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Article

Differential Expression of miRNAs and Behavioral Change in the Cuprizone-Induced Demyelination Mouse Model

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Supplementary Figures and Table

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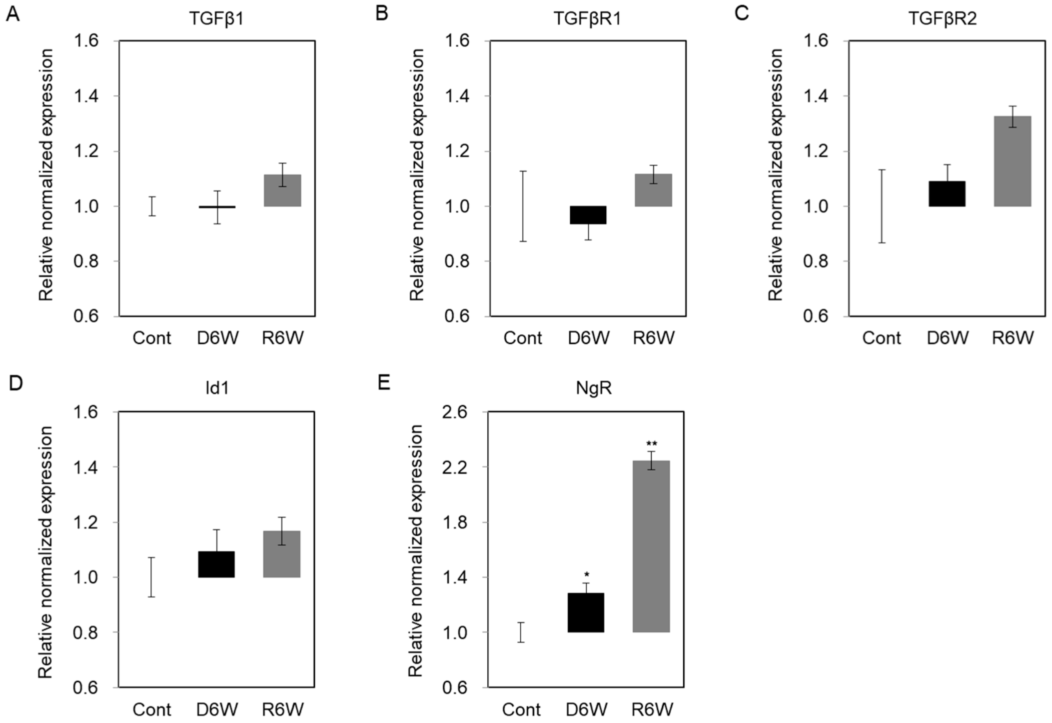

Figure S1. Analysis of miRNA target gene expression by qPCR. (**A**–**D**) The expression levels of TGFβ1, TGFβR1, TGFβR1 and Id1 were not significantly altered in demyelinated mice (D6W) compared to control mice (Cont) by real-time PCR analysis. (**E**) The expression level of NgR was significantly upregulated in D6W compared to Cont. The differences between groups are expressed as $*p < 0.05$, $**p < 0.01$.

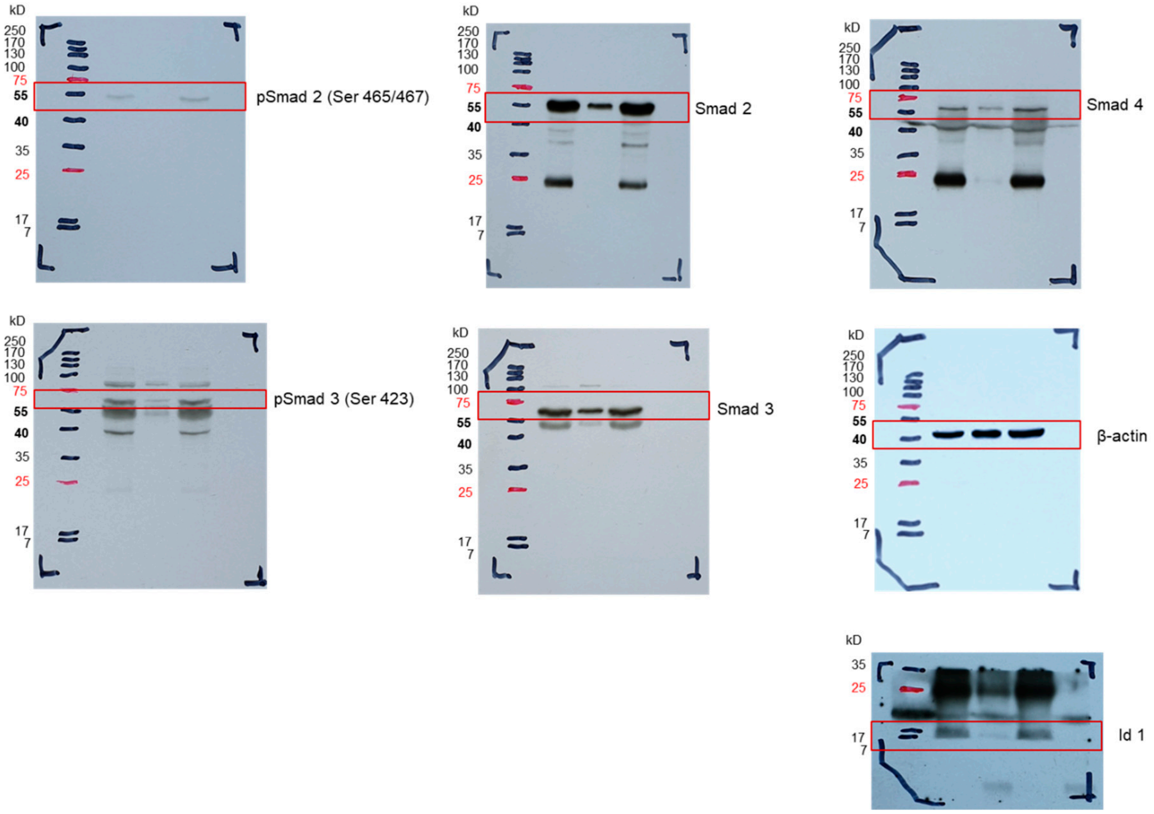

Figure S2. The uncut original western blot images of Figure 8A.

Table S1. The quantitative PCR primers of miRNAs and target genes.

Oligo Name	Length (mer)	Sequence (5' – 3')
Upregulated miRNA		
mmu-miR-146a-5p	22	TGAGAACTGAATTCCATGGGTT
mmu-miR-20a-5p	23	TAAAGTGCTTATAGTGCAGGTAG
mmu-miR-155-5p	23	TTAATGCTAATTGTGATAGGGGT
Downregulated miRNA		
mmu-miR-145a-5p	23	GTCCAGTTTTCCCAGGAATCCCT
mmu-miR-219a-2-3p	22	AGAATTGTGGCTGGACATCTGT
mmu-miR-338-5p	22	AACAATATCCTGGTGCTGAGTG
Predicted taget genes		
TGFβ1	21	CTATGACAAGTTCAAGCAGAG
TGFβR1	20	GTGAAGCCTTGAGAGTAATG
TGFβR2	18	AATATAACACCAGCAATC
Id1	18	TGTTACTCACGCCTCAAG
NgR	18	ACGGCAACCGCATCTCCA
GAPDH	18	GGTATCGTGGAAGGACTC