAGTGGCAGAT	74
mNkx2.2-R	GAGTTCTATCCTCTCCAAAAGTTCAAA	
mCnp-F	GTTCTGAGACCCTCCGAAAA	108
mCnp-R	CCTTGGGTTCATCTCCAGAA	
mMal-F	TCACACTGGATGCAGCCTACC	71
mMal-R	CAGGGCTTCCAGAACTGAGG	
mMog-F	ATGAAGGAGGCTACACCTGC	123
mMog-R	CAAGTGCGATGAGAGTCAGC	
mMag-F	AACCAGTATGGCCAGAGAGC	133
mMag-R	GTTCCGGGTTGGATTTTACC	
mMbp-F	CCCGTGGAGCCGTGATC	81
mMbp-R	TCTTCAAACGAAAAGGGA	
mPlp-F	GTATAGGCAGTCTCTGCGCTGAT	201
mPlp-R	AAGTGGCAGCAATCATGAAGG	
mGapdh-F	ACCCAGAAGACTGTGGATGG	171
mGapdh-R	CACATTGGGGGTAGGAACAC	