Proteomics-level analysis of myelin formation and regeneration in a mouse model for Vanishing White Matter disease

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Supplementary Material:

Supplementary Figures

Supplementary Tables

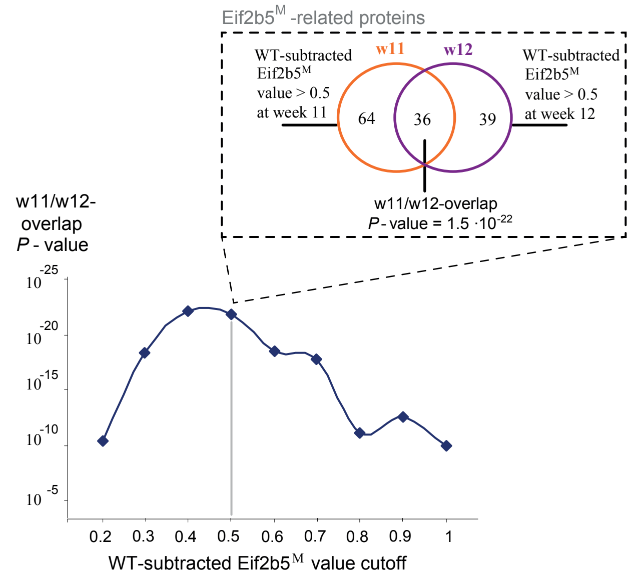
Supplementary Figures

Supp. Fig. 1. Consistency between the proteome profiles at 11 and 12 weeks of age in normal-diet-fed mice. **Top**: a Van-diagram representation of the overlap between the 100 proteins whose absolute WT-subtracted Eif2b^M value is higher than 0.5 at 11 weeks of age (orange) and the 75 proteins whose absolute WT-subtracted Eif2b^M value is higher than 0.5 at 12 weeks of age (purple) (w11/w12 overlap P value $< 1.5 \cdot 10^{-22}$; hyper-geometric test; see **Methods**). The unified set of all 139 proteins in the two circles are referred to as 'Eif2b-related proteins'. **Bottom**: A scatter plot of the hyper-geometric P-value (y axis) for different WT-subtracted Eif2b^M value cutoffs (x axis). The calculation of the overlap P-value for the case of 0.5 cutoff is illustrated in **a**. For all cutoffs, P-values are smaller (more significant) than 10^{-9}.

Supp. Fig. 2. Correlation matrices of protein responses between different diets and genotypes. Two matrices depicting the Pearson correlations between each two response profiles (that is, developmental myelination or remyelination response, either in WT or in Eif2b^M) that were calculated across all 1831 measured proteins (**a**) or across a subset of proteins with at least one absolute response value that is higher than 0.4 (**b**). In both cases, the correlations indicate a high resemblance between 'developmental myelination response' in the mutant strain and 'remyelination response' in WT.

Supp. Fig. 3: (**a**) *Glycolysis and gluconeogenesis.* The matrix presents all proteins related to glycolysis and gluconeogenesis (rows) across experiments (columns, shown as detailed in **Fig. 4**). (**b**) *Non-ETC proteins.* The matrix presents proteins that are in the inner mitochondrial membrane but are not part of the *ETC* (rows) across experiments (columns, shown as detailed in **Fig. 4**).

SFigure 1


Eif2b5^{M} -related proteins
w11
w12
WT-subtracted Eif2b5^{M} value > 0.5 at week 11
WT-subtracted Eif2b5^{M} value > 0.5 at week 12
64
36
39
w11/w12-overlap P- value = 1.5 $\cdot 10^{-22}$
w11/w12-overlap P - value
10^{-25}
10^{-20}
10^{-15}
10^{-10}
10^{-5}
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
WT-subtracted Eif2b5^{M} value cutoff

SFigure 2

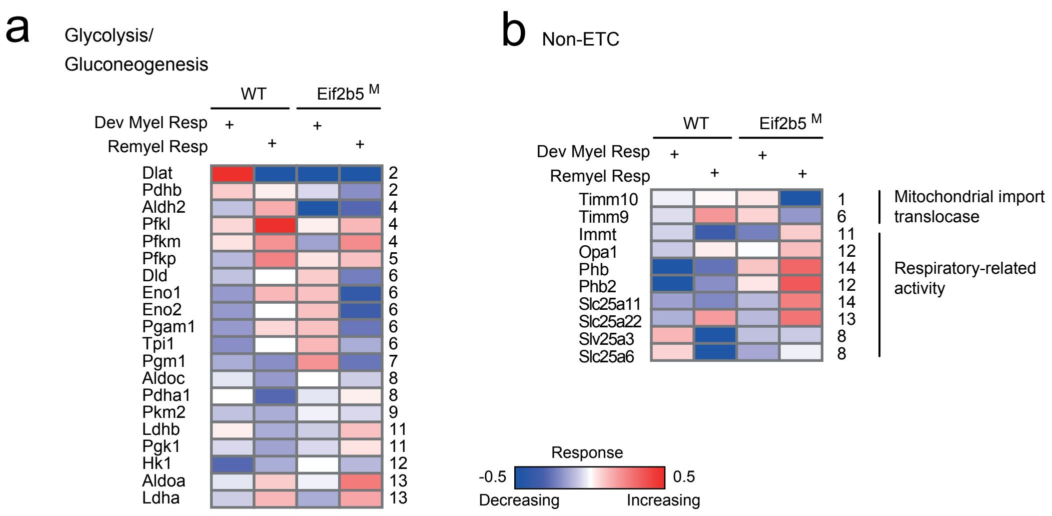
a

		Remyel Resp		Dev Myel Resp	
		Eif2b5^M	WT	Eif2b5^M	WT
Remyel Resp	Eif2b5^M	1			
	WT	0.06	1		
Dev Myel Resp	Eif2b5^M	0.11	**0.59**	1	
	WT	-0.32	-0.38	-0.38	1

b

		Remyel Resp		Dev Myel Resp	
		Eif2b5^M	WT	Eif2b5^M	WT
Remyel Resp	Eif2b5^M	1			
	WT	0.19	1		
Dev Myel Resp	Eif2b5^M	0.39	**0.54**	1	
	WT	-0.45	-0.36	-0.29	1

SFigure 3


a
Glycolysis/
Gluconeogenesis
WT
Eif2b5 M
Dev Myel Resp + +
Remyel Resp + +
Dlat 2
Pdhb 2
Aldh2 4
Pfkl 4
Pfkm 4
Pfkp 5
Dld 6
Eno1 6
Eno2 6
Pgam1 6
Tpi1 6
Pgm1 7
Aldoc 8
Pdha1 8
Pkm2 9
Ldhb 11
Pgk1 11
Hk1 12
Aldoa 13
Ldha 13
b
Non-ETC
WT
Eif2b5 M
Dev Myel Resp + +
Remyel Resp + +
Timm10 1
Timm9 6
Immt 11
Opa1 12
Phb 14
Phb2 12
Slc25a11 14
Slc25a22 13
Slv25a3 8
Slc25a6 8
Mitochondrial import translocase
Respiratory-related activity
Response
-0.5
0.5
Decreasing
Increasing

Supplementary Tables

Supplementary Table 1. Protein levels in all eight experiments. The experiment depicted only highly abundant proteins. For all 1831 measured proteins, shown are UniProt ID (column 1), entrez ID in mouse (column 2), symbol name (column 3) and protein levels (H/L ratio) in all eight experiments (columns 4-11).

Supplementary Table 2. Developmental myelination and remyelination responses. Shown are 802 proteins for which response data is available (column 1), their cluster identifier (column 2) and responses during developmental myelination in WT (column 3) and eIF2B5$^{R132H/R132H}$ mutant (column 5) as well as remyelination responses in WT (column 4) and mutant (column 6). Response values are presented as fold changes (w12/w11 ratio). Note that only highly abundant proteins are shown.

Supplementary Table 3. Functional enrichments in all protein that were measured under normal diet. For four experiments (Mut in week 11, WT in week 11, Mut in week 12 and WT in week 12, in columns 1-4, respectively), presented are functional categories (left) and their enrichment hyper-geometric P values (right) for all 1831 measured proteins. The functional categories are sorted based on the P-values in each column separately. P-values were calculated and corrected for multiple testing by the IPA software.

Supplementary Table 4. eIF2B-related proteins. Shown are the 139 eIF2B-related proteins (column 1), the cluster for each protein (column 2) and their protein levels (H/L ratio) in WT (week 11 and 12 in columns 3 and 4, respectively) and mutant Eif2b5$^{R132H/R132H}$ mice (week 11 and 12 in columns 5 and 6, respectively).

*Supplementary Table 5. Functional enrichments of the eIF2B-related proteins***.** Shown are broad and specific functional categories (columns 1 and 2) and the P-value of statistical significance (column 3). The number of eIF2B-related proteins and the particular symbols in each category are specified in columns 4 and 5, respectively.

Supp. Table 1

			Developmental Myelination				**Remyelination**			
Uniprot identifier	Entrez identifier	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
P56379	70257	2010107E04Rik		0.99	0.99	0.97	0.95	1.03	1.22	0.96
Q3UHJ0	269774	Aak1	3.65	1.14	1.18	3.46	2.46	1.04	2.83	1.07
Q8BGQ7	234734	Aars	1.00	1.02	0.89	0.94	0.83	0.99	0.90	0.95
P61922	268860	Abat	0.85	0.99	0.81	0.96	1.22	1.02	1.18	0.99
P61222	24015	Abce1		1.12	0.99		0.98	1.00		0.98
Q99LR1	76192	Abhd12		1.04	1.13	1.25	1.02	1.08	1.22	1.08
Q8R2Y0	66082	Abhd6		1.51	1.19	1.71	1.04	1.22	2.15	0.99
Q8CBW3	11308	Abi1	1.45		1.08			0.97		1.29
P62484	329165	Abi2	1.16	1.13	1.15		0.97	0.98		1.11
Q5SSL4	109934	Abr	1.21	1.08	1.11	1.32	0.87	1.21	1.22	1.21
Q5SWU9	107476	Acaca			1.34					
Q8JZN5	229211	Acad9		1.11						
P51174	11363	Acadl		1.08	0.86			0.87		0.92
P50544	11370	Acadvl	0.82	0.93	0.89	0.93	0.90	0.96	1.01	0.97
Q8QZT1	110446	Acat1	1.01	1.09	0.97	1.05	0.98	0.98	0.99	0.93
Q91V92	104112	Acly	0.96	0.91	0.90	0.95	0.85	0.91	0.99	0.93
P28271	11428	Aco1		1.11	0.84	0.79	0.81	1.14	0.72	0.96
Q99KI0	11429	Aco2	0.93	1.01	0.97	0.92	0.95	0.97	0.92	0.98
Q9CQR4	66834	Acot13	1.08	1.03	0.82	0.99	0.97	0.96	0.97	0.94
Q91V12	70025	Acot7	0.95	0.92	0.92	0.98	1.14	1.01	1.23	0.92
Q9R0X4	64833|563	Acot9	2.48	1.04	1.41			0.99		1.04
Q99PU5	94180	Acsbg1	0.93	0.91	0.95	1.11	1.53	1.12		0.85
Q8VCW8	264895	Acsf2	0.97	0.93		1.09	0.65	0.91	1.07	1.08
P41216	14081	Acsl1						1.23		
Q9CZW4	74205	Acsl3	0.70				0.65			
Q91WC3	216739	Acsl6	0.90	1.00	0.88	1.13	0.85	1.00	1.06	0.95
Q8BFZ3	238880	Actbl2		0.96	0.91	0.71		0.72	0.26	0.99
P68033	11464	Actc1	0.93	0.99	0.98	0.98	1.02	0.96	0.94	1.03
Q7TPR4	109711	Actn1	0.63	0.89	1.04	0.83	1.14	0.89	0.99	1.22
P57780	60595	Actn4	0.70	0.94	1.10	0.90	1.27	0.86	1.06	1.25
P61164	54130	Actr1a	1.02			0.95	1.03		1.08	
Q8R5C5	226977	Actr1b	1.06	0.97	1.10	1.04	0.98	0.99	0.96	1.04
P61161	66713	Actr2	1.38	0.90	1.15	1.16	0.98	1.15	1.22	1.10
Q99JY9	74117	Actr3	1.41	1.03	1.02	1.13	0.86	0.99	1.16	1.03
Q641P0	242894	Actr3b	1.74	1.11	1.14	1.42	1.36	1.03	1.14	1.09
P56376	66204	Acyp1	0.95	0.86	0.96	0.96	0.98	0.90	0.77	0.90
P56375	75572	Acyp2	0.86	0.94	0.91	0.82	0.86	0.88	1.08	0.85
Q9R1V6	11496	Adam22	0.94	0.94	0.97		1.13	0.98	0.72	0.90
Q9R1V7	23792	Adam23	0.92	0.82	0.98	0.95	1.10	0.94	0.97	1.00
P51830	11515	Adcy9		0.69				2.64		
Q9QYC0	11518	Add1	1.12	1.03	1.10	1.10	0.97	1.05	1.09	1.06
Q9QYB8	11519	Add2	1.80	1.05	1.04	1.52	1.56	1.05	1.32	1.08
Q9QYB5	27360	Add3	1.07	1.09	1.39		0.99	0.96	0.66	
P28474	11532	Adh5		1.01	1.41		1.29	0.93		0.83
P54923	11544	Adprh		0.99	1.11			0.84		0.90
Q8CG72	100206	Adprhl2			1.35			1.05		1.01

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q99MK8	110355	Adrbk1	1.48	0.96	1.04		1.21	0.93		1.02
Q8JZQ2	69597	Afg3l2	1.10	0.94	0.94	1.02	1.00	1.04	0.97	0.93
Q3UHD9	216439	Agap2	1.48	1.10	1.25		1.68	1.23		1.12
Q9ESW4	69923	Agk		1.16	1.02		1.18	1.05		1.09
P50247	269378	Ahcy	0.84	0.91	0.87	0.90	1.21	0.88	0.92	0.91
Q80SW1	229709	Ahcyl1	1.00	0.95	0.92	1.06	0.93	0.97	0.94	0.94
Q68FL4	74340	Ahcyl2			1.32					
Q9Z0X1	26926	Aifm1	1.04	0.92	0.92	1.26	0.90	1.06	1.27	0.87
P31230	13722	Aimp1			2.69		0.96	0.88	1.20	
Q8R010	231872	Aimp2	1.37		1.08			1.20	1.39	1.11
Q9R0Y5	11636	Ak1	1.03	1.06	1.03	0.99	0.84	0.93	1.08	1.02
Q9WTP7	56248	Ak3	1.22	1.06	0.97	0.97	0.67	0.97	1.32	1.05
Q9WUR9	11639	Ak4	1.23	1.14	1.00		0.85	0.97	0.77	0.95
Q920P5	229949	Ak5	1.12	1.07	0.95		1.11	0.96	1.04	1.11
Q9WTQ5	83397	Akap12	3.63	1.12	0.84	2.48			5.89	0.86
O55074	432442	Akap7	1.07	0.95	0.96	0.91	0.74	0.97	1.39	0.97
Q70FJ1	100986	Akap9		1.30				1.10		
Q9JII6	58810	Akr1a1	0.90	1.06	0.96	0.85		0.95	0.93	1.03
P45376	11677	Akr1b1	0.97	0.95	0.98			0.96	1.03	0.96
P21300	11997	Akr1b7	0.88	0.96	0.88			0.93	0.88	0.82
Q8CG76	110198	Akr7a2		1.01	0.95			0.94		0.95
Q60823	11652	Akt2			1.02					
Q61490	11658	Alcam	0.97	1.01	1.08	0.88	1.22	0.88	0.74	0.99
Q9Z110	56454	Aldh18a1		0.96	1.34		1.07	1.21	0.92	1.02
P24549	11668	Aldh1a1							1.20	
Q9CZS1	72535	Aldh1b1	1.00		1.09	1.69	1.44		1.20	
Q8R0Y6	107747	Aldh1l1	0.83	1.16	0.92	0.96	1.10	1.05	0.96	1.04
P47738	11669	Aldh2	1.56	0.97	0.95	0.90	0.99	0.83	0.97	1.08
Q8CHT0	212647	Aldh4A1	0.83				1.21		0.92	
Q8BWF0	214579	Aldh5A1	0.86	0.93	0.81	0.82	1.00	1.01	0.95	0.88
Q9EQ20	104776	Aldh6A1		1.16	1.03			0.94	1.10	1.06
Q9DBF1	110695	Aldh7A1		1.03	1.40			1.08		1.40
P05064	11674	Aldoa	1.00	1.01	0.99	0.97	0.82	0.99	0.92	1.00
P05063	11676	Aldoc	0.84	0.85	0.86	0.86	0.99	0.96	1.01	0.91
Q9DBE8	56737	Alg2			0.99	1.06		1.06		0.99
O08583	21681	Alyref	1.26	1.20	1.14	1.03		1.08		0.91
Q7TQF7	218038	Amph	2.12	1.08	1.02	2.10	2.37	0.94	1.82	1.04
Q02357	11733	Ank1	1.09	0.92	1.01	0.71		1.25	1.35	0.99
Q8C8R3	109676	Ank2	1.02	1.03	1.05	1.19	1.31	1.14	1.08	1.14
O35381	11737	Anp32a	1.04	1.00	0.90	1.02	1.25	0.87	1.12	1.01
P97822	66471	Anp32e	1.08				1.38	0.84	1.15	
P97449	16790	Anpep	1.02	0.84		0.80	1.35	1.01	0.96	
P10107	16952	Anxa1		0.79	0.79			0.75		0.83
P07356	12306	Anxa2					1.39			
P48036	11747	Anxa5	0.83	0.95	0.87	0.76	1.25	0.96	0.91	0.99
P14824	11749	Anxa6	0.92	0.92	1.00	1.00	1.12	0.94	0.95	0.98

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
O35643	11764	Ap1b1	1.54	1.01	0.98	1.32	1.30	1.00	1.48	1.02
P22892	11765	Ap1g1	2.02		1.05		1.28		1.39	0.25
P17426	11771	Ap2A1	1.42	1.01	1.02	1.30	1.16	0.96	1.16	1.02
P17427	11772	Ap2A2	1.08	1.02	0.98	1.08	1.07	0.91	0.98	1.02
Q9DBG3	71770	Ap2b1	1.03	1.04	1.02	1.08	0.97	0.97	0.98	1.03
P84091	11773	Ap2M1	0.95	1.02	1.03	1.40	1.00	0.95	1.23	1.02
P62743	232910	Ap2S1	0.98	1.10	1.15	1.05	0.87	1.00	0.73	0.88
Q9JME5	11775	Ap3b2	0.99	1.04	0.99	1.09	1.03	1.00	1.07	1.05
O54774	11776	Ap3d1	1.57	1.09	1.04	1.56	1.53	1.02	1.34	1.01
Q8R2R9	64933	Ap3M2			1.54	1.08		1.34		1.19
Q8R146	235606	Apeh			0.76					
P28352	11792	Apex1	1.23	1.19	1.24		1.82	1.45	1.36	1.18
Q03157	11803	Aplp1			1.40					0.96
Q00623	11806	Apoa1	0.86		1.23	0.51				
Q8K4Z3	246703	Apoa1bp	0.99	1.10	0.99	1.13	0.76	1.01	1.18	1.02
P09813	11807	Apoa2	0.50							
P08226	11816	Apoe		0.82	0.84			1.08	0.95	0.90
Q9DCZ4	621156|68	Apoo	1.21	0.98	0.94	1.25	1.14	1.07	1.17	0.97
Q78IK4	68117	Apool				1.04				
P12023	11820	App				0.95		3.57		0.85
Q8K3H0	72993	Appl1	1.84	0.89	1.09		1.85	1.08	0.90	0.97
P55088	11829	Aqp4	0.68	0.90		0.61			0.69	
Q8BSL7	11841	Arf2	1.01		0.83					1.11
P61205	11842	Arf3	1.02	0.99	1.00	1.02	0.90	1.01	1.01	1.04
P61750	11843	Arf4		1.21				0.87		
P84084	11844	Arf5	1.00	0.99	1.07	1.02	0.88	1.07	0.93	1.06
P62331	11845	Arf6	0.97	0.79	1.01	1.04	0.88	0.98	1.15	0.99
Q5FWK3	228359	Arhgap1	1.16			1.15	1.48		1.32	
Q91YM2	232906	Arhgap35			1.56			1.44		1.19
P97393	11855	Arhgap5		0.96	0.93					
Q99PT1	192662	Arhgdia	1.14	0.97	0.94	1.07	1.60	0.96	1.17	0.99
Q60875	16800	Arhgef2	1.11	1.03	1.33	1.10	1.13	0.98	1.03	1.15
P61211	104303	Arl1	1.20		1.13		0.82	3.48	1.05	1.08
Q9WUL7	56350	Arl3	1.05	0.98	1.01	1.04	1.09	0.96	1.20	0.91
O88848	56297	Arl6						0.88		0.91
Q8VEH3	68724	Arl8A	1.00	1.24	0.90	1.06	0.83	1.14		1.10
Q9CQW2	67166	Arl8b	0.94	1.00	0.92	1.04	0.90	1.11	0.98	0.97
Q9D0L7	67211	Armc10	1.01					1.14		
Q8BNU0	76813	Armc6							1.31	
Q9R0Q6	56443	Arpc1a	0.95	1.05	1.28	1.20	0.88	1.18	0.93	1.09
Q9CVB6	76709	Arpc2	1.19	1.01	1.10	1.07	0.99	1.01	0.95	1.03
Q9JM76	56378	Arpc3	1.15	1.06	1.05	1.06	0.87	1.03	1.03	1.00
P59999	68089	Arpc4	1.01	1.01	1.03	1.06	1.08	0.99	1.02	1.04
Q9CPW4	67771	Arpc5		1.11	0.97		0.90	1.06	1.04	1.07
Q9D898	74192	Arpc5l		0.99			1.01	0.98		1.14
P56212	59046	Arpp19		0.92	0.99	1.80		1.23		0.96

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q9WV54	11886	Asah1	1.05		0.96			1.04		1.03
Q9QWY8	13196	Asap1		0.94	1.08			0.97		
O54984	56495	Asna1	0.95	1.20	1.02	1.11	2.30	0.95	1.32	1.08
Q8R3P0	11484	Aspa		0.78	0.68			0.69		0.58
Q80VP9	72898	Asphd2			1.15			1.19		1.07
Q8C0M9	66514	Asrgl1	0.99	1.00	0.87	1.00	0.71	0.96	1.01	0.96
P16460	11898	Ass1	0.71	1.31			0.84		1.28	0.98
Q61137	11899	Astn1	1.08		1.13	0.98	0.88	0.87	0.92	
Q925I1	108888	Atad3A/Atad3b		0.96	1.12		1.10	1.49		1.00
Q9D906	74244	Atg7	1.06		0.80		0.94	1.20		1.35
Q9CWJ9	108147	Atic	1.00	0.96	1.08	0.87	0.98	0.87		0.92
Q8BH66	73991	Atl1	1.39	0.97	1.48	1.12	0.94	1.01	0.91	1.15
Q6PA06	56298	Atl2				1.22		1.05		0.94
O08997	11927	Atox1	1.04	0.92				0.92	1.03	
Q8VDN2	11928	Atp1a1	0.91	1.00	1.21	0.77	0.76	1.10	0.81	1.07
Q6PIE5	98660	Atp1a2	0.78	0.94	0.79	0.77	0.74	0.91	0.97	0.88
Q6PIC6	232975	Atp1A3	0.78	0.90	0.87	0.67	0.70	0.90	0.94	0.92
P14094	11931	Atp1b1	0.90	0.98	1.01	0.83	0.89	1.01	0.98	0.98
P14231	11932	Atp1b2	1.06	0.89	0.78	0.95	0.97	0.89	1.00	0.85
O55143	11938	Atp2a2	1.08	1.04	1.07	0.89	0.81	1.14	0.87	1.14
Q9R0K7	11941	Atp2b2	1.08	1.00	1.10	1.09	0.96	1.07	0.98	1.02
Q03265	11946	Atp5a1	1.01	0.99	1.01	1.01	0.92	0.95	1.13	0.98
P56480	11947	Atp5b	0.94	0.97	1.02	0.93	1.19	1.03	1.03	1.00
Q91VR2	11949	Atp5c1	1.11	1.02	1.01	1.02	0.97	1.08	1.15	0.98
Q9D3D9	66043	Atp5d		1.12	0.96	0.99	1.00	1.07		1.30
P56382	67126	Atp5e	1.11	0.90	0.94	0.96	1.05	0.95	1.11	0.96
Q9CQQ7	11950	Atp5f1	1.13	1.04	1.02	0.99	1.00	1.10	1.07	0.98
Q9DCX2	71679	Atp5h	1.00	1.01	1.01	0.94	1.02	1.03	1.11	0.98
Q06185	11958	Atp5I	0.94	1.04	0.99	0.92	1.03	0.99	0.97	1.00
P97450	11957	Atp5J	0.98	1.00	1.02	0.92	1.14	0.99	1.02	0.92
P56135	57423	Atp5j2	0.84	0.92	0.96	0.94	0.71	0.94	1.02	0.95
Q9CPQ8	27425	Atp5l	1.03	0.98	0.96	0.99	0.93	1.00	0.99	0.93
Q9DB20	28080	Atp5o	1.00	0.99	0.97	0.92	0.89	1.02	1.04	0.97
Q9CRA7	68055	Atp5s	1.00	1.12	1.01		0.86	0.93	0.95	0.83
Q9CYN9	70495	Atp6Ap2		0.90	0.98	0.68	1.06	0.95	1.11	0.98
Q9Z1G4	11975	Atp6v0a1	0.97	0.94	1.07	0.68	0.83	1.01	1.06	1.01
P63082	10003963	Atp6v0c	0.93	1.02	1.08	0.73	0.78	1.10	1.04	1.04
P51863	11972	Atp6v0d1	0.96	0.97	1.11	1.02	0.82	1.06	1.00	1.03
P50516	11964	Atp6v1a	0.94	0.98	0.98	0.93	0.99	0.97	0.89	1.00
P62814	11966	Atp6v1b2	1.01	1.07	1.06	0.90	0.95	1.05	0.96	1.08
Q9Z1G3	66335	Atp6v1c1	1.03	0.96	1.02	0.97	0.97	0.98	1.01	0.99
P57746	73834	Atp6v1d	1.00	1.00	1.04	0.94	1.10	0.95	1.07	1.07
P50518	11973	Atp6v1e1	1.05	0.97	1.00	0.93	0.98	0.97	1.11	1.00
Q9D1K2	66144	Atp6v1f	1.11	1.03	1.04	1.13	0.88	1.00	1.06	0.95
Q9CR51	66290	Atp6v1g1	1.19	1.28	1.08	1.13	1.03	0.89	1.43	1.12
Q9WTT4	66237	Atp6v1g2	0.95	0.99	1.01	1.00	0.95	0.98	0.97	1.06

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q8BVE3	108664	Atp6v1h	1.21	0.97	1.10	1.13	1.06	1.09	1.05	1.14
P03930	17706	Atp8	1.04	1.00	1.02	1.19	0.94	0.94	1.04	0.96
O35143	11983	Atpif1	0.97	0.98	0.97	0.97	1.26	0.95	0.95	0.96
Q9JLZ3	11992	Auh	0.97	1.06	0.57	0.90	0.85	0.98	1.03	0.88
Q8BKX1	108100	Baiap2	1.46	1.29	1.00	1.47	1.73	1.52	1.15	1.31
Q91XV3	70350	Basp1	1.06	1.01	1.11	1.83	1.52	1.00	0.85	1.08
Q61361	12032	Bcan	0.97	0.90	0.89	0.91		0.86	0.93	0.97
Q61335	27061	Bcap31		0.89	1.10	0.58		1.20		0.99
Q80YN3	76960	Bcas1	1.26	0.92	0.96			1.09	0.89	0.76
Q8CCN5	192197	Bcas3					1.24			
P24288	12035	Bcat1					0.20	1.26		
Q6P3A8	12040	Bckdhb				1.25			1.44	
P59017	94044	Bcl2l13								1.42
Q80XN0	71911	Bdh1	1.03	1.12	1.09	1.14		1.02	0.92	1.03
O08539	30948	Bin1	4.14	1.04	1.04	3.44	4.23	1.01	1.62	1.02
Q8R016	104184	Blmh		1.02	1.03			1.07		
Q9CY64	109778	Blvra		1.10	1.12			0.95		0.93
Q8BGS2	66162	Bola2/Bola2B		1.03	0.94				1.36	
Q8R164	68021	Bphl	1.05	1.05	1.01	0.91	1.03	1.02	1.38	1.24
Q9Z0S1	23827	Bpnt1	1.01	1.01	0.89	1.16	1.00	0.97	0.91	0.93
Q91VR8	101314	Brk1					0.88	1.22	1.05	
Q9D023	70456	Brp44	1.02	1.02	1.11	0.98	0.88	1.12	1.34	1.09
P63030	55951	Brp44l		1.07	0.95	1.92		1.31		1.06
Q5RJI5	381979	Brsk1		2.68						1.18
P18572	12215	Bsg	1.27		1.25		1.49	1.02	1.08	1.11
O88737	12217	Bsn	2.03	1.30	1.28	2.18	1.62	1.49	1.00	1.24
Q80TK0	231570	Btbd8				1.13				
Q9CQH7	70533	Btf3l4	1.31	1.06	0.93		1.84	1.09	1.34	1.01
Q91V76	70984	C11Orf54			1.47			1.16		1.09
Q8R0P4	66273	C11Orf67		1.01	0.93	1.17		0.99		0.95
Q8BZA9	319801	C12Orf5	1.03				0.24			
O35127	14790	C12Orf57			0.98			0.92		
Q9CQE8	68045	C14Orf166	1.10	1.06	1.04	0.97	1.20	0.99	1.17	1.05
Q9CR41	67693	C15Orf63		1.13	1.05			1.05		1.06
Q9CPT4	28106	C19Orf10		1.01	0.72	0.90	0.99			0.91
Q8R404	224904	C19Orf70	1.30	1.00	0.92	1.08	0.89	1.05	1.02	0.97
Q8BHG2	74098	C1Orf123		0.99	0.89			0.99		0.90
O35658	12261	C1Qbp	0.88	0.96	0.92	0.84	1.37	1.00	0.91	0.92
Q02105	12262	C1Qc								1.35
Q9D1K7	67326	C20Orf27	1.29	1.20	1.03	1.12		1.01		
Q9D7N9	71881	C20Orf3	1.07							
Q9D172	28295	C21Orf33	0.98	1.02	0.96	1.00	1.13	1.03	1.08	0.94
Q99LF4	28088	C22Orf28	1.01		0.94		1.12		0.83	
Q9DB10	69029	C22Orf32		1.07	0.98			0.96		1.15
Q80X80	71764	C2Cd2l		1.11	1.14			1.02		0.70
Q8BR90	106064	C5Orf51	1.19				0.79		0.98	

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Gen	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
P00920	12349	Ca2	0.87	0.83	0.84	0.73	0.66	0.69	0.57	0.59
Q06138	12283	Cab39	0.93	1.19	1.06	1.02	1.06	1.04	0.70	1.06
Q61290	12290	Cacna1e		0.91	1.21			1.12		1.00
O08532	12293	Cacna2d1	0.92	0.99	1.06	0.75	1.12	1.01	0.92	1.01
Q6PHS9	56808	Cacna2d2	0.79							
Q9Z1L5	12294	Cacna2d3	1.01	0.82	1.20	0.68	1.20	1.17	0.85	1.10
Q9CXW3	12301	Cacybp	1.32	1.03	0.94		1.67	0.99	1.44	1.02
Q8R5M8	54725	Cadm1		1.00	1.00			0.78		1.13
Q8BLQ9	239857	Cadm2	0.93	0.98	1.07	0.98	1.27	1.00	0.87	0.98
Q99N28	94332	Cadm3	0.98	0.98	1.05	0.93	1.08	1.01	0.98	0.94
Q80TJ1	27062	Cadps	0.99	1.04	1.00	0.95	1.03	0.99	1.12	1.02
Q8BYR5	320405	Cadps2							1.67	
P12658	12307	Calb1	1.15	1.03	1.07	1.10	1.12	0.96	1.11	0.98
Q08331	12308	Calb2	0.81	1.05	0.50	0.59	0.79	0.67	1.27	0.74
P14211	12317	Calr	1.03	1.01	1.05	0.95	1.49	1.01	0.86	1.14
Q8BW96	227541	Camk1d		1.04	1.07			1.00		1.12
P11798	12322	Camk2a	0.96	1.20	1.12	1.10	1.12	0.87	0.96	1.33
P28652	12323	Camk2b	1.10	1.26	1.17	1.11	1.20	1.04	1.24	1.39
Q6PHZ2	108058	Camk2d	1.15	1.27	0.98	1.03	1.18		1.06	1.33
Q923T9	12325	Camk2g	1.12	1.03	1.18	1.13	0.99	1.03	1.18	1.41
Q6QWF9	66259	Camk2N1		1.37	1.20			1.16		
P08414	12326	Camk4	1.20	0.96		0.99	0.96		0.98	1.13
Q8C078	207565	Camkk2	1.25		1.27	1.23	1.20	1.14	0.98	
Q3UHL1	235604	Camkv	1.87	1.04	1.15	1.90	1.57	1.12	1.29	1.06
Q8C1B1	67886	Camsap2			1.13			1.49		1.05
Q80VC9	69697	Camsap3	0.94							
Q6ZQ38	71902	Cand1	1.02	1.00	0.92	1.11	0.95	0.88	1.01	0.92
P35564	12330	Canx	0.95	1.01	0.93	0.84	1.21	0.97	1.05	0.95
P40124	12331	Cap1	3.39	1.02	1.14	3.12	3.73	0.92	2.94	1.06
Q9CYT6	67252	Cap2	1.12	1.02	1.19	1.22	0.94	1.16	1.19	1.27
O08529	12334	Capn2	0.87	0.90	1.00		0.85	1.03	1.18	0.91
O08688	12337	Capn5	1.30	1.27	1.13		1.13	1.39		0.91
O88456	12336	Capns1		1.16				0.95		
Q60865	53872	Caprin1	1.56	1.37	1.15			1.14	1.01	1.15
P47754	12343	Capza2	0.96	1.04	1.05	0.98	1.02	0.93	0.99	1.11
P47757	12345	Capzb	0.86	0.97	1.00	1.05	0.93	0.94	0.98	1.07
Q9CR86	52502	Carhsp1	1.03	0.86				0.94		
Q9CZ42	69225	Carkd	1.12	0.89			0.97	1.05	1.15	
Q9ER72	27267	Cars			1.11			0.98		1.42
O70589	12361	Cask		1.10	1.01			1.08		1.02
Q6P9K8	268932	Caskin1	3.36	1.12	1.12	2.02	1.24	1.10	1.06	1.03
P24270	12359	Cat							0.75	
P48758	12408	Cbr1	1.07	0.98	0.91	1.00	1.10	0.88	1.07	0.89
P23198	12417	Cbx3	1.03			1.21	0.87		0.87	
Q8CI71	73288	Ccdc132	1.13	1.14	1.09	1.17	1.30	0.89	1.37	1.23
Q8K003	66167|100	Ccdc72		0.86	1.09			0.81		0.93

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Gen	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q8BGU5	67974	Ccny		1.13	1.32			1.10		1.17
P80314	12461	Cct2	0.93	0.94	0.92	0.91	0.97	1.02	0.98	1.01
P80318	12462	Cct3	1.00	0.98	0.91	1.01	0.74	0.92	1.04	0.99
P80315	12464	Cct4	1.07	1.02	1.01	1.12	0.98	0.82	0.94	1.07
P80316	12465	Cct5	0.95	0.98	0.97	0.86	0.72	0.90	1.10	1.02
P80317	12466	Cct6a	1.09	1.01	0.95	1.15	0.90	1.11	1.11	1.04
P80313	12468	Cct7	1.06	0.93	0.90	1.03	0.92	1.16	1.06	0.88
P42932	12469	Cct8	0.81	1.02	0.91		0.86	0.88	1.16	0.96
O54901	17470	Cd200	1.46					0.95		
Q61735	16423	Cd47	0.91	1.18	1.06	0.81	1.14	1.12	0.87	0.89
P35762	12520	Cd81	0.81	0.86	0.84	0.98	0.74	0.91	0.93	0.78
P40240	12527	Cd9	0.67	0.83		0.80	0.71	0.65	0.64	0.67
Q61081	12539	Cdc37	1.23	0.96	0.85	1.12	1.73	0.91	1.42	0.99
P60766	12540	Cdc42	1.02	1.01	1.07	1.09	1.17	0.99	1.04	1.03
Q7TT50	217866	Cdc42bpb		1.10	1.31	2.00		1.17	0.91	1.00
Q8BGH7	72729	Cdc42se2		1.10				0.98		
P15116	12558	Cdh2	1.18	1.25	1.02	1.09	1.03	1.18	1.13	1.22
Q8VDP6	52858	Cdipt			1.16			1.23		
Q80YP0	69681	Cdk3		7.99				10.19		
P49615	12568	Cdk5	0.98	0.94	0.92	0.93	1.01	0.93	1.03	0.94
Q99L43	110911	Cds2	0.99	1.30		0.88	0.80	1.16	1.11	
Q9Z0H4	14007	Celf2		0.86	1.09	1.24	0.63		1.06	1.05
Q9JKC6	57754	Cend1	1.21	1.01	0.96	1.03	1.24	1.07	1.38	0.93
Q569L8	219103	Cenpj		19.00				17.72		
Q9CXS4	73139	Cenpv	1.39		1.06			0.90		0.70
Q6A065	545389	Cep170			1.32					
P18760	12631	Cfl1	1.02	0.97	0.99	1.00	0.87	0.98	1.03	1.00
P45591	12632	Cfl2	0.92	0.97	0.87	1.01	0.86	0.96	1.46	0.91
P46061	19387	Chadl		3.15	1.10			0.90		1.12
Q9CRB9	66075	Chchd3	0.94	1.09	1.00	0.86	0.90	1.17	1.51	1.06
Q91VN4	66098	Chchd6	1.03	0.99	1.00	1.07	1.17	0.93	1.24	
P70232	12661	Chl1		1.17	1.00			1.34		1.02
Q9D8B3	75608	Chmp4b	1.54	1.28			1.11	1.18	1.20	1.05
Q8R1T1	105513	Chmp7				1.45			1.38	
P61022	56398	Chp			0.85		1.10			
Q91WS0	52637	Cisd1	1.07	0.99	0.96	0.99	1.14	1.02	1.06	0.93
Q9CQB5	67006	Cisd2								1.00
P49025	12704	Cit		1.16	0.75			0.91	1.25	0.96
Q8BMK4	216197	Ckap4		0.97	1.03			2.28		1.13
A2AGT5	75786	Ckap5	1.72	1.00	0.99	1.62	1.02	1.09	1.56	0.87
Q04447	12709	Ckb	0.94	0.99	0.99	0.97	0.94	0.99	0.94	0.92
P30275	12716	Ckmt1a/Ck	1.08	1.04	0.97	1.03	1.20	1.04	1.08	0.97
Q80TV8	76707	Clasp1		0.77						
Q8BRT1	76499	Clasp2	1.28	1.05	1.12	1.05	0.94	1.03	1.22	0.97
Q60771	18417	Cldn11	0.83	0.76	0.64	0.77	0.45	0.67	1.03	0.46
Q9QYB1	29876	Clic4	0.83	0.90	0.81			1.00	0.89	0.82

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q922J3	56430	Clip1		0.93	1.05			0.98		1.10
Q9Z0H8	269713	Clip2	1.18	0.93	1.07	1.32	0.90	0.91		1.28
O88696	53895	Clpp		0.99			1.76	1.14		1.08
O08585	12757	Clta	1.13	1.10	1.03	1.25	1.08	1.00	0.90	1.06
Q6IRU5	74325	Cltb	1.41	1.08	1.04	1.37	1.40	0.96	0.99	1.00
Q68FD5	67300	Cltc	0.99	1.03	1.00	0.88	0.85	0.97	0.99	1.00
Q06890	12759	Clu						1.26		
Q8R4N0	69634	Clybl			1.00			0.96	1.27	
Q9CPZ8	67899	Cmc1		0.95	0.85			1.08		
Q9DBP5	66588	Cmpk1	0.95	1.06	0.92	0.97	0.76	0.95	0.97	0.98
Q9D6G9	67272	Cmtm5						1.22		
Q9D1A2	66054	Cndp2				1.35			1.00	
Q9DAW9	71994	Cnn3	1.12				0.96		1.85	1.35
Q6ZQ08	234594	Cnot1	1.08			1.07	0.97		1.48	
P16330	12799	Cnp	0.88	0.80	0.77	0.77	0.54	0.81	0.85	0.68
Q5M8N0	380686	Cnrip1	1.03	0.96	1.06	1.09	0.97	0.99	0.90	1.11
P12960	12805	Cntn1	0.85	0.96	1.01	0.79	1.02	1.06	0.88	1.05
Q61330	21367	Cntn2		1.20	1.17			1.37		0.68
O54991	53321	Cntnap1	1.17	0.79		0.87	0.87		0.92	
Q9CPW0	66797	Cntnap2	1.06	0.93	0.84	0.75	0.95	0.91	0.98	1.04
Q3V4B5	66200	Commd6					0.98		0.88	
Q8K2Q0	76501	Commd9	1.12		1.12			0.98	0.89	0.97
O88587	12846	Comt								1.22
Q8CIE6	12847	Copa	0.70	0.96	1.21	1.14	0.97	1.07	1.22	1.03
Q9JIF7	70349	Copb1		1.14	1.07	1.08	1.07	1.49	1.28	1.21
O55029	50797	Copb2		1.00				0.85		1.28
Q9QZE5	54161	Copg1	1.10	0.99	1.19		1.18	0.87	0.63	1.07
P61202	12848	Cops2	1.32	1.01	1.02	1.17	1.11		1.08	0.95
O88543	26572	Cops3			1.18	0.92	0.81	1.47	1.28	
O88544	26891	Cops4	1.10	0.84	0.98	1.22	0.83	0.90	1.21	0.95
O35864	26754	Cops5	1.52	1.03	1.11	1.12		0.97	1.05	1.06
O88545	26893	Cops6	0.99	0.96	1.00	1.20		0.94	1.06	1.00
Q9CZ04	26894	Cops7a		0.92	0.81	1.04		0.87	1.02	0.93
Q8BV13	26895	Cops7b						1.08		
Q8VBV7	108679	Cops8	0.91	1.09			0.72	0.89	1.07	0.92
P61924	56447	Copz1	1.13	1.46	1.08		0.88	1.33	1.06	
Q8K1Z0	67914	Coq9		1.00				0.94		0.89
O89053	12721	Coro1a	1.06	1.10	1.16	1.25	1.12	1.07	1.01	1.26
Q9WUM4	23790	Coro1C	0.73	0.91	0.84	0.74	0.89	0.83	1.06	0.86
Q9CQI6	72042	Cotl1	0.98	0.99	0.99	0.99	1.01	0.98	1.01	0.96
P56394	12856	Cox17		1.33	1.18			1.08		
P00405	17709	Cox2	0.96	0.97	1.03	0.84	0.81	1.10	1.20	1.02
P19783	12857	Cox4l1	1.04	0.96	0.95	0.87	1.04	1.02	1.04	0.99
P12787	12858	Cox5a	1.02	0.96	1.03	0.78	1.00	1.00	1.06	0.95
P19536	12859	Cox5b	1.04	0.96	1.02	0.82	0.80	1.07	1.28	0.98
P43024	12861	Cox6a1	0.99		1.01	1.31	0.99	1.01	1.04	0.68

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
P56391	110323	Cox6b1	0.93	0.95	1.03	0.67	1.06	0.99	1.02	0.97
Q9CPQ1	621837|12	Cox6C	0.96	0.93	1.00	0.65	1.00	1.00	1.01	1.01
P48771	12866	Cox7a2	1.00	0.98	1.01	1.02		1.11	1.77	1.00
P56393	66142	Cox7b		1.08	1.27					
P17665	12867|100	Cox7C/gm10012		1.04	1.06					1.12
P63040	12889	Cplx1	1.16	1.03	1.03	1.32	1.21	1.04	1.11	1.05
P84086	12890	Cplx2	0.97	1.07	1.01		1.26		0.88	1.01
Q9Z140	12891	Cpne6	1.37	0.96	1.21	1.08	1.21	1.07	0.98	1.17
Q1RLL3	211232	Cpne9				0.89				
P47934	12908	Crat		0.93				0.99		1.22
Q9DCT8	68337	Crip2	1.53	1.11	1.13	1.21	1.39	1.16	1.31	1.08
Q64010	12928	Crk	0.82	1.03	1.13	1.30	0.80	1.17	0.81	1.09
P47941	12929	Crkl	1.89					1.03		
P97427	12933	Crmp1	1.07	1.01	1.07	1.05	0.94	1.02	1.04	1.04
Q9DC50	74114	Crot	0.83	0.97						
P23927	12955	Cryab	0.75	0.84	0.78	0.85	0.22	0.84	0.86	0.70
O54983	12971	Crym	0.95	0.93	0.95	0.90	0.99	0.88	0.82	0.91
P47199	12972	Cryz	1.05	1.05	2.08			1.08	1.10	1.12
Q921W4	66609	Cryzl1	1.15		0.80					
Q9CZU6	12974	Cs	1.01	1.00	0.97	0.99	0.86	0.97	1.07	0.93
Q9ERK4	110750	Cse1l	1.03	1.10	1.25	1.00	0.92	1.01	0.97	0.97
Q8BK63	93687	Csnk1a1	0.95	4.41	0.90			2.27	0.98	1.63
Q60737	12995	Csnk2a1	1.39	1.07	1.21	1.40	1.27	1.03	1.32	0.97
O54833	13000	Csnk2a2	1.11	0.93	1.15	1.25	0.90	0.97	1.00	0.95
P67871	13001	Csnk2b			1.31					
Q71M36	29873	Cspg5	0.99							
P97315	13007	Csrp1	0.88	0.92	0.82	1.14	0.96	0.95	0.99	0.86
P21460	13010	Cst3	1.02	0.84	1.09		0.88	0.82		1.02
Q62426	13014	Cstb	1.02	1.01	0.97	1.15	0.84	1.00	0.81	0.91
O88712	13016	Ctbp1	1.41	1.07	1.12		1.08	1.14	1.37	1.15
Q61301	12386	Ctnna2	1.22	1.28	1.01	1.13	1.25	1.20	1.11	1.36
Q02248	12387	Ctnnb1	1.25	1.06	1.09	1.33	0.96	1.11	1.34	1.15
O35927	18163	Ctnnd2		1.31	1.45			1.19		0.99
P10605	13030	Ctsb	0.93	1.13	1.14	0.89	1.06	0.90	0.86	1.09
P18242	13033	Ctsd	1.23	1.15	1.15	1.32	1.23	1.37	2.09	1.15
Q60598	13043	Cttn	1.47	1.07	1.18	1.67	1.28	1.14	1.00	1.09
Q9WTX6	26965	Cul1	1.09							
Q9D4H8	71745	Cul2		0.91	0.94			0.83		0.89
Q9JLV5	26554	Cul3	0.93	1.00	0.93	1.02	1.06	0.92	0.93	0.94
Q3TCH7	99375	Cul4a		1.00	1.16			1.08		0.86
Q9D5V5	75717	Cul5	1.11	1.07	0.92	1.02	0.91	0.93	0.83	0.83
P56395	109672	Cyb5a		1.07	0.78		1.09	1.41		1.08
Q9CQX2	66427	Cyb5b	0.91	1.00	0.95	0.91	1.03	0.96	0.98	1.00
Q9DB73	72017	Cyb5R1				1.83		1.12		1.04
Q9DCN2	109754	Cyb5R3	0.92	0.98	0.89	0.84	1.45	1.00	0.98	1.06
Q9D0M3	66445	Cyc1	0.94	0.94	0.95	0.85	1.07	1.03	1.06	1.00

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Gen	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
P62897	13063	Cycs	0.98	0.98	0.92	0.98	1.04	0.98	0.92	0.91
Q7TMB8	20430	Cyfip1	1.09	1.03		1.18	0.90	1.09	1.10	1.11
Q5SQX6	76884	Cyfip2	1.12	1.03	1.00	1.10	1.01	1.01	1.11	1.05
Q9CX80	114886	Cygb			0.76		0.88			
Q3UHC7	69601	Dab2Ip								1.08
Q922B2	226414	Dars								1.42
P31786	13167	Dbi	0.67	0.96	0.84	0.71	1.01	0.81	0.91	0.89
Q9QXS6	56320	Dbn1	1.52	1.10	1.23	1.72	1.14	0.97	1.34	1.17
Q62418	13169	Dbnl	0.58	1.06	1.10	1.33	1.22	0.97	1.28	1.01
Q9JLM8	13175	Dclk1	1.11	1.05	1.19	1.33	0.95	0.95	1.01	1.06
Q6PGN3	70762	Dclk2	1.13	0.75			0.84			
O08788	13191	Dctn1	0.70	1.05	0.94	0.92	0.65	0.92	0.76	0.91
Q99KJ8	69654	Dctn2	1.11	0.98	1.09	1.05	0.98	0.93	1.09	0.96
Q9Z0Y1	53598	Dctn3		0.95	0.92			0.94		0.90
Q9QZB9	59288	Dctn5								1.26
Q9WUB4	22428	Dctn6	1.08	0.98	2.06		0.96		0.95	1.08
Q9CWS0	69219	Ddah1	0.95	1.01	0.98	1.10	1.09	0.87	1.10	0.99
Q99LD8	51793	Ddah2		1.07	1.10	1.14		0.90	1.33	1.00
Q3U1J4	13194	Ddb1	0.82	0.90	0.87	0.77	1.03	0.93	0.72	0.87
O35215	13202	Ddt	0.83	0.96	0.83	0.86	0.98	0.92	0.91	0.80
Q91VR5	104721	Ddx1	0.94	1.06	1.00	1.19	1.05	1.03	1.01	1.07
Q9Z1N5	53817	Ddx39b	1.25	1.01	1.18	1.02		1.13	1.01	0.95
Q62167	13205	Ddx3X	1.23	0.94	1.13	1.23	1.02	1.02	1.18	1.02
Q61496	13206	Ddx4	0.98	0.92	0.91		0.98	0.94		0.73
Q61656	13207	Ddx5	1.24	1.03	1.04		1.08	1.03		1.05
P54823	13209	Ddx6	1.83		1.14	2.05	1.64		1.40	
Q9CQ62	67460	Decr1	0.72	0.98	0.84	1.19	1.53	0.97		0.92
Q9CQJ6	68184	Denr		1.12						
Q6NS52	217480	Dgkb	1.25	0.99	1.50		1.16	1.11		1.07
O35286	13204	Dhx15		1.82				1.24		1.09
Q6PGC1	218629	Dhx29				1.55				
O70133	13211	Dhx9	0.97	0.89	0.94	0.89	0.85	0.97	0.93	1.04
O08808	13367	Diaph1	1.09							
Q3UH60	239667	Dip2b		0.83				0.91		
Q5PR73	68203	Diras2	1.26	0.92	1.14		0.92	1.11	0.95	1.04
Q8BMF4	235339	Dlat	2.17	1.04	0.91	1.78	2.47	1.02	2.28	1.00
O08749	13382	Dld	0.96	1.02	0.98	0.94	1.07	0.93	0.94	0.96
Q811D0	13383	Dlg1	0.99	0.86	1.16	1.02	1.08	1.30	1.34	1.01
P70175	53310	Dlg3	1.12	1.01	1.09	1.30	1.20	1.00	1.02	1.14
Q62108	13385	Dlg4	1.05	1.23	1.17	1.01	1.14	1.14	1.06	1.30
Q9D2G2	78920	Dlst	0.09	0.94		0.08	0.86	0.91	0.16	0.91
Q6PNC0	240283	Dmxl1				1.63				
Q8BPN8	235380	Dmxl2	1.17	1.09	1.15	1.23	0.96	1.20	0.95	1.08
P63037	15502	Dnaja1	0.94	1.06	1.05		1.07	0.98	1.18	0.94
Q9QYJ0	56445	Dnaja2	1.52	1.01	1.01	1.43	1.11	0.93	1.00	1.02
Q99M87	83945	Dnaja3				1.06	1.55		1.08	

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
O54946	23950	Dnajb6		1.30	1.16			0.95		
Q9CQV7	67713	Dnajc19			1.12			1.03		
P60904	13002	Dnajc5	1.48	1.09	1.00	1.03	2.30	1.00	1.30	1.00
Q80TZ3	72685	Dnajc6	1.24	1.08	1.12	1.17	1.21	1.10	1.14	1.08
Q05A62	105000	Dnal1			1.22			0.88		1.10
P39053	13429	Dnm1	1.00	1.02	1.02	1.07	0.95	0.97	0.94	1.01
Q8K1M6	74006	Dnm1l	1.06	1.02	1.02	1.00	1.00	0.97	0.98	1.00
P39054	13430	Dnm2	0.93	0.96	0.98		0.71	0.99	0.94	1.00
Q8BZ98	103967	Dnm3	0.88	0.94	0.83	0.92	0.84	0.89	1.01	0.86
Q8CIQ7	208869	Dock3	1.33	1.29		1.45			1.05	
P59764	238130	Dock4				0.92		1.23		
Q8R1A4	67299	Dock7					0.80		0.80	
Q6NXK7	269109	Dpp10	0.66	1.01	1.00	0.73	0.95	0.87	0.92	1.10
Q99KK7	75221	Dpp3	0.98	1.23	0.94		1.11	0.97	0.67	1.00
Q9Z218	13483	Dpp6	0.98	1.01	0.84	1.06	1.24	1.00	0.72	0.98
Q80YA7	74388	Dpp8					0.93		1.12	
Q99LT0	66310	Dpy30		0.94	0.84			0.83		1.16
O08553	12934	Dpysl2	1.15	1.01	0.97	1.05	1.01	0.94	1.02	0.94
Q62188	22240	Dpysl3	1.18	1.24	1.19	1.14	1.05	1.13	1.49	1.13
O35098	26757	Dpysl4	1.06	1.00	0.99	1.01	0.86	1.00	1.07	1.02
Q9EQF6	65254	Dpysl5	1.08	1.04	0.97	1.03	0.97	1.00	1.16	0.98
Q91ZU6	13518	Dst				1.75		0.85		
Q9R0P5	56431	Dstn	1.00	0.98	0.95	0.91	1.02	0.96	0.99	0.99
Q9D2N4	13527	Dtna	1.44	1.17	1.10		1.32	1.04		1.05
Q9D7X3	72349	Dusp3	1.46	1.02	1.10	1.14	0.97	1.08	1.16	1.01
Q9JHU4	13424	Dync1h1	0.98	1.01	1.01	0.99	0.96	1.02	0.85	1.00
O88485	13426	Dync1l1	0.91	0.92	0.86	0.92	0.91	0.93	0.98	0.96
O88487	13427	Dync1l2	0.83	1.07	0.96		1.15	0.90		0.87
Q8R1Q8	235661	Dync1li1	1.08	1.03	0.98	1.14	1.00	1.01	1.14	1.01
Q6PDL0	234663	Dync1li2	1.34	0.86	1.04	1.45	1.03	1.20	1.09	1.05
P63168	56455	Dynll1	1.35	1.08	1.20	1.25	0.98	1.13	1.04	1.16
Q9D0M5	68097	Dynll2	1.04	1.00	1.03	0.98	1.02	0.99	0.99	0.96
P62627	67068	Dynlrb1	0.98	1.00	1.03	1.03	0.88	0.98	1.01	0.92
O35459	51798	Ech1		1.27	1.29	0.83		1.05		0.76
Q8BH95	93747	Echs1	0.92	1.00	0.89	0.95	0.95	0.97	1.03	0.92
P42125	13177	Eci1	0.85	1.04	0.92	0.84	1.16	0.95	1.01	0.91
Q9WUR2	23986	Eci2						1.02		
Q8BL66	216238	Eea1	1.07	1.08	0.98	0.89	1.25	1.05	1.12	1.02
P10126	13627	Eef1a1	1.01	0.99	0.95	0.95	0.94	0.94	1.22	1.02
P62631	13628	Eef1a2	0.93	0.98	0.95	0.93	1.03	0.85	1.09	0.94
O70251	55949	Eef1b2	1.00	1.02	0.93	0.95	1.00	0.95	0.98	1.02
P57776	66656	Eef1d		1.24	1.25			1.00		1.12
Q9D8N0	67160	Eef1g	1.04	0.94	0.94	1.14	1.21	0.96	0.94	0.99
P58252	13629	Eef2	0.88	0.99	1.01	0.93	1.03	0.97	0.92	1.01
Q9D8Y0	27984	Efhd2	1.01	0.93	0.94	1.02	1.50	0.92	1.07	1.02
Q8BG67	76740	Efr3a							1.12	

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q6ZQ18	668212	Efr3b		1.49						
O08810	20624	Eftud2				1.26	0.87	1.12	0.92	
Q9QXY6	57440	Ehd3	0.94	0.96	1.04	0.96	0.98	0.84	0.98	0.98
P48024	20918	Eif1	0.96	0.95	0.99	0.30	0.54	0.96	1.17	0.97
Q8BMJ3	66235	Eif1ax	1.09	0.97			1.26	0.73	0.80	1.23
Q99LD9	217715	Eif2b2	0.90	0.72	0.95			0.67	1.15	0.91
Q6ZWX6	13665	Eif2s1	0.95	1.00	1.23	1.01		0.87	1.03	1.35
P23116	13669	Eif3a	1.26	1.00	0.91	1.21	1.02	1.04	1.34	1.05
Q8JZQ9	27979	Eif3b						1.84		1.53
Q8R1B4	56347	Eif3c/Eif3c	1.32	1.14	1.20	1.35	1.30	0.92	1.24	1.06
Q9DCH4	66085	Eif3f					1.11			
Q91WK2	68135	Eif3h	0.98	0.91	1.16		0.90	0.92	0.88	0.97
Q9QZD9	54709	Eif3l		1.17						
Q99JX4	98221	Eif3M	1.01			1.17	1.13	1.24	1.05	
P60843	13681	Eif4a1	1.01	0.85	0.99		1.23	1.02	1.09	1.08
P10630	13682	Eif4a2	1.17	1.08	1.10	1.06	1.09	1.11	1.16	1.07
Q91VC3	192170	Eif4a3	0.85						1.08	
Q8BGD9	75705	Eif4b	1.29	1.05	1.02	1.27	1.12	0.98	1.04	1.01
P63073	13684	Eif4e	1.06	1.02	1.00	1.19	0.98	1.05	1.08	1.08
Q6NZJ6	208643	Eif4g1	1.70	1.10	1.06	1.53		1.13	1.33	1.17
Q62448	13690	Eif4g2		1.56				0.97		
Q80XI3	230861	Eif4g3		1.11	1.02	2.55		0.94	1.30	1.02
Q9WUK2	22384	Eif4h	1.15	1.00				0.95	0.94	1.03
P63242	276770	Eif5a	0.91	0.92	1.01	0.85	1.03	0.93	0.98	0.96
P70372	15568	Elavl1	0.89	0.91				1.06	0.95	0.89
Q8BHL5	140579	Elmo2		1.30	1.23			0.99		1.28
P17182	13806|433	Eno1	0.93	1.00	1.03	0.93	1.23	0.96	0.93	1.01
P17183	13807	Eno2	0.94	1.02	1.00	0.90	1.26	1.00	0.97	0.99
Q8BGB7	67870	Enoph1	0.59	0.97	0.24		0.96	0.59	0.61	0.88
Q8BGN3	320981	Enpp6	1.10			0.65	0.66		0.81	
P60840	56205	Ensa	1.02	0.99	1.15	1.01	1.23	1.06		0.92
Q9JIX0	223527	Eny2		1.03				0.87		
Q9Z2H5	13821	Epb41l1	1.29	1.14	1.07	1.19	1.04	1.09	1.00	1.01
O70318	13822	Epb41l2	1.21	1.19	0.98	1.31	1.31	0.91	1.22	1.11
Q9WV92	13823	Epb41l3	1.02	0.91	0.88	0.92	0.99	0.92	1.16	0.92
Q9WV69	13829	Epb49			1.07					1.25
Q99M71	105298	Epdr1			1.14			0.76		0.80
Q03137	13838	Epha4						1.45		
Q8VEH5	77781	Epm2aip1	1.13			1.65	0.73	1.94	1.11	
Q80VP1	13854	Epn1	1.56	1.01	1.09	1.37	1.28	0.98	1.14	1.00
Q8CHU3	13855	Epn2	1.72			1.18	1.27		1.13	
Q91W69	71889	Epn3			1.15			1.04		1.08
Q8R0W0	223650	Eppk1		0.95						
Q8CGC7	107508	Eprs	1.39	0.94	1.07	1.23	1.06	1.12	1.41	1.15
Q60902	13859	Eps15l1		4.72			1.05			1.26
Q6PH08	238988	Erc2	1.30	1.26	1.08	1.08	1.08	1.23	0.99	1.52

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q9DC16	67458	Ergic1		1.06		2.00		1.04		0.94
P84089	13877	Erh	1.01	0.99	1.09		1.07	1.02	0.93	1.08
Q8BFZ9	244373	Erlin2								0.97
Q5EBJ4	77767	Ermn		2.43	0.90					0.71
P57759	67397	Erp29		0.90	0.89	0.84		1.07	0.90	1.10
Q9R0P3	13885	Esd	1.20	0.88		0.45		1.03		0.84
Q99LC5	110842	Etfa	0.88	0.99	0.88	1.02	0.99	0.97	1.03	0.90
Q9DCW4	110826	Etfb	0.99	0.95	0.82	0.92	0.88	0.91	0.94	0.85
Q921G7	66841	Etfdh		0.91	0.85	0.77	1.09	0.93	0.90	0.88
P70429	14026	Evl	1.19	0.63	0.99		0.99		1.40	1.04
Q9D952	14027	Evpl		1.20	0.83			1.18		0.55
Q8R3S6	69940	Exoc1		1.02	0.97			1.00		0.90
Q9D4H1	66482	Exoc2			0.94			0.91		
O35382	20336	Exoc4	1.12	1.03	1.10	1.00	1.06	0.98	1.00	1.12
Q3TPX4	105504	Exoc5			1.53					1.31
O35250	53413	Exoc7			0.81					
Q6PGF7	102058	Exoc8	1.18	0.99	1.02		1.00	0.90	1.54	1.05
Q8C163	208194	Exog	1.38		1.38			1.12		1.09
Q0VAV2	320051	Exph5			4.07					
P26040	22350	Ezr	0.95	0.91	0.97	0.94	1.64	1.00	0.93	1.04
O08914	14073	Faah	1.22			0.93	1.02		1.12	
P11404	14077	Fabp3	1.06	0.99	1.03	1.05	1.09	1.05		1.08
Q05816	16592	Fabp5	1.06	0.93	0.81	1.07	1.13	1.01	0.89	1.00
P51880	12140	Fabp7	1.27	1.51	1.22	1.36	1.42	1.02	1.32	1.15
Q8R0F8	68636	Fahd1	0.77	0.93	0.86		0.81	0.79	0.92	0.97
Q3TC72	68126	Fahd2a	0.97	0.90	0.83		0.96	0.87		0.89
Q6A0A9	218236	Fam120a	1.57	1.00	1.23	1.86	1.27	1.06	1.42	1.19
Q9CR98	66488	Fam136a		0.86	0.92	2.05		0.88		0.94
Q9D6U8	70186	Fam162a	0.87	0.90	0.90	1.51		1.01	1.85	0.99
Q3UGS4	192173	Fam195b	0.61	0.88	1.14	0.26		0.94	0.58	0.97
Q8BGY7	108654	Fam210a	0.99		0.92					0.94
Q9CYH2	70564	Fam213a	0.94	1.19	0.99	0.97	0.79	1.03	0.84	1.17
Q9DB60	66469	Fam213b	1.30	1.00	0.91			0.88	1.19	0.94
Q8BHZ0	76820	Fam49a			1.35	1.19	0.78	0.90	0.90	1.23
Q921M7	223601	Fam49b	1.23	0.91	1.01	1.12	0.99	0.98	1.14	1.01
Q9CWE0	76824	Fam54b							1.68	
Q3V2J0	436062	Fam92b		1.04	0.91			0.60		0.71
Q80VD1	68215	Fam98b		1.09			1.08	1.17		1.00
Q8C0C7	66590	Farsa	1.36			1.02			1.13	
P19096	14104	Fasn	0.96	1.00	0.93	0.85	0.77	1.06	0.93	0.86
P62862	14109	Fau	1.68	1.09	0.98	1.82	1.88	0.91	1.68	1.15
Q80UW2	230904	Fbxo2		0.95	0.76			1.04		0.93
Q920E5	110196	Fdps	0.91	0.96	0.99	1.34	0.80	0.83	0.91	0.88
Q8CIB5	218952	Fermt2			1.88		0.90			
P97807	14194	Fh	1.04	1.03	0.93	0.92	0.95	1.04	1.08	0.97
Q9CQ92	66437	Fis1 (Inclu	0.85	1.00	0.83	1.00	1.01	0.98	0.97	0.92

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
P26883	14225	Fkbp1a		0.85	0.91	0.98	1.13	0.89		0.93
P45878	14227	Fkbp2	1.07	1.01	0.78	0.91	1.23	0.98	0.87	0.96
Q62446	30795	Fkbp3	0.87	1.04	0.83	0.98	1.12	0.93	0.99	1.01
P30416	14228	Fkbp4		1.12	0.99	1.12		0.61	0.95	1.04
Q8BTM8	192176	Flna		1.02		1.35		1.11	2.40	1.18
O08917	14251	Flot1			1.04		0.69	1.19		
Q8K274	238024	Fn3Krp		0.98	1.01			1.03		1.02
Q64731	14241	Foxl1	7.60	1.05				1.20		
Q61553	14086	Fscn1	0.98	0.93	1.10	1.23	0.95	0.98	0.97	1.03
P09528	14319	Fth1	0.88	0.97	0.84	0.71	1.02	1.07	0.90	0.87
Q91WJ8	51886	Fubp1	2.13	0.88	1.12		2.17	1.18	1.70	0.92
Q9DB70	72018	Fundc1							0.97	
Q9D6K8	67391	Fundc2	1.32		1.26	0.89	0.99		0.94	0.89
P56959	233908	Fus	1.03	1.00	1.03	1.13	1.12	1.00	0.91	0.99
Q9D164	59095	Fxyd6	1.64	1.22	1.02	1.62	1.10	1.05	1.62	1.06
P97379	23881	G3bp2	1.24	0.94	0.98		1.11	0.95		1.05
Q00612	14381	G6Pd			0.90	0.66			1.07	
Q9DCD6	56486	Gabarap		1.08				0.91		0.92
Q8R3R8	57436	Gabarapl1		0.94		0.96		1.71		1.00
P60521	93739	Gabarapl2	1.03	1.10	0.86	1.10	1.02	0.95		0.93
P48318	14415	Gad1	1.01	1.00			0.88	0.91	1.01	1.12
P48320	14417	Gad2		1.09				0.72		0.84
Q99KY4	231580	Gak		0.99	0.83			0.81		0.86
Q9R0N0	14635	Galk1				1.62				
Q8BHN3	14376	Ganab		0.99	1.02	0.90		0.92	0.83	
P06837	14432	Gap43	1.43	1.01	0.88	1.68	1.27	0.81	1.65	0.95
P16858	100042025	Gapdh/loc1	0.96	0.97	0.95	0.96	0.69	0.95	1.00	0.96
Q6PAR5	66691	Gapvd1		1.01	1.30					1.08
Q9CZD3	353172	Gars	1.03	1.06	0.90		1.03	0.94	1.09	0.98
Q60780	14457	Gas7	0.82							
O55126	14467	Gbas	0.97	1.01	0.83	0.91	1.03	0.92	1.19	1.02
Q9D6Y9	74185	Gbe1			1.47			0.84		
Q60759	270076	Gcdh	0.87							
P97494	14629	Gclc		1.01				0.72		0.98
Q9R111	14544	Gda	1.09	0.94	1.06	1.16	1.08	0.91	0.87	1.06
O88741	14545	Gdap1	0.92	1.07	1.03	1.11	1.28	1.11	0.97	0.98
Q8VE33	228858	Gdap1l1							1.09	
Q9JL56	56209	Gde1								1.12
P50396	14567	Gdi1	0.99	1.03	0.96	0.94	0.99	0.92	0.98	1.01
Q61598	14569	Gdi2	1.01	1.04	1.02	1.10	1.07	1.10	0.98	1.08
Q9CRY7	66569	Gdpd1	0.99				0.45	0.88		
P03995	14580	Gfap	1.14	1.06	1.04	0.75	1.97	3.18	1.61	2.73
P56213	11692	Gfer			1.20			1.42		0.88
P47856	14583	Gfpt1						1.03		
Q8R0H9	106039	Gga1			0.89					
Q8BMI3	260302	Gga3		1.26			1.02	0.86		

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
P06880	14599	Gh1								99.76
Q68FF6	216963	Git1				1.04			1.03	
P23242	14609	Gja1	0.87	0.80			0.59	1.15		
Q64516	14933	Gk		0.87	1.11		0.98		1.37	
Q8K3I9	170772	Glcci1					0.80			
Q9CPU0	109801	Glo1	0.97	1.03	0.91	0.87	1.08	0.93	0.99	0.97
Q9CPV4	67201	Glod4	0.91	1.02	0.87	0.88	1.19	0.89	0.81	0.95
Q9QUH0	93692	Glrx	0.97	1.01	1.06	1.34	1.03	0.98	0.98	
Q9CQM9	30926	Glrx3	1.20		1.11		1.37	1.04	1.44	1.37
Q80Y14	73046	Glrx5	1.15	1.15	0.93	0.83	0.92	0.96		0.95
Q9JL62	56356	Gltp	1.13	0.89	0.81	0.98	0.58	0.84	1.04	0.80
P26443	14661	Glud1	0.84	1.01	0.87	0.92	0.89	0.96	0.94	0.94
P15105	14645	Glul	1.13	0.91	0.89		0.98	0.78	0.87	0.84
P47963	270106|10(	Gm10071/Rpl13			1.44	1.00		1.23	0.97	1.15
Q80SZ7	100043507	Gm15776/Gng5		0.91	0.94			0.96		0.92
Q9CQI3	63985	Gmfb	1.08	0.91	0.99	1.31	0.84	0.93	1.02	0.95
Q9DCZ1	66355	Gmpr	1.05	0.97	0.99	1.04			0.99	1.01
Q3THK7	229363	Gmps	0.91	1.33	1.09		0.96	0.92	1.27	1.02
P21278	14672	Gna11	0.88	1.04	1.01		0.99	1.06	0.91	1.11
P30677	14675	Gna14		0.92						0.92
P08752	14678	Gnai2	1.07	1.08	1.04	1.09	1.00	1.00	1.29	1.01
Q8CGK7	14680	Gnal	1.14	1.01	1.25		0.94			1.03
P18872	14681	Gnao1	1.03	0.98	1.03	1.10	1.07	1.00	0.97	1.01
P21279	14682	Gnaq	0.97	0.96	0.99	1.00	0.89	0.96	1.09	0.96
Q6R0H7	14683	Gnas	0.89	1.10			1.12	1.04		
O70443	14687	Gnaz	0.87	1.00	1.37		1.02	1.11	0.97	0.95
P62874	14688	Gnb1	0.90	0.99	1.05	1.01	0.78	0.92	0.95	0.99
P68040	14694	Gnb2l1	1.64	1.08	1.04	1.18	1.04	1.01		1.02
P62881	14697	Gnb5	0.98	0.86	1.04		1.07	1.07	1.11	1.11
Q9DAS9	14701	Gng12	0.90	1.48	0.92			0.94	0.95	
P63213	14702	Gng2	0.87	0.94	0.93	1.31	1.26	0.92	0.71	1.17
P63216	14704	Gng3	1.04	0.96	1.03	1.04	0.90	1.00	0.88	0.96
P50153	14706	Gng4		1.29	1.10			0.68		1.76
Q61016	14708	Gng7	0.99	0.91	0.98			0.87	0.90	1.12
P36916	14670	Gnl1								0.95
Q91W53	57437	Golga7		0.90	1.30			0.89		0.94
P05201	14718	Got1	0.94	0.96	0.93	0.91	1.06	0.97	0.91	0.95
P05202	14719	Got2	0.97	0.99	0.97	0.97	1.05	1.03	1.03	0.98
P13707	14555	Gpd1	1.12	0.92	0.97	0.95		1.14	1.26	1.13
Q3ULJ0	333433	Gpd1l	1.18	1.05	1.03	0.99		0.97	0.98	1.02
Q64521	14571	Gpd2	1.00	1.05	1.03	1.04	1.01	1.02	0.90	1.01
Q8BUV3	268566	Gphn	0.82	0.88	0.93	1.10		0.99	1.15	0.98
P06745	14751	Gpi	0.92	0.98	0.96	0.90	1.06	0.93	0.99	0.98
P35802	234267	Gpm6a	0.97	0.95	1.09	1.01	0.91	0.99	0.81	0.93
P35803	14758	Gpm6b	1.00	0.99	1.19	1.00	1.06	1.05	0.80	1.04
Q8C419	241263	Gpr158	2.25	1.69	1.39	1.49	1.82	1.57	1.92	1.25

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Gen	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q3UNH4	26913	Gprin1	4.04	1.11	1.23	3.52	2.45	0.84	2.44	1.01
O70325	625249	Gpx4		0.85	1.16	0.84	0.86	0.90	0.99	1.14
Q60631	14784	Grb2	1.10	0.97	1.01	1.06	1.02	0.98	1.20	0.91
Q91Z53	76238	Grhpr	0.88	0.99	1.20	0.87			0.81	0.99
P23818	14799	Gria1		1.21				1.31		
P23819	14800	Gria2	1.25	1.15	1.42	1.25	1.14	1.31	1.01	1.23
Q9Z2W9	53623	Gria3		1.11	1.33					1.51
Q01097	14812	Grin2b			1.25					
Q8VD04	54645	Gripap1		0.88				1.10		0.93
Q9QYS2	108069	Grm3	1.11	1.01	1.33	1.12	0.91	1.25	0.95	1.13
Q99LP6	17713	Grpel1		1.04	1.05			0.97		0.91
Q9WV60	56637	Gsk3b	1.25	1.47	1.02		0.94		0.92	1.10
P13020	227753	Gsn	0.90	0.94	0.94		0.94	1.06	1.00	0.97
Q8R050	14852	Gspt1	1.07	1.11	0.89		0.92	0.86		0.99
P24472	14860	Gsta4	0.95	1.01	0.86	0.79	0.87	0.89	0.83	0.82
Q9DCM2	76263	Gstk1	1.05	1.07	0.99		0.89	0.98	1.30	0.95
P48774	14866	Gstm3	0.95	0.95	0.93	0.91	0.73	0.81	0.89	0.84
P10649	14862	Gstm5	0.92	0.95	0.91	0.98	0.83	0.90	0.99	0.92
O09131	14873	Gsto1		0.97				0.86		
P19157	100042625	Gstp1	0.99	0.99	0.87	0.87	0.78	0.87	0.87	0.85
Q9WVL0	14874	Gstz1	1.14	1.05	0.84		1.04	1.14	1.02	0.93
Q8K284	233863	Gtf3c1								0.83
O08582	14904	Gtpbp1			0.94					
O54865	54195	Gucy1b3	0.97	1.37	1.00	1.18	0.74	1.29	0.94	0.98
Q64520	14923	Guk1	1.09	0.96	0.98	1.00	1.06	1.00	1.08	1.00
P10922	14958	H1f0	18.53	1.39	1.43			2.35	19.62	1.24
Q8R1M2	232440	H2afj	1.56	1.08	1.24	1.38	1.10	2.12	2.22	0.99
P27661	15270	H2afx							2.57	
P0C0S6	51788	H2afz		1.20		1.12				0.98
Q61425	15107	Hadh	0.86	0.92	1.02		1.20	0.84	0.90	0.91
Q8BMS1	97212	Hadha	0.97	1.01	0.89	0.90	0.95	1.03	0.95	0.94
Q99JY0	231086	Hadhb	0.89	0.95	0.86	1.15		1.03	0.92	
Q99KB8	14651	Hagh	0.86	0.98	0.99	1.00	1.25	0.94	0.89	1.19
O35668	15114	Hap1		1.18	0.30				2.38	0.75
Q9QUP5	12950	Hapln1		0.89	0.98			0.93		0.86
Q61035	15115	Hars				0.93			1.09	
Q9D1L9	68576	Hbxip		0.92	1.13			1.15		0.64
O88704	15165	Hcn1		1.08	0.93					
O88703	15166	Hcn2							0.93	
P70288	15182	Hdac2						1.29		1.12
Q9D114	68695	Hddc3						14.14		
P51859	15191	Hdgf	0.97	1.36	1.15			1.07	1.07	1.01
Q9JMG7	29877	Hdgfrp3			1.02			1.08		1.06
Q3UGR5	76987	Hdhd2	0.98	0.94	0.90	0.87	1.11	0.92	0.98	0.98
Q9CYW4	72748	Hdhd3		1.28				0.72		
Q8VDJ3	110611	Hdlbp	1.20							

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Gen	Symbol	Mut- w11	Mut- w12	WT- w11	WT- w12	Mut- w11	Mut- w12	WT- w11	WT- w12
Q9R257	15199	Hebp1	1.27	4.20	4.27		2.49	2.77	3.74	2.88
Q69ZR2	207304	Hectd1		0.96	1.61	0.77		0.83		1.02
Q640R3	72927	Hepacam	1.57	1.33	0.84	1.03	2.09	1.07	1.50	0.95
Q99LI8	15239	Hgs		0.85	1.12			1.03		1.06
Q99L13	58875	Hibadh	0.82	1.17	0.93	0.91	1.25	0.98	0.89	0.95
Q8QZS1	227095	Hibch	0.96	1.03	0.90	0.90	0.74	0.94	1.12	0.92
P70349	15254	Hint1	1.02	1.03	0.92	1.02	1.03	0.97	0.88	0.95
Q9D0S9	68917	Hint2	1.21	1.13	0.81		1.15	0.95	1.22	0.91
Q9CPS6	66847	Hint3	1.30	0.87	0.77	1.10		0.89	1.28	0.77
Q9JKY5	29816	Hip1r	1.21	1.05	1.20	1.94	1.04	0.97	1.02	1.02
P15864	50708	Hist1h1c		1.10	1.67	0.70		2.56	2.53	1.18
P43274	50709	Hist1h1e		1.06	1.68			2.95		1.19
P17710	15275	Hk1	0.95	0.96	0.94	0.78	1.02	0.95	1.07	0.99
P63158	15289	Hmgb1	1.10	1.01	1.01	0.87	2.03	0.95	0.89	1.03
O70252	15369	Hmox2		0.90	0.97			0.98		0.92
P49312	15382	Hnrnpa1	1.14	0.97	1.05	0.92	0.99	1.02	0.98	1.07
O88569	53379	Hnrnpa2b1	0.92	0.97	0.97	1.01	1.02	1.02	0.85	1.08
Q8BG05	229279	Hnrnpa3	0.96	1.04	0.98	1.11	0.75	1.06	1.13	1.07
Q99020	15384	Hnrnpab	1.28	1.12	1.02	0.93		1.09	1.29	1.08
Q9Z204	15381	Hnrnpc	0.89	0.95	1.12	1.18	0.94	1.16	0.94	0.97
Q60668	11991	Hnrnpd	0.99	1.01	0.97		1.09	0.99	1.46	1.04
O35737	59013	Hnrnph1	1.16		1.01	1.33	0.97	1.00	0.92	1.11
P61979	15387	Hnrnpk	1.17	1.05	1.05	1.08	1.03	1.02	1.03	1.11
Q8R081	15388	Hnrnpl	1.18	0.96	1.00	1.37	1.16	0.97	1.11	1.04
Q9D0E1	76936	Hnrnpm	1.07	0.93	1.27		1.03	1.07	1.54	1.13
Q8VEK3	51810	Hnrnpu	1.97	1.04	0.97	1.77	1.65	0.99	1.68	1.00
Q00PI9	68693	Hnrnpul2		1.12	0.93		0.14	1.01		1.05
Q921F4	72692	Hnrpll	1.63	1.09	1.01	1.62	1.28	1.15	1.08	1.21
Q9Z2Y3	26556	Homer1	1.46	1.90	1.29		1.12	1.15	1.04	1.39
Q3TEA8	15441	Hp1bp3	2.80	1.08	1.20			1.01		1.06
P84075	15444	Hpca	1.09	0.92	1.03	0.93	1.02	1.08	0.89	1.04
P62748	53602	Hpcal1	1.06	1.03	0.87	1.03	1.05	0.71		0.83
Q8BGZ1	170638	Hpcal4	1.34	1.11	1.31	1.36	1.24	1.12	1.02	1.13
P00493	15452	Hprt1	1.06	1.00	0.82	1.32	0.99	0.91	1.21	0.91
Q61411	15461	Hras	1.08	1.04	1.03	1.08	0.94	0.98	1.04	0.99
P52760	15473	Hrsp12	0.90	0.86	1.19	0.91	1.02	1.21	1.08	
O08756	15108	Hsd17b10	1.04	0.98	1.22		0.95	1.05	1.00	1.04
O70503	56348	Hsd17b12	1.02	1.09	1.34	1.20	1.10	1.20	1.19	1.03
Q8BTX9	72552	Hsdl1	0.96		0.82					0.89
P07901	15519	Hsp90aa1	1.03	1.01	0.98	1.08	1.00	0.97	1.02	0.96
P11499	15516	Hsp90ab1	1.01	0.96	0.98	1.03	0.99	0.98	0.97	0.97
P08113	22027	Hsp90b1	0.92	1.02	0.95	0.96	0.94	0.97	0.99	1.01
Q8K0U4	73442	Hspa12a	1.01	0.96	0.95	1.15	0.88	1.01	1.02	0.99
Q9CZJ2	72630	Hspa12b	1.05	0.98		0.98	0.82	0.97		1.11
P17879	193740|15	Hspa1a/Hs	0.72	0.98		1.08	0.77	0.80		0.74
P17156	15512	Hspa2	0.97	0.99	1.00	1.25	0.85	0.85	1.14	1.06

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q61316	15525	Hspa4	1.93	1.03	0.91	1.78	2.29	0.98	1.70	0.96
P48722	18415	Hspa4l	0.90	1.02	0.87	0.89	0.98	1.01	0.95	0.89
P20029	14828	Hspa5	1.01	1.03	1.00	0.97	1.10	1.02	1.00	1.03
P63017	15481	Hspa8	0.92	0.99	0.98	0.96	0.98	0.97	0.94	0.98
P38647	15526	Hspa9	1.00	1.02	0.94	1.03	0.98	1.01	1.01	0.99
P14602	15507	Hspb1			0.94		1.07			
P63038	15510	Hspd1	0.94	1.03	0.96	0.86	0.95	0.95	1.02	0.95
Q64433	15528	Hspe1	0.90	1.02	0.96	0.94	1.12	0.95	0.95	0.93
Q61699	15505	Hsph1	1.42	1.04	0.99	1.39	1.28	1.04	1.26	0.95
P42859	15194	Htt	1.51	1.10	0.97	1.76		1.34	1.14	1.18
Q7TMY8	59026	Huwe1		1.22	1.09	1.40		1.11		0.95
Q9JKR6	12282	Hyou1	1.14	0.98	0.92	1.12	1.37	0.98	1.37	0.97
Q8BU30	105148	Iars	1.97	1.33		1.44	0.72			
Q8BIJ6	381314	Iars2	0.92	1.05	0.98	0.98	0.79	1.08	0.92	0.98
Q60625	15898	Icam5		1.02	1.24		0.90		0.70	0.94
O88844	15926	Idh1	1.10	0.95	0.97	1.19	0.88	1.00	0.98	1.01
P54071	269951	Idh2	0.88	1.01	0.94		1.09	0.92	1.35	0.91
Q9D6R2	67834	Idh3a	0.98	1.03	0.98	0.63	0.42	0.96	1.11	0.98
P70404	15929	Idh3g	0.93	1.05	1.00	0.99	1.16	1.04	1.03	1.00
P58044	319554	Idi1	0.81	0.83			0.98	0.72		
Q8R366	140559	Igsf8		0.79	0.80			0.80		0.81
Q8CAQ8	76614	Immt	1.13	0.97	0.99	0.95	1.04	1.11	1.28	1.00
O55023	55980	Impa1	0.97	0.94	0.93	0.91	1.04	0.94	0.85	0.91
P46660	226180	Ina	1.04	0.86	0.80	0.60	0.67	1.09	1.05	1.09
P49442	16329	Inpp1		1.77	0.96					1.10
Q9EPW0	269180	Inpp4a	1.25	0.96	0.97			0.98		1.06
Q8BKC5	70572	Ipo5	0.95	0.92	0.96	1.03	0.98	0.99	1.02	1.09
Q9EPL8	233726	Ipo7	1.34	1.02	1.13	1.06	1.17	1.03	1.10	1.09
Q91YE6	226432	Ipo9		1.04	1.62	1.18	3.35	0.99		
Q8R0S2	232227	Iqsec1	1.21	0.95	0.97	1.32	1.26	1.03	1.04	1.25
Q5DU25	245666	Iqsec2		0.83	0.96					1.00
Q8VIM9	210146	Irgq					0.84	1.21		
Q9D924	69046	Isca1		1.03	0.83	1.26	1.11	0.99	1.22	0.93
Q9DCB8	74316	Isca2			0.93	1.44		1.01		
Q91V64	66307	Isoc1	0.89		0.88		1.14	1.02	0.91	0.94
P85094	664994	Isoc2	0.93	1.03	0.86		0.93	1.01	1.09	0.95
Q9D892	16434	Itpa	0.90	0.93	1.03	1.15	1.52	0.94	1.08	0.92
P11881	16438	Itpr1	1.31	1.12	1.28	1.22	0.87	1.37	1.02	1.10
Q9Z0R4	16443	Itsn1	1.68	0.98	0.93	1.83		0.83	1.69	1.04
Q99MN1	85305	Kars	0.85	0.78	0.97	1.30	1.23	1.12	1.11	0.90
Q8BNW9	74901	Kbtbd11	1.16			1.15	1.20		1.22	
P62482	16498	Kcnab2	0.93	0.94	0.94	0.97	0.91	1.13	0.94	0.93
Q9JM63	16513	Kcnj10						1.34	2.42	
Q60749	20218	Khdrbs1		0.89	1.01			1.62		0.97
Q3U0V1	16549	Khsrp	1.20	0.90	1.06			1.07	1.21	1.06
Q80U49	217882	Kiaa0284			1.17	1.54			1.39	1.87

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q6PDI5	230249	Kiaa0368	1.40	0.97	0.91	1.22		0.93	1.42	1.10
Q8R0A7	234797	Kiaa0513	0.88					0.75	1.32	
Q80TL4	230085	Kiaa1045		3.48	1.03				1.06	
Q9DBN4	97820	Kiaa1191								0.84
A2AQ25	208618	Kiaa1217	1.73	1.19	1.00		1.23	1.18	1.39	1.33
Q3UGY8	215821	Kiaa1244	2.01	0.95	1.22	1.52				1.21
Q6ZPU9	72320	Kiaa1279		1.06						
Q148V7	227446	Kiaa1468	1.40	1.17	1.05	1.00	0.64	0.85	0.96	0.97
Q7TQ95	69605	Kiaa1715							3.05	
Q8VDP4	219158	Kiaa1967		1.42	0.98	1.95		1.16	2.16	0.93
P33173	16560	Kif1a	1.79	1.11	0.97	1.11		1.07	1.02	1.04
Q9QXL2	16564	Kif21a	1.32	0.98	0.97	1.08	1.23	1.09	1.03	0.98
P28740	16563	Kif2a		1.04				1.19		1.18
P28741	16568	Kif3a	1.78				1.93			
Q61768	16573	Kif5b	1.36	1.07	0.93	0.97	0.83	0.94	1.54	0.78
P28738	16574	Kif5c	1.01	0.98	0.84	0.98	0.90	0.97	0.96	0.94
O88447	16593	Klc1		0.99	0.87	1.96	1.29	0.91		1.15
O88448	16594	Klc2						0.49		
Q60960	16646	Kpna1						1.26		
O35343	16649	Kpna4			0.98					
P70168	16211	Kpnb1	0.96	1.11	0.98	0.97	1.09	0.94	1.00	1.07
Q61781	16664	Krt14		0.98	0.97			0.95		0.81
Q3UV17	77055	Krt76	14.01	26.17	8.87		11.32	25.51		18.32
Q61595	16709	Ktn1	1.15	1.51	1.08	1.67	1.12	1.02	1.38	1.09
P11627	16728	L1cam	0.96	1.03	1.08	0.87	1.65	0.95	1.07	1.04
Q9EP89	80907	Lactb				1.08			1.10	
P19137	16772	Lama1	0.99	1.03	1.04	0.95	1.48	1.05	0.86	
Q9CQ22	66508	Lamtor1					1.01			
O88653	56692	Lamtor3	1.26	1.07				1.01	1.23	
O89112	14768	Lancl1	1.24	0.97	1.10			1.15		1.09
Q9JJK2	71835	Lancl2	1.15	0.95	1.19	1.22	1.19	1.20	1.07	1.11
Q9CPY7	66988	Lap3	0.85			0.64			0.97	
Q8BMJ2	107045	Lars	0.28	0.80	1.07	1.28	0.81	0.83		0.79
Q61792	16796	Lasp1	1.84	1.03	1.15	0.21	0.57	1.08	1.83	1.04
Q61233	18826	Lcp1					1.84			
P06151	16828	Ldha	1.09	1.01	1.10	1.06	0.89	1.01	0.95	1.04
P16125	16832	Ldhb	0.99	0.95	0.95	0.99	0.88	0.96	1.04	0.96
Q9Z2I0	56384	Letm1	1.04	1.07	1.00	0.92	1.22	1.05	1.05	0.97
P16045	16852	Lgals1		1.04	1.91			0.99	0.80	1.22
Q8VED9	216551	Lgalsl	1.25	0.93	0.93	0.92	1.60	0.97	0.93	0.91
Q9JIA1	56839	Lgi1	0.87	0.95	1.05		0.82	1.14		1.11
O89017	19141	Lgmn	0.87							
Q9D7I5	76429	Lhpp	1.05						0.82	
Q8JZS0	108030	Lin7a	1.17	1.05	1.13		1.00	1.09		1.12
O88952	22343	Lin7c		1.07	0.92			1.15		1.00
Q8BT35	67885	Linc00116			1.20			1.41		

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Gen	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q9D1T0	235402	Lingo1		1.01					1.66	
P48678	16905	Lmna	1.13	1.07	1.10	0.92	1.39	1.07	1.04	1.06
P14733	16906	Lmnb1	1.82	1.08	1.09	1.54	1.45	1.02	0.82	1.23
P21619	16907	Lmnb2	1.27	1.03	0.99	1.35	1.17	0.95	1.63	0.89
Q8C129	240028	Lnpep	1.07						1.06	
Q8CGK3	74142	Lonp1	1.18	1.07	1.02	1.32	1.46	1.08	1.15	0.96
Q80TR1	330814	Lphn1	1.72		1.19		0.85			0.97
Q91ZX7	16971	Lrp1	1.00	1.00	1.06	0.89	1.01	1.13	0.94	1.04
Q6PB66	72416	Lrpprc	1.11	1.01	0.87	1.02	0.98	0.98	1.21	1.00
Q9D1G5	66606	Lrrc57	1.46	0.94	1.11	1.17	1.13	1.07	1.10	1.06
Q922Q8	98238	Lrrc59			1.13					1.00
Q8BLK3	268890	Lsamp	0.91	0.86	1.02	0.91	0.92	0.98	0.93	0.97
P62313	78651	Lsm6		1.04	0.92	1.06		1.00		0.94
P24527	16993	Lta4h	0.98	0.95	0.91	1.35	0.90	1.01	1.04	0.89
P70202	17035	Lxn	0.95	1.00	1.05	0.89	0.79	1.16	0.89	1.07
Q9WUC3	23934	Ly6h	1.15		1.17			1.03	0.88	1.21
Q9WTL7	26394	Lypla2	0.87	1.24	1.02	1.15		1.02		1.01
Q8K215	380840	Lyrm4		1.13	1.03	0.94	1.06	0.89	1.26	
Q9JHQ5	93730	Lztfl1								1.09
Q9QXZ0	11426	Macf1	1.25	1.42	1.21	1.21	1.60	1.11	1.22	1.19
Q3UYG8	72899	Macrod2	1.97	0.89	1.03					1.03
Q80U28	228355	Madd	2.16	1.06	1.31	1.50		1.30		1.11
P20917	17136	Mag	0.86	0.87	0.83	0.70	0.76	0.88	0.70	0.69
Q6RHR9	14924	Magi1							1.44	
P61327	17149	Magoh								0.54
Q8BW75	109731	Maob		1.11	0.78	1.11			1.21	1.35
Q9QYR6	17754	Map1a	2.09	0.96	0.99	1.96	4.30	0.98	2.32	0.96
P14873	17755	Map1b	2.91	1.01	0.97	4.02	0.71	1.02	3.84	0.98
Q91VR7	66734	Map1lc3a	1.03	1.01	0.98	1.29	0.89	0.89	0.89	0.91
Q9CQV6	67443	Map1lc3b	0.95	0.91	0.87	1.05	0.82	0.80	0.78	0.83
Q8C052	270058	Map1s		1.03	1.02				1.01	1.12
P20357	17756	Map2	1.02	1.03	0.94	0.91	1.25	1.00	0.84	0.97
P31938	26395	Map2K1	1.14	1.00	0.98	1.22	1.08	0.97	0.96	0.98
P47809	26398	Map2k4	1.09	0.99	1.42		0.77	0.78		1.05
P27546	17758	Map4	1.66	1.03	1.09		1.09	1.08	1.72	0.95
Q7TSJ2	17760	Map6	1.38	1.00	1.02	2.26	1.37	1.02	1.30	0.95
A2AJI0	245877	Map7d1	4.06	0.89	0.74		3.22	0.89		0.97
A2AG50	78283	Map7d2	1.51	0.74	0.64	0.86	0.84		1.26	0.79
P63085	26413	Mapk1	1.06	0.99	0.97	1.01	1.10	0.94	0.99	0.99
Q63844	26417	Mapk3	1.12				0.69			
Q61166	13589	Mapre1	1.58	1.07	1.00	1.51	1.92	0.97	1.61	1.04
Q8R001	212307	Mapre2	1.45	0.95	0.96		1.15	1.01	1.33	0.88
Q6PER3	100732	Mapre3	1.47	1.00	0.97	1.34	1.73	0.98	1.47	0.95
P10637	17762	Mapt	1.59	0.78	0.99	2.00	1.13	0.93	1.69	0.87
Q922Q1	67247	March2	1.30	1.21	1.38	1.22	1.14	1.43	1.63	1.41
P26645	17118	Marcks	1.70	0.99	0.90	1.35	1.49	0.88	1.91	0.91

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
P28667	17357	Marcksl1		1.09	1.30			0.98		1.15
Q8VHJ5	226778	Mark1		1.12	1.34			1.00		1.22
Q03141	17169	Mark3			1.12		3.01		0.96	1.17
Q99LB6	108645	Mat2b				1.15			1.01	
Q8K310	17184	Matr3	1.32	1.05	1.10	1.25	1.18	1.09	1.26	1.13
P04370	17196	Mbp	0.78	0.73	0.69	0.71	0.47	0.77	0.82	0.62
Q5HZI9	230125	Mcart1			1.39					0.84
Q8R3F5	223722	Mcat						0.77		
Q9D1I5	73724	Mcee		0.91				0.97		
Q9DB27	68995	Mcts1	0.88	1.16	1.24	1.08	1.40	1.03	0.98	1.22
Q3UMR5	215999	Mcu	1.13				0.69	1.54	0.87	
P14152	17449	Mdh1	0.92	0.95	0.95	0.88	1.02	0.90	0.91	0.94
P08249	17448	Mdh2	0.85	1.02	0.98	0.87	1.14	0.98	0.92	0.97
Q9D967	67881	Mdp1	0.84		1.20		1.30	0.99	0.89	
P06801	17436	Me1	0.93	0.84		0.85	1.40	0.96	0.95	0.85
Q8BMF3	109264	Me3	0.93		1.11	1.02	1.01		1.51	1.83
Q80U63	170731	Mfn2	1.58		1.15					
Q9EQQ9	76055	Mgea5		1.01		1.05	1.02	0.97	1.05	1.08
O35678	23945	Mgll			1.81			1.24		1.34
Q9CPU4	66447	Mgst3	1.13	1.11	1.10	0.92	0.77	1.42	0.84	1.14
Q8CJ19	194401	Mical3			0.91					
Q8VCX5	216001	Micu1	1.15						1.01	
P34884	17319	Mif							0.97	
Q9JM52	50932	Mink1	2.08	1.60	1.42	1.49	1.64	1.41	0.96	1.24
Q7TNS2	433771	Minos1			1.11			1.18		
Q9QZQ1	17356	Mllt4		1.18	1.22	1.92			2.73	1.42
Q8C7H1	109136	Mmaa								1.04
Q8K273	236792	Mmgt1		1.04						
Q9CQY6	67267	Mnf1	0.84				0.94			1.96
Q9D2P8	17433	Mobp	1.30	0.77	0.76		0.99	0.96	1.71	0.59
Q61885	17441	Mog	0.78	0.78	0.73	0.66	0.47	0.85	0.88	0.64
Q80TL7	67074	Mon2	1.30			1.19		1.08	1.40	1.05
Q9WV34	50997	Mpp2	0.94	1.12	1.59		1.60		1.01	1.59
O88910	13384	Mpp3					1.27	1.06		1.00
Q99J99	246221	Mpst	1.07		1.03	1.06	0.96	1.05	0.97	1.24
O08989	17532	Mras	1.17	1.00	1.09	1.21	1.37	1.05	0.88	1.02
Q9DB15	56282	Mrpl12	1.15	1.03	0.90	1.08		0.98		0.95
Q9D1H8	68499	Mrpl53				1.17				
Q9CPX7	66242	Mrps16	1.48					1.35		
Q9CQX8	66128	Mrps36	1.73	0.99	0.97	1.90	1.63	0.98	2.50	0.94
P26041	17698	Msn		1.22			1.22	1.31	1.03	1.15
Q791V5	56428	Mtch2	0.96	1.04	1.04	0.95	1.05	1.20	1.06	1.09
Q9CRB8	67900	Mtfp1	1.17				1.39	1.21	1.30	
Q922D8	108156	Mthfd1	0.93	0.86	0.86			0.94		0.83
Q3V3R1	270685	Mthfd1l	1.87	1.03	1.12	1.17		1.01		1.05
Q9Z2C4	53332	Mtmr1			1.07			1.16		0.81

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q9JLN9	56717	Mtor	1.40	0.91		1.22	1.28	1.04	1.41	
P62774	14489	Mtpn	1.11	0.94	1.03	1.06	1.02	0.93	0.88	0.99
P47802	17827	Mtx1							0.89	
O88441	53375	Mtx2	1.11	1.11	0.96	0.88	1.11	1.09	1.15	0.97
Q8VCM5	68350	Mul1		1.05	1.20			0.92		0.84
P16332	17850	Mut	1.29	0.94	0.87		0.87	0.90		0.93
P09922	17858|178	Mx1	0.90		1.63	1.11	0.88		0.85	
Q8C854	17876	Myef2	1.37	1.05	1.02		0.93	1.09	1.35	1.07
Q5SX40	17879	Myh1						4.40		
Q61879	77579	Myh10	0.98	1.04	1.02	1.00	0.90	1.08	1.11	1.04
Q6URW6	71960	Myh14	1.57		0.83	0.94	1.02		1.20	0.84
Q8VDD5	17886	Myh9	1.23	1.16	1.22	1.23	0.97	1.26	1.32	1.14
P05977	17901	Myl1		0.78	0.93			0.97		1.01
Q3THE2	67938	Myl12b	1.37	1.14	1.10		1.36	1.06	1.35	1.11
Q60605	17904	Myl6	1.14	1.03	0.97	1.30	1.05	0.97	1.09	1.10
Q9JMH9	360013	Myo18a	0.99	0.93	1.17	0.97	0.90	1.10	1.10	0.96
Q99104	17918	Myo5a	0.89	0.91	1.01	1.01	0.97	0.99	1.02	1.03
Q64331	17920	Myo6	0.85	1.12	0.78	1.09	1.07	0.79	1.61	1.22
Q6PGB6	72117	Naa50					1.29	1.09		1.19
P70670	17938	Naca	1.21	0.96	1.02	1.06	1.50	0.99	1.08	0.97
P28656	53605	Nap1l1	0.98		1.05	1.13	1.05	1.01	1.07	
Q78ZA7	17955	Nap1l4	1.17				1.57		1.08	
Q9DB05	108124	Napa	1.24	1.10	1.07	1.11	0.98	1.05	1.14	0.97
P28663	17957	Napb	1.21	1.05	1.07	1.24	1.02	0.99	1.11	1.01
Q9CWZ7	108123	Napg	1.05	1.01	1.01	1.04	0.57	0.99	1.08	0.99
Q8BP47	70223	Nars	1.19	1.09	1.05	1.11	0.88	1.31	1.34	0.99
Q9EPN1	26422	Nbea	1.25	1.14	1.21	1.25	0.99	1.19	0.94	1.10
Q91X97	52589	Ncald	1.03	0.99	1.15	1.03	1.22	1.07	0.88	1.06
P13595	17967	Ncam1	0.90	1.04	0.94	0.79	1.12	0.91	0.98	0.93
O35136	17968	Ncam2	1.02	1.03	0.96	1.06	1.37	0.96	1.00	0.92
P55066	13004	Ncan	2.09	1.07	1.14	1.94		1.43	1.76	1.01
Q9Z0E0	26562	Ncdn	1.08	1.02	0.97	1.10	0.84	0.96	0.93	1.00
Q8BLF1	320024	Nceh1	1.36			1.05	0.99		0.84	
P28660	50884	Nckap1	1.10	1.03	1.01	1.07	0.99	1.08	0.93	1.05
Q9ESJ4	80987	Nckipsd	1.27	1.10	0.92	1.48	1.10	1.07	1.15	1.06
P09405	17975	Ncl	5.92	1.04	1.04	5.48	5.56	1.09	4.36	1.06
Q8BNY6	14299	Ncs1	0.93	1.44	0.96	0.88	1.05	1.06		1.09
P57716	59287	Ncstn		0.99	1.21			1.18		1.53
P03888	17716	Nd1	0.98	0.98	1.54	0.70	0.85	1.11	1.23	1.27
P03911	17719	Nd4	0.93	1.02	0.93	0.66	0.95	1.25	1.13	1.15
Q62433	17988	Ndrg1	1.26							
Q9QYG0	29811	Ndrg2	0.92	1.06	0.80	0.88	0.88	0.99	1.10	0.94
Q9QYF9	29812	Ndrg3	1.20				1.32	1.33	1.33	
Q8BTG7	234593	Ndrg4	0.86	1.18				1.12		1.00
O35683	54405	Ndufa1					0.89			
Q99LC3	67273	Ndufa10	0.99	0.91	1.02	0.77	0.88	1.07	1.01	1.02

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Gen	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q9D8B4	239760|69	Ndufa11					1.02			
Q7TMF3	66414	Ndufa12	0.94	0.90	1.04	0.74	0.80	1.09	1.07	1.01
Q9ERS2	67184	Ndufa13	1.03	0.91	0.92	0.90	0.80	1.06	1.11	1.00
Q9CQ75	17991	Ndufa2	1.01	0.97	1.06	0.70	0.81	1.07	1.04	0.98
Q9CQ91	66091	Ndufa3			0.93			1.08		
Q62425	17992	Ndufa4	1.11	1.04	1.04	1.16	0.89	0.97	1.06	1.02
Q9CPP6	68202	Ndufa5	0.91	0.94	1.01	0.78	0.79	1.06		0.94
Q9CQZ5	67130	Ndufa6	0.98	0.93	0.97	0.88	0.91	1.02	0.99	1.01
Q9Z1P6	66416	Ndufa7	1.15	0.91	0.95	0.89	0.95	1.06	1.24	1.02
Q9DCJ5	68375	Ndufa8	0.93	0.95	1.00	0.67	0.78	1.11	1.18	1.04
Q9DC69	66108	Ndufa9	0.94	0.97	1.01	0.81	0.87	1.11	1.06	0.97
Q9CR21	70316	Ndufab1	0.86	0.99	0.97	0.66		1.04	1.14	0.98
Q9D1H6	68493	Ndufaf4		0.98				1.27		
Q9DCS9	68342	Ndufb10	1.38	1.12	1.36	0.99	1.17	1.17	1.47	1.18
O09111	104130	Ndufb11		0.88	1.04			1.17		0.95
Q9CQZ6	66495	Ndufb3	0.94	0.91	1.02	0.75	0.95	1.07	1.12	0.99
Q9CQC7	10004127	Ndufb4	1.06	0.97	0.96	0.88	0.80	1.03	1.12	1.02
Q9CQH3	66046	Ndufb5	0.88	0.90	0.98	0.74	0.90	1.15	1.23	1.00
Q3UIU2	230075	Ndufb6	1.06	0.98	1.01	0.62	0.81	1.08	1.10	1.00
Q9CR61	66916	Ndufb7		0.92	1.04			1.04		
Q9D6J5	67264	Ndufb8	0.99	0.99	1.10	0.65		1.22		1.08
Q9CQJ8	66218	Ndufb9			1.14					
Q9CQ54	68197	Ndufc2	1.18	0.94	1.01	0.83	0.97	1.09	1.27	0.97
Q91VD9	227197	Ndufs1	0.95	0.92	0.99	0.73	0.93	1.09	1.18	1.01
Q91WD5	226646	Ndufs2	1.01	0.97	1.05	0.93	0.97	1.08	1.19	0.97
Q9DCT2	68349	Ndufs3	0.98	0.94	1.05	0.68	0.90	1.08	1.16	1.02
Q9CXZ1	17993	Ndufs4	1.03	0.91	1.02		0.87	1.05	1.14	0.99
Q99LY9	595136	Ndufs5	1.00	0.94	0.94	0.86	0.92	1.03	1.08	0.97
P52503	623286|40	Ndufs6	1.06	0.95	1.02	0.81	0.98	1.12	1.05	0.97
Q9DC70	75406	Ndufs7	0.91	0.96	1.00	0.99	0.87	1.11	1.09	0.99
Q8K3J1	225887	Ndufs8	1.14	0.94	0.99	0.96	1.08	1.17	1.29	0.97
Q91YT0	17995	Ndufv1	0.98	0.90	1.02	0.87	1.30	1.16	1.16	1.00
Q9D6J6	72900	Ndufv2	1.03	0.98	1.13		1.00	1.13	1.15	1.07
Q8BK30	78330	Ndufv3	1.15	0.96	1.00	0.83	1.10	1.02	1.38	1.02
Q9CR95	67602	Necap1	0.92	0.95	1.01	1.12	1.17	0.92	1.24	0.98
P46935	17999	Nedd4	0.99			1.02	1.14	1.08		
P29595	18002	Nedd8	0.95	1.01	1.00	1.03	1.01	0.94	0.97	0.95
P19246	380684	Nefh	1.38	0.69	0.62	1.09	1.11	0.99	2.16	0.93
P08551	18039	Nefl	1.03	0.79	0.78	0.76	0.65	1.20	1.11	1.04
P08553	18040	Nefm	1.03	0.81	0.77	0.79	0.66	1.11	1.13	1.10
Q80Z24	320840	Negr1	0.87	0.98	1.18		1.17	1.03	1.15	1.03
Q04690	18015	Nf1 (Includ	1.15	0.97	1.00	1.06	0.94	1.09	0.95	1.00
Q810U3	269116	Nfasc	0.94	0.94	0.89	0.86	1.11	1.02	0.95	0.98
Q9QZ23	56748	Nfu1			1.08					0.86
Q8CHT1	53972	Ngef	0.94	1.00	1.46			1.12	1.24	1.21
Q9EQ80	65102	Nif3l1						1.02		

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Gen	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
O55125	18082	Nipsnap1	1.09	1.05	0.94	0.94	0.89	0.92	1.04	0.97
Q9CQE1	66536	Nipsnap3a	0.84		2.25		1.39		1.16	1.09
Q69ZK9	216856	Nlgn2		1.12	0.92			1.07		0.99
Q8BYM5	245537	Nlgn3			0.88			0.72		1.03
Q91YP2	75805	Nln	1.04	1.16	1.09	1.36	1.31	0.87	1.06	0.95
P15532	18102	Nme1 (Incl	0.94	0.96	0.88	0.96	0.93	0.90	0.96	0.94
Q01768	18103	Nme2	0.93	0.95	0.89	0.97	0.94	0.99	0.90	0.95
Q8K2T1	67824	Nmral1	0.94						0.74	
Q99K48	53610	Nono	0.97	0.99	1.05	1.26				
Q9Z0J4	18125	Nos1		1.17	0.91	0.94	1.56	0.98		0.85
Q11011	19155	Npepps	0.93	0.95	0.88	1.03	0.90	0.92	1.02	0.95
P60670	217365	Nploc4	0.97			0.91	1.08			
Q61937	18148	Npm1		1.05	1.04	3.11		1.00		1.08
P97300	20320	Nptn	0.88	0.98	1.20		1.26	1.14	0.69	1.12
Q62443	18164	Nptx1	1.03		1.45		1.54			
P08556	18176	Nras		1.39	1.39	2.05				1.23
Q810U4	319504	Nrcam	0.82	0.94	1.03	0.93	1.35	0.98	0.75	1.00
P60761	64011	Nrgn		0.92	1.10	1.27	0.91	1.22		1.08
Q8CFV4	68404	Nrn1	1.41	0.99	1.28	1.33		1.28	0.96	
Q9CS84	18189	Nrxn1	0.90			0.68		1.32		0.93
Q9R1J0	18194	Nsdhl						0.87		0.95
P46460	18195	Nsf	1.03	0.97	0.99	0.97	0.94	0.96	1.01	1.02
Q9CZ44	386649	Nsfl1c		1.25	1.20		1.37	0.77	1.25	0.84
Q9JM14	50773	Nt5c	3.81	0.98	1.04		1.20	0.95	1.16	0.96
Q3UHB1	103466	Nt5dc3	0.73		0.80	0.86		1.41	0.81	0.75
Q99PJ0	235106	Ntm	0.93	1.00	1.25	1.03	1.13	1.18	1.01	1.07
P15209	18212	Ntrk2	0.90	1.10	1.01	0.91	1.19	1.19	1.04	1.07
O35685	18221	Nudc		0.92	0.99			1.06		0.92
Q9CQF3	68219	Nudt21	1.15	1.09	1.12	0.96	0.95	1.04	0.97	1.17
Q8BJ71	71805	Nup93							1.08	
P61971	621832|10(	Nutf2	1.10	0.99	0.99	1.21	0.85	0.97	1.08	
P29758	18242	Oat							0.65	1.41
Q9CRD0	68095	Ociad1	2.49	1.24	0.91		2.19	1.11	2.11	1.03
Q9D8W7	433904	Ociad2	1.18	0.99	1.16		1.25	1.18	1.41	1.08
Q60597	18293	Ogdh	0.86	0.96	0.90	0.81	0.87	0.96	0.92	0.97
Q8VE52	70155	Ogfrl1	1.19							
Q8CGY8	108155	Ogt	1.17	1.07	1.12	1.17	0.89	1.09	1.07	1.05
Q9CZ30	67059	Ola1	0.94	0.97	1.02	0.83	1.10	1.00	0.94	1.12
P58281	74143	Opa1	1.02	1.02	1.06	1.00	1.01	1.09	0.99	1.01
Q8K010	75475	Oplah		0.97				0.79		
Q3B7Z2	76303	Osbp					1.32		0.95	
Q8BWU5	66246	Osgep	0.85						0.58	
Q62422	20409	Ostf1						1.14		
Q8BGT0	14628	Ostm1				1.71				
Q7TQI3	107260	Otub1	0.97	1.00	0.98	0.97	0.81	0.95	0.92	0.96
Q9D0K2	67041	Oxct1	0.96	0.91	0.99	1.01	0.89	0.97	0.86	0.97

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q4KMM3	170719	Oxr1	1.39	0.99	1.16	1.40	1.21	1.04	1.39	1.04
P09103	18453	P4hb	1.04	0.96	0.98	0.85	1.19		0.97	1.15
P50580	18813	Pa2g4		1.08				0.96		1.26
P29341	18458	Pabpc1	1.06	1.02	1.00	1.21	1.04	1.00	0.94	1.00
Q8K212	107975	Pacs1	1.40	1.03	1.15	1.17	1.20	1.00	1.29	1.01
Q61644	23969	Pacsin1	0.99	1.00	1.01	1.00	1.35	0.91	0.96	0.99
P63005	18472	Pafah1b1	0.94	1.00	1.02		0.89	1.07	1.05	0.91
Q9DCL9	67054	Paics	0.98	0.97	0.94	1.07	0.83	1.09	0.89	1.06
O88643	18479	Pak1	1.20	1.02	0.95	1.21	1.08	0.93	1.12	0.97
Q61036	18481	Pak3	0.90	1.05	1.10	0.86	0.89	0.59	0.96	0.95
Q9Z0P4	18483	Palm	1.95	0.89	1.17		1.29	1.16	1.45	1.19
Q9CQV1	66449	Pam16		1.39				1.13		
Q99LX0	57320	Park7	0.96	0.96	0.90	1.02	1.00	0.94	1.11	0.93
Q05920	18563	Pc	0.95	0.95	0.84	1.05	0.88	0.95	1.05	0.88
P60335	23983	Pcbp1	1.13	1.12	1.13		1.18	1.09	1.18	0.97
Q61990	18521	Pcbp2		1.04	0.90		1.07	1.12		1.06
Q91ZA3	110821	Pcca	1.09	1.06	0.90		0.78	0.95	0.86	0.94
Q99MN9	66904	Pccb	1.05	1.02	1.06				1.20	1.12
Q8BH04	74551	Pck2	1.07	1.06		1.56	1.29		1.30	0.97
Q9QYX7	26875	Pclo	1.32	1.26	1.41	1.56	1.80	1.45	1.70	1.20
P23506	18537	Pcmt1	0.91	0.92	0.96	0.94	0.94	0.95	0.94	0.92
P63054	18546	Pcp4	1.16	1.01	0.98	0.98	1.09	0.97		
Q6W8Q3	66425	Pcp4l1	1.32	1.09	0.91		1.22	0.94		1.08
Q9CQF9	66881	Pcyox1	0.87				1.15		0.90	
Q3UHX2	231887	Pdap1	1.42	1.08	1.02	1.77	1.77	0.99	1.18	1.09
Q8VE70	56426	Pdcd10	1.13				1.41		1.39	
P56812	100042424	Pdcd5	1.14	0.98	1.01		0.95	0.90		0.92
P12815	18570	Pdcd6	1.02	0.97	1.04	0.97	0.74	0.91	1.02	0.99
Q9WU78	18571	Pdcd6ip	2.19	0.93	0.85	2.56	1.14	1.05	1.17	0.97
Q8CA95	23984	Pde10a	0.90	1.03	0.87		0.90	1.04	1.04	0.96
Q61481	18573	Pde1a	1.00	0.96	1.02			0.96		1.01
Q01065	18574	Pde1b	1.19	1.04	1.03		1.38		0.99	1.28
Q922S4	207728	Pde2a	1.19	0.99	0.94		1.50	0.86	1.01	1.08
P35486	18597	Pdha1	1.04	1.04	1.02	1.03	1.03	1.06	1.17	0.97
Q9D051	68263	Pdhb	1.05	1.02	1.00	1.06	1.14	1.01	0.98	1.01
Q8BKZ9	27402	Pdhx			0.84					
P27773	14827	Pdia3	1.05	0.99	1.02	0.94	1.26	1.34	1.02	0.99
P08003	12304	Pdia4	0.88	0.95	0.96	1.22	1.58	1.12		1.01
Q922R8	71853	Pdia6						1.04	0.97	
Q8K183	216134	Pdxk	0.88	0.99	0.85	0.84		0.85	1.00	0.91
Q62048	18611	Pea15	1.06	0.96	0.93	1.16	1.05	0.82	0.80	0.91
P70296	23980	Pebp1	1.07	0.97	0.95	1.10	1.09	0.96	1.00	1.08
Q8BFY6	67898	Pef1						1.34		
Q5SUR0	237823	Pfas	1.05	1.10	1.18	1.04			1.25	
Q9CWM4	67199	Pfdn1		0.88	0.88	0.86		0.83		0.92
O70591	18637	Pfdn2		1.34	0.97					0.96

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q9WU28	56612	Pfdn5	1.00	0.82	1.24		0.95	0.91	1.42	1.11
Q03958	14976	Pfdn6		0.96	0.94	1.10		0.84		0.84
P12382	18641	Pfkl	0.90	0.92	1.03	1.08	0.89	0.98	0.68	0.99
P47857	18642	Pfkm	1.03	0.94	0.98	1.02	0.86	1.01	0.83	0.97
Q9WUA3	56421	Pfkp	0.96	1.00	1.05	0.98	0.93	1.01	0.85	1.01
P62962	18643	Pfn1	1.03	0.96	1.00	1.04	1.12	1.03	0.73	1.00
Q9JJV2	18645	Pfn2	1.01	0.88	0.91	1.02	0.81	0.99	0.63	0.90
Q9DBJ1	18648	Pgam1	0.90	0.98	0.91	0.82	1.11	0.95	0.89	0.95
Q9DCD0	110208	Pgd	0.92			0.95	0.84		1.23	
P09411	18655	Pgk1	1.01	0.98	0.97	0.95	0.96	1.01	1.06	0.97
Q9CQ60	66171	Pgls	0.91	0.93	0.99		0.89	0.93	1.12	0.98
Q9D0F9	72157	Pgm1	0.81	0.95	0.77	0.71	1.05	0.89	0.95	0.84
Q8CAA7	70974	Pgm2l1	1.03	0.96	1.02	1.12	0.87	0.92	0.87	0.98
Q8CHP8	67078	Pgp		0.94	0.94	1.06		0.84		0.93
O55022	53328	Pgrmc1	1.15	1.00	0.94	0.91	1.03	0.86		1.01
Q2M3X8	218194	Phactr1		0.97						
Q501J7	100169	Phactr4		1.03	0.93	1.30		1.06		0.98
P67778	18673	Phb	0.95	1.02	1.11	0.79	0.93	1.16	1.26	1.06
O35129	12034	Phb2	1.05	1.08	1.09	0.74	0.91	1.16	1.19	1.05
Q61753	236539	Phgdh	1.38	1.02	0.94		0.93	0.93		0.86
Q9DAK9	75454	Phpt1	1.16	0.89	0.90	0.99	1.05	0.86	0.82	0.92
Q8K0S0	105653	Phyhip	1.04	0.92	1.10			1.05	0.95	1.05
Q7M6Y3	233489	Picalm	1.25	1.11	1.18	1.09	0.66	1.29	1.07	0.94
Q6PF93	225326	Pik3c3						0.70		0.66
P26450	18708	Pik3R1			0.96					
Q9QUR7	23988	Pin1	0.95	1.15	1.02	0.93	1.08	0.97	1.08	1.08
O70172	18718	Pip4K2a	0.94	1.23		0.92	1.21	1.51	0.91	0.93
Q91XU3	117150	Pip4K2c		0.97						1.55
O70161	18717	Pip5K1c	1.26	0.99	1.42	1.31	0.98	1.18	1.01	0.81
Q8BWR2	66193	Pithd1	0.91				1.00	1.07	1.04	
P53810	18738	Pitpna	0.94	0.95	0.95	0.96	1.28	0.96	1.07	0.92
P53811	56305	Pitpnb				0.90				
O35954	18739	Pitpnm1	1.51		1.04	1.84	1.63			1.00
Q6ZPQ6	19679	Pitpnm2	7.11			1.43				
Q8K411	69617	Pitrm1	0.23							
P63248	18767	Pkia		1.02	0.83					
P52480	18746	Pkm2	0.96	0.96	0.91	0.87	0.87	0.84	1.02	0.94
Q9Z1B3	18795	Plcb1	1.60	1.02	1.06	1.46	1.89	0.87	1.29	1.09
Q62077	18803	Plcg1							1.07	
Q8K394	224860	Plcl2		1.11						
Q8BLJ3	239318	Plcxd3	0.91	0.99	0.96	1.09	0.97	0.76	1.01	0.96
Q9QXS1	18810	Plec	1.07	0.99	1.04	1.08	1.10	1.21	1.01	1.24
P60202	18823	Plp1	0.72	0.76	0.72	0.63	0.46	0.88	0.69	0.66
Q99K51	102866	Pls3	1.06	1.12	1.02	1.55	0.89	0.90	1.01	0.93
P70206	18844	Plxna1	1.20	0.94	1.17	1.19		1.11	1.26	0.90
Q80UG2	243743	Plxna4	1.28	0.98	0.96	1.05		1.20	0.94	0.98

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Gen	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
O35621	29858	Pmm1		0.95				0.78		1.05
Q9QYK9	93843	Pnck	1.63							
O35691	18949	Pnn							2.52	
P23492	667034|18	Pnp	0.93	1.15	1.04	0.96		0.90		1.30
Q6R3M4	26447	Poli			0.98					0.82
P37040	18984	Por	1.04	1.25	0.94	0.90	1.74	0.96	1.11	0.89
Q9D819	67895	Ppa1	1.06	1.02	1.11	1.25	1.04	1.03	1.07	1.04
Q91VM9	74776	Ppa2 (Includes eg:		1.00	0.95			0.92		1.07
Q99JY8	67916	Ppap2b							1.29	
Q8BSS9	327814	Ppfia2	1.42		1.34	1.54		3.23	1.29	1.19
P60469	76787	Ppfia3	1.16	1.09	1.02	1.01	1.02	1.06	1.13	1.01
P17742	268373	Ppia	0.89	0.99	0.92	0.88	0.98	0.93	0.86	0.95
P24369	19035	Ppib	0.90	0.97	1.09	0.94	0.85	0.96	0.99	1.04
Q9CR16	67738	Ppid		1.29	0.89			1.07		
Q99KR7	105675	Ppif		0.99	0.86			0.92		0.94
Q80TL0	320472	Ppm1e		1.18	0.98		2.25	1.13		1.08
Q3UYC0	319468	Ppm1h				1.35			0.93	
Q8BVQ5	72590	Ppme1	1.15	1.05	1.37		1.10		0.85	1.09
P62137	19045	Ppp1ca	1.22	0.99	1.16	1.37	1.05	0.99	1.17	1.12
P63087	19047	Ppp1cc	0.99	1.01	1.02	1.02		0.91	1.21	1.06
Q9DBR7	17931	Ppp1R12a				2.03		0.96		
Q91VC7	68458	Ppp1R14a		0.78	0.75			0.82		0.66
Q9ERT9	58200	Ppp1R1a (Includes eg:5502			1.10			1.01		
Q60829	19049	Ppp1R1b		0.83			1.13	1.01		0.96
Q9DCL8	66849	Ppp1R2		0.88	0.91	1.45		0.79		0.96
Q3TDD9	73825	Ppp1R21								1.06
Q3UM45	66385	Ppp1R7	1.05	1.22	1.18	1.09	0.94	1.06	1.07	0.86
Q6R891	217124	Ppp1R9b	0.89	0.91	0.98	1.44	1.29	0.99	1.20	0.99
P62715	19053	Ppp2cb		1.10			1.18	1.03	1.11	
Q76MZ3	51792	Ppp2r1a	1.16	0.96	1.01	1.04	0.97	0.97	1.03	1.04
Q6P1F6	71978	Ppp2R2a	0.83		0.95	1.15	0.83		0.89	1.03
P58389	110854	Ppp2R4	1.07	1.03	0.86	1.12		0.88	1.05	1.04
Q60996	26931	Ppp2R5c	1.38	0.94	1.07			1.30		1.17
Q61151	26932	Ppp2r5e	0.96			0.97	0.73		1.05	
P63328	19055	Ppp3ca	1.12	0.70	1.17	1.12	0.98	1.09	0.95	0.73
P48453	19056	Ppp3cb	1.15		1.14				1.24	1.32
Q63810	19058	Ppp3R1	1.09	0.99	1.11	1.20	0.98	1.05	0.85	1.04
Q60676	19060	Ppp5c	1.12		0.86				0.95	
Q9CQR6	67857	Ppp6c			1.05		1.03	1.01	1.12	0.97
Q8R3Q2	71474	Ppp6R2		0.89	1.14			1.07		1.00
Q922D4	52036	Ppp6R3				1.27				
P35700	18477	Prdx1	0.89	0.96	0.93	0.90	0.89	1.01	0.92	0.95
Q61171	21672	Prdx2	0.89	0.93	1.01	0.92	0.90	0.93	0.89	0.92
P20108	11757	Prdx3	0.86	1.14	0.96		1.37	1.02	0.94	0.98
P99029	54683	Prdx5	0.88	1.02	0.87	0.85	1.05	0.99	1.01	0.95
O08709	11758	Prdx6	0.99	1.05	1.14	1.10	1.11	1.14	1.01	1.13

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q9QUR6	19072	Prep	0.96	0.85	1.01		1.44	1.30		0.99
Q69ZK0	277360	Prex1		1.02	0.94	1.14		0.94		1.12
Q5EG47	105787	Prkaa1						0.96		
P05132	18747	Prkaca	0.96	0.99	1.00	0.96	0.84	0.99	0.98	0.99
P68181	18749	Prkacb	0.93	1.10	1.04	0.93	0.85	1.01	0.86	1.01
Q9DBC7	19084	Prkar1a			1.33	0.98	0.87	1.03	1.31	
P12367	19087	Prkar2a	1.40	1.13			1.15	0.81		
P31324	19088	Prkar2b	1.17	1.01	1.01	1.47	1.19	0.92	1.08	0.98
P20444	18750	Prkca		1.17	1.51	1.08		1.73		1.25
P68404	18751	Prkcb	1.38	1.13	1.37	1.19	0.78	1.32	1.25	1.08
P28867	18753	Prkcd		1.04	1.05		0.87	1.56		1.04
P16054	18754	Prkce	1.04	1.01	1.21	1.12	0.98	0.94	0.82	0.99
P63318	18752	Prkcg	1.17	0.96	1.22	0.95	0.81	1.13	0.84	0.99
O08795	19089	Prkcsh	0.94	0.97	0.97			0.88		0.94
Q9WTX2	23992	Prkra	0.87	1.21						
A2AHG0	241638	Prosapip1								1.31
Q9Z2Y8	114863	Prosc	1.13	0.96	0.93	0.86	1.34	0.93	1.01	0.91
Q99KP6	28000	Prpf19	0.96	1.17	0.96		1.04		1.19	1.43
Q99PV0	192159	Prpf8				1.02		1.16		
Q9D7G0	19139	Prps1		0.95	0.90			0.86		0.99
Q8R574	212627	Prpsap2	0.90	1.23	0.89		0.61	0.88		1.62
Q8BIW1	229589	Prune				1.30			1.14	
Q61207	19156	Psap		1.00	0.99	0.99		1.06		1.01
Q99K85	107272	Psat1	1.10	1.03	0.94	0.88	1.43	1.23	1.40	1.06
Q2PFD7	234353	Psd3	0.74	0.87	0.82	0.91	1.25	0.65	0.99	1.04
Q99JF8	101739	Psip1			0.88			0.81		
Q9R1P4	26440	Psma1	0.84	0.99	0.98	0.91	1.45	0.93	0.90	1.01
P49722	19166	Psma2	0.95	0.99	0.99	0.96	1.14	0.98	0.89	1.05
O70435	19167	Psma3	1.03	0.96	0.92	0.83	1.47	0.97	0.85	0.95
Q9R1P0	26441	Psma4			0.97	0.91		0.89	1.06	0.99
Q9Z2U1	26442	Psma5	0.95	1.05	1.05	0.98	1.13	0.99	1.00	0.99
Q9QUM9	26443	Psma6	1.09	1.13	1.01	0.85	1.17	1.00	0.85	0.98
Q9Z2U0	26444	Psma7	0.87	0.95	0.95	0.87	1.23	0.97	0.81	0.98
Q9CWH6	73677	Psma8		1.00	1.00			0.98		1.01
O09061	19170	Psmb1	0.98	1.08	1.14	0.94	1.15	0.97	0.89	0.96
Q9R1P3	26445	Psmb2	1.12	1.06	0.93	0.93	1.28	0.96	1.19	0.95
Q9R1P1	26446	Psmb3	0.93	0.95	0.97	0.98	1.16	0.97	0.82	0.98
P99026	19172	Psmb4	0.97	1.06	0.92	0.92	1.20	1.05	0.85	0.95
O55234	19173	Psmb5	0.89	1.01	1.00	0.94	1.20	1.05	0.87	0.92
Q60692	19175	Psmb6	0.91					0.94	0.86	0.93
P70195	19177	Psmb7	0.83	0.98	0.90		1.37	1.04	0.83	0.90
P62192	19179	Psmc1			2.29	1.16			0.97	1.63
O88685	19182	Psmc3	1.45				0.95		1.17	
P62196	19184	Psmc5	1.02		1.25		0.83	1.14		1.32
Q3TXS7	70247	Psmd1	1.06	1.12		0.99	0.83		0.94	0.97
Q8BG32	69077	Psmd11	0.93	1.00	1.02	0.82	1.03	1.15	0.98	1.13

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q9D8W5	66997	Psmd12				1.23				
Q9WVJ2	23997	Psmd13	1.26	1.01	0.96			0.97		0.90
O35593	59029	Psmd14	1.17	1.03	0.96	1.05		0.99	1.19	
Q8VDM4	21762	Psmd2	1.06	0.99	1.03	0.98	0.98	0.97	0.89	1.05
P14685	22123	Psmd3								0.15
O35226	19185	Psmd4						1.08		1.01
P26516	17463	Psmd7	1.39	1.09	1.07		0.97	0.92	1.37	1.14
Q9CX56	57296	Psmd8	1.30		1.52			0.92	1.19	0.90
Q9CR00	67151	Psmd9				0.83				
P97371	19186	Psme1		1.04	1.06	1.44		1.02	1.35	0.98
P97372	19188	Psme2	0.99						1.01	
Q8R326	66645	Pspc1	1.11	1.44	1.06		1.13	1.00		1.09
Q99LS3	100678	Psph						1.17		
Q91Z31	56195	Ptbp2	1.25							
O09114	19215	Ptgds	0.98		1.29			0.90	0.75	0.97
Q8VDQ1	77219	Ptgr2	0.94	0.86	0.91	1.09		0.95	1.23	0.87
P34152	14083	Ptk2 (Includes eg:1		1.13	1.40			1.28		
Q9QVP9	19229	Ptk2b (Incl	1.43	1.11	1.26	1.29	1.30	0.97	1.04	1.02
P26350	19231	Ptma	0.84	1.03	0.98		1.17	0.92	1.01	0.92
Q9D0J8	69202	Ptms	0.96	0.98	1.08	1.08	1.13	1.13	0.95	1.08
Q63739	19243	Ptp4a1		2.19	1.54	1.16		0.91		0.99
O70274	19244	Ptp4a2	0.86							0.72
Q8K2C9	57874	Ptplad1	0.92	1.01		0.78		0.82	1.17	3.07
Q66GT5	66461	Ptpmt1	0.93							
P35235	19247	Ptpn11		1.02	0.90		0.94			1.19
P54830	19259	Ptpn5			0.94					
O35239	56294	Ptpn9						1.14		
B0V2N1	19280	Ptprs	0.96	1.14	1.30		1.07	1.07		1.03
Q8R2Y8	217057	Ptrh2	1.01	0.83	0.85		1.39	1.16		0.98
P42669	19290	Pura	1.14	0.92	0.99	1.07	0.80	1.04	0.95	0.96
O35295	19291	Purb	1.21	1.05	1.09		0.97	1.02	0.89	1.06
P32848	19293	Pvalb	0.74	0.71	0.77	0.65	0.81	0.99	0.84	0.75
Q922Q4	69051	Pycr2	1.15	1.00	1.13	1.18	0.78	0.88		1.00
Q9DCC4	66194	Pycrl						1.41		
Q8CI94	110078	Pygb	0.91	0.96	0.89	0.93	0.86	0.97	0.92	0.93
Q9WUB3	19309	Pygm	0.87	0.88	0.66	0.81	0.73	0.97	1.13	0.77
Q8BVI4	110391	Qdpr	0.80	0.86	0.84	0.65	0.76	0.82	0.76	0.70
P61027	19325	Rab10	0.98	0.99	1.01	0.95	0.94	1.17		1.13
P46638	19326	Rab11b	1.00	1.00	1.05	1.04	1.09	0.98	0.96	1.00
Q8R361	52055	Rab11fip5			0.90			1.57		0.93
P35283	19328	Rab12		1.00	0.97					1.12
Q91V41	68365	Rab14	1.12	1.04	1.05	1.09	1.17	1.04	1.07	1.04
P35293	19330	Rab18	1.10	1.00	0.99	1.05	1.23	0.97	1.12	0.99
P62821	19324	Rab1a (Inc	0.97	1.01	1.01	1.05	1.04	1.03	0.99	1.00
Q9D1G1	76308	Rab1b	1.05	0.98	1.03	1.02	1.05	1.05	0.86	1.02
P35282	216344	Rab21		1.28	0.97			0.95	1.14	1.05

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
P35285	19334	Rab22a	0.96		0.83		1.30	1.39	1.34	
P35288	19335	Rab23	0.79			1.01	1.20		1.21	
P35290	19336	Rab24	1.67	0.93	1.08	1.10	1.36	1.24	1.85	0.86
Q99P58	80718	Rab27b						1.14		
P53994	59021	Rab2a	1.06	1.00	0.92	1.16	1.11	0.96	0.96	0.99
Q6PHN9	77407	Rab35	0.94	1.11	1.15	1.01	0.99	1.14	0.81	1.08
Q8BHD0	270160	Rab39a	0.90	1.00	1.08	0.94	0.98	1.00	0.77	1.14
Q8BHC1	67790	Rab39b		2.15	2.27	1.27		1.05		1.64
P63011	19339	Rab3a	0.94	0.96	1.06	1.02	1.14	0.97	0.88	0.98
Q9CZT8	69908	Rab3b	1.00	0.97	1.24	1.10	1.04	0.84	1.06	0.98
P62823	67295	Rab3c (Inc	0.99	1.07	1.20	1.08	1.09	1.11	1.05	0.99
P35276	19340	Rab3d	0.93	0.94	0.95	0.89	1.05	0.89	0.84	0.91
Q80UJ7	226407	Rab3gap1	1.18	0.93	0.87	0.92	0.91	2.11	1.24	0.98
Q8BMG7	98732	Rab3gap2	1.28			0.79	0.77		1.15	0.84
Q9CQD1	271457	Rab5a	1.06	0.99	1.04	1.07	1.00	1.04	1.05	0.95
P61021	19344	Rab5b	0.99	1.03	1.00	0.94	0.91	1.02	0.99	0.95
P35278	19345	Rab5c	0.92	1.06	1.05	1.03	1.03	1.05	0.98	1.12
P35279	19346	Rab6a	0.86	1.39	0.85		0.92	1.09	1.02	0.95
P61294	270192	Rab6b	1.06	1.02	0.98	1.07	0.90	0.99	0.92	0.99
P51150	19349	Rab7a	1.04	1.07	1.05	1.02	1.14	1.09	0.94	0.99
P55258	17274	Rab8a		1.29	0.94	0.90	0.84	1.21	0.87	1.08
O35551	54189	Rabep1		0.96				1.29		
A2AWA9	227800	Rabgap1	1.58			1.48	1.36		1.74	
P63001	19353	Rac1	0.85	0.98	1.04	0.85	0.91	0.99	0.86	0.97
P60764	170758	Rac3	0.91			1.30	1.23			
P54728	19359	Rad23b			1.20					
P63321	56044	Rala	1.09	0.94	1.04	0.93	1.02	0.92	0.99	0.87
Q8BQZ4	228850	Ralgapb			1.07					
Q64012	19383	Raly		1.14	0.94					1.10
P62827	19384	Ran	0.91	1.03	1.01	0.83	1.05	1.07	0.96	1.01
P34022	19385	Ranbp1	0.55	1.03	0.91	4.32	4.23	1.03	3.59	0.96
Q9CT10	71810	Ranbp3	0.86	1.06	0.90		1.05	1.30	1.05	0.97
P62835	109905	Rap1a		0.78	0.88		1.11			
Q99JI6	215449	Rap1b	0.94	0.91	0.97	0.96	1.01	0.95	0.92	0.90
Q5SVL6	380711	Rap1gap2	1.10	0.94	0.97		1.04	1.06	1.01	1.13
Q80ZJ1	76108	Rap2a	1.17	0.98	1.14	1.21	0.95	1.06	1.19	1.04
P61226	74012	Rap2b	0.98	1.01	1.04	1.08	1.15	1.02	1.03	1.02
Q8CHG7	76089	Rapgef2	1.36	1.09	1.29	0.95	0.87	1.22	1.21	1.04
Q9EQZ6	56508	Rapgef4	1.37	1.16		1.00		1.16		
Q9D0I9	104458	Rars					0.95			
Q9Z268	19415	Rasal1	1.15	1.14	1.23	1.01	1.09	1.08	0.89	1.05
Q9QUG9	19395	Rasgrp2						1.00		
O88851	26450	Rbbp9	1.05	0.88	0.91		1.03	1.01		0.80
Q8VH51	170791	Rbm39						1.11		
Q9CWZ3	60365	Rbm8a		1.12						
O35479	19656	Rbmxl1		1.53	1.32			1.05		1.27

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
P62878	56438	Rbx1	1.08	0.95	0.98	1.12	0.82	0.92		0.89
Q8BP92	26611	Rcn2 (Inclu	1.11							
P26043	19684	Rdx	1.03	1.03	0.85		1.60	1.00	1.20	1.10
Q60870	13476	Reep5		0.88	0.88	0.85	1.47	0.65		1.02
Q9CQE5	67865	Rgs10	1.51	1.02	1.11	1.17	1.50	0.75	1.29	0.85
Q9Z2H2	50779	Rgs6				0.93			1.04	
O54829	24012	Rgs7	1.07	1.05	1.20	1.09	1.07	0.86	0.99	1.09
Q921J2	19744	Rheb (Mou	1.00	1.06	1.06	1.03	1.26	0.82		0.96
Q9QUI0	11848	Rhoa	0.99	0.94	0.95	1.22	1.06	1.03	1.13	0.87
P84096	56212	Rhog	0.74	0.85	0.77	0.79	0.56	0.73	0.88	0.63
Q8BG51	59040	Rhot1	1.13	1.12	0.94			1.16		1.14
Q921Q7	225870	Rin1	1.33	0.98	1.17		1.00		1.15	1.18
Q8BZ36	72772	Rint1	0.05							
Q8VCT3	215615	Rnpep	1.25	1.01	1.03	1.20	0.96	1.09	1.09	1.06
P70336	19878	Rock2	1.07	0.95	0.95	1.02	1.08	1.00	0.95	0.98
Q3TDK6	66049	Rogdi	1.30			1.14	1.05	0.91	1.62	1.27
P47708	19894	Rph3a	3.07	0.91	1.11	0.26	3.21	1.04	3.50	1.06
Q6ZWV3	110954	Rpl10	1.24	0.99	1.04		0.93	1.19	1.07	1.03
P53026	19896	Rpl10a	1.18	1.02	0.99	1.24	1.00	1.03	1.09	0.95
Q9CXW4	67025	Rpl11	1.16	1.04	1.04	1.09	0.88	1.04	1.05	1.02
P35979	269261	Rpl12		0.97	1.00	1.02		1.08		1.03
P19253	22121	Rpl13a		1.04	1.10	0.88		1.13		1.07
Q9CR57	67115	Rpl14		1.03	1.12	1.13		1.23		1.16
Q9CZM2	66480	Rpl15	1.02	0.98	1.00	1.58	0.89	0.99	0.97	0.97
Q9CPR4	319195	Rpl17	1.00	1.19	1.08	0.78	0.87	1.17	1.11	1.03
P35980	19899	Rpl18	1.05	1.06	1.00	0.99	0.84	1.14	1.10	1.03
P62717	76808	Rpl18a		1.13	1.14	1.15		1.17		1.07
P84099	19921	Rpl19		0.94	0.80			0.91		0.91
O09167	19933	Rpl21 (Incl	1.25	1.01	0.93	1.03	0.82	1.25	0.91	0.96
P67984	19934	Rpl22		1.05	1.01			0.95		1.05
Q9D7S7	68028	Rpl22l1				1.00		0.87		0.99
P62830	65019	Rpl23		1.01	0.88	1.22	0.81	1.10		1.01
P62751	100043755	Rpl23a	1.47	0.97	0.95	1.25	1.67	1.03	1.38	0.95
Q8BP67	68193	Rpl24	1.18	1.15	1.00	1.21	0.66	0.89		0.95
P61255	19941	Rpl26	0.97	1.16	0.95	0.98		1.24	0.89	1.10
P61358	19942	Rpl27	0.94		1.27	1.24	1.16	0.94	1.01	0.93
P14115	26451	Rpl27a	1.16		0.78	0.85		0.90	1.11	0.96
P41105	19943	Rpl28	0.99	1.05	1.45		0.81	1.14	1.14	1.05
P47915	383770|66	Rpl29 (Includes Ot		1.15	0.99			1.06	1.40	1.12
P62889	19946|666	Rpl30		0.96	1.12	1.28	1.19	1.07	0.78	0.99
P62900	114641|10	Rpl31	0.96	0.99	0.97	1.07	0.90	0.98	1.12	1.00
P62911	19951	Rpl32	0.97	0.94	0.90			1.16		0.97
Q9D1R9	100043876	Rpl34			1.07	1.14	0.79	1.00		0.99
Q6ZWV7	66489	Rpl35	1.14	0.95	1.13	1.02	1.18	1.03	1.00	1.05
P47964	54217	Rpl36		1.02		1.31	1.12	1.08	0.97	
Q9JJI8	67671	Rpl38	1.01	0.96	1.05	1.02	0.97	1.01	1.00	1.17

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ge	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q9D8E6	67891	Rpl4		1.35	1.03			1.10		1.10
P47962	1.01E+08	Rpl5	0.98			0.86	1.04	0.94	0.99	1.11
P47911	432502|19	Rpl6	1.20	0.99	1.13			1.21		1.11
P14148	19989	Rpl7	1.16	1.01	0.99	1.00	0.80	1.08	1.04	1.06
P12970	27176	Rpl7a	1.18	0.99	0.98	1.06	1.11	1.04	1.04	1.03
P62918	26961	Rpl8	1.24	1.13	1.07	1.08	1.34	1.14	0.98	1.19
P51410	20005	Rpl9	1.00	1.05		1.05	0.77	1.17	0.99	0.89
P14869	11837	Rplp0	1.47	0.97	0.98	1.46	1.59	1.00	1.44	1.03
P47955	56040	Rplp1	3.42	1.01	0.96		2.13	0.96	0.48	0.99
P99027	67186	Rplp2	1.84	1.07	1.00	1.83	1.78	1.04		1.06
Q91YQ5	103963	Rpn1		0.93	1.07		1.04	1.20	0.98	1.01
P63325	67097	Rps10	1.05	1.06	0.95	0.97	1.17	1.06	1.21	1.06
P62281	27207	Rps11	1.08	0.94	0.92	1.05	0.71	1.03		0.98
P63323	20042	Rps12	1.00	0.91	1.20		0.87	1.05	0.85	1.00
P62301	68052	Rps13	1.07	1.08	1.06	0.84	1.00	0.98	1.08	1.02
P62264	20044	Rps14	1.30	1.44	0.93	1.10	1.00	0.95	1.30	
P62843	20054	Rps15	0.97	1.01	1.04			0.95	1.01	1.14
P62245	267019	Rps15a	1.07	0.97	0.99	1.11	0.93	1.02	0.92	1.02
P14131	20055	Rps16	0.87	1.12	0.95	1.05	0.79	1.00	1.02	1.04
P63276	20068	Rps17	1.11	0.99	0.95	1.15	0.92	0.99	1.09	1.01
P62270	20084	Rps18	1.15	0.98	1.04	0.99	0.83	0.98	0.92	1.09
Q9CZX8	20085	Rps19	0.94	0.99	0.96	1.04	1.00	0.93	0.91	1.05
P25444	16898	Rps2	1.02	1.12	0.97	0.95	0.93	1.08	0.88	0.97
P60867	67427	Rps20	1.34	1.03	0.94	1.01	0.85	0.97	0.88	1.07
Q9CQR2	66481	Rps21			0.97			1.08		
P62267	66475	Rps23	1.08	1.01	1.04	1.09	1.00	1.12	0.81	1.06
P62849	20088	Rps24	0.95	0.99	0.97	1.13	0.82	0.95	0.96	1.04
P62852	75617	Rps25	1.00	1.08	1.35	1.01		1.42	0.84	1.01
P62855	27370	Rps26	1.19	1.10	1.42	1.53	1.04	1.21	1.19	1.30
Q6ZWU9	57294|100	Rps27	1.47	1.06	1.14	1.08		1.04	0.88	0.99
P62983	78294	Rps27a	0.99	1.07	0.95	0.98	1.12	1.04	1.09	1.13
P62858	54127	Rps28					1.01			
P62274	20090	Rps29		1.05	1.05		0.84	0.96		
P62908	27050	Rps3	1.00	0.95	1.06	1.05	0.93	1.03	1.00	1.09
P97351	20091	Rps3a	1.21	1.03	1.00	1.06	1.24	0.95	0.97	0.95
P62702	20102	Rps4x	1.26	1.04	0.98	1.09	1.02	1.13	1.11	1.01
P97461	20103	Rps5	1.31				1.39		1.19	
P62754	20104|667	Rps6	0.82	1.13	1.18	1.22	1.19	0.85	1.05	0.99
P62082	20115	Rps7	1.06	1.07	1.14	1.14	0.87	1.13	1.10	1.04
P62242	20116|100	Rps8	1.04	1.31	1.11	1.05	0.83	1.15	0.91	1.09
Q6ZWN5	76846	Rps9	1.01	1.08	0.99	1.04	0.89	1.14	1.05	0.95
P14206	16785	Rpsa	1.07	1.07	1.03	0.88	1.00	1.06	0.93	1.04
P62071	66922	Rras2			1.08					
Q8K0T0	104001	Rtn1	2.00	0.95	1.00	2.15	1.78	0.96	1.93	0.95
Q9ES97	20168	Rtn3	1.35	1.03	1.06	1.30	1.19	1.00	1.36	1.02
Q99P72	68585	Rtn4 (Inclu	1.72	1.16	1.09	1.09	1.02	1.10	1.92	1.09

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q9D394	52822	Rufy3	1.01	0.93	0.86		0.98	0.84	1.30	0.96
P56565	20193	S100a1		0.94	0.96			0.90	0.80	1.12
P97352	20196	S100a13		0.93	1.05			0.90		
P63084	20199	S100a5		29.35						
Q9JLC8	50720	Sacs		0.92				0.68		
Q9R1T2	56459	Sae1						0.96		
P36536	20224	Sar1a	1.07	1.11	1.08	0.83	1.15	1.09	1.06	1.07
Q9CQC9	66397	Sar1b	0.92	1.07	1.21		1.06	0.89	1.19	0.98
Q9D1J3	66118	Sarnp				1.15				
P26638	20226	Sars	1.07	1.06	0.97	1.04	1.20	1.06	1.00	1.01
Q6ZPE2	77980	Sbf1	1.18	1.12	1.10	1.09		1.36	1.07	1.05
Q8K021	107767	Scamp1	1.16	0.87	1.07	1.13	1.15	1.13	1.10	1.07
Q9JKD3	56807	Scamp5		1.02	1.12	1.03	1.13	0.90	0.94	1.09
Q8R127	109232	Sccpdh							1.33	
Q8BRF7	76983	Scfd1	1.39			1.57	0.69			
Q03517	20254	Scg2		1.05	0.59			0.65		0.66
Q56A07	72821	Scn2b	1.20	1.14	1.21		1.13	1.12	0.85	1.13
Q9WTU3	20273	Scn8a	1.24	0.96	1.12	0.73	0.89	1.04		0.92
Q62205	20274	Scn9a	1.04	0.98	1.43	1.04	1.00	1.33	1.30	1.05
Q78YZ6	56367	Scoc		0.88	0.94			0.91		0.88
P32020	20280	Scp2	1.24	1.04	0.95	1.08	1.01	0.92		0.99
Q9CZC8	69938	Scrn1	1.01	0.93		0.92	0.90	0.82	1.14	0.77
Q8CFE4	213326	Scyl2								1.00
Q8K2B3	66945	Sdha (Inclu	1.15	1.04	0.95	1.04	1.18	1.03	1.03	0.99
Q9CQA3	67680	Sdhb	1.07	1.06	0.97	1.01	1.06	0.97	1.12	0.95
Q9CZB0	66052	Sdhc	1.46	0.82		0.86	0.90	1.10	1.04	
Q63918	20324	Sdpr						0.92		
O08547	20333	Sec22b	1.84	1.17	1.20	1.20	1.41	1.11	1.41	1.15
Q01405	20334	Sec23a	0.97	1.12			1.26	0.87		
Q3UPL0	69162	Sec31a	1.29	0.99	1.10	1.40	1.16	1.17	2.02	0.91
Q9CQS8	66212	Sec61b		1.05	1.00			1.03		
Q8C650	103080	Sept10						1.13		
Q8C1B7	52398	Sept11	0.94	0.89	1.00	1.18	1.11	1.03	0.91	0.98
Q9Z1S5	24050	Sept3	0.97	0.97	0.96	1.09	0.88	1.03	0.94	0.98
P28661	18952	Sept4	1.17						1.18	0.84
Q9Z2Q6	18951	Sept5	1.10	1.01	1.01	1.09	0.98	1.00	0.97	0.96
Q9R1T4	56526	Sept6	1.00	1.01	1.10	1.02	1.16	1.10	0.97	1.08
O55131	235072	Sept7	1.06	0.95	1.02	1.07	1.00	1.00	0.88	0.96
Q8CHH9	20362	Sept8	1.15	0.98	1.01	1.53	0.84	1.04	1.09	1.00
Q80UG5	53860	Sept9	1.47	1.21	1.25	1.45	0.96	1.08	1.20	1.34
P63300	20364	Sepw1						1.21		
Q9CY58	66870	Serbp1	1.28	0.97	0.90	2.86	1.41		1.64	1.15
P07758	20703|207	Serpina1	0.77		1.71	0.58			0.18	
Q8BYY9	238395|27	Serpina3a								1.01
Q60854	20719	Serpinb6				1.01			0.91	
Q9EQU5	56086	Set	0.98	1.09	1.08		4.12	1.13	1.08	1.08

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q6P1D5	56747	Sez6l	1.15	0.84				0.97	1.04	1.05
Q8K4Z5	67465	Sf3a1					1.42		1.98	
Q99NB9	81898	Sf3b1	1.20			1.20	1.32	1.09	1.26	
P59708	66055	Sf3b14						1.22		
Q923D4	66125	Sf3b5					0.79	1.09		
O70456	55948	Sfn	0.89	1.01	0.96	0.93	0.83	1.01	0.74	0.94
Q8VIJ6	71514	Sfpq	1.06	1.04	1.01	1.15	1.03	1.03	1.05	0.99
Q99JR1	14057	Sfxn1	1.45	0.93		0.88	0.86	1.05	1.23	0.93
Q91V61	94280	Sfxn3	1.17	1.12	1.32	1.07	1.22	1.40	1.06	1.26
Q925N0	94282	Sfxn5	0.99	0.93	0.90	0.96	0.83	1.16	1.30	1.12
Q8VD37	73094	Sgip1	1.18	0.86	0.95	1.13	1.08	0.86	1.26	1.00
Q8BPQ7	52850	Sgsm1		1.06	0.96	1.60	1.12			0.87
Q8BJU0	52551	Sgta		1.16	1.04			0.95		0.99
Q8VD33	218544	Sgtb	1.52	1.02	1.05			1.00	0.90	
Q9JJU8	56726	Sh3bgrl	1.05	0.91	0.98	1.03	1.12	0.84		0.92
Q8BG73	212531	Sh3bgrl2	0.78	1.04	1.70	1.28	0.83		0.86	
Q91VW3	73723	Sh3bgrl3	0.69	0.92	1.03		0.47	0.84	0.80	1.16
Q62420	20404	Sh3gl2	1.13	1.12	1.25	1.16	1.13	1.12	1.06	1.10
Q8R3V5	227700	Sh3glb2		1.08	1.33					1.06
Q6P4S6	70661	Sik3		0.95					1.61	
P97797	19261	Sirpa	1.74	0.98	1.27	1.24	2.22	1.11	1.17	1.10
Q8VDQ8	64383	Sirt2	0.97	0.81	0.81	0.91	0.86	0.88	1.01	0.73
Q9WTX5	21402	Skp1/Skp1	1.06	1.03	1.01	0.99	1.11	0.96	1.05	1.04
P55012	20496	Slc12a2		1.47				1.31		
Q91V14	57138	Slc12a5	1.10	1.07	1.17	0.88	1.01	1.10	0.95	0.96
P53986	20501	Slc16a1				0.63				
Q3TXX4	72961	Slc17a7	1.11	0.97	1.21	1.32	1.05	1.00	1.31	0.99
P43006	20511	Slc1a2	0.83	0.92	1.06	0.65	0.77	1.00	0.87	0.94
P56564	20512	Slc1a3	1.04	0.86	0.94	1.03	0.90		0.81	1.02
Q9CR62	67863	Slc25a11	1.05	0.97	0.98	0.88	0.92	1.09	1.08	0.94
Q8BH59	78830	Slc25a12	0.94	0.97	0.94	0.86	0.84	1.07	1.00	0.94
Q9QXX4	50799	Slc25a13	1.06	0.89	0.97	0.97	0.92	0.73	0.92	0.98
Q9DB41	71803	Slc25a18					0.49			
Q9D6M3	68267	Slc25a22	1.14	1.07	1.23	1.13	0.97	1.18	0.98	1.12
Q6GQS1	66972	Slc25a23			1.21					0.05
Q8VEM8	18674	Slc25a3	0.99	0.93	0.96	1.05	1.03	0.98	1.28	0.92
Q3V132	73333	Slc25a31		0.89	0.94			0.91		0.89
P48962	11739	Slc25a4	0.97	0.91	0.96	0.93	0.86	0.93	1.21	0.94
P51881	11740	Slc25a6	1.04	0.94	0.98	1.02	0.98	0.97	1.44	0.95
P17809	20525	Slc2a1	1.17			0.65	0.84			
P32037	20527	Slc2a3	0.73	1.05	0.92	1.12	0.81	0.94	1.09	0.96
O35633	22348	Slc32a1	1.03	1.31	0.78	0.75		0.48	1.42	0.90
P10852	17254	Slc3a2	1.15	1.11	0.98	0.97	1.28	1.23	1.19	1.24
Q5DTL9	94229	Slc4a10	1.21	1.02	1.26	1.08	1.13	1.25	1.13	1.03
O88343	54403	Slc4a4	0.92	1.02	0.82	0.70	0.88	1.10	1.46	0.96
P31648	232333	Slc6a1	0.93	0.95	0.94	0.74	0.87	1.00	1.16	0.91

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
P31650	243616	Slc6a11	0.68	0.94	0.56		0.55	0.70	1.68	0.71
P70414	20541	Slc8a1	0.84		0.97	0.84	0.88	1.07	0.83	0.95
P70441	26941	Slc9a3R1	2.03	1.15	1.12	1.73		1.09	2.03	1.00
O54988	20874	Slk	1.33	1.00	0.89	1.34	1.10	0.93	1.20	0.91
Q3TKT4	20586	Smarca4			0.86					
Q9CU62	24061	Smc1a							0.80	
P60879	20614	Snap25	1.21	1.09	1.20	1.28	1.38	1.37	1.16	1.16
Q8R570	67826	Snap47	1.16				0.61	1.03	0.86	0.93
Q61548	20616	Snap91	1.47	1.02	1.03	1.48	1.21	0.94	1.39	0.99
O55042	20617	Snca	0.41	0.37	0.49	0.61	0.47	0.44	0.10	0.32
Q91ZZ3	104069	Sncb	1.09	1.19	1.10	1.16	1.03	1.09	1.02	1.20
Q9Z0F7	20618	Sncg	0.75	1.01	0.65	0.71	0.81	1.15	1.08	0.66
Q78PY7	56463	Snd1	0.95	0.98	0.93	0.92	1.31	1.06	0.97	1.03
P62315	20641	Snrpd1	1.03			0.86				
P62317	107686	Snrpd2	1.02	1.04	0.89	1.19	0.95	1.00	0.87	1.04
P62305	20643	Snrpe						1.15	1.06	
Q9WV80	56440	Snx1		1.08	0.93		0.96	1.14		1.06
O70493	55988	Snx12	0.96	1.02	1.07	1.03	1.22	1.01	1.06	1.03
Q9CWK8	67804	Snx2	1.16	1.22	1.05		0.63	0.99		1.24
O70492	54198	Snx3		0.95	0.91	0.81		0.95		
P08228	20655	Sod1	0.74	0.91	0.84	0.81	0.99	0.83	0.84	0.90
P09671	20656	Sod2	0.97	1.16	1.00	0.98	1.12	1.08	1.09	1.03
Q6NZL0	67412	Soga3				1.26	1.44	1.20	1.48	
Q64442	20322	Sord	0.86	0.91	0.83		1.17	1.01	0.86	0.91
Q62245	20662	Sos1							1.05	
P70663	13602	Sparcl1	1.51	0.97	0.89	1.37	1.70	1.02	1.28	0.82
Q3UMC0	57815	Spata5		0.88				1.01		
Q64105	20751	Spr	0.78	0.92	0.89	0.68	1.08	0.90	0.88	
P16546	20740	Sptan1	0.97	0.96	1.03	0.96	1.07	1.01	0.97	1.04
P15508	20741	Sptb	1.23			0.86	1.04	1.74	0.56	0.89
Q62261	20742	Sptbn1	1.00	0.96	0.99	1.04	0.96	0.97	1.04	1.04
Q9QWI6	56013	Srcin1	1.68	1.18	1.14	1.35	1.14	1.19	1.33	1.22
Q812A2	259302	Srgap3	1.10	1.03	0.96	1.49	0.87	0.78	1.06	0.98
Q6P069	109552	Sri		0.93	0.89	1.12		0.90		0.96
Q8BMA6	217337	Srp68 (Incl	1.07	0.95	0.84		0.90	0.94	1.48	0.91
Q9QZX7	27364	Srr	1.08	1.03	1.26	1.23		1.01	0.84	1.04
Q6PDM2	110809	Srsf1					1.43		1.18	
Q62093	20382	Srsf2	1.03	1.09	1.10	0.95		1.10	0.91	1.11
P32067	20823	Ssb			1.29		1.04	1.04	1.19	1.15
Q9CYR0	381760	Ssbp1	1.10	1.03	0.87	1.20	1.48	1.05	1.16	0.99
Q62186	20832	Ssr4								1.08
P60041	20604	Sst		0.71	0.87			0.68		1.23
Q99L47	70356	St13	0.96	0.99	0.95		1.47	0.98		0.94
P70297	20844	Stam	1.46	1.31	1.31		0.91	1.08		1.29
Q60864	20867	Stip1	0.93	0.97	0.96	0.92	0.96	0.91	0.93	0.95
Q9Z2W1	59041	Stk25	1.11				1.10			

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q8QZV4	57740	Stk32c			0.97					
Q9Z1W9	53416	Stk39			0.87	2.37		1.02		1.07
P54227	16765	Stmn1	0.86	0.90	0.92	0.88	0.91	0.83	0.83	0.96
P55821	20257	Stmn2		0.79	1.00			0.79		1.01
Q9ER00	100226	Stx12	1.23	1.05	1.23	0.91	1.31	1.17	1.22	1.09
O35526	20907	Stx1a	1.15	1.01	1.18	1.07	1.79	1.07	0.92	1.12
P61264	56216	Stx1b	0.92	0.86	0.90	0.89	1.13	0.81	0.99	0.92
O08599	20910	Stxbp1	0.97	0.99	0.97	0.95	0.89	0.99	0.90	0.97
Q8K400	78808	Stxbp5	1.18	0.93	1.09		0.76	1.39		1.22
Q5DQR4	207227	Stxbp5l	1.19			1.18	1.84	1.52		
P11031	20024	Sub1		1.13	1.53			1.25		1.15
Q9Z2I9	20916	Sucla2	1.08	1.00	0.91	1.13	1.03	1.00	1.09	0.95
Q9WUM5	56451	Suclg1	0.97	0.96	0.90	0.94	0.93	0.96	1.05	0.92
Q8CH09	234373	Sugp2					0.99		1.24	
Q9CX34	67955	Sugt1	1.09	1.00	1.11		1.04	1.08	1.32	1.05
P63166	22218	Sumo1				1.09				
P61957	170930	Sumo2	1.13	1.04	0.96		1.32	0.96		1.02
Q62383	20926	Supt6h		1.04	0.78			0.87		0.91
Q9JIS5	64051	Sv2a	0.96	0.94	0.91	0.95	0.78	0.91	0.96	0.91
Q8BG39	64176	Sv2b		1.01	1.05	1.28	1.10	0.96		1.05
O88935	20964	Syn1	3.05	1.05	1.15	1.45	2.72	1.03	0.85	0.99
Q64332	20965	Syn2	1.75	1.11	1.11	1.77	1.07	0.95	1.48	1.02
Q7TMK9	56403	Syncrip	1.14	1.86	1.36	1.02	1.24	1.09	1.02	1.08
Q6ZWR6	64009	Syne1	0.97	0.97		1.09	1.10	1.29	0.82	
O55100	20972	Syngr1	0.97	0.90	1.01	0.92	0.98	0.86	0.94	0.86
Q8CHC4	104015	Synj1	1.28	1.05	1.03	1.21	1.19	1.02	1.22	1.00
Q9D6K5	24071	Synj2bp		0.95	0.88			0.95		0.88
Q8CC35	104027	Synpo	1.14	1.13	1.29		1.25	1.06		1.28
Q62277	20977	Syp	0.77	0.96	0.97	0.76	0.89	0.93	0.88	0.93
P46096	20979	Syt1 (Inclu	0.99	1.02	1.18	0.96	1.17	1.00	0.90	1.03
P46097	20980	Syt2	1.04	0.98		0.97	1.87	0.99	0.89	0.88
Q8K0Z7	70207	Taco1						1.02	1.07	
Q9WVA4	21346	Tagln2		1.24				1.62		
Q9R1Q8	56370	Tagln3	0.96	0.96	1.00	1.02	1.22	0.95	1.02	1.05
Q93092	21351	Taldo1	0.91	0.97	0.94	0.82	1.01	0.94	0.99	0.94
Q921F2	230908	Tardbp	1.19	1.14	1.58	2.26	1.06	1.10	1.34	1.14
Q9D0R2	110960	Tars	1.16	1.08	0.94		0.94	0.85		0.87
P48428	21371	Tbca	0.92	0.96	0.86	0.94	0.95	0.88		0.77
Q9D1E6	66411	Tbcb			0.98	1.26		0.92	1.02	0.92
Q8R0A5	66104|594	Tceal3	2.42	1.00	1.08	1.20	1.87	0.86	1.83	0.98
Q8CCT4	331532	Tceal5	2.03	1.06	1.06	2.24	1.95	1.01	1.49	1.09
P83940	67923	Tceb1	1.12	1.06	0.99	1.11	0.90	0.98	0.94	1.00
P62869	67673	Tceb2	1.04	0.87	0.85	1.06	0.98	0.95	0.94	0.90
Q8CGF7	56070	Tcerg1				1.78				
P11983	21454	Tcp1	0.93	1.05	0.98	1.19	0.83	0.98	1.00	1.00
Q921I1	22041	Tf	0.89	0.53	1.15	0.91	0.50	0.60	0.75	0.61

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q62351	22042	Tfrc			0.95					0.71
Q3UUI3	75778	Them4	1.13	1.39	1.28		0.95	1.20	1.05	1.27
Q8BH55	208967	Thnsl1		0.60						1.54
Q8C1A5	50492	Thop1	0.90	1.01	0.94		1.06	0.89	0.92	0.98
Q569Z6	230753	Thrap3		1.23		2.02				
P01831	21838	Thy1	0.96	0.93	1.17	0.80	0.99	1.14	0.98	1.07
P62073	30059	Timm10	0.91	0.94	0.99	0.97	1.39	0.88	0.99	1.00
P62075	30055	Timm13		1.01	0.97	1.06	1.21	0.99		1.01
Q9CQ85	56322	Timm22					1.50			
O35857	21856	Timm44	0.73	1.11	1.44			1.09	1.34	1.00
Q9D880	66525	Timm50	1.13	1.16	1.12		0.80	1.05	1.22	1.09
P62077	30057	Timm8b						1.01		
Q9WV98	30056	Timm9	0.96	1.01	0.97	0.95	1.07	0.96	0.87	0.99
Q8BH58	226591	Tiprl	1.32						1.04	
P40142	21881	Tkt	0.79	0.91	0.81	0.75	1.00	0.86	0.76	0.83
P26039	21894	Tln1	1.42	1.07		1.36	1.19	1.29	1.35	1.27
Q71LX4	70549	Tln2	1.40	1.17	1.11	1.77	1.16	1.15	1.17	0.99
Q9D1D4	100042773	Tmed10	0.97	1.10	1.07	0.86	1.09	1.10	1.05	0.99
Q9R0Q3	56334	Tmed2		0.87						
Q99KF1	67511	Tmed9	1.02	1.06				1.13		1.09
Q99KI3	66087	Tmem111					0.87			
Q9D8Y1	66271	Tmem126a		1.32				1.18		
Q8VEK0	69981	Tmem30a							0.95	
Q4VAE3	74868	Tmem65	0.90	1.03	0.94	0.97	1.26	0.98	0.92	1.16
Q9JKK7	50876	Tmod2	0.92	0.91	0.98	1.09	1.14	0.84	1.00	0.98
Q6ZWY8	19240|399	Tmsb10/Tr	1.35	0.96	1.00	0.92	1.31	0.82	1.19	1.20
Q8C0L0	52837	Tmx4			0.74			1.04	0.84	
P58871	228140	Tnks1bp1		1.17	1.48			1.55		1.04
Q99LG2	212999	Tnpo2	0.79	1.02	0.95	1.13	1.12	1.06	1.18	
Q6P2B1	320938	Tnpo3		1.19		1.08	1.09		1.01	
Q8BYI9	21960	Tnr	0.92	1.00	0.93	0.80	0.98	1.01	0.90	0.98
Q9QZ06	54473	Tollip		1.04	1.06	1.00	0.84	0.93	0.97	0.98
Q9DCC8	67952	Tomm20	1.40	1.31	1.63	1.01	1.55	1.15		
Q9CPQ3	223696	Tomm22				1.04	1.11	1.18	0.99	
Q9QYA2	53333	Tomm40	1.08							
B1AXP6	68512	Tomm5		0.98				0.99		1.02
Q9CZW5	28185	Tomm70a	1.23	0.98	0.96	1.18	1.13	1.01	1.38	0.99
Q62393	21985	Tpd52	0.98	1.07	1.17		1.30	1.02	0.99	1.02
Q9CYZ2	66314	Tpd52l2	0.95	0.85	0.98	1.27		0.98	1.13	1.17
P17751	21991	Tpi1	0.91	1.00	1.00	0.89	1.05	0.97	0.97	0.98
P58771	22003	Tpm1 (Incl	0.87	1.02	1.06	1.00	1.45	1.02	0.95	1.06
P21107	59069	Tpm3	1.04	1.04	1.01	1.01	1.26	0.97	0.96	1.08
Q6IRU2	326618	Tpm4		1.44				0.92		
Q64514	22019	Tpp2	1.17	1.07	0.93	1.03	0.90	0.96	1.08	0.96
Q7TQD2	72948	Tppp	0.97	1.02	0.97	1.22	1.07	0.96	1.09	0.91
Q9CRB6	67971	Tppp3	1.05	0.94	0.62	0.75	0.97	0.75	1.22	0.74

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
Q9DBS2	67808	Tprg1l	1.14		0.96	1.42		1.00	1.07	1.04
P63028	22070	Tpt1 (Inclu	1.04	0.94	0.98	0.93	0.87	0.93	1.01	1.02
Q9CQN1	68015	Trap1		0.82					1.10	
Q9JME7	59005	Trappc2l			1.38			1.03		0.99
O55013	27096	Trappc3		1.16	1.00	0.94	1.55	0.94		1.02
Q9D289	78232	Trappc6b	1.10	0.93	0.76		0.89	1.06		
Q3U0M1	76510	Trappc9	1.13			1.15	1.06			
Q9ESN6	80890	Trim2	1.66	1.18	1.03	1.88	2.16	1.04	1.50	0.97
Q8BGX0	81003	Trim23		0.82	0.86			0.99		0.98
Q62318	21849	Trim28		1.02	0.96			0.99		1.15
Q9R1R2	55992	Trim3	1.35	1.05	0.96	1.87	1.88	0.96		0.98
Q0KL02	223435	Trio	1.26	1.10	1.41	1.39		1.09	1.33	1.05
P62500	21807	Tsc22d1	0.71					0.99		
Q9CZR8	66399	Tsfm	0.97							
Q62348	22099	Tsn	0.90	1.00	0.92		0.75	0.84	0.88	0.96
Q9QZE7	53424	Tsnax	1.17				1.23			1.00
Q922J6	70747	Tspan2	1.10	0.78		1.24		0.84	0.75	0.53
Q62283	21912	Tspan7		0.91	1.09			0.87		0.85
Q8C8T8	69499	Tsr2 (Inclu	0.98		0.91					0.94
P52196	22117	Tst	0.91	0.94	0.99	0.81	0.96	0.86	0.79	0.86
A2ASS6	22138	Ttn (Includ	1.12	1.03				1.37	0.82	1.14
P07309	22139	Ttr	0.98		1.73		0.65			
P68368	22145	Tuba4a		0.98				0.93		1.08
P99024	22154	Tubb	1.10	1.03	1.04	1.01	0.92	0.99	0.95	1.06
Q7TMM9	22151	Tubb2a	1.00	1.03	0.99	1.01	0.89	0.94	0.98	1.01
Q9CWF2	73710	Tubb2b						1.05		
Q9ERD7	22152	Tubb3	0.98	0.99	0.96	0.96	0.88	0.94	0.95	0.98
Q9D6F9	22153	Tubb4a	1.03	0.93	0.99	1.03	0.85	0.98	0.92	1.00
P68372	227613	Tubb4b	0.94	0.94	0.94	0.61	0.94	0.92		0.97
Q8BFR5	233870	Tufm	1.07	1.03	1.04	1.07	0.88	1.03	1.27	0.98
Q91YR1	19230	Twf1 (Includes eg:1		0.89	1.08					1.37
Q9Z0P5	23999	Twf2	1.04	1.03	1.15	1.83	1.12	1.00	0.99	1.20
P10639	22166	Txn (Includ	1.03	0.98	0.98	1.09	0.93	0.91	0.99	0.91
Q9CQU0	66073	Txndc12		0.90	1.24	1.08		1.09		1.08
Q9CQM5	52700	Txndc17	1.09	0.94	0.92	1.16	0.98	0.92		0.97
Q8CDN6	53382	Txnl1	1.18	1.05	0.97	0.83		0.98	1.06	0.91
Q02053	22201	Uba1	0.92	0.96	0.94	0.82	1.03	0.92	0.84	0.95
Q8C7R4	231380	Uba6				0.88	0.97	0.83		
Q80X50	74383	Ubap2l		1.15				1.08		1.12
P61079	66105	Ube2d3		0.92	0.85	1.17		0.89		0.89
P68037	22195	Ube2l3	0.86	1.01	0.91	0.87	0.78	0.93	1.04	0.93
P61082	22192	Ube2M		0.95	1.11	1.10		0.80		1.12
P61089	93765	Ube2N	1.03	1.00	0.91	0.94	0.99	0.94	1.02	0.95
Q6ZPJ3	217342	Ube2o	1.54	1.07	1.17	1.24	1.16	1.14	1.81	1.09
Q9CZY3	66589	Ube2v1		0.91	0.99			0.85		
Q9D2M8	70620	Ube2v2	0.84	0.97		0.91	0.67	0.99	0.79	

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
P21126	27643	Ubl4a		1.08	1.09			0.96	1.31	0.89
Q8R317	56085	Ubqln1						0.99	1.34	1.02
Q9QZM0	54609	Ubqln2	1.55	1.02	0.97	1.42	1.99	0.94	1.23	0.96
A2AN08	69116	Ubr4		1.11	1.38	1.34	1.28	1.20	0.86	1.16
Q99PL6	66530	Ubxn6		1.02	1.11				0.95	0.71
Q6P5G6	224111	Ubxn7						1.05		
Q9R0P9	22223	Uchl1	1.01	1.04	0.87	0.90	1.05	0.97	1.11	0.97
Q9JKB1	50933	Uchl3	0.93	1.06	1.10	1.04		0.96	0.89	0.91
Q9WUP7	56207	Uchl5		0.93	1.15		1.53	1.00		
Q9CR09	66155	Ufc1	0.70	0.82	0.86	0.80	0.64	0.93	0.92	0.86
P61961	67890	Ufm1	1.25		0.90			0.85	1.14	
Q6P5E4	320011	Uggt1	1.20	1.12	0.83	0.91	0.98	0.94		0.84
Q91ZJ5	216558	Ugp2	1.07	1.01	1.11	1.12	1.07	1.07	1.07	1.06
Q4KUS2	382018	Unc13a	2.04	1.12	1.41	1.48		1.46	1.22	
Q9EPU0	19704	Upf1		1.15	1.21	0.92				0.95
Q8R1I1	66152	Uqcr10	1.05	1.11	1.01	0.96	1.46	0.90	1.03	
Q9D855	67530	Uqcrb	0.96	0.94	0.96	0.99	0.97	0.98	0.85	0.99
Q9CZ13	22273	Uqcrc1	1.04	0.99	1.07	0.91	0.97	1.07	1.20	1.05
Q9DB77	67003	Uqcrc2	0.97	0.96	1.04	0.88	1.10	1.07	1.07	1.00
Q9CR68	66694	Uqcrfs1	1.00	0.93	0.99		0.99	1.06	1.10	0.94
Q9CQ69	22272	Uqcrq	0.85	0.90	0.99	0.95	0.75	1.01	1.08	0.90
Q78IK2	66477	Usmg5	0.92	1.00	0.95	1.06	0.96	1.04	0.90	0.91
Q9Z1Z0	56041	Uso1	1.13	0.89	1.18	0.97	1.57	0.86	0.98	1.10
Q9JMA1	59025	Usp14				0.96			1.10	
Q8R5H1	14479	Usp15			1.37	0.94		1.23	1.16	
P56399	22225	Usp5	0.96	0.98	0.95	0.92	0.92	0.96	0.90	0.92
Q6A4J8	252870	Usp7	0.94	1.05	1.30	1.14	1.00	0.93	0.91	1.02
P70398	22284	Usp9X	1.16	1.06	1.02	1.00	0.97	1.12	1.03	0.87
Q62442	22317	Vamp1	1.16	1.14	0.87	0.79	1.31	1.43	1.55	1.07
P63044	22318	Vamp2	1.30	1.29	1.16	1.26	1.27	1.19	1.08	1.28
O70480	53330	Vamp4		1.11				1.07		
Q9WV55	30960	Vapa	1.37	1.00	1.02	1.13	1.30	1.00	1.45	1.01
Q9QY76	56491	Vapb	1.38	1.19	0.99	1.34	1.14	1.06	1.35	1.06
Q9Z1Q9	22321	Vars	1.12	0.92	0.84	0.92	1.00	0.97	0.95	0.98
Q62465	26949	Vat1		1.02	0.63		0.32	0.86		0.83
Q80TB8	270097	Vat1l	1.25	0.85	0.50	0.76	1.01	0.66	1.33	0.70
Q62059	13003	Vcan	1.21	1.02	1.08	0.98	1.05	1.68	1.17	1.39
Q64727	22330	Vcl	0.92	1.10	0.95	1.12	1.08	1.01	1.09	1.09
Q01853	269523	Vcp	0.91	0.98	0.98	0.85	1.08	0.88	0.90	0.99
Q8CDG3	70675	Vcpip1	1.37	0.95	1.32	1.24	1.18	0.91		1.06
Q60932	22333	Vdac1	0.98	1.02	0.99	0.75	1.00	1.06	1.11	1.02
Q60930	22334	Vdac2	0.89	0.97	0.92	0.78	0.86	1.06	1.05	0.99
Q60931	22335	Vdac3	0.86	1.03	0.95	0.79	0.96	1.06	1.28	0.98
P20152	22352	Vim	1.14		1.03	0.86	0.93		1.84	1.98
Q8BX70	320528	Vps13c	1.40	0.90	1.29	1.65	1.03	1.33		1.71
Q9CQ80	28084	Vps25 (Includes eg:28084)			0.82					

Supp. Table 1 (cont.)

			Developmental Myelination				Remyelination			
Uniprot_ID	Entrez Ger	Symbol	Mut-w11	Mut-w12	WT-w11	WT-w12	Mut-w11	Mut-w12	WT-w11	WT-w12
P40336	30930	Vps26a	1.17	1.02	3.48		0.84	1.43	0.82	0.80
Q8C0E2	69091	Vps26b	0.98	1.16	1.04	1.24	1.03	1.03	1.26	1.16
Q9D1C8	66914	Vps28 (Includes eg:300052)						1.17		
Q9QZ88	56433	Vps29 (Inc	0.96	1.00	0.96			1.04		0.99
P59016	233405	Vps33b	0.91				1.02		1.20	
Q9EQH3	65114	Vps35	1.11	1.03	1.02	0.98	0.99	1.02	1.07	1.00
P97390	22365	Vps45						1.04		1.12
P62761	26950	Vsnl1	1.03	0.96	1.08	0.95	1.12	1.09	1.08	1.03
Q9CR26	66201	Vta1 (Includes eg:292640)				0.51				
O88384	53612	Vti1b						0.87		
P32921	22375	Wars							1.02	
Q8R5H6	83767	Wasf1	1.75	1.09	1.25	1.69	1.31	1.02	1.61	1.08
Q8VHI6	245880	Wasf3		0.79	0.70			0.89		1.07
Q91YD9	73178	Wasl		1.09				1.15		0.81
P97765	22378	Wbp2		0.97						0.79
Q6VNB8	72145	Wdfy3	1.04	0.95			0.96		1.08	
O88342	22388	Wdr1	0.95	1.00	1.05	0.88	0.91	0.99	0.86	1.09
Q8CBE3	207615	Wdr37							1.06	
Q8CGF6	99512	Wdr47		1.01			0.88	1.10	0.89	
Q8BH57	67561	Wdr48			0.84					
P61965	140858	Wdr5			1.40			1.17		
Q9ERF3	66317	Wdr61					0.84			
Q920I9	104082	Wdr7	1.26	1.12	1.10	1.22	0.91	1.10	1.19	1.08
Q6P1B1	170750	Xpnpep1	1.11	1.09	0.97	0.94	0.96	1.07	1.01	0.87
Q6P5F9	103573	Xpo1	1.06	0.99	0.98	1.14	0.83	1.03	1.07	1.15
Q924C1	72322	Xpo5		2.46				2.53		
Q9EPK7	65246	Xpo7	1.33	0.96	1.20	1.03	0.95	1.03	0.87	1.00
Q91WQ3	107271	Yars	1.00	0.80	1.02	1.13	1.03	0.79	0.84	0.92
Q9CQW1	56418	Ykt6	1.18	1.01	1.10	1.08	1.03	1.09	2.26	1.02
Q9CQV8	54401	Ywhab	1.06	1.03	0.97	1.05	1.01	1.01	1.06	1.01
P62259	22627	Ywhae	1.02	1.01	0.99	0.97	0.98	0.98	0.95	0.98
P61982	22628	Ywhag	1.00	1.00	0.99	0.94	1.00	0.98	1.04	0.97
P68510	22629	Ywhah	1.07	1.03	1.10	1.00	0.96	1.04	1.01	1.03
P68254	22630	Ywhaq	0.99	1.03	0.96	0.94	0.91	0.98	1.10	1.01
P63101	22631	Ywhaz	0.97	1.02	1.07	1.01	0.95	1.00	0.96	1.05
Q80ZJ6	227693	Zer1					0.90			
Q5SSH7	195018	Zzef1				1.65				

Supp. Table 2

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^{M}, developmental myelination response	eIF2B^{M}, remyelination response
Ahcy	1	1.04	0.99	1.08	0.73
Macf1	1	1.00	0.98	1.13	0.69
Rps6	1	1.03	0.94	1.37	0.72
Asna1	1	1.09	0.82	1.26	0.41
Ccdc132	1	1.07	0.89	1.02	0.68
Itpa	1	1.12	0.85	1.03	0.62
Ncam2	1	1.10	0.92	1.00	0.70
Nln	1	1.25	0.90	1.11	0.66
Pacsin1	1	0.99	1.02	1.01	0.67
Psd3	1	1.11	1.05	1.17	0.52
Stx1b	1	0.99	0.93	0.94	0.72
Timm10	1	0.99	1.01	1.03	0.63
Tmod2	1	1.11	0.98	0.99	0.73
Atpif1	1	1.00	1.02	1.01	0.75
Fabp7	1	1.11	0.87	1.18	0.71
Pitpna	1	1.00	0.86	1.01	0.75
Plcxd3	1	1.13	0.95	1.09	0.79
Por	1	0.96	0.80	1.20	0.55
Fkbp3	1	1.19	1.02	1.20	0.83
Cul3	1	1.10	1.01	1.07	0.87
Gdap1	1	1.08	1.02	1.16	0.86
Nedd8	1	1.03	0.98	1.07	0.93
Rab1a	1	1.04	1.01	1.04	0.99
Rps27a	1	1.03	1.04	1.08	0.93
C14Orf166	1	0.94	0.90	0.96	0.82
Cdc42	1	1.02	0.98	0.99	0.85
Rap2b	1	1.04	0.99	1.03	0.88
Skp1/Skp1	1	0.97	0.99	0.97	0.87
Snx12	1	0.96	0.97	1.06	0.83
Syngr1	1	0.91	0.92	0.93	0.88
Tagln3	1	1.01	1.03	1.00	0.78
Arhgdia	2	1.14	0.85	0.85	0.60
Efhd2	2	1.10	0.96	0.92	0.61
Dnajc5	2	1.03	0.76	0.74	0.43
Plcb1	2	1.38	0.84	0.64	0.46
Ubqln2	2	1.46	0.78	0.66	0.47
Pdap1	2	1.75	0.93	0.76	0.56
LgalsI	2	0.99	0.97	0.74	0.60
Naca	2	1.03	0.90	0.79	0.66
Rps3a	2	1.06	0.97	0.85	0.77
Prosc	2	0.92	0.90	0.84	0.69
Basp1	2	1.65	1.26	0.96	0.66
Dlg3	2	1.19	1.11	0.90	0.84
Fkbp2	2	1.17	1.10	0.95	0.79
Pea15	2	1.25	1.14	0.91	0.78
Twf2	2	1.60	1.21	0.99	0.90

Supp. Table 2 (cont.)

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^{M}, developmental myelination response	eIF2B^{M}, remyelination response
Cltb	2	1.32	1.00	0.76	0.69
Eef1g	2	1.22	1.05	0.90	0.79
Pebp1	2	1.16	1.08	0.90	0.88
Rab2a	2	1.26	1.03	0.94	0.86
Ank2	2	1.14	1.05	1.01	0.87
Ap2a2	2	1.10	1.04	0.94	0.86
Arpc4	2	1.03	1.02	1.00	0.92
Mapk1	2	1.05	0.99	0.93	0.85
Pdhb	2	1.07	1.03	0.97	0.89
Rab14	2	1.04	0.97	0.93	0.89
Rap1b	2	0.99	0.98	0.97	0.94
Sars	2	1.07	1.01	1.00	0.88
Hint1	2	1.11	1.08	1.01	0.94
Map1a	2	1.97	0.41	0.46	0.23
Hyou1	2	1.21	0.71	0.85	0.71
Anp32a	2	1.13	0.90	0.96	0.70
Eif3c/Eif3c	2	1.13	0.86	0.87	0.70
Epb41l2	2	1.35	0.92	0.98	0.70
Lonp1	2	1.29	0.83	0.91	0.74
Ssbp1	2	1.38	0.85	0.94	0.71
Cbr1	2	1.11	0.83	0.91	0.80
Rab18	2	1.06	0.88	0.90	0.79
Cdc37	2	1.31	0.70	0.78	0.53
Hepacam	2	1.23	0.63	0.85	0.51
Rgs10	2	1.05	0.66	0.67	0.50
Trim2	2	1.82	0.65	0.71	0.48
Ppp1R9b	2	1.47	0.83	1.03	0.77
Ddx1	2	1.19	1.06	1.12	0.98
Nme1	2	1.09	0.98	1.02	0.97
Cdk5	2	1.02	0.91	0.96	0.92
Ckmt1a/Ck	2	1.07	0.89	0.96	0.87
Cycs	2	1.06	0.99	1.00	0.95
Mrps36	2	1.95	0.38	0.57	0.60
Cend1	2	1.07	0.68	0.83	0.87
Tppp3	2	1.20	0.61	0.89	0.77
Lmnb2	2	1.37	0.54	0.81	0.81
Gap43	2	1.91	0.58	0.71	0.64
Marcks	2	1.50	0.48	0.58	0.59
Vat1L	2	1.52	0.53	0.68	0.66
Ap2M1	2	1.36	0.83	1.07	0.96
Cand1	2	1.21	0.91	0.98	0.94
Csrp1	2	1.39	0.86	1.04	1.00
Dync1Li1	2	1.16	0.89	0.95	1.01
Fdps	2	1.35	0.97	1.06	1.04
Hspa2	2	1.25	0.93	1.02	0.99
Kars	2	1.34	0.81	0.92	0.91

Supp. Table 2 (cont.)

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^{M}, developmental myelination response	eIF2B^{M}, remyelination response
Npepps	2	1.18	0.93	1.02	1.02
Rhoa	2	1.28	0.77	0.94	0.97
Sucla2	2	1.24	0.87	0.92	0.97
Hprt1	2	1.61	0.75	0.94	0.92
Tardbp	2	1.43	0.86	0.95	1.03
Auh	2	1.58	0.85	1.09	1.16
Pls3	2	1.52	0.92	1.06	1.01
Cisd1	2	1.03	0.89	0.93	0.89
Hsp90aa1	2	1.10	0.94	0.98	0.97
Park7	2	1.12	0.83	1.00	0.94
Sfpq	2	1.14	0.95	0.98	1.00
Txn	2	1.12	0.92	0.96	0.98
Ube2n	2	1.03	0.92	0.97	0.95
Dync1l1	2	1.08	0.98	1.01	1.02
Hspa9	2	1.10	0.98	1.02	1.03
Epb41l3	2	1.05	0.79	0.90	0.93
Aak1	2	2.94	0.38	0.31	0.42
Gprin1	2	2.87	0.41	0.27	0.34
Ncl	2	5.27	0.24	0.18	0.20
Rtn1	2	2.15	0.50	0.47	0.54
Pak1	2	1.28	0.87	0.85	0.87
Synj1	2	1.17	0.82	0.82	0.86
Hsph1	2	1.41	0.76	0.73	0.81
Snap91	2	1.43	0.72	0.69	0.77
Sgip1	2	1.18	0.79	0.73	0.80
Hnrnpu	2	1.84	0.59	0.53	0.60
Map6	2	2.23	0.73	0.72	0.75
Acot13	2	1.21	0.97	0.95	0.98
Hip1r	2	1.62	1.00	0.87	0.94
Map1Lc3a	2	1.32	1.03	0.98	1.01
Nckipsd	2	1.60	0.92	0.86	0.97
Ppa1	2	1.12	0.98	0.96	0.99
Cap1	2	2.75	0.36	0.30	0.25
Mapre1	2	1.51	0.65	0.67	0.50
Mapre3	2	1.38	0.64	0.68	0.56
Rplp0	2	1.49	0.72	0.66	0.63
Ap3d1	2	1.49	0.75	0.70	0.67
Amph	2	2.05	0.57	0.51	0.40
Fau	2	1.87	0.68	0.65	0.48
Hspa4	2	1.95	0.56	0.54	0.43
Rpl23a	2	1.32	0.69	0.66	0.62
Sparcl1	2	1.54	0.64	0.65	0.60
Dlat	2	1.95	0.44	0.48	0.41
Bpnt1	2	1.31	1.02	1.00	0.97
Srgap3	2	1.56	0.93	0.94	0.89
Prkar2b	2	1.45	0.91	0.86	0.77

Supp. Table 2 (cont.)

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^M, developmental myelination response	eIF2B^M, remyelination response
Cplx1	2	1.29	0.95	0.89	0.86
Calb1	2	1.03	0.89	0.89	0.85
Bin1	2	3.30	0.63	0.25	0.24
Actr3b	2	1.24	0.96	0.64	0.75
Ap2a1	2	1.27	0.88	0.71	0.82
Epn1	2	1.25	0.88	0.65	0.77
Tceal3	2	1.11	0.54	0.41	0.46
Camkv	2	1.65	0.83	0.55	0.71
Add2	2	1.47	0.82	0.58	0.67
Tceal5	2	2.11	0.73	0.52	0.52
Baiap2	2	1.47	1.14	0.89	0.88
Fabp5	2	1.31	1.13	0.88	0.90
Hnrnpl	2	1.36	0.94	0.81	0.84
Eif4b	2	1.25	0.98	0.81	0.87
Map2k1	2	1.24	1.02	0.88	0.90
Myl6	2	1.34	1.01	0.90	0.92
Dnajc6	2	1.05	0.95	0.87	0.91
Sdha	2	1.09	0.96	0.90	0.88
Snrpd2	2	1.33	1.20	1.02	1.06
Sept11	2	1.18	1.08	0.94	0.93
Map1Lc3b	2	1.21	1.06	0.95	0.98
Pabpc1	2	1.21	1.07	0.96	0.96
Mapt	2	2.02	0.51	0.49	0.83
Apoo	2	1.33	0.83	0.81	0.94
Atp1b2	2	1.21	0.85	0.83	0.92
Eif3a	2	1.33	0.79	0.79	1.01
Fxyd6	2	1.58	0.66	0.75	0.95
Slk	2	1.50	0.76	0.75	0.85
Syn2	2	1.59	0.69	0.63	0.89
Ap1b1	2	1.34	0.69	0.65	0.76
Csnk2A1	2	1.15	0.73	0.77	0.81
Oxr1	2	1.20	0.74	0.71	0.86
Rtn3	2	1.23	0.75	0.77	0.84
Tomm70a	2	1.24	0.72	0.80	0.89
Vapa	2	1.11	0.69	0.73	0.77
Wasf1	2	1.35	0.67	0.62	0.77
Atp8	2	1.16	0.93	0.96	1.00
Rpl10a	2	1.25	0.88	0.86	1.03
Tln2	2	1.60	0.85	0.83	0.99
Vapb	2	1.35	0.79	0.86	0.93
Rpl15	2	1.59	1.00	0.96	1.11
Cyfip2	2	1.10	0.95	0.92	1.00
Ywhab	2	1.09	0.95	0.97	0.99
Pdcd6lp	2	3.02	0.83	0.43	0.93
Dbn1	2	1.40	0.88	0.72	0.85
Fam120a	2	1.51	0.84	0.63	0.83

Supp. Table 2 (cont.)

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^M, developmental myelination response	eIF2B^M, remyelination response
Crip2	2	1.07	0.82	0.73	0.84
Pacs1	2	1.02	0.78	0.74	0.83
Gmfb	2	1.32	0.94	0.85	1.11
Tceb2	2	1.25	0.96	0.84	0.97
Dpysl2	2	1.08	0.93	0.88	0.93
Guk1	2	1.01	0.93	0.88	0.94
Sept5	2	1.08	0.99	0.92	1.03
Ahcyl1	2	1.15	1.00	0.95	1.04
Cul5	2	1.11	1.00	0.96	1.03
Eif4e	2	1.18	1.00	0.96	1.07
Hsp90ab1	2	1.05	1.00	0.95	0.99
Nme2	2	1.09	1.05	1.02	1.06
Sptbn1	2	1.05	1.01	0.97	1.01
Atp5e	2	1.02	0.87	0.81	0.91
Matr3	2	1.14	0.90	0.79	0.92
Napb	2	1.16	0.91	0.86	0.97
Ppp1ca	2	1.18	0.96	0.82	0.95
Caskin1	3	1.80	0.97	0.33	0.89
Sec22b	3	1.00	0.81	0.64	0.79
Bsn	3	1.70	1.24	0.64	0.92
Cttn	3	1.42	1.09	0.72	0.89
Dnaja2	3	1.41	1.02	0.66	0.84
Hnrpll	3	1.60	1.11	0.67	0.90
Ipo7	3	0.94	0.99	0.77	0.87
Ugp2	3	1.02	0.99	0.94	1.00
Sept7	3	1.04	1.08	0.89	0.99
Sept9	3	1.16	1.11	0.82	1.11
Atp6v1h	3	1.03	1.08	0.80	1.03
Dclk1	3	1.12	1.05	0.94	1.00
Epb41l1	3	1.12	1.01	0.88	1.05
Fscn1	3	1.12	1.06	0.95	1.03
Ipo5	3	1.07	1.07	0.97	1.01
Lancl2	3	1.03	1.03	0.83	1.01
Pgm2l1	3	1.11	1.13	0.94	1.05
Ppp2r1a	3	1.03	1.01	0.82	1.00
Rock2	3	1.08	1.04	0.88	0.93
Rpl7a	3	1.08	0.99	0.84	0.94
Rps15a	3	1.12	1.10	0.90	1.10
Snap25	3	1.07	1.00	0.90	0.99
Vars	3	1.09	1.03	0.82	0.97
Kif21a	3	1.12	0.95	0.74	0.89
Scamp1	3	1.06	0.97	0.75	0.99
Lrrc57	3	1.05	0.96	0.64	0.95
Snca	3	1.25	3.06	0.92	0.94
Syn1	3	1.26	1.17	0.34	0.38
Sirpa	3	0.98	0.93	0.56	0.50

Supp. Table 2 (cont.)

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^{M}, developmental myelination response	eIF2B^{M}, remyelination response
Ptk2b	3	1.02	0.97	0.77	0.74
Slc25a13	3	1.00	1.07	0.84	0.79
Tmsb10/Tr	3	0.91	1.01	0.71	0.63
Cct4	3	1.11	1.14	0.95	0.84
Clta	3	1.21	1.17	0.97	0.92
Dpp6	3	1.26	1.35	1.03	0.81
Gda	3	1.09	1.22	0.87	0.84
Gng2	3	1.41	1.64	1.07	0.73
Mink1	3	1.05	1.29	0.77	0.86
Iqsec1	3	1.36	1.20	0.78	0.81
Lmnb1	3	1.41	1.50	0.59	0.70
Mras	3	1.11	1.16	0.86	0.77
Phpt1	3	1.09	1.13	0.77	0.82
Yars	3	1.11	1.09	0.80	0.77
Adam23	3	0.96	1.04	0.89	0.85
Acyp1	3	1.00	1.17	0.91	0.92
Ctnna2	3	1.12	1.23	1.05	0.96
Pfn1	3	1.04	1.36	0.93	0.92
Rpl8	3	1.01	1.21	0.91	0.86
Vamp2	3	1.08	1.19	1.00	0.94
Ap2b1	3	1.05	1.05	1.01	1.00
Dnm1	3	1.05	1.07	1.02	1.02
Fus	3	1.09	1.09	0.97	0.90
Gdi2	3	1.07	1.10	1.03	1.02
Gnao1	3	1.07	1.05	0.95	0.93
Hpcal4	3	1.04	1.11	0.82	0.91
Mtpn	3	1.03	1.12	0.84	0.91
Slc3a2	3	0.99	1.05	0.96	0.96
Erc2	4	0.99	1.54	0.97	1.14
Pfkl	4	1.05	1.46	1.03	1.09
Gria2	4	0.88	1.22	0.92	1.14
Nudt21	4	0.86	1.20	0.95	1.10
Aldh2	4	0.95	1.11	0.62	0.84
Cpne6	4	0.89	1.19	0.70	0.88
Dnm1l	4	0.98	1.02	0.95	0.97
Rpl35	4	0.91	1.05	0.83	0.87
Camk2g	4	0.95	1.20	0.92	1.04
Cnrip1	4	1.03	1.23	0.93	1.02
Dync1h1	4	0.99	1.17	1.03	1.07
Pfn2	4	1.12	1.44	0.87	1.23
Plec	4	1.03	1.23	0.93	1.10
Ppp3r1	4	1.07	1.22	0.91	1.07
Psmd2	4	0.95	1.18	0.93	0.98
Rab1b	4	1.00	1.18	0.94	1.00
Rps23	4	1.05	1.31	0.93	1.13
Uqcrb	4	1.03	1.16	0.97	1.00

Supp. Table 2 (cont.)

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^M, developmental myelination response	eIF2B^M, remyelination response
Actr1b	4	0.95	1.08	0.92	1.01
Arpc2	4	0.98	1.08	0.85	1.03
Atl1	4	0.76	1.27	0.70	1.07
Cntnap2	4	0.89	1.07	0.87	0.96
Exoc4	4	0.92	1.12	0.92	0.92
Gpm6a	4	0.93	1.14	0.98	1.09
Hnrnpa1	4	0.88	1.10	0.85	1.02
Hnrnpk	4	1.03	1.08	0.89	0.99
Hpca	4	0.91	1.17	0.84	1.06
Nckap1	4	1.05	1.12	0.93	1.09
Oxct1	4	1.01	1.13	0.95	1.09
Pfkm	4	1.05	1.16	0.91	1.17
Rpl38	4	0.97	1.17	0.95	1.04
Rps20	4	1.08	1.21	0.77	1.14
Tubb	4	0.97	1.12	0.94	1.08
Xpo7	4	0.86	1.15	0.72	1.09
Cacna2d3	5	0.57	1.29	0.81	0.98
Cox6b1	5	0.65	0.95	1.02	0.94
Ap2s1	5	0.92	1.21	1.12	1.15
Cntn1	5	0.78	1.20	1.13	1.03
Fam213a	5	0.99	1.40	1.27	1.31
Gpm6b	5	0.84	1.29	0.99	0.99
Pfkp	5	0.93	1.19	1.04	1.08
Rab35	5	0.87	1.33	1.18	1.16
Rasal1	5	0.82	1.18	0.99	0.99
Sfn	5	0.97	1.26	1.13	1.22
Wdr1	5	0.84	1.26	1.05	1.09
Atp6v1b2	5	0.85	1.12	1.06	1.10
Ntm	5	0.82	1.07	1.07	1.05
Psmd11	5	0.80	1.16	1.07	1.11
Rac1	5	0.82	1.13	1.15	1.08
Ran	5	0.82	1.05	1.13	1.03
Rpsa	5	0.85	1.12	1.01	1.06
Syp	5	0.79	1.06	1.24	1.04
Tnr	5	0.86	1.09	1.09	1.04
Aco2	5	0.96	1.05	1.08	1.01
Cadm3	5	0.88	0.96	1.00	0.94
Eif5a	5	0.84	0.97	1.01	0.90
Sh3gl2	5	0.93	1.04	0.99	0.99
Sptan1	5	0.93	1.08	0.99	0.94
Arhgef2	5	0.82	1.12	0.94	0.87
Prkce	5	0.92	1.21	0.97	0.96
Atp6v1g2	5	0.99	1.09	1.03	1.03
Prdx6	5	0.96	1.12	1.06	1.03
Ywhae	5	0.97	1.04	0.99	0.99
Ywhaz	5	0.94	1.09	1.06	1.05

Supp. Table 2 (cont.)

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^M, developmental myelination response	eIF2B^M, remyelination response
Cab39	6	0.96	1.50	1.29	0.98
Dlg4	6	0.86	1.23	1.17	1.00
Rab39A	6	0.87	1.49	1.10	1.02
Cacna2d1	6	0.70	1.09	1.08	0.90
Ctsb	6	0.78	1.27	1.22	0.85
Ddb1	6	0.88	1.20	1.09	0.90
Ola1	6	0.82	1.19	1.03	0.91
Psma6	6	0.84	1.15	1.04	0.86
Syt1	6	0.81	1.14	1.03	0.86
Uba1	6	0.87	1.12	1.05	0.90
Usp7	6	0.87	1.12	1.11	0.94
Sar1a	6	0.76	1.01	1.04	0.94
Tst	6	0.82	1.09	1.03	0.90
Sept6	6	0.93	1.12	1.01	0.94
Atp6v1a	6	0.95	1.12	1.05	0.97
Ezr	6	0.96	1.11	0.96	0.61
Hmgb1	6	0.86	1.15	0.91	0.47
Psma3	6	0.90	1.11	0.93	0.66
Stx1a	6	0.90	1.22	0.88	0.60
Uso1	6	0.82	1.12	0.79	0.54
Actc1	6	0.99	1.10	1.07	0.95
Anxa6	6	0.99	1.04	1.00	0.84
Atp6v1d	6	0.90	1.00	1.00	0.86
Dstn	6	0.96	1.00	0.98	0.94
Eef1b2	6	1.02	1.04	1.02	0.95
Ehd3	6	0.93	1.00	1.02	0.85
Gdi1	6	0.98	1.03	1.03	0.93
Got1	6	0.98	1.05	1.02	0.91
Hdhd2	6	0.97	0.99	0.96	0.83
Hspa5	6	0.97	1.03	1.02	0.93
Impa1	6	0.97	1.07	0.97	0.90
Mdh1	6	0.92	1.04	1.03	0.89
Nfasc	6	0.98	1.04	1.00	0.92
Rab11b	6	0.99	1.04	0.99	0.90
Rab7a	6	0.98	1.05	1.03	0.96
Alcam	6	0.81	1.34	1.04	0.72
Cadm2	6	0.91	1.12	1.06	0.79
Calr	6	0.91	1.33	0.97	0.68
Camk2a	6	0.98	1.38	1.25	0.78
Capza2	6	0.94	1.12	1.08	0.92
Crym	6	0.94	1.11	0.99	0.89
Cyb5r3	6	0.95	1.08	1.06	0.69
Eno1	6	0.91	1.10	1.08	0.78
Glod4	6	1.02	1.18	1.13	0.75
Hagh	6	1.00	1.34	1.14	0.75
Map2	6	0.96	1.16	1.01	0.80

Supp. Table 2 (cont.)

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^{M}, developmental myelination response	eIF2B^{M}, remyelination response
Ncald	6	0.90	1.21	0.96	0.88
Nrcam	6	0.91	1.33	1.14	0.73
Psma1	6	0.92	1.12	1.17	0.64
Psma2	6	0.97	1.18	1.04	0.86
Psma7	6	0.92	1.20	1.09	0.79
Psmb3	6	1.01	1.19	1.03	0.84
Psmb4	6	1.01	1.12	1.10	0.87
Rab3a	6	0.97	1.11	1.02	0.85
Rab3d	6	0.94	1.09	1.01	0.85
Rgs7	6	0.90	1.10	0.98	0.81
Snd1	6	0.98	1.06	1.03	0.81
Stmn1	6	0.96	1.16	1.05	0.92
Timm9	6	0.97	1.14	1.05	0.89
Tmem65	6	1.02	1.26	1.15	0.78
Tpm1	6	0.95	1.12	1.18	0.70
Tpm3	6	1.00	1.12	1.00	0.77
Vcp	6	0.87	1.11	1.08	0.82
Lmna	6	0.83	1.02	0.95	0.77
Coro1a	6	1.07	1.24	1.04	0.96
Hnrnpa2b1	6	1.04	1.27	1.05	1.01
Rps19	6	1.09	1.16	1.06	0.94
Sncb	6	1.06	1.18	1.09	1.06
Gpd2	6	1.01	1.12	1.05	1.01
Ptms	6	1.00	1.13	1.02	1.00
Atp5l	6	0.92	1.03	1.11	0.97
Cyb5b	6	0.96	1.02	1.11	0.93
Hspa8	6	0.98	1.05	1.08	0.99
Pin1	6	0.90	1.00	1.21	0.90
Stip1	6	0.95	1.02	1.04	0.95
Actn1	6	0.80	1.22	1.41	0.78
Actn4	6	0.82	1.18	1.34	0.68
Anxa5	6	0.87	1.09	1.14	0.76
C1Qbp	6	0.92	1.00	1.09	0.73
Camk2b	6	0.95	1.13	1.14	0.87
Dpp10	6	0.74	1.19	1.53	0.91
Eef2	6	0.91	1.09	1.12	0.94
Hibadh	6	0.97	1.07	1.43	0.78
Kpnb1	6	0.99	1.07	1.15	0.87
Mcts1	6	0.87	1.24	1.32	0.74
Mdh2	6	0.89	1.06	1.20	0.86
Pgam1	6	0.90	1.06	1.09	0.85
Ppia	6	0.95	1.11	1.12	0.94
Psmb1	6	0.82	1.08	1.10	0.84
Psmb5	6	0.94	1.06	1.13	0.87
Sod1	6	0.96	1.07	1.23	0.83
Syncrip	6	0.75	1.07	1.64	0.88

Supp. Table 2 (cont.)

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^M, developmental myelination response	eIF2B^M, remyelination response
Tkt	6	0.93	1.09	1.15	0.86
Cd47	6	0.76	1.02	1.30	0.98
Dld	6	0.95	1.02	1.07	0.87
Eno2	6	0.90	1.02	1.09	0.80
Tpi1	6	0.89	1.02	1.10	0.92
L1Cam	7	0.81	0.97	1.08	0.58
Aldh1l1	7	1.04	1.08	1.40	0.96
Rab5c	7	0.98	1.13	1.16	1.02
Capzb	7	1.05	1.09	1.13	1.00
Eci1	7	0.91	0.90	1.23	0.82
Hsp90b1	7	1.01	1.02	1.10	1.03
Hspe1	7	0.98	0.98	1.13	0.85
Idh3g	7	0.99	0.98	1.13	0.90
Ntrk2	7	0.90	1.03	1.22	1.01
Pgm1	7	0.92	0.89	1.17	0.85
Prdx5	7	0.97	0.94	1.16	0.94
Psma5	7	0.94	0.99	1.10	0.87
Sod2	7	0.98	0.94	1.20	0.97
Atp5b	7	0.91	0.97	1.04	0.87
Atp5j	7	0.90	0.91	1.02	0.87
Canx	7	0.90	0.90	1.07	0.80
Eea1	7	0.91	0.91	1.01	0.84
Glo1	7	0.95	0.99	1.06	0.86
Gpi	7	0.94	0.99	1.07	0.88
Letm1	7	0.92	0.93	1.03	0.86
Myo5a	7	1.00	1.01	1.03	1.01
Rab3b	7	0.89	0.92	0.97	0.81
Taldo1	7	0.87	0.96	1.06	0.93
Dbi	7	0.84	0.97	1.43	0.80
Pak3	7	0.78	0.99	1.16	0.67
Ncam1	7	0.84	0.95	1.15	0.81
Sec31a	8	1.27	0.45	0.76	1.00
Ctsd	8	1.15	0.55	0.93	1.12
Ykt6	8	0.98	0.45	0.86	1.06
Cfl2	8	1.15	0.63	1.05	1.11
Pc	8	1.25	0.84	1.00	1.08
Acsl6	8	1.29	0.90	1.12	1.17
Echs1	8	1.07	0.90	1.09	1.02
Aldoc	8	0.99	0.90	1.01	0.97
Arl3	8	1.04	0.76	0.94	0.89
Atp5a1	8	1.00	0.86	0.98	1.03
Dpysl5	8	1.06	0.85	0.97	1.02
Eef1a1	8	1.00	0.84	0.98	1.00
Gnai2	8	1.04	0.78	1.01	0.99
Pdha1	8	1.01	0.83	0.99	1.03
Suclg1	8	1.04	0.88	0.99	1.04

Supp. Table 2 (cont.)

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^{M}, developmental myelination response	eIF2B^{M}, remyelination response
Cd81	8	1.17	0.85	1.06	1.22
Dnm3	8	1.11	0.85	1.07	1.06
Gstm5	8	1.08	0.93	1.04	1.08
Ndrg2	8	1.10	0.85	1.15	1.12
Rpl31	8	1.10	0.90	1.02	1.09
Tcp1	8	1.21	1.00	1.13	1.18
Usmg5	8	1.12	1.00	1.09	1.08
Grb2	8	1.05	0.76	0.88	0.96
Slc25a3	8	1.09	0.72	0.94	0.95
Slc25a6	8	1.05	0.66	0.91	0.99
Acyp2	9	0.90	0.79	1.09	1.03
Chchd3	9	0.85	0.70	1.16	1.30
Dpysl3	9	0.96	0.76	1.05	1.08
Hsd17b12	9	0.90	0.87	1.07	1.09
Ppp1r7	9	0.93	0.80	1.16	1.14
Rhog	9	1.02	0.71	1.15	1.30
Slc4a4	9	0.84	0.66	1.10	1.24
Vamp1	9	0.91	0.69	0.98	1.09
Vdac3	9	0.84	0.77	1.20	1.11
Sncg	9	1.09	0.61	1.35	1.42
Acadvl	9	1.05	0.96	1.13	1.06
Aldh5a1	9	1.01	0.93	1.07	1.01
Copa	9	0.94	0.85	1.37	1.11
Coro1c	9	0.89	0.81	1.24	0.94
Glud1	9	1.05	1.00	1.21	1.08
Hspa4l	9	1.02	0.94	1.13	1.02
Slc2a3	9	1.23	0.88	1.43	1.16
Atp5h	9	0.93	0.89	1.02	1.01
Bphl	9	0.90	0.90	1.00	0.99
Cadps	9	0.95	0.91	1.05	0.96
Hspd1	9	0.89	0.93	1.09	1.00
Mtx2	9	0.92	0.85	1.00	0.98
Ndufv1	9	0.85	0.86	0.92	0.89
Pcmt1	9	0.99	0.97	1.01	1.01
Pkm2	9	0.95	0.92	1.00	0.97
Rab3C	9	0.90	0.95	1.08	1.01
Ywhag	9	0.94	0.92	1.00	0.98
Atp1a2	9	0.97	0.90	1.21	1.23
Ckb	9	0.98	0.98	1.05	1.06
Ube2l3	9	0.96	0.90	1.18	1.19
Ywhaq	9	0.97	0.92	1.04	1.07
Rps16	9	1.10	1.02	1.28	1.27
Ranbp1	10	4.73	0.27	1.87	0.24
Abat	10	1.19	0.84	1.16	0.84
Calb2	10	1.17	0.58	1.30	0.84
Ddah1	10	1.12	0.90	1.06	0.80

Supp. Table 2 (cont.)

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^{M}, developmental myelination response	eIF2B^{M}, remyelination response
Myo6	10	1.39	0.75	1.32	0.73
Necap1	10	1.11	0.79	1.03	0.79
Pclo	10	1.11	0.71	0.95	0.81
Psmb2	10	0.99	0.80	0.95	0.75
Tppp	10	1.26	0.83	1.05	0.90
Ktn1	10	1.55	0.79	1.31	0.91
Acat1	10	1.08	0.95	1.08	1.01
Ap3b2	10	1.09	0.97	1.05	0.97
Ddt	10	1.03	0.88	1.16	0.94
Etfa	10	1.16	0.88	1.13	0.98
Fis1	10	1.22	0.95	1.18	0.98
Vcl	10	1.18	0.99	1.19	0.93
Vps26b	10	1.20	0.92	1.18	0.99
Dbnl	10	1.21	0.79	1.83	0.80
Acot7	10	1.07	0.74	0.98	0.89
Atp6v1g1	10	1.05	0.78	1.07	0.87
C21Orf33	10	1.05	0.87	1.04	0.91
Cotl1	10	1.00	0.94	1.01	0.97
Eef1a2	10	0.98	0.86	1.06	0.83
Gbas	10	1.10	0.86	1.04	0.89
Got2	10	1.00	0.95	1.02	0.99
Psat1	10	0.94	0.76	0.94	0.86
Rps10	10	1.02	0.87	1.00	0.91
Sdhb	10	1.04	0.85	0.99	0.91
Uchl1	10	1.04	0.88	1.03	0.92
H2afj	11	1.12	0.44	0.69	1.92
Cldn11	11	1.19	0.44	0.92	1.49
Kif5b	11	1.04	0.51	0.79	1.13
Rtn4	11	1.00	0.57	0.67	1.08
Nars	11	1.05	0.74	0.92	1.50
Akap7	11	0.94	0.70	0.88	1.30
Slc25a4	11	0.96	0.78	0.95	1.09
Nipsnap1	11	0.99	0.94	0.96	1.04
Pgk1	11	0.98	0.91	0.97	1.04
Ppfia3	11	1.00	0.90	0.94	1.04
Rab5a	11	1.03	0.91	0.93	1.04
Arl8b	11	1.13	0.99	1.06	1.23
Asrgl1	11	1.16	0.95	1.01	1.36
Atp5c1	11	1.01	0.85	0.92	1.12
Atp5l	11	1.02	0.95	0.95	1.07
Atp6v1f	11	1.08	0.89	0.93	1.14
Cct3	11	1.11	0.95	0.98	1.24
Cs	11	1.02	0.86	0.99	1.13
Dynlrb1	11	1.00	0.91	1.02	1.12
Fh	11	0.99	0.89	0.99	1.09
Gnaq	11	1.00	0.89	0.99	1.08

Supp. Table 2 (cont.)

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^{M}, developmental myelination response	eIF2B^{M}, remyelination response
Hibch	11	1.01	0.82	1.08	1.26
Ldhb	11	1.03	0.92	0.96	1.09
Rps9	11	1.05	0.91	1.07	1.28
Tufm	11	1.03	0.77	0.97	1.17
Usp9x	11	0.98	0.85	0.91	1.15
Xpnpep1	11	0.96	0.86	0.98	1.12
Apoa1bp	11	1.14	0.86	1.11	1.32
Hnrnpa3	11	1.14	0.95	1.09	1.41
Pygm	11	1.21	0.68	1.01	1.33
Cct7	11	1.14	0.82	0.88	1.26
Clasp2	11	0.94	0.79	0.82	1.09
Gltp	11	1.21	0.76	0.79	1.46
Immt	11	0.96	0.79	0.86	1.06
Napa	11	1.03	0.85	0.89	1.07
Ndufs8	11	0.96	0.76	0.82	1.08
Ndufv3	11	0.83	0.74	0.84	0.92
Rab24	11	1.01	0.46	0.56	0.91
Ube2o	11	1.06	0.60	0.70	0.98
Ckap5	11	1.63	0.56	0.58	1.06
Nefh	11	1.76	0.43	0.50	0.89
Map1b	11	4.15	0.25	0.35	1.44
Gpr158	11	1.07	0.65	0.75	0.86
Lrpprc	11	1.18	0.83	0.91	1.00
Rps17	11	1.21	0.93	0.89	1.08
Aifm1	11	1.37	0.69	0.89	1.18
Sept8	11	1.51	0.92	0.85	1.24
Lta4h	11	1.49	0.86	0.96	1.13
Dctn2	11	0.96	0.88	0.88	0.95
Hras	11	1.05	0.95	0.96	1.04
Acly	11	1.06	0.93	0.95	1.07
Cct6a	11	1.21	0.94	0.93	1.23
Etfb	11	1.13	0.90	0.96	1.03
Hspa12a	11	1.21	0.97	0.96	1.14
Kif5c	11	1.17	0.98	0.97	1.08
Ndufa4	11	1.11	0.96	0.94	1.09
Cops4	11	1.24	0.79	0.77	1.08
Ctnnb1	11	1.23	0.86	0.85	1.16
Sirt2	11	1.11	0.72	0.83	1.02
Slc17a7	11	1.10	0.75	0.88	0.95
Tpp2	11	1.10	0.88	0.92	1.06
Rpl21	11	1.10	1.06	0.81	1.53
Rala	11	0.90	0.88	0.86	0.90
Sept3	11	1.13	1.04	0.99	1.17
Abr	11	1.19	1.00	0.89	1.39
Pura	11	1.08	1.01	0.81	1.30
Rpl11	11	1.05	0.98	0.90	1.19

Supp. Table 2 (cont.)

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^M, developmental myelination response	eIF2B^M, remyelination response
Rps24	11	1.16	1.08	1.05	1.16
Wdr7	11	1.11	0.91	0.89	1.21
Xpo1	11	1.17	1.08	0.94	1.25
Add1	11	1.00	0.98	0.92	1.08
Cstb	11	1.18	1.12	0.99	1.19
Dynll1	11	1.04	1.12	0.79	1.15
Idh1	11	1.23	1.03	0.86	1.13
Ncdn	11	1.14	1.07	0.95	1.14
Nf1	11	1.06	1.06	0.85	1.16
Rab6b	11	1.09	1.08	0.97	1.10
Rps26	11	1.08	1.09	0.93	1.16
Tceb1	11	1.12	1.06	0.95	1.09
Actr2	11	1.01	0.90	0.66	1.18
Actr3	11	1.10	0.89	0.73	1.15
Afg3l2	11	1.09	0.96	0.86	1.03
Arf6	11	1.03	0.86	0.82	1.12
C19Orf70	11	1.18	0.95	0.77	1.18
Csnk2a2	11	1.09	0.95	0.83	1.08
Ddx3x	11	1.08	0.86	0.76	1.00
Dusp3	11	1.03	0.87	0.70	1.11
Dync1li2	11	1.39	0.96	0.64	1.16
Eprs	11	1.14	0.81	0.68	1.05
Fam49b	11	1.11	0.89	0.74	1.00
Rap2a	11	1.07	0.87	0.83	1.12
Rnpep	11	1.17	0.97	0.81	1.14
Rps4x	11	1.11	0.91	0.82	1.11
Srcin1	11	1.18	0.92	0.70	1.04
Ppp3ca	11	0.96	0.76	0.62	1.11
Atp1a1	12	0.64	1.32	1.10	1.44
Atp6v0a1	12	0.64	0.95	0.97	1.23
Atp6v0c	12	0.68	1.00	1.09	1.41
Cox6c	12	0.65	1.00	0.97	1.00
Eif1	12	0.30	0.83	0.99	1.78
Nd1	12	0.45	1.03	0.99	1.30
Nd4	12	0.71	1.02	1.10	1.32
Ndufa12	12	0.71	0.94	0.96	1.37
Ndufa2	12	0.66	0.94	0.97	1.32
Ndufa8	12	0.67	0.88	1.02	1.42
Ndufb6	12	0.62	0.91	0.92	1.32
Ndufs3	12	0.65	0.88	0.96	1.20
Phb2	12	0.68	0.88	1.03	1.27
Slc1a2	12	0.61	1.09	1.11	1.31
Thy1	12	0.68	1.10	0.97	1.15
Lasp1	12	0.18	0.57	0.56	1.89
Rph3a	12	0.24	0.30	0.29	0.32
Atp1a3	12	0.78	0.98	1.15	1.29

Supp. Table 2 (cont.)

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^M, developmental myelination response	eIF2B^M, remyelination response
Atp1b1	12	0.82	1.00	1.09	1.14
Cltc	12	0.88	1.00	1.03	1.14
Cox5a	12	0.76	0.90	0.94	0.99
Cse1l	12	0.80	1.00	1.07	1.10
Fth1	12	0.84	0.96	1.10	1.05
Mag	12	0.85	0.99	1.01	1.15
Ndufa10	12	0.76	1.00	0.92	1.22
Ndufb3	12	0.74	0.88	0.97	1.12
Ndufs6	12	0.79	0.92	0.90	1.15
Qdpr	12	0.77	0.93	1.08	1.08
Rpl17	12	0.72	0.92	1.19	1.36
Slc12a5	12	0.76	1.01	0.98	1.09
Tmed10	12	0.80	0.94	1.14	1.01
Vdac1	12	0.75	0.92	1.04	1.06
Arpc1a	12	0.93	1.18	1.10	1.33
Lrp1	12	0.84	1.10	1.00	1.12
Lxn	12	0.85	1.21	1.06	1.46
Ogdh	12	0.90	1.06	1.12	1.10
Ppib	12	0.87	1.05	1.09	1.12
Prkacb	12	0.90	1.18	1.18	1.19
Rps2	12	0.98	1.10	1.10	1.16
Rps8	12	0.94	1.20	1.26	1.38
Dctn1	12	0.98	1.20	1.50	1.42
Cyc1	12	0.89	0.95	1.00	0.96
Gsta4	12	0.91	0.99	1.06	1.03
Hk1	12	0.83	0.93	1.01	0.94
Prdx2	12	0.91	1.03	1.05	1.03
Rps13	12	0.79	0.95	1.01	0.98
Uqcrc2	12	0.84	0.93	0.99	0.98
Vsnl1	12	0.87	0.96	0.94	0.97
Stx12	12	0.74	0.90	0.85	0.89
Gnb1	12	0.96	1.05	1.10	1.17
Mtch2	12	0.92	1.03	1.08	1.14
Prdx1	12	0.98	1.03	1.08	1.14
Ca2	12	0.86	1.03	0.95	1.05
Cct2	12	0.99	1.03	1.01	1.05
Opa1	12	0.95	1.02	1.00	1.08
Usp5	12	0.97	1.02	1.02	1.03
Ina	13	0.75	1.04	0.83	1.64
Itpr1	13	0.96	1.08	0.85	1.58
Mgst3	13	0.84	1.36	0.99	1.84
Vcan	13	0.91	1.19	0.84	1.60
Slc4a10	13	0.85	0.91	0.85	1.11
Gfap	13	0.72	1.69	0.93	1.61
Arf5	13	0.96	1.14	0.99	1.21
Atp2a2	13	0.84	1.30	0.97	1.41

Supp. Table 2 (cont.)

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^{M}, developmental myelination response	eIF2B^{M}, remyelination response
Grm3	13	0.84	1.20	0.91	1.37
Prkcg	13	0.78	1.18	0.82	1.39
Sfxn3	13	0.82	1.19	0.96	1.15
Slc25a22	13	0.92	1.13	0.93	1.21
Crk	13	1.15	1.36	1.26	1.46
Atp6v1c1	13	0.95	0.98	0.93	1.01
Cox4l1	13	0.92	0.95	0.92	0.98
Dynll2	13	0.96	0.97	0.96	0.97
Pdia3	13	0.92	0.97	0.94	1.06
Aldoa	13	0.98	1.08	1.01	1.21
Cap2	13	1.03	1.06	0.91	1.23
Kiaa1468	13	0.95	1.01	0.84	1.32
Ndufa6	13	0.91	1.02	0.95	1.13
Paics	13	1.14	1.20	0.99	1.31
Atp2b2	13	0.98	1.04	0.93	1.11
Crmp1	13	0.98	1.00	0.94	1.09
Dhx9	13	0.95	1.12	0.92	1.14
Dmxl2	13	1.07	1.14	0.93	1.24
Gng3	13	1.01	1.08	0.92	1.11
Ldha	13	0.97	1.10	0.92	1.13
Lsamp	13	0.89	1.04	0.94	1.06
Nbea	13	1.03	1.17	0.91	1.20
Nsf	13	0.98	1.01	0.95	1.02
Rps18	13	0.95	1.18	0.85	1.18
Rps3	13	1.00	1.09	0.95	1.10
Stxbp1	13	0.98	1.08	1.02	1.11
Tpt1	13	0.95	1.01	0.91	1.07
Tubb3	13	0.99	1.03	1.01	1.07
Tubb4a	13	1.03	1.09	0.90	1.16
Ywhah	13	0.92	1.02	0.97	1.08
Tf	13	0.79	0.81	0.59	1.20
Ak3	14	1.00	0.79	0.87	1.45
Cnp	14	1.01	0.80	0.91	1.51
Mbp	14	1.03	0.76	0.94	1.65
Mog	14	0.90	0.73	1.01	1.80
Nefl	14	0.97	0.94	0.77	1.85
Nefm	14	1.03	0.98	0.78	1.68
Picalm	14	0.93	0.88	0.89	1.95
Prkcb	14	0.87	0.87	0.82	1.70
Cryab	14	1.09	0.81	1.12	3.79
Napg	14	1.03	0.92	0.96	1.72
Rab3gap1	14	1.05	0.79	0.79	2.31
March2	14	0.89	0.86	0.93	1.26
Dlg1	14	0.89	0.75	0.87	1.21
Ndufb4	14	0.92	0.91	0.91	1.28
Ndufc2	14	0.82	0.77	0.80	1.12

Supp. Table 2 (cont.)

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^{M}, developmental myelination response	eIF2B^{M}, remyelination response
Ndufs5	14	0.91	0.90	0.94	1.12
Rapgef2	14	0.74	0.86	0.80	1.40
Slc25a11	14	0.90	0.87	0.93	1.19
Atp6v1e1	14	0.93	0.90	0.92	0.99
Eif4a2	14	0.96	0.92	0.92	1.02
Vps35	14	0.97	0.94	0.93	1.03
Aars	14	1.06	1.05	1.01	1.18
Arpc3	14	1.01	0.98	0.93	1.18
Atp5f1	14	0.97	0.92	0.92	1.10
Cdh2	14	1.06	1.08	1.06	1.14
Cfl1	14	1.01	0.98	0.95	1.13
Dpysl4	14	1.03	0.95	0.94	1.17
Gapdh/Loc	14	1.01	0.96	1.02	1.39
Gstm3	14	0.98	0.94	0.99	1.10
Gstp1	14	1.00	0.97	1.01	1.12
Hnrnpc	14	1.05	1.03	1.07	1.23
Kcnab2	14	1.03	0.98	1.01	1.24
Myh9	14	1.01	0.86	0.94	1.30
Ndufa13	14	0.97	0.90	0.89	1.32
Ogt	14	1.04	0.98	0.91	1.23
Pdcd6	14	0.93	0.97	0.95	1.24
Rpl18	14	1.00	0.94	1.01	1.37
Rpl7	14	1.01	1.02	0.87	1.35
Rps7	14	1.00	0.95	1.01	1.30
Sfxn5	14	1.07	0.86	0.94	1.39
Sv2a	14	1.04	0.94	0.97	1.17
Arf3	14	1.02	1.03	0.97	1.11
Tubb2a	14	1.03	1.03	1.02	1.06
Ndufa7	14	0.94	0.82	0.79	1.12
Pip5k1c	14	0.93	0.81	0.78	1.20
Idh3a	14	0.65	0.89	1.04	2.27
Gucy1b3	14	1.18	1.05	1.40	1.74
Plp1	14	0.88	0.96	1.04	1.92
Brp44	14	0.89	0.81	1.00	1.28
Cct5	14	0.89	0.93	1.03	1.26
Cox2	14	0.81	0.86	1.02	1.36
Cox5b	14	0.80	0.77	0.93	1.33
Fasn	14	0.92	0.92	1.04	1.39
Myo18a	14	0.83	0.87	0.94	1.22
Ndufa9	14	0.80	0.91	1.03	1.28
Ndufb5	14	0.76	0.82	1.02	1.29
Ndufs1	14	0.74	0.85	0.97	1.17
Ndufs2	14	0.88	0.81	0.97	1.12
Phb	14	0.72	0.84	1.07	1.24
Pvalb	14	0.84	0.89	0.97	1.23
Scn9a	14	0.73	0.81	0.95	1.33

Supp. Table 2 (cont.)

Symbol	Cluster	WT, developmental myelination response	WT, remyelination response	eIF2B^M, developmental myelination response	eIF2B^M, remyelination response
Slc25a12	14	0.91	0.93	1.03	1.28
Slc6a1	14	0.78	0.78	1.02	1.15
Uqcrc1	14	0.85	0.88	0.95	1.10
Uqcrq	14	0.96	0.84	1.06	1.34
Vdac2	14	0.85	0.94	1.09	1.22
Ndufb10	14	0.73	0.80	0.81	1.00
Ak1	14	0.96	0.94	1.03	1.10
Atp5J2	14	0.98	0.93	1.10	1.32
Atp5o	14	0.95	0.93	0.99	1.15
Atp6v0d1	14	0.92	1.04	1.01	1.29
Cmpk1	14	1.06	1.01	1.11	1.26
Hadha	14	1.02	0.99	1.05	1.08
Iars2	14	1.00	1.06	1.15	1.36
Myh10	14	0.98	0.94	1.06	1.19
Ndufs7	14	0.99	0.91	1.06	1.27
Otub1	14	1.00	1.04	1.04	1.17
Prkaca	14	0.96	1.01	1.03	1.19
Pygb	14	1.05	1.02	1.06	1.13
Rab5b	14	0.94	0.96	1.04	1.12
Ufc1	14	0.93	0.94	1.17	1.44

Supp. Table 3

Eif2b5^{M}, w11		WT, w11		Eif2b5^{M}, w12		WT, w12	
Movement Disorders	1.97E-63	Movement Disorders	9.41E-69	Movement Disorders	1.09E-70	Movement Disorders	6.42E-65
disorder of basal ganglia	2.09E-59	disorder of basal ganglia	2.95E-67	disorder of basal ganglia	5.79E-66	disorder of basal ganglia	1.40E-58
neuromuscular disease	1.98E-51	neuromuscular disease	7.43E-60	neuromuscular disease	1.91E-57	neuromuscular disease	5.05E-50
neurological signs	7.54E-46	Huntington's Disease	1.84E-52	Huntington's Disease	7.84E-52	neurological signs	2.18E-43
Huntington's Disease	2.83E-45	neurological signs	1.31E-51	neurological signs	1.01E-49	Huntington's Disease	4.02E-42
dyskinesia	1.17E-43	dyskinesia	1.24E-49	organization of cytoplasm	2.21E-49	dyskinesia	6.20E-41
organization of cytoplasm	2.36E-42	organization of cytoplasm	6.28E-44	dyskinesia	4.91E-49	organization of cytoplasm	2.95E-40
organization of cytoskeleton	6.42E-40	organization of cytoskeleton	1.31E-42	organization of cytoskeleton	1.26E-47	organization of cytoskeleton	4.26E-40
microtubule dynamics	4.81E-39	microtubule dynamics	6.88E-41	microtubule dynamics	4.38E-46	microtubule dynamics	5.15E-38
formation of cellular protrusions	1.77E-34	formation of cellular protrusions	4.58E-33	formation of cellular protrusions	9.22E-37	formation of cellular protrusions	2.01E-33
development of neurons	4.59E-32	development of neurons	6.38E-31	development of neurons	7.18E-36	development of neurons	1.57E-30
formation of plasma membrane projections	2.53E-30	neuritogenesis	3.96E-30	neuritogenesis	2.12E-34	formation of plasma membrane projections	2.10E-29
neuritogenesis	4.58E-30	formation of plasma membrane projections	1.81E-29	formation of plasma membrane projections	1.51E-33	neuritogenesis	2.62E-29
necrosis	7.78E-27	transport of molecule	2.73E-29	transport of molecule	1.38E-28	transport of molecule	1.41E-28
cell death	7.70E-26	cell death	4.51E-28	Schizophrenia	4.32E-28	Viral Infection	2.10E-24
transport of molecule	1.16E-25	necrosis	4.87E-26	cell death	1.05E-26	morphogenesis of neurons	1.34E-23
transport of vesicles	4.23E-25	long-term potentiation	5.52E-26	neurotransmission	1.83E-25	Schizophrenia	3.37E-23
metabolism of nucleic acid component or derivative	4.49E-24	Schizophrenia	2.41E-25	long-term potentiation	1.45E-24	neurotransmission	3.52E-23
transport of synaptic vesicles	1.54E-23	secretory pathway	5.28E-25	necrosis	5.05E-24	long-term potentiation	6.84E-23
Schizophrenia	2.92E-23	metabolism of nucleic acid component or derivative	1.76E-24	morphogenesis of neurons	6.55E-24	morphogenesis of neurites	8.17E-23
morphogenesis of neurons	3.10E-23	transport of vesicles	3.15E-24	growth of neurites	1.76E-23	shape change of neurons	1.39E-22
Viral Infection	1.05E-22	exocytosis	3.37E-24	behavior	1.79E-23	branching of neurons	1.47E-22
morphogenesis of neurites	1.59E-22	neurotransmission	1.04E-23	synaptic transmission	1.88E-23	synaptic transmission	3.03E-22
secretory pathway	1.74E-22	endocytosis	4.13E-23	secretory pathway	1.94E-23	endocytosis	3.45E-22
exocytosis	2.09E-22	Viral Infection	7.03E-23	exocytosis	2.02E-23	necrosis	5.67E-22
long-term potentiation	3.83E-22	formation of filaments	7.13E-23	development of cytoplasm	2.58E-23	secretory pathway	7.92E-22
proliferation of cells	5.70E-22	tauopathy	1.01E-22	morphogenesis of neurites	2.95E-23	cell death	9.27E-22
neurotransmission	8.30E-22	development of cytoplasm	3.43E-22	Viral Infection	6.27E-23	exocytosis	1.11E-21
behavior	2.88E-21	synaptic transmission	1.26E-21	proliferation of cells	9.68E-23	dendritic growth/branching	3.46E-21
metabolism of purine nucleotide	3.92E-21	Dementia	2.80E-21	metabolism of nucleic acid component or derivative	1.39E-22	branching of neurites	5.15E-21
tauopathy	5.52E-21	outgrowth of neurites	3.14E-21	outgrowth of neurites	2.43E-22	morphology of nervous tissue	9.86E-21
endocytosis	6.55E-21	proliferation of cells	3.90E-21	formation of filaments	9.15E-22	progressive motor neuropathy	1.50E-20
synaptic transmission	7.93E-21	amyloidosis	4.12E-21	outgrowth of cells	1.56E-21	morphology of neurons	1.65E-20
metabolism of nucleotide	2.16E-20	transport of synaptic vesicles	5.38E-21	tauopathy	7.98E-21	morphology of neurites	3.37E-20
neuronal cell death	3.70E-20	metabolism of nucleotide	6.76E-21	proliferation of neuronal cells	1.31E-20	tauopathy	3.94E-20
metabolism of nucleoside triphosphate	4.98E-20	progressive motor neuropathy	6.91E-21	morphology of nervous tissue	2.82E-20	transport of synaptic vesicles	4.09E-20
outgrowth of neurites	5.89E-20	neuronal cell death	8.92E-21	morphology of neurons	3.20E-20	synaptic depression	5.60E-20

Supp. Table 3 (cont.)

Eif2b5^{M}, w11		WT, w11		Eif2b5^{M}, w12		WT, w12	
branching of neurons	1.06E-19	behavior	1.20E-20	endocytosis	4.25E-20	metabolism of nucleoside triphosphate	6.33E-20
shape change of neurons	1.09E-19	outgrowth of cells	1.81E-20	transport of synaptic vesicles	7.92E-20	metabolism of nucleic acid component or derivative	1.20E-19
growth of neurites	1.84E-19	morphogenesis of neurons	2.34E-20	transport of protein	9.62E-20	outgrowth of neurites	1.43E-19
amyloidosis	2.16E-19	growth of neurites	2.40E-20	transport of vesicles	1.30E-19	development of cytoplasm	1.44E-19
morphology of nervous tissue	3.05E-19	Alzheimer's disease	2.69E-20	formation of cytoskeleton	1.33E-19	growth of neurites	1.85E-19
formation of filaments	4.03E-19	metabolism of purine nucleotide	8.92E-20	metabolism of nucleotide	1.73E-19	transport of vesicles	1.96E-19
morphology of neurons	4.22E-19	metabolism of nucleoside triphosphate	9.05E-20	cognition	2.48E-19	outgrowth of cells	3.36E-19
Dementia	5.01E-19	morphogenesis of neurites	1.00E-19	branching of neurons	2.61E-19	neuronal cell death	4.64E-19
outgrowth of cells	7.04E-19	transport of protein	1.00E-19	amyloidosis	2.82E-19	Dementia	4.67E-19
polymerization of protein	1.38E-18	exocytosis by cells	3.35E-19	translation	2.93E-19	amyloidosis	5.27E-19
branching of neurites	2.42E-18	formation of cytoskeleton	5.01E-19	shape change of neurons	2.95E-19	Parkinson's disease	1.04E-18
development of cytoplasm	2.55E-18	hydrolysis of nucleotide	7.06E-19	apoptosis	4.37E-19	formation of filaments	1.79E-18
translation	2.91E-18	apoptosis	9.04E-19	synaptic depression	4.47E-19	metabolism of purine nucleotide	2.54E-18
dendritic growth/branching	4.38E-18	translation	1.31E-18	neuronal cell death	4.47E-19	exocytosis by cells	4.96E-18
exocytosis by cells	4.54E-18	proliferation of neuronal cells	2.57E-18	progressive motor neuropathy	5.55E-19	morphology of cellular protrusions	5.89E-18
Alzheimer's disease	6.36E-18	cell death of tumor cell lines	6.88E-18	Dementia	5.73E-19	Alzheimer's disease	8.68E-18
progressive motor neuropathy	2.40E-17	engulfment of cells	7.47E-18	exocytosis by cells	2.47E-18	organization of actin cytoskeleton	1.00E-17
morphology of neurites	2.69E-17	Parkinson's disease	8.13E-18	learning	2.50E-18	behavior	1.39E-17
proliferation of neuronal cells	3.82E-17	morphology of nervous tissue	8.90E-18	dendritic growth/branching	2.64E-18	abnormal morphology of neurons	1.77E-17
cognition	5.45E-17	morphology of neurons	1.07E-17	branching of neurites	4.39E-18	proliferation of neuronal cells	3.11E-17
morphology of nervous system	8.21E-17	branching of neurons	1.90E-17	shape change of neurites	4.93E-18	branching of cells	3.52E-17
organization of actin cytoskeleton	1.97E-16	synaptic depression	2.17E-17	Alzheimer's disease	5.32E-18	replication of Influenza A virus	5.23E-17
hydrolysis of nucleotide	2.39E-16	cognition	2.74E-17	polymerization of protein	5.84E-18	translation	6.85E-17
endocytosis of vesicles	2.61E-16	learning	2.78E-17	organization of actin cytoskeleton	7.17E-18	metabolism of nucleotide	7.84E-17
learning	2.63E-16	synthesis of protein	3.28E-17	morphology of neurites	8.22E-18	morphology of nervous system	7.97E-17
abnormal morphology of neurons	4.52E-16	morphology of plasma membrane projections	5.93E-17	synthesis of protein	1.01E-17	formation of cytoskeleton	8.90E-17
transport of protein	6.13E-16	dendritic growth/branching	6.49E-17	metabolism of purine nucleotide	1.07E-17	abnormal morphology of plasma membrane	8.98E-17
organization of organelle	6.82E-16	organismal death	1.34E-16	morphology of nervous system	1.22E-17	transport of protein	1.30E-16
morphology of cellular protrusions	8.14E-16	morphology of neurites	2.41E-16	synaptic transmission of cells	1.82E-17	proliferation of cells	2.34E-16
formation of cytoskeleton	1.30E-15	branching of neurites	3.07E-16	replication of Influenza A virus	2.50E-17	abnormal morphology of neurites	2.40E-16
synaptic depression	1.33E-15	shape change of neurites	3.28E-16	metabolism of nucleoside triphosphate	3.13E-17	morphology of axons	2.56E-16
cell death of tumor cell lines	1.48E-15	translation of protein	4.89E-16	abnormal morphology of neurons	4.28E-17	sprouting	4.68E-16
metabolism of ATP	1.67E-15	metabolism of protein	7.63E-16	polymerization of filaments	4.53E-17	synthesis of protein	5.22E-16
synthesis of protein	1.76E-15	organization of organelle	1.17E-15	translation of protein	1.18E-16	endocytosis of vesicles	5.90E-16

Supp. Table 3 (cont.)

Eif2b5^M, w11		WT, w11		Eif2b5^M, w12		WT, w12	
apoptosis	2.00E-15	synaptic transmission of cells	1.20E-15	Parkinson's disease	1.29E-16	engulfment of cells	1.15E-15
metabolism of protein	2.30E-15	organization of actin cytoskeleton	1.61E-15	metabolism of protein	1.41E-16	metabolism of protein	2.63E-15
exocytosis of vesicles	2.91E-15	endocytosis of vesicles	1.81E-15	hydrolysis of nucleotide	1.85E-16	metabolism of ATP	3.80E-15
synaptic transmission of cells	3.07E-15	morphology of nervous system	2.11E-15	cell death of tumor cell lines	1.91E-16	myopathy	3.86E-15
translation of protein	5.31E-15	morphology of cellular protrusions	2.13E-15	organismal death	3.73E-16	synaptic transmission of cells	4.52E-15
quantity of cellular protrusions	5.52E-15	polymerization of filaments	2.18E-15	morphology of cellular protrusions	4.57E-16	abnormal morphology of axons	4.73E-15
organismal death	7.37E-15	metabolism of ATP	2.36E-15	abnormal morphology of plasma membrane	8.79E-16	replication of RNA virus	5.29E-15
morphology of axons	7.56E-15	expression of protein	3.19E-15	expression of protein	9.18E-16	organization of organelle	5.45E-15
abnormal morphology of plasma membrane	9.00E-15	polymerization of protein	3.52E-15	quantity of cellular protrusions	1.41E-15	formation of neurites	7.62E-15
seizure disorder	1.03E-14	quantity of cellular protrusions	7.31E-15	abnormal morphology of neurites	1.48E-15	polymerization of protein	7.86E-15
catabolism of purine nucleotide	1.09E-14	morphology of cells	1.15E-14	morphology of axons	2.24E-15	quantity of vesicles	1.25E-14
abnormal morphology of neurites	1.17E-14	quantity of vesicles	1.17E-14	organization of organelle	3.25E-15	quantity of synaptic vesicles	1.33E-14
abnormal morphology of axons	1.48E-14	abnormal morphology of neurons	1.25E-14	engulfment of cells	6.65E-15	release of neurotransmitter	1.35E-14
branching of cells	1.86E-14	catabolism of purine nucleotide	1.48E-14	axonogenesis	7.40E-15	metabolism of dicarboxylic acid	1.36E-14
Parkinson's disease	1.94E-14	morphology of axons	1.66E-14	replication of RNA virus	8.35E-15	cognition	1.75E-14
cell death of neuroblastoma cell lines	3.56E-14	conformational modification of protein	1.73E-14	branching of cells	9.12E-15	abnormal morphology of nervous system	3.42E-14
apoptosis of neurons	4.58E-14	apoptosis of neurons	2.18E-14	Mood Disorders	1.04E-14	translation of protein	3.50E-14
replication of Influenza A virus	5.98E-14	myopathy	2.34E-14	cell death of neuroblastoma cell lines	1.75E-14	exocytosis of vesicles	4.03E-14
abnormal morphology of nervous system	7.54E-14	hydrolysis of GTP	2.37E-14	stabilization of filaments	1.87E-14	learning	4.36E-14
morphology of cells	7.56E-14	infection of cells	3.98E-14	seizure disorder	2.20E-14	polymerization of filaments	4.56E-14
expression of protein	9.87E-14	folding of protein	4.33E-14	long term depression	2.46E-14	replication of virus	6.73E-14
myopathy	1.02E-13	replication of Influenza A virus	4.75E-14	abnormal morphology of axons	2.89E-14	quantity of cellular protrusions	7.15E-14
metabolism of dicarboxylic acid	1.02E-13	replication of RNA virus	5.96E-14	seizures	2.92E-14	infection of cells	1.28E-13
formation of neurites	1.30E-13	long-term potentiation of synapse	8.28E-14	endocytosis of vesicles	3.44E-14	long term depression	1.37E-13
release of neurotransmitter	1.40E-13	branching of cells	9.05E-14	release of neurotransmitter	3.49E-14	apoptosis	1.56E-13
polymerization of filaments	1.95E-13	plasticity of synapse	1.10E-13	abnormal morphology of nervous system	6.41E-14	expression of protein	1.64E-13
engulfment of cells	2.01E-13	axonogenesis	1.38E-13	plasticity of synapse	1.08E-13	cell death of neuroblastoma cell lines	2.01E-13
sprouting	2.12E-13	seizure disorder	1.65E-13	replication of virus	1.13E-13	hydrolysis of nucleotide	2.81E-13
seizures	2.37E-13	release of neurotransmitter	1.69E-13	conformational modification of protein	1.28E-13	Mood Disorders	3.26E-13
infection of cells	2.43E-13	abnormal morphology of axons	2.07E-13	morphology of cells	1.73E-13	axonogenesis	3.36E-13
quantity of vesicles	2.85E-13	Mood Disorders	2.22E-13	locomotion	1.76E-13	cell death of tumor cell lines	3.70E-13
replication of RNA virus	3.12E-13	seizures	2.43E-13	hydrolysis of GTP	2.03E-13	catabolism of ATP	3.78E-13
endocytosis of synaptic vesicles	3.13E-13	abnormal morphology of neurites	2.58E-13	formation of neurites	2.57E-13	seizure disorder	4.20E-13
excitatory postsynaptic current	4.21E-13	exocytosis of vesicles	2.89E-13	targeting of protein	2.69E-13	formation of vesicles	6.47E-13
Mood Disorders	1.02E-12	abnormal morphology of plasma membrane	3.43E-13	folding of protein	3.22E-13	apoptosis of neurons	1.27E-12

Supp. Table 3 (cont.)

Eif2b5^{M}, w11		WT, w11		Eif2b5^{M}, w12		WT, w12	
stabilization of filaments	1.54E-12	catabolism of ATP	6.25E-13	sprouting	3.55E-13	long-term potentiation of synapse	1.30E-12
catabolism of ATP	6.08E-13	cell death of neuroblastoma cell lines	3.19E-13	exocytosis of vesicles	2.85E-13	assembly of cell-cell contacts	7.36E-13
locomotion	1.64E-12	replication of virus	6.96E-13	quantity of filaments	5.32E-13	synaptogenesis	1.37E-12
quantity of synaptic vesicles	1.76E-12	long term depression	1.01E-12	quantity of vesicles	5.39E-13	endocytosis of synaptic vesicles	1.48E-12
long-term potentiation of synapse	1.93E-12	long-term potentiation of brain	1.04E-12	morphology of central nervous system	9.89E-13	assembly of intercellular junctions	2.51E-12
targeting of protein	3.31E-12	endocytosis of synaptic vesicles	1.35E-12	long-term potentiation of brain	1.02E-12	organismal death	2.73E-12
infection by RNA virus	3.64E-12	targeting of protein	1.55E-12	metabolism of ATP	1.16E-12	infection by RNA virus	2.75E-12
assembly of cell-cell contacts	3.89E-12	abnormal morphology of nervous system	1.60E-12	apoptosis of tumor cell lines	1.69E-12	formation of plasma membrane	4.14E-12
axonogenesis	4.62E-12	locomotion	1.69E-12	infection of cells	1.70E-12	morphology of cells	4.67E-12
infection by Dengue virus 2	4.82E-12	infection by RNA virus	2.08E-12	stabilization of microtubules	1.85E-12	targeting of protein	5.01E-12
replication of virus	4.90E-12	morphology of central nervous system	2.52E-12	potentiation of synapse	2.80E-12	folding of protein	6.12E-12
recycling of synaptic vesicles	7.83E-12	quantity of filaments	2.72E-12	cell movement	3.11E-12	development of gap junctions	6.27E-12
benign neoplasia	8.53E-12	sprouting	3.03E-12	assembly of cell-cell contacts	3.13E-12	seizures	8.75E-12
assembly of intercellular junctions	1.22E-11	trafficking of vesicles	3.38E-12	apoptosis of neurons	3.16E-12	paralysis	1.86E-11
hydrolysis of GTP	1.24E-11	apoptosis of tumor cell lines	3.41E-12	bipolar disorder	4.54E-12	abnormal quantity of synaptic vesicles	2.94E-11
synaptogenesis	1.41E-11	size of body	3.63E-12	spatial learning	5.03E-12	recycling of synaptic vesicles	3.54E-11
development of gap junctions	1.82E-11	stabilization of filaments	3.83E-12	synaptogenesis	5.03E-12	plasticity of synapse	5.58E-11
quantity of filaments	1.92E-11	formation of neurites	4.25E-12	catabolism of purine nucleotide	6.20E-12	infection by Dengue virus 2	6.05E-11
excitatory postsynaptic potential	2.23E-11	spatial learning	5.15E-12	formation of vesicles	6.35E-12	transport of inorganic cation	7.12E-11
conformational modification of protein	2.91E-11	cell movement	5.67E-12	long-term potentiation of synapse	8.22E-12	morphology of central nervous system	7.23E-11
paralysis	3.51E-11	cell death of fibroblast cell lines	7.46E-12	development of gap junctions	8.41E-12	Diamond-Blackfan anemia	7.45E-11
stabilization of microtubules	3.65E-11	quantity of synaptic vesicles	1.03E-11	metabolism of dicarboxylic acid	9.18E-12	synthesis of purine nucleotide	8.08E-11
spatial learning	5.70E-11	excitatory postsynaptic potential	1.19E-11	assembly of intercellular junctions	9.43E-12	benign neoplasia	8.10E-11
infection of hepatoma cell lines	5.96E-11	infection of tumor cell lines	1.21E-11	formation of microtubules	1.04E-11	excitatory postsynaptic current	1.01E-10
cell death of brain	6.95E-11	morphology of brain	1.25E-11	morphology of brain	1.20E-11	infection of tumor cell lines	1.52E-10
formation of plasma membrane	7.70E-11	formation of actin filaments	1.33E-11	myopathy	1.26E-11	Neurodegeneration	1.60E-10
formation of vesicles	7.71E-11	synthesis of purine nucleotide	1.42E-11	synthesis of purine nucleotide	1.39E-11	cell death of central nervous system cells	1.81E-10
folding of protein	7.94E-11	synaptogenesis	2.05E-11	formation of plasma membrane	1.98E-11	cell death of brain	2.25E-10
biosynthesis of purine ribonucleotide	1.01E-10	recycling of synaptic vesicles	3.04E-11	polymerization of actin filaments	2.61E-11	long-term potentiation of brain	2.25E-10
long term depression	1.01E-10	formation of vesicles	3.40E-11	endocytosis of synaptic vesicles	3.01E-11	biosynthesis of purine ribonucleotide	2.26E-10
cell movement	1.32E-10	biosynthesis of purine ribonucleotide	3.41E-11	recycling of synaptic vesicles	3.01E-11	cell movement	2.30E-10
infection of tumor cell lines	1.34E-10	bundling of filaments	3.59E-11	infection by RNA virus	3.21E-11	locomotion	2.54E-10
autosomal dominant neuropathy	1.44E-10	long-term potentiation of cerebral cortex	3.66E-11	biosynthesis of purine ribonucleotide	3.35E-11	metabolism of NADH	2.71E-10
cell death of cervical cancer cell lines	1.48E-10	mitochondrial disorder	4.64E-11	chronic psoriasis	3.58E-11	morphology of intercellular junctions	2.87E-10
morphology of central nervous system	1.57E-10	stabilization of microtubules	6.45E-11	fusion of synaptic vesicles	4.08E-11	formation of microtubules	3.06E-10

Supp. Table 3 (cont.)

Eif2b5^{M}, w11		WT, w11		Eif2b5^{M}, w12		WT, w12	
cell death of central nervous system cells	1.66E-10	autosomal dominant neuropathy	6.75E-11	cell movement of neurons	5.46E-11	cell spreading	3.49E-10
abnormal quantity of synaptic vesicles	1.51E-10	translation of RNA	6.19E-11	formation of actin filaments	3.93E-11	formation of filopodia	2.90E-10
polymerization of actin filaments	1.77E-10	formation of microtubules	7.28E-11	size of body	5.53E-11	spatial learning	4.46E-10
chronic psoriasis	1.78E-10	cell death of central nervous system cells	9.69E-11	translation of RNA	6.05E-11	stabilization of filaments	4.52E-10
formation of lamellipodia	2.13E-10	leukoencephalopathy	9.90E-11	abnormal morphology of central nervous system	6.07E-11	translation of RNA	4.61E-10
size of body	2.39E-10	development of gap junctions	1.18E-10	infection of tumor cell lines	6.33E-11	quantity of filaments	4.75E-10
paired-pulse facilitation	2.40E-10	cell death of brain	1.24E-10	trafficking of vesicles	6.75E-11	hydrolysis of GTP	5.23E-10
Diamond-Blackfan anemia	2.51E-10	amyotrophic lateral sclerosis	1.29E-10	quantity of synaptic vesicles	1.09E-10	amyotrophic lateral sclerosis	5.28E-10
movement of organelle	2.58E-10	assembly of cell-cell contacts	1.29E-10	cell death of fibroblast cell lines	1.15E-10	infection of hepatoma cell lines	5.46E-10
cell death of fibroblast cell lines	2.80E-10	organization of filaments	1.36E-10	organization of filaments	1.33E-10	chronic psoriasis	6.35E-10
fatty acid metabolism	3.65E-10	morphology of cerebral cortex	1.39E-10	morphology of cerebral cortex	1.36E-10	mitochondrial disorder	6.60E-10
formation of microtubules	4.41E-10	metabolism of dicarboxylic acid	1.43E-10	migration of cells	1.45E-10	excitatory postsynaptic potential	8.01E-10
mitochondrial disorder	4.45E-10	abnormal morphology of central nervous system	1.48E-10	cell death of cervical cancer cell lines	1.54E-10	fusion of synaptic vesicles	8.36E-10
miniature excitatory postsynaptic currents	5.00E-10	exocytosis by pheochromocytoma cell lines	1.66E-10	exocytosis by pheochromocytoma cell lines	1.65E-10	polymerization of actin filaments	9.26E-10
neurogenic muscular atrophy	5.43E-10	long-term potentiation of hippocampus	1.70E-10	long-term potentiation of cerebral cortex	1.74E-10	exocytosis by pheochromocytoma cell lines	1.03E-09
peripheral neuropathy	6.16E-10	cell survival	1.81E-10	migration of neurons	1.85E-10	morphology of brain	1.06E-09
synthesis of purine nucleotide	6.18E-10	polymerization of actin filaments	1.83E-10	excitatory postsynaptic current	1.86E-10	trafficking of vesicles	1.36E-09
formation of actin filaments	6.63E-10	abnormal morphology of brain	2.12E-10	abnormal morphology of brain	2.04E-10	cell death of cerebral cortex cells	1.42E-09
cell spreading	7.95E-10	formation of plasma membrane	2.18E-10	mitochondrial disorder	2.18E-10	abnormal morphology of central nervous system	1.63E-09
metabolism of NADH	8.10E-10	bundling of microtubules	2.66E-10	catabolism of ATP	2.21E-10	migration of cells	1.78E-09
apoptosis of tumor cell lines	8.19E-10	neurogenic muscular atrophy	2.81E-10	abnormal morphology of hippocampus layer	2.64E-10	benign thyroid nodule	1.78E-09
paired-pulse facilitation of synapse	8.21E-10	assembly of intercellular junctions	3.66E-10	excitatory postsynaptic potential	2.72E-10	metabolism of medium chain dicarboxylic acid	1.78E-09
plasticity of synapse	9.25E-10	benign neoplasia	4.17E-10	cell spreading	3.76E-10	degeneration of nervous system	2.02E-09
cell survival	1.03E-09	migration of cells	4.17E-10	benign neoplasia	3.99E-10	organization of filaments	2.13E-09
morphology of brain	1.29E-09	translation of mRNA	4.51E-10	formation of filopodia	4.17E-10	paired-pulse facilitation	2.35E-09
Charcot-Marie-Tooth disease	1.47E-09	engulfment of tumor cell lines	6.02E-10	translation of mRNA	4.42E-10	formation of actin filaments	2.48E-09
abnormal morphology of hippocampus layer	1.48E-09	Charcot-Marie-Tooth disease	6.84E-10	bundling of filaments	4.80E-10	cell death of fibroblast cell lines	2.53E-09
Neurodegeneration	1.49E-09	formation of lamellipodia	8.08E-10	leukoencephalopathy	5.64E-10	extension of cellular protrusions	2.55E-09
bundling of filaments	1.57E-09	Neurodegeneration	9.97E-10	paralysis	6.21E-10	cell survival	2.57E-09
cell movement of neurons	1.99E-09	necrosis of kidney	9.98E-10	morphology of intercellular junctions	7.39E-10	bipolar disorder	3.11E-09
abnormal morphology of central nervous system	2.22E-09	formation of focal adhesions	1.08E-09	cell death of central nervous system cells	7.75E-10	degeneration of cells	3.66E-09
idiopathic dilated cardiomyopathy	2.27E-09	formation of cellular inclusion bodies	1.27E-09	long-term potentiation of hippocampus	8.04E-10	translation of mRNA	4.01E-09

Supp. Table 3 (cont.)

Eif2b5^{M}, w11		WT, w11		Eif2b5^{M}, w12		WT, w12	
transport of inorganic cation	2.46E-09	movement of organelle	1.50E-09	invasion of cells	8.45E-10	allergic pulmonary eosinophilia	4.19E-09
fusion of synaptic vesicles	2.23E-09	cell death of cervical cancer cell lines	1.11E-09	formation of lamellipodia	7.92E-10	formation of dendrites	3.86E-09
cell death of brain cells	2.51E-09	cell movement of neurons	1.72E-09	cell death of brain	9.75E-10	abnormal morphology of brain	4.99E-09
exocytosis by pheochromocytoma cell lines	3.06E-09	cell movement of central nervous system cells	1.95E-09	long term depression of cells	1.06E-09	cell death of cervical cancer cell lines	5.11E-09
migration of cells	3.71E-09	peripheral neuropathy	2.17E-09	cell movement of tumor cell lines	1.19E-09	small GTPase mediated signal transduction	5.34E-09
long-term potentiation of brain	3.81E-09	transport of inorganic cation	2.19E-09	movement of organelle	1.48E-09	ataxia	5.55E-09
cell movement of central nervous system cells	4.32E-09	infection by Dengue virus 2	2.24E-09	tremor	1.79E-09	tremor	6.84E-09
abnormal morphology of brain	4.65E-09	cell death of kidney cells	2.26E-09	cell movement of central nervous system cells	1.92E-09	cell movement of central nervous system cells	7.30E-09
cell death of cerebral cortex cells	4.67E-09	small GTPase mediated signal transduction	2.32E-09	metabolism of NADH	1.97E-09	idiopathic dilated cardiomyopathy	7.46E-09
trafficking of vesicles	5.49E-09	bipolar disorder	2.37E-09	transport of inorganic cation	2.13E-09	apoptosis of tumor cell lines	7.72E-09
metabolism of medium chain dicarboxylic acid	5.88E-09	infection of hepatoma cell lines	2.68E-09	infection by Dengue virus 2	2.22E-09	leukoencephalopathy	8.06E-09
formation of filopodia	6.36E-09	cell death of brain cells	3.10E-09	synaptic transmission of nervous tissue	2.87E-09	inclusion body myopathy	8.79E-09
ataxia	6.88E-09	cell spreading	3.11E-09	cell death of cerebral cortex cells	3.10E-09	differentiation of cells	9.60E-09
migration of neurons	7.26E-09	cell death of cerebral cortex cells	3.17E-09	amyotrophic lateral sclerosis	4.03E-09	formation of lamellipodia	1.06E-08
tremor	8.02E-09	morphology of intercellular junctions	4.04E-09	cell survival	4.20E-09	paired-pulse facilitation of synapse	1.13E-08
differentiation of cells	8.75E-09	degeneration of cells	4.17E-09	abnormal morphology of cerebral cortex	4.69E-09	cell death of brain cells	1.17E-08
bipolar disorder	9.09E-09	internalization of protein	4.41E-09	growth of axons	4.78E-09	degradation of mitochondria	1.17E-08
migration of central nervous system cells	9.22E-09	proliferation of tumor cell lines	4.56E-09	synthesis of ADP	4.93E-09	degeneration of neurites	1.18E-08
exocytosis of synaptic vesicles	9.95E-09	abnormal morphology of hippocampus layer	4.66E-09	formation of dendrites	5.37E-09	long-term potentiation of cerebral cortex	1.25E-08
invasion of cells	1.22E-08	abnormal morphology of cerebral cortex	4.79E-09	ataxia	5.64E-09	transport of metal	1.26E-08
leukoencephalopathy	1.32E-08	fusion of synaptic vesicles	4.96E-09	autosomal dominant neuropathy	6.22E-09	morphology of cerebral cortex	1.30E-08
organization of filaments	1.46E-08	synthesis of ADP	4.96E-09	disassembly of filaments	6.96E-09	movement of organelle	1.46E-08
sensory neuropathy	1.55E-08	migration of brain cells	5.19E-09	cell movement of brain cells	7.13E-09	stabilization of microtubules	1.55E-08
organization of cellular membrane	1.59E-08	infection of cervical cancer cell lines	5.48E-09	abnormal quantity of synaptic vesicles	7.62E-09	disruption of filaments	1.61E-08
morphology of intercellular junctions	1.66E-08	migration of neurons	5.58E-09	expression of mRNA	7.63E-09	degeneration of axons	1.70E-08
length of plasma membrane projections	1.71E-08	degeneration of nervous system	6.08E-09	extension of cellular protrusions	8.28E-09	conditioning	1.88E-08
allergic pulmonary eosinophilia	1.83E-08	excitatory postsynaptic current	6.69E-09	quantity of plasma membrane projections	8.34E-09	fatty acid metabolism	2.01E-08
extension of cellular protrusions	1.88E-08	cell movement of brain cells	7.24E-09	paired-pulse facilitation	9.46E-09	growth of axons	2.01E-08
hereditary motor and sensory neuropathy	2.08E-08	abnormal quantity of synaptic vesicles	7.69E-09	inborn error of amino acid metabolism	1.10E-08	fusion of vesicles	2.41E-08
migration of brain cells	2.08E-08	expression of mRNA	7.81E-09	proliferation of tumor cell lines	1.16E-08	autosomal dominant neuropathy	2.46E-08
cell movement of brain cells	2.12E-08	cell death of kidney cell lines	8.11E-09	infection of cervical cancer cell lines	1.19E-08	cytokinesis	2.62E-08
demyelinating peripheral neuropathy	2.45E-08	chronic psoriasis	9.21E-09	oligomerization of protein	1.43E-08	infection by HIV-1	2.89E-08

Supp. Table 3 (cont.)

Eif2b5^{M}, w11		WT, w11		Eif2b5^{M}, w12		WT, w12	
infection by HIV-1	2.54E-08	cell viability	9.27E-09	differentiation of cells	1.59E-08	miniature excitatory postsynaptic currents	3.34E-08
growth of axons	2.20E-08	Charcot-Marie-Tooth disease type 2	8.93E-09	gliosis	1.28E-08	mammary tumor	2.68E-08
oligomerization of protein	2.58E-08	paired-pulse facilitation	9.57E-09	Neurodegeneration	1.80E-08	receptor-mediated endocytosis	3.41E-08
small GTPase mediated signal transduction	2.79E-08	migration of central nervous system cells	1.39E-08	infection of hepatoma cell lines	1.84E-08	Nonaka myopathy	3.95E-08
polymerization of actin	2.94E-08	synaptic transmission of nervous tissue	1.39E-08	length of plasma membrane projections	1.87E-08	sporadic amyotrophic lateral sclerosis	4.35E-08
inborn error of amino acid metabolism	3.16E-08	synthesis of nucleotide	1.81E-08	neurogenic muscular atrophy	2.05E-08	morphology of central nervous system cells	4.68E-08
long-term potentiation of cerebral cortex	3.32E-08	miniature excitatory postsynaptic currents	1.86E-08	fatty acid metabolism	2.07E-08	cell movement of neurons	4.74E-08
degeneration of nervous system	3.38E-08	demyelinating peripheral neuropathy	1.89E-08	internalization of protein	2.11E-08	bundling of filaments	4.91E-08
translation of RNA	3.69E-08	length of plasma membrane projections	1.90E-08	Diamond-Blackfan anemia	2.25E-08	fragmentation of mitochondria	4.91E-08
long-term potentiation of hippocampus	3.97E-08	receptor-mediated endocytosis	1.98E-08	cell death of brain cells	2.28E-08	cell movement of brain cells	4.94E-08
mammary tumor	4.33E-08	formation of filopodia	2.09E-08	psoriasis	2.28E-08	fragmentation of Golgi apparatus	5.27E-08
synaptic transmission of nervous tissue	4.41E-08	fatty acid metabolism	2.14E-08	fusion of vesicles	2.37E-08	synthesis of ADP	5.69E-08
formation of dendrites	4.74E-08	sensory neuropathy	2.14E-08	migration of brain cells	2.57E-08	disassembly of filaments	6.40E-08
benign neoplasm of female genital organ	5.03E-08	Diamond-Blackfan anemia	2.26E-08	small GTPase mediated signal transduction	2.74E-08	length of plasma membrane projections	6.68E-08
morphology of central nervous system cells	5.37E-08	infection by HIV-1	2.60E-08	paired-pulse facilitation of synapse	2.98E-08	engulfment of tumor cell lines	7.48E-08
amyotrophic lateral sclerosis	5.51E-08	hereditary motor and sensory neuropathy	2.60E-08	formation of cellular inclusion bodies	3.24E-08	transport of monovalent inorganic cation	7.50E-08
Charcot-Marie-Tooth disease type 2	5.68E-08	extension of cellular protrusions	2.67E-08	X-linked mental retardation	3.90E-08	long-term potentiation of hippocampus	7.56E-08
engulfment of tumor cell lines	6.04E-08	paralysis	2.79E-08	organization of actin filaments	4.08E-08	biosynthesis of nucleoside triphosphate	7.74E-08
translation of mRNA	7.27E-08	organization of cellular membrane	2.96E-08	synthesis of nucleotide	4.16E-08	degeneration of neurons	8.52E-08
internalization of protein	7.50E-08	secretion of molecule	2.98E-08	morphology of central nervous system cells	4.48E-08	posttetanic potentiation	8.79E-08
fusion of cellular membrane	7.60E-08	paired-pulse facilitation of synapse	3.01E-08	fusion of cellular membrane	4.66E-08	cell movement of tumor cell lines	9.60E-08
abnormal morphology of metencephalon	7.60E-08	cell death of connective tissue cells	3.24E-08	mammary tumor	4.71E-08	size of body	9.74E-08
necrosis of kidney	7.90E-08	transmembrane potential of mitochondria	3.24E-08	Charcot-Marie-Tooth disease	5.18E-08	organization of plasma membrane	1.02E-07
degeneration of cells	8.16E-08	invasion of cells	3.93E-08	conditioning	5.74E-08	abnormal morphology of hippocampus layer	1.06E-07
uterine leiomyoma	8.32E-08	X-linked mental retardation	3.95E-08	allergic pulmonary eosinophilia	6.00E-08	exchange of nucleotide	1.06E-07
cell death of kidney cells	8.80E-08	cell viability of tumor cell lines	4.09E-08	mitochondrial respiratory chain deficiency	6.06E-08	synaptic transmission of nervous tissue	1.12E-07
cell death of kidney cell lines	9.42E-08	development of central nervous system	4.10E-08	respiratory rhythm	6.06E-08	gliosis	1.22E-07
cell viability	9.68E-08	quantity of plasma membrane projections	4.12E-08	migration of central nervous system cells	6.22E-08	concentration of glutathione	1.24E-07
mitochondrial respiratory chain deficiency	1.13E-07	morphology of central nervous system cells	4.56E-08	migration of tumor cell lines	6.33E-08	Breast Cancer and Tumors	1.25E-07
length of neurites	1.21E-07	transport of metal	5.94E-08	idiopathic dilated cardiomyopathy	8.91E-08	degeneration of brain	1.46E-07

Supp. Table 3 (cont.)

Eif2b5^{M}, w11		WT, w11		Eif2b5^{M}, w12		WT, w12	
abnormal morphology of rhombencephalon	1.23E-07	allergic pulmonary eosinophilia	6.06E-08	infection by HIV-1	9.48E-08	cell death of hippocampal cells	1.46E-07
degeneration of axons	1.20E-07	organization of nervous tissue	5.23E-08	exchange of nucleotide	6.79E-08	cellular degradation	1.41E-07
development of cerebral cortex	1.13E-07	fusion of cellular membrane	4.71E-08	bundling of microtubules	6.79E-08	metabolism of reactive oxygen species	1.36E-07
elongation of neurites	1.16E-07	mammary tumor	4.98E-08	endocytosis of protein	6.79E-08	psoriasis	1.40E-07
cytokinesis	1.25E-07	mitochondrial respiratory chain deficiency	6.12E-08	transmembrane potential of mitochondria	9.49E-08	breast cancer	1.53E-07
conditioning	1.25E-07	respiration of fibroblast cell lines	6.30E-08	length of neurites	1.01E-07	morphology of dendrites	1.54E-07
benign thyroid nodule	1.26E-07	endocytosis of protein	6.84E-08	abnormal respiratory rhythm	1.08E-07	transport of ion	1.54E-07
sporadic amyotrophic lateral sclerosis	1.26E-07	exchange of nucleotide	6.84E-08	cell viability	1.10E-07	infection of cervical cancer cell lines	1.57E-07
transport of mitochondria	1.26E-07	inclusion body myopathy	7.44E-08	depolymerization of filaments	1.12E-07	ruffling	1.70E-07
synthesis of ADP	1.33E-07	metabolism of NADH	7.99E-08	degeneration of axons	1.13E-07	long term depression of synapse	1.76E-07
autosomal dominant disease	1.48E-07	degeneration of central nervous system	8.03E-08	Breast Cancer and Tumors	1.17E-07	exocytosis of dense-core vesicles	1.80E-07
prepulse inhibition	1.51E-07	tremor	8.48E-08	polymerization of actin	1.18E-07	migration of neurons	1.86E-07
glycolysis of cells	1.56E-07	degradation of DNA	8.55E-08	miniature excitatory postsynaptic currents	1.18E-07	proliferation of tumor cell lines	1.94E-07
coordination	1.73E-07	idiopathic dilated cardiomyopathy	8.99E-08	secretion of molecule	1.21E-07	extension of plasma membrane projections	1.97E-07
Breast Cancer and Tumors	1.79E-07	formation of dendrites	9.01E-08	cell death of connective tissue cells	1.21E-07	organization of nervous tissue	2.11E-07
primary cardiomyopathy	1.82E-07	metabolism of reactive oxygen species	9.47E-08	long term depression of neurons	1.31E-07	internalization of protein	2.13E-07
proliferation of tumor cell lines	1.83E-07	degeneration of axons	1.14E-07	breast cancer	1.31E-07	synthesis of ATP	2.77E-07
leiomyomatosis	2.07E-07	polymerization of actin	1.19E-07	engulfment of tumor cell lines	1.35E-07	autosomal dominant disease	2.82E-07
breast cancer	2.09E-07	phagocytosis	1.21E-07	transport of metal	1.41E-07	processing of RNA	2.86E-07
fragmentation of Golgi apparatus	2.21E-07	Breast Cancer and Tumors	1.23E-07	metabolism of glutamine family amino acid	1.46E-07	rearrangement of cytoskeleton	2.88E-07
cell death of hippocampal cells	2.33E-07	fusion of vesicles	1.33E-07	degeneration of cells	1.49E-07	long term depression of cells	2.90E-07
infection of cervical cancer cell lines	2.55E-07	breast cancer	1.38E-07	neurotransmission of brain cells	1.62E-07	expression of mRNA	3.01E-07
morphology of cerebellum	2.72E-07	autosomal dominant Charcot-Marie-Tooth disease type 2	1.39E-07	biosynthesis of nucleoside triphosphate	1.80E-07	distal myopathy	3.01E-07
expression of mRNA	2.73E-07	apoptosis of kidney cell lines	1.45E-07	cell death of kidney cells	1.84E-07	follicular adenoma	3.01E-07
morphology of cerebral cortex	2.79E-07	modification of reactive oxygen species	1.47E-07	necrosis of kidney	1.87E-07	modification of reactive oxygen species	3.01E-07
quantity of filopodia	2.85E-07	disassembly of filaments	1.49E-07	polymerization of microtubules	1.90E-07	cell viability	3.10E-07
rearrangement of cytoskeleton	3.15E-07	conditioning	1.73E-07	apoptosis of cervical cancer cell lines	2.10E-07	invasion of cells	3.33E-07
bundling of microtubules	3.33E-07	degeneration of brain	1.81E-07	Mitochondrial complex I deficiency	2.11E-07	migration of brain cells	3.35E-07
endocytosis of protein	3.33E-07	cell movement of tumor cell lines	1.82E-07	formation of focal adhesions	2.16E-07	diffuse B-cell lymphoma	3.53E-07
exchange of nucleotide	3.33E-07	biosynthesis of nucleoside triphosphate	1.82E-07	disruption of filaments	2.21E-07	transport of metal ion	3.57E-07
gliosis	3.34E-07	gliosis	1.86E-07	export of protein	2.33E-07	secretion of neurotransmitter	3.62E-07
cell death of connective tissue cells	3.34E-07	degradation of mitochondria	1.92E-07	morphology of dendrites	2.35E-07	formation of cellular inclusion bodies	4.03E-07
synthesis of ATP	3.97E-07	release of catecholamine	2.23E-07	secretion of neurotransmitter	2.78E-07	exocytosis of synaptic vesicles	4.57E-07

Supp. Table 3 (cont.)

Eif2b5^M, w11		WT, w11		Eif2b5^M, w12		WT, w12	
abnormal morphology of cerebellum	4.06E-07	disruption of filaments	2.23E-07	morphology of hippocampus	2.84E-07	oxidation of protein	4.57E-07
ruffling	3.42E-07	differentiation of cells	1.98E-07	receptor-mediated endocytosis	2.52E-07	peripheral neuropathy	4.11E-07
degeneration of brain	3.63E-07	inborn error of amino acid metabolism	2.08E-07	degeneration of nervous system	2.68E-07	retraction of cellular protrusions	4.31E-07
Cytosis	3.69E-07	Mitochondrial complex I deficiency	2.12E-07	rearrangement of cytoskeleton	2.77E-07	Cytosis	4.54E-07
receptor-mediated endocytosis	4.06E-07	Nonaka myopathy	2.25E-07	metabolism of medium chain dicarboxylic acid	2.96E-07	formation of dendritic spines	4.71E-07
exocytosis of dense-core vesicles	4.19E-07	export of protein	2.35E-07	sporadic amyotrophic lateral sclerosis	2.96E-07	quantity of dendritic spines	4.71E-07
mitochondrial leukoencephalopathy	4.47E-07	morphology of dendrites	2.37E-07	cell death of kidney cell lines	3.19E-07	metabolism of oxalacetic acid	4.72E-07
inclusion body myopathy	4.76E-07	rearrangement of cytoskeleton	2.80E-07	cell spreading of tumor cell lines	3.24E-07	quantity of plasma membrane projections	4.84E-07
disassembly of filaments	4.98E-07	secretion of neurotransmitter	2.83E-07	metabolism of amino acids	3.50E-07	thyroid adenoma	5.06E-07
Leigh syndrome	5.17E-07	benign thyroid nodule	2.98E-07	quantity of actin filaments	3.52E-07	migration of central nervous system cells	5.16E-07
transport of metal	5.34E-07	metabolism of medium chain dicarboxylic acid	2.98E-07	exocytosis of synaptic vesicles	3.52E-07	organization of cellular membrane	5.23E-07
retraction of cellular protrusions	5.53E-07	sporadic amyotrophic lateral sclerosis	2.98E-07	quantity of microtubules	3.52E-07	neurogenic muscular atrophy	5.31E-07
head and neck neoplasia	5.78E-07	transport of mitochondria	2.98E-07	organization of nervous tissue	3.89E-07	size of axons	5.58E-07
transmembrane potential of mitochondria	5.83E-07	binding of GTP	3.28E-07	metabolism of amino acid analogs	4.00E-07	systemic light chain amyloidosis	5.58E-07
formation of cellular inclusion bodies	5.86E-07	ataxia	3.42E-07	synaptic transmission of brain cells	4.10E-07	cell death of connective tissue cells	5.72E-07
biosynthesis of nucleoside triphosphate	5.98E-07	exocytosis of synaptic vesicles	3.55E-07	sensory neuropathy	4.22E-07	cell spreading of tumor cell lines	6.12E-07
organization of actin filaments	5.98E-07	quantity of microtubules	3.55E-07	synthesis of ATP	4.43E-07	neurodegeneration of central nervous system	6.24E-07
disruption of filaments	6.14E-07	cellular degradation	3.70E-07	elongation of neurites	4.80E-07	abnormal morphology of cerebral cortex	6.55E-07
glioblastoma cancer	6.15E-07	neurodegeneration of central nervous system	3.72E-07	metabolism of acidic amino acid	4.90E-07	length of neurites	6.66E-07
metabolism of reactive oxygen species	6.15E-07	cytokinesis	3.82E-07	emotional behavior	5.08E-07	fusion of cellular membrane	6.90E-07
endoplasmic reticulum stress response	6.70E-07	respiratory rhythm	4.14E-07	size of brain	5.13E-07	stabilization of protein	7.64E-07
emotional behavior	6.72E-07	transformation of fibroblast cell lines	4.20E-07	long term depression of synapse	5.31E-07	elongation of neurites	7.88E-07
organization of plasma membrane	6.77E-07	synthesis of ATP	4.49E-07	hereditary motor and sensory neuropathy	5.44E-07	retraction of plasma membrane projections	8.26E-07
quantity of plasma membrane projections	7.09E-07	cognitive impairment	4.54E-07	long term depression of brain cells	5.56E-07	transformation of fibroblast cell lines	8.61E-07
respiratory rhythm	7.72E-07	degeneration of neurons	4.80E-07	fusion of myoblasts	5.58E-07	shape change of tumor cell lines	8.64E-07
long term depression of synapse	8.50E-07	elongation of neurites	4.85E-07	homotetramerization of protein	5.58E-07	breast or ovarian cancer	8.75E-07
development of central nervous system	8.50E-07	size of brain	5.20E-07	development of central nervous system	5.62E-07	mitochondrial leukoencephalopathy	8.95E-07
distal myopathy	8.53E-07	length of neurites	5.39E-07	nuclear export of protein	5.72E-07	oligomerization of protein	9.43E-07
follicular adenoma	8.53E-07	long term depression of cells	5.52E-07	shape change of tumor cell lines	5.90E-07	M phase	9.45E-07
formation of endocytotic vesicle	8.53E-07	fragmentation of mitochondria	5.60E-07	demyelinating peripheral neuropathy	6.22E-07	reorganization of cytoskeleton	9.58E-07
modification of reactive oxygen species	8.53E-07	cell death of pheochromocytoma cell lines	5.60E-07	fusion of muscle cells	6.22E-07	sensory neuropathy	9.81E-07
organization of nervous tissue	8.61E-07	homotetramerization of protein	5.64E-07	extension of plasma membrane projections	6.82E-07	abnormal morphology of metencephalon	1.10E-06
glycolysis	9.23E-07	growth of axons	6.89E-07	prepulse inhibition	7.00E-07	mitochondrial respiratory chain deficiency	1.23E-06

Supp. Table 3 (cont.)

Eif2b5^{M}, w11		WT, w11		Eif2b5^{M}, w12		WT, w12	
breast or ovarian cancer	9.40E-07	extension of plasma membrane projections	6.93E-07	homo-oligomerization of protein	7.26E-07	transport of H+	1.23E-06
Mitochondrial complex I deficiency	8.99E-07	nuclear export of protein	5.76E-07	quantity of dendritic spines	6.96E-07	cell movement of kidney cell lines	1.10E-06
release of vesicles	8.99E-07	transmembrane potential	6.75E-07	concentration of glutathione	7.00E-07	morphology of tumor cell lines	1.23E-06
morphology of dendrites	1.00E-06	transport of monovalent inorganic cation	7.03E-07	metabolism of reactive oxygen species	7.67E-07	HIV infection	1.27E-06
homotetramerization of protein	1.03E-06	concentration of glutathione	7.08E-07	exocytosis of dense-core vesicles	8.29E-07	bundling of microtubules	1.39E-06
size of axons	1.03E-06	breast or ovarian cancer	7.45E-07	disassembly of focal adhesions	8.32E-07	endocytosis of protein	1.39E-06
systemic light chain amyloidosis	1.03E-06	organization of actin filaments	7.61E-07	contraction of heart	8.83E-07	abnormal morphology of rhombencephalon	1.41E-06
abnormal morphology of cerebral cortex	1.05E-06	proliferation of fibroblast cell lines	7.64E-07	polarization of cells	8.83E-07	extension of neurites	1.41E-06
growth of organism	1.08E-06	abnormal respiratory rhythm	7.65E-07	transport of metal ion	9.05E-07	primary cardiomyopathy	1.45E-06
instability of microtubules	1.09E-06	major depression	7.73E-07	release of catecholamine	9.06E-07	axonal transport	1.46E-06
metabolism of oxalacetic acid	1.09E-06	growth of organism	8.06E-07	density of dendritic spines	9.17E-07	synthesis of reactive oxygen species	1.46E-06
psoriasis	1.11E-06	phagocytosis of tumor cell lines	8.10E-07	outgrowth of axons	9.75E-07	dystonia	1.54E-06
autosomal dominant Charcot-Marie-Tooth disease type 2	1.13E-06	exocytosis of dense-core vesicles	8.33E-07	Renal Cancer and Tumors	9.95E-07	hereditary motor and sensory neuropathy	1.57E-06
synthesis of nucleotide	1.13E-06	viral entry by Influenza virus	8.47E-07	export of molecule	1.02E-06	Leigh syndrome	1.57E-06
tetramerization of protein	1.15E-06	development of cerebral cortex	8.67E-07	peripheral neuropathy	1.02E-06	necrosis of kidney	1.59E-06
cellular degradation	1.18E-06	polarization of cells	8.98E-07	quantity of actin stress fibers	1.03E-06	production of reactive oxygen species	1.59E-06
epilepsy	1.21E-06	transport of metal ion	9.25E-07	degeneration of central nervous system	1.04E-06	organization of actin filaments	1.62E-06
formation of focal adhesions	1.22E-06	oligomerization of protein	9.78E-07	depolymerization of microtubules	1.04E-06	Charcot-Marie-Tooth disease	1.63E-06
infection of embryonic cell lines	1.34E-06	neurotransmission of brain cells	1.02E-06	breast or ovarian cancer	1.07E-06	Ewing's sarcoma	1.63E-06
infection of epithelial cell lines	1.34E-06	Renal Cancer and Tumors	1.03E-06	memory	1.10E-06	plasma cell dyscrasia	1.80E-06
morphology of brain cells	1.34E-06	quantity of actin stress fibers	1.04E-06	inclusion body myopathy	1.11E-06	abnormal morphology of cerebellum	1.81E-06
mitochondrial encephalomyopathy	1.35E-06	morphology of hippocampus	1.05E-06	length of dendritic spines	1.11E-06	synthesis of nucleotide	1.82E-06
dystonia	1.38E-06	processing of RNA	1.08E-06	cytokinesis	1.14E-06	density of dendritic spines	1.83E-06
cell movement of tumor cell lines	1.39E-06	length of dendritic spines	1.11E-06	Cytosis	1.17E-06	coordination	1.84E-06
transport of ion	1.40E-06	fragmentation of DNA	1.20E-06	myelination	1.18E-06	osteosarcoma	1.88E-06
quantity of microtubules	1.41E-06	cell death of hippocampal cells	1.21E-06	cell death of hippocampal cells	1.19E-06	release of catecholamine	1.90E-06
infection of kidney cell lines	1.50E-06	cell death of muscle cells	1.23E-06	shape change of fibroblast cell lines	1.19E-06	cell death of kidney cell lines	1.92E-06
abnormal respiratory rhythm	1.59E-06	psoriasis	1.28E-06	abnormal morphology of hippocampus	1.20E-06	cell death of pheochromocytoma cell lines	1.93E-06
transport of metal ion	1.68E-06	cell death of muscle	1.32E-06	carcinoma in larynx	1.22E-06	Waldenstrom's macroglobulinemia	1.99E-06
thyroid adenoma	1.71E-06	quantity of neurites	1.35E-06	quantity of neurites	1.34E-06	formation of cytoplasmic aggregates	2.02E-06
neurotransmission of brain cells	1.77E-06	mitochondrial leukoencephalopathy	1.40E-06	formation of membrane ruffles	1.35E-06	mitochondrial encephalomyopathy	2.07E-06
transport of carboxylic acid	2.18E-06	localization of protein	1.43E-06	action potential of cells	1.51E-06	modification of hydrogen peroxide	2.22E-06

Supp. Table 3 (cont.)

Eif2b5^{M}, w11		WT, w11		Eif2b5^{M}, w12		WT, w12	
Nonaka myopathy	2.47E-06	renal cancer	1.44E-06	activation of enzyme	1.52E-06	refractory classical Hodgkin lymphoma	2.22E-06
degeneration of neurons	1.80E-06	polymerization of microtubules	1.40E-06	mitochondrial leukoencephalopathy	1.39E-06	polymerization of actin	2.07E-06
HIV infection	1.85E-06	Leigh syndrome	1.40E-06	renal cancer	1.39E-06	cell death of kidney cells	2.17E-06
quantity of actin filaments	1.96E-06	binding of microtubules	1.40E-06	Leigh syndrome	1.39E-06	glycolysis of cells	2.21E-06
systemic amyloidosis	2.47E-06	infection of embryonic cell lines	1.47E-06	transmembrane potential	1.65E-06	relapsed classical Hodgkin lymphoma	2.22E-06
shape change of tumor cell lines	2.63E-06	infection of epithelial cell lines	1.47E-06	organization of cellular membrane	1.67E-06	reactive gliosis	2.26E-06
outgrowth of axons	2.75E-06	action potential of cells	1.53E-06	size of axons	1.70E-06	length of dendritic spines	2.57E-06
neurodegeneration of central nervous system	2.90E-06	HIV infection	1.62E-06	systemic light chain amyloidosis	1.70E-06	apoptosis of pheochromocytoma cell lines	2.61E-06
shape change of plasma membrane	2.96E-06	depressive disorder	1.68E-06	shape of cells	1.77E-06	neurotransmission of brain cells	2.65E-06
cell viability of tumor cell lines	3.00E-06	quantity of actin filaments	1.70E-06	degradation of DNA	1.89E-06	dilated cardiomyopathy	3.00E-06
apoptosis of cervical cancer cell lines	3.14E-06	size of axons	1.71E-06	organic aciduria	1.90E-06	renal cancer	3.01E-06
abnormal morphology of cells	3.15E-06	infection of kidney cell lines	1.78E-06	ruffling	1.93E-06	metabolism of fructose-1,6-diphosphate	3.19E-06
concentration of glutathione	3.58E-06	shape change of tumor cell lines	1.89E-06	cell death of pheochromocytoma cell lines	1.94E-06	metabolism of malic acid	3.19E-06
organic aciduria	3.69E-06	ruffling	1.95E-06	Charcot-Marie-Tooth disease type 2	1.97E-06	size of synapse	3.19E-06
transport of monovalent inorganic cation	3.71E-06	distal myopathy	1.98E-06	distal myopathy	1.97E-06	paralysis of limb	3.25E-06
cell viability of neuroblastoma cell lines	3.79E-06	follicular adenoma	1.98E-06	modification of reactive oxygen species	1.97E-06	cell-cell adhesion	3.26E-06
metabolism of amino acid analogs	3.79E-06	formation of endocytotic vesicle	1.98E-06	abnormal morphology of metencephalon	1.99E-06	quantity of phosphatidylinositol 4,5-diphosphate	3.30E-06
secretion of neurotransmitter	3.80E-06	production of reactive oxygen species	2.06E-06	coordination	2.02E-06	release of vesicles	3.30E-06
viral entry by Influenza virus	3.86E-06	actin capping	2.15E-06	degradation of amino acids	2.08E-06	prepulse inhibition	3.31E-06
atrophy of muscle	3.96E-06	instability of microtubules	2.15E-06	actin capping	2.14E-06	Renal Cancer and Tumors	3.38E-06
reorganization of cytoskeleton	4.05E-06	morphology of brain cells	2.29E-06	instability of microtubules	2.14E-06	blood protein disorder	3.38E-06
cell spreading of tumor cell lines	4.06E-06	cell viability of neuroblastoma cell lines	2.31E-06	long term depression of Purkinje cells	2.14E-06	abnormal morphology of cerebellar cortex	3.55E-06
aplastic anemia	4.10E-06	elongation of cellular protrusions	2.49E-06	metabolism of oxalacetic acid	2.14E-06	diffuse small-cell lymphoma	3.62E-06
fusion of vesicles	4.10E-06	retraction of cellular protrusions	2.49E-06	bone sarcoma	2.24E-06	inclusion body myositis	3.74E-06
astrocytoma	4.21E-06	size of embryo	2.51E-06	release of vesicles	2.24E-06	morphology of hippocampus	4.16E-06
memory	4.22E-06	synaptic transmission of brain cells	2.56E-06	degeneration of brain	2.26E-06	formation of endocytotic vesicle	4.22E-06
organization of mitochondria	4.38E-06	synthesis of reactive oxygen species	2.58E-06	morphology of brain cells	2.26E-06	development of hippocampal neurons	4.23E-06
abnormal morphology of cerebellar cortex	4.39E-06	atrophy of muscle	2.64E-06	cognitive impairment	2.45E-06	shape change of plasma membrane	4.27E-06
reactive gliosis	4.65E-06	contraction of heart	2.65E-06	retraction of cellular protrusions	2.46E-06	M phase of cervical cancer cell lines	4.31E-06
production of reactive oxygen species	4.73E-06	Cytosis	2.74E-06	Ewing's sarcoma	2.64E-06	long term depression of brain cells	4.55E-06
concentration of ATP	5.31E-06	autosomal dominant disease	3.23E-06	abnormal morphology of rhombencephalon	3.13E-06	long term depression of neurons	4.99E-06

Supp. Table 3 (cont.)

Eif2b5^{M}, w11		WT, w11		Eif2b5^{M}, w12		WT, w12	
M phase	5.70E-06	emotional behavior	3.28E-06	Waldenstrom's macroglobulinemia	3.35E-06	cell viability of neuroblastoma cell lines	5.37E-06
synthesis of reactive oxygen species	4.77E-06	localization of mitochondria	2.96E-06	development of cerebral cortex	2.77E-06	tetramerization of protein	4.77E-06
synaptic transmission of brain cells	4.81E-06	formation of actin stress fibers	2.97E-06	formation of actin stress fibers	2.92E-06	quantity of cellular inclusion bodies	4.90E-06
modification of hydrogen peroxide	5.05E-06	organization of plasma membrane	3.03E-06	fusion of cells	2.92E-06	transport of L-glutamic acid	4.90E-06
polarization of neurons	5.05E-06	prepulse inhibition	3.21E-06	organization of plasma membrane	3.00E-06	size of brain	4.97E-06
association of vesicles	5.87E-06	fusion of myoblasts	3.38E-06	infection of embryonic cell lines	3.36E-06	quantity of intermediate filaments	5.39E-06
metabolism of fructose-1,6-diphosphate	5.87E-06	Waldenstrom's macroglobulinemia	3.40E-06	infection of epithelial cell lines	3.36E-06	formation of focal adhesions	5.48E-06
metabolism of malic acid	5.87E-06	apoptosis of fibroblast cell lines	3.45E-06	epilepsy	3.42E-06	inborn error of amino acid metabolism	5.55E-06
fatty acid oxidation disorder	5.98E-06	oxidation of protein	3.52E-06	oxidation of protein	3.50E-06	quantity of neurites	5.69E-06
Clathrin mediated endocytosis	6.09E-06	M phase	3.61E-06	M phase	3.55E-06	phagocytosis	6.24E-06
length of dendritic spines	6.44E-06	Clathrin mediated endocytosis	3.84E-06	primary cardiomyopathy	3.81E-06	disassembly of focal adhesions	6.29E-06
organization of actin	6.64E-06	apoptosis of pheochromocytoma cell lines	4.02E-06	phagocytosis	3.97E-06	outgrowth of axons	6.41E-06
export of protein	6.85E-06	action potential of neurons	4.11E-06	infection of kidney cell lines	4.01E-06	binding of filaments	6.60E-06
homo-oligomerization of protein	6.86E-06	endoplasmic reticulum stress response	4.11E-06	action potential of neurons	4.05E-06	polymerization of microtubules	6.60E-06
quantity of actin stress fibers	6.98E-06	abnormal morphology of hippocampus	4.34E-06	reorganization of cytoskeleton	4.21E-06	endocrine gland tumor	6.61E-06
size of brain	7.02E-06	mitochondrial encephalomyopathy	4.42E-06	production of reactive oxygen species	4.26E-06	synthesis of phosphatidylinositol 4,5-diphosphate	6.69E-06
extension of plasma membrane projections	7.13E-06	thyroid adenoma	4.55E-06	cell viability of tumor cell lines	4.28E-06	morphology of synapse	6.70E-06
respiratory system tumor	7.37E-06	synaptic transmission of cerebral cortex cells	4.84E-06	mitochondrial encephalomyopathy	4.38E-06	glycolysis	6.82E-06
density of dendritic spines	7.65E-06	activation of vesicles	4.85E-06	benign thyroid nodule	4.50E-06	reorganization of actin cytoskeleton	7.02E-06
failure of bone marrow	7.65E-06	formation of endosomes	4.85E-06	elongation of filaments	4.50E-06	docking of vesicles	7.13E-06
long term depression of cells	7.70E-06	systemic amyloidosis	4.85E-06	transport of mitochondria	4.50E-06	cognitive impairment	7.20E-06
morphology of hippocampus	8.07E-06	density of dendritic spines	4.91E-06	thyroid adenoma	4.52E-06	secretion of molecule	7.48E-06
Waldenstrom's macroglobulinemia	8.29E-06	neurodegeneration of brain	4.91E-06	Growth Failure	4.73E-06	abnormal morphology of white matter	7.54E-06
hypertrophy of heart	8.70E-06	fragmentation of Golgi apparatus	4.95E-06	tetramerization of protein	4.75E-06	cell death of pyramidal neurons	7.54E-06
morphology of mitochondria	9.64E-06	quantity of dendritic spines	4.95E-06	synaptic transmission of cerebral cortex cells	4.80E-06	density of filaments	7.54E-06
apoptosis of kidney cell lines	9.68E-06	cell spreading of tumor cell lines	5.01E-06	Nonaka myopathy	4.82E-06	phagocytosis by macrophage cancer cell lines	7.54E-06
paralysis of limb	9.69E-06	docking of vesicles	5.36E-06	activation of vesicles	4.82E-06	quantity of lamellipodia	7.54E-06
myelination	1.01E-05	head and neck neoplasia	5.80E-06	systemic amyloidosis	4.82E-06	branching of axons	7.58E-06
congenital aplastic anemia	1.01E-05	cell movement of kidney cell lines	6.22E-06	transport of monovalent inorganic cation	4.87E-06	formation of membrane ruffles	7.58E-06
development of hippocampus	1.03E-05	electrophysiology of nervous system	6.24E-06	invasion of tumor cell lines	4.96E-06	transmembrane potential of mitochondria	7.60E-06
release of catecholamine	1.13E-05	quantity of filopodia	6.49E-06	transformation of fibroblast cell lines	5.84E-06	contraction of heart	8.25E-06

Supp. Table 3 (cont.)

Eif2b5^M, w11		WT, w11		Eif2b5^M, w12		WT, w12	
metabolism of amino acids	1.19E-05	accumulation of vesicles	6.77E-06	astrocytoma	5.85E-06	polarization of cells	8.25E-06
quantity of intermediate filaments	1.10E-05	morphology of tumor cell lines	6.45E-06	cell movement of breast cancer cell lines	5.84E-06	quantity of actin stress fibers	8.17E-06
synthesis of acyl-coenzyme A	1.05E-05	excitatory postsynaptic potential of neurons	6.36E-06	dystonia	5.05E-06	metabolism of monosaccharide	7.80E-06
abnormal morphology of hippocampus	1.05E-05	phagocytosis of cells	6.36E-06	myogenesis	5.25E-06	synaptic transmission of brain cells	7.88E-06
disruption of Golgi apparatus	1.10E-05	morphology of fibroblast cell lines	6.41E-06	docking of vesicles	5.32E-06	morphology of brain cells	7.98E-06
priming of vesicles	1.10E-05	transport of ion	6.43E-06	cellular degradation	5.58E-06	adrenal gland tumor	8.07E-06
formation of actin stress fibers	1.20E-05	apoptosis of cervical cancer cell lines	7.14E-06	branching of axons	6.13E-06	Clathrin mediated endocytosis	8.34E-06
transmembrane potential	1.23E-05	blebbing	7.41E-06	morphology of cerebellum	6.14E-06	myelination	8.42E-06
cell death of hippocampal neurons	1.28E-05	uterine leiomyoma	7.68E-06	apoptosis of kidney cell lines	6.27E-06	carcinoma in larynx	8.57E-06
oxidation of protein	1.33E-05	concentration of ATP	7.90E-06	transport of ion	6.27E-06	loss of neurites	8.57E-06
quantity of cellular inclusion bodies	1.33E-05	posttetanic potentiation	8.02E-06	aciduria	6.30E-06	metabolism of carbohydrate	8.87E-06
transport of L-glutamic acid	1.33E-05	migration of tumor cell lines	8.33E-06	morphology of fibroblast cell lines	6.35E-06	contextual conditioning	9.44E-06
fragmentation of mitochondria	1.35E-05	actin capping of filament barbed ends	8.36E-06	quantity of filopodia	6.45E-06	binding of lipid	9.48E-06
development of muscle	1.57E-05	reactive gliosis	8.36E-06	reorganization of actin cytoskeleton	6.50E-06	epilepsy	9.56E-06
secretion of molecule	1.58E-05	phosphorylation of nucleotide	8.81E-06	shape change of axons	6.99E-06	chronic kidney disease	9.67E-06
neuroepithelial tumor	1.59E-05	carcinoma in larynx	9.12E-06	degeneration of neurons	7.54E-06	replenishment of vesicles	9.95E-06
cell death of muscle cells	1.60E-05	binding of filaments	9.16E-06	binding of GTP	7.81E-06	abnormal morphology of dendrites	9.97E-06
autosomal recessive Charcot-Marie-Tooth disease type 2	1.63E-05	myelination	9.40E-06	posttetanic potentiation	7.98E-06	cytokinesis of cervical cancer cell lines	9.97E-06
replenishment of vesicles	1.63E-05	cell movement of fibroblast cell lines	9.45E-06	HIV infection	8.02E-06	homotetramerization of protein	9.97E-06
synthesis of phosphatidylinositol 4,5-diphosphate	1.65E-05	association of vesicles	9.65E-06	development of muscle	8.04E-06	hydrolysis of ATP	9.97E-06
density of filaments	1.69E-05	dissociation of microtubules	9.65E-06	actin capping of filament barbed ends	8.32E-06	concentration of ATP	1.01E-05
phagocytosis by macrophage cancer cell lines	1.69E-05	metabolism of fructose-1,6-diphosphate	9.65E-06	reactive gliosis	8.32E-06	failure of bone marrow	1.03E-05
quantity of lamellipodia	1.69E-05	degradation of amino acids	9.74E-06	abnormal morphology of cerebellum	8.60E-06	neurodegeneration of brain	1.03E-05
glioma	1.77E-05	modification of hydrogen peroxide	9.86E-06	myelodysplastic syndrome	8.61E-06	accumulation of neurofilaments	1.06E-05
disassembly of focal adhesions	1.85E-05	mitochondrial myopathy	9.87E-06	metastatic occult primary cancer of head and neck	8.75E-06	adult-onset amyotrophic lateral sclerosis	1.06E-05
elongation of axons	1.85E-05	metabolism of DNA	9.92E-06	metastatic squamous cell cancer of the ethmoid sinus	8.75E-06	binding of actin cytoskeleton	1.06E-05
retraction of plasma membrane projections	1.88E-05	binding of lipid	1.02E-05	metastatic squamous cell cancer of the glottis	8.75E-06	formation of clathrin-coated vesicles	1.06E-05
Growth Failure	1.89E-05	infection by Flaviviridae	1.09E-05	metastatic squamous cell cancer of the hypopharynx	8.75E-06	cell death of hippocampal neurons	1.12E-05
docking of vesicles	1.92E-05	organic aciduria	1.11E-05	metastatic squamous cell cancer of the lip	8.75E-06	quantity of phosphatidylinositol diphosphate	1.12E-05
degradation of mitochondria	2.11E-05	shape of cells	1.26E-05	recurrent occult primary cancer of head and neck	8.75E-06	nonischemic cardiomyopathy	1.15E-05

Supp. Table 3 (cont.)

Eif2b5^{M}, w11		WT, w11		Eif2b5^{M}, w12		WT, w12	
synaptic transmission of synapse	2.14E-05	outgrowth of axons	1.30E-05	recurrent squamous cell cancer of the ethmoid sinus	8.75E-06	shape of cells	1.15E-05
myelination of cells	2.11E-05	formation of actin bundles	1.26E-05	phosphorylation of nucleotide	8.75E-06	size of plasma membrane projections	1.13E-05
nuclear export of protein	1.92E-05	cell death of heart cells	1.13E-05	metastatic squamous cell cancer of the maxillary sinus	8.75E-06	autosomal dominant motor neuron disease	1.13E-05
adult-onset amyotrophic lateral sclerosis	1.95E-05	benign neoplasm of female genital organ	1.17E-05	metastatic squamous cell cancer of the oropharynx	8.75E-06	instability of microtubules	1.13E-05
formation of clathrin-coated vesicles	1.95E-05	cell death of hippocampal neurons	1.23E-05	metastatic squamous cell cancer of the supraglottis	8.75E-06	long term depression of Purkinje cells	1.13E-05
fusion of muscle cells	2.20E-05	mental retardation	1.31E-05	recurrent squamous cell cancer of the glottis	8.75E-06	depressive disorder	1.19E-05
actin capping	2.29E-05	coordination	1.31E-05	recurrent squamous cell cancer of the hypopharynx	8.75E-06	heart rate	1.21E-05
autosomal dominant motor neuron disease	2.29E-05	hypertrophy of heart	1.33E-05	recurrent squamous cell cancer of the lip	8.75E-06	migration of tumor cell lines	1.24E-05
size of plasma membrane projections	2.29E-05	activation of enzyme	1.35E-05	recurrent squamous cell cancer of the maxillary sinus	8.75E-06	degeneration of cerebral cortex	1.25E-05
Renal Cancer and Tumors	2.41E-05	fatty acid oxidation disorder	1.36E-05	recurrent squamous cell cancer of the oropharynx	8.75E-06	binding of cytoskeleton	1.27E-05
polarization of cells	2.49E-05	abnormal morphology of cells	1.37E-05	recurrent squamous cell cancer of the supraglottis	8.75E-06	disruption of microtubules	1.27E-05
loss of neurites	2.51E-05	M phase of cervical cancer cell lines	1.46E-05	unresectable occult primary cancer of head and neck	8.75E-06	elongation of filaments	1.27E-05
pinocytosis	2.52E-05	release of L-glutamic acid	1.46E-05	unresectable squamous cell cancer of the ethmoid sinus	8.75E-06	loss of intercellular junctions	1.27E-05
quantity of neurites	2.63E-05	long term depression of synapse	1.52E-05	unresectable squamous cell cancer of the glottis	8.75E-06	transport of mitochondria	1.27E-05
morphology of synapse	2.68E-05	depolymerization of filaments	1.53E-05	unresectable squamous cell cancer of the hypopharynx	8.75E-06	infection of kidney cell lines	1.28E-05
transport of H+	2.70E-05	fusion of muscle cells	1.53E-05	unresectable squamous cell cancer of the lip	8.75E-06	infection of embryonic cell lines	1.29E-05
organization of Golgi apparatus	2.74E-05	function of neurons	1.54E-05	unresectable squamous cell cancer of the maxillary sinus	8.75E-06	infection of epithelial cell lines	1.29E-05
elongation of filaments	2.84E-05	release of amino acids	1.54E-05	unresectable squamous cell cancer of the oropharynx	8.75E-06	endoplasmic reticulum stress response	1.31E-05
loss of intercellular junctions	2.84E-05	morphology of head	1.57E-05	unresectable squamous cell cancer of the supraglottis	8.75E-06	X-linked mental retardation	1.31E-05
lung tumor	2.85E-05	Ewing's sarcoma	1.62E-05	viral entry by Influenza virus	8.75E-06	binding of microtubules	1.42E-05
migration of tumor cell lines	2.88E-05	inborn error of lipid metabolism	1.66E-05	head and neck neoplasia	8.84E-06	homo-oligomerization of protein	1.46E-05
branching of axons	3.24E-05	memory	1.67E-05	degradation of mitochondria	9.09E-06	atrophy of muscle	1.53E-05
axonal transport	3.35E-05	epilepsy	1.70E-05	long-term potentiation of cerebral cortex cells	9.09E-06	nasopharyngeal cancer	1.53E-05
formation of actin bundles	3.35E-05	leiomyomatosis	1.72E-05	synthesis of reactive oxygen species	9.25E-06	small cell lung cancer	1.53E-05
transport of Ca2+	3.54E-05	primary cardiomyopathy	1.91E-05	neurodegeneration of central nervous system	9.78E-06	metastatic squamous cell cancer of the lip	1.54E-05

Supp. Table 3 (cont.)

Eif2b5^M, w11		WT, w11		Eif2b5^M, w12		WT, w12	
renal cancer	3.61E-05	metabolism of monosaccharide	1.94E-05	metabolism of GABA	9.81E-06	metastatic squamous cell cancer of the maxillary sinus	1.54E-05
shape of cells	3.35E-05	formation of cytoplasmic aggregates	1.73E-05	morphology of head	9.35E-06	formation of actin stress fibers	1.53E-05
processing of RNA	3.37E-05	shape change of fibroblast cell lines	1.79E-05	association of vesicles	9.62E-06	accumulation of filaments	1.54E-05
fusion of myoblasts	3.40E-05	hydrolysis of ATP	1.84E-05	dissociation of microtubules	9.62E-06	metastatic occult primary cancer of head and neck	1.54E-05
hydrolysis of ATP	3.40E-05	abnormal morphology of metencephalon	1.84E-05	linkage of cytoskeleton	9.62E-06	metastatic squamous cell cancer of the ethmoid sinus	1.54E-05
size of embryo	3.44E-05	refolding of protein	1.85E-05	metabolism of fructose-1,6-diphosphate	9.62E-06	metastatic squamous cell cancer of the glottis	1.54E-05
Ewing's sarcoma	3.53E-05	morphology of synapse	1.89E-05	movement of rodents	9.70E-06	metastatic squamous cell cancer of the hypopharynx	1.54E-05
extension of neurites	3.70E-05	tetramerization of protein	1.96E-05	modification of hydrogen peroxide	9.81E-06	metastatic squamous cell cancer of the oropharynx	1.54E-05
accumulation of filaments	3.74E-05	fusion of early endosomes	1.96E-05	refractory classical Hodgkin lymphoma	9.81E-06	metastatic squamous cell cancer of the supraglottis	1.54E-05
development of cerebral cortex cells	3.74E-05	priming of vesicles	1.96E-05	relapsed classical Hodgkin lymphoma	9.81E-06	recurrent occult primary cancer of head and neck	1.54E-05
metastatic occult primary cancer of head and neck	3.74E-05	quantity of intermediate filaments	1.96E-05	elongation of cellular protrusions	1.01E-05	recurrent squamous cell cancer of the ethmoid sinus	1.54E-05
metastatic squamous cell cancer of the ethmoid sinus	3.74E-05	necrosis of epithelial tissue	1.97E-05	growth of organism	1.09E-05	recurrent squamous cell cancer of the glottis	1.54E-05
metastatic squamous cell cancer of the glottis	3.74E-05	bone sarcoma	2.04E-05	synaptic transmission of synapse	1.10E-05	recurrent squamous cell cancer of the hypopharynx	1.54E-05
metastatic squamous cell cancer of the hypopharynx	3.74E-05	release of vesicles	2.04E-05	morphology of mitochondria	1.10E-05	recurrent squamous cell cancer of the lip	1.54E-05
metastatic squamous cell cancer of the lip	3.74E-05	metabolism of glutathione	2.13E-05	neuroepithelial tumor	1.11E-05	recurrent squamous cell cancer of the maxillary sinus	1.54E-05
metastatic squamous cell cancer of the maxillary sinus	3.74E-05	formation of membrane processes	2.20E-05	binding of microtubules	1.16E-05	recurrent squamous cell cancer of the oropharynx	1.54E-05
metastatic squamous cell cancer of the oropharynx	3.74E-05	synthesis of acyl-coenzyme A	2.20E-05	localization of protein	1.17E-05	recurrent squamous cell cancer of the supraglottis	1.54E-05
metastatic squamous cell cancer of the supraglottis	3.74E-05	abnormal morphology of telencephalon	2.25E-05	glioma	1.17E-05	unresectable occult primary cancer of head and neck	1.54E-05
phosphorylation of nucleotide	3.74E-05	dystonia	2.31E-05	cell viability of neuroblastoma cell lines	1.20E-05	unresectable squamous cell cancer of the ethmoid sinus	1.54E-05
recurrent occult primary cancer of head and neck	3.74E-05	degeneration of cerebral cortex	2.34E-05	organization of Golgi apparatus	1.22E-05	unresectable squamous cell cancer of the glottis	1.54E-05
recurrent squamous cell cancer of the ethmoid sinus	3.74E-05	dysfunction of mitochondria	2.34E-05	motor function	1.25E-05	unresectable squamous cell cancer of the hypopharynx	1.54E-05
recurrent squamous cell cancer of the glottis	3.74E-05	synthesis of nitric oxide	2.38E-05	axonal transport	1.25E-05	unresectable squamous cell cancer of the lip	1.54E-05
unresectable squamous cell cancer of the glottis	3.74E-05	abnormal morphology of rhombencephalon	2.63E-05	release of L-glutamic acid	1.45E-05	export of molecule	1.90E-05

Supp. Table 3 (cont.)

Eif2b5^{M}, w11		WT, w11		Eif2b5^{M}, w12		WT, w12	
unresectable squamous cell cancer of the hypopharynx	3.74E-05	extension of neurites	2.63E-05	M phase of cervical cancer cell lines	1.45E-05	motor function	1.90E-05
recurrent squamous cell cancer of the hypopharynx	3.74E-05	viral entry by virus	2.39E-05	concentration of L-glutamic acid	1.25E-05	unresectable squamous cell cancer of the maxillary sinus	1.54E-05
recurrent squamous cell cancer of the lip	3.74E-05	activation of permeability transition pores	2.44E-05	mental retardation	1.29E-05	unresectable squamous cell cancer of the oropharynx	1.54E-05
recurrent squamous cell cancer of the maxillary sinus	3.74E-05	autosomal recessive Charcot-Marie-Tooth disease type 2	2.44E-05	endoplasmic reticulum stress response	1.30E-05	unresectable squamous cell cancer of the supraglottis	1.54E-05
recurrent squamous cell cancer of the oropharynx	3.74E-05	replenishment of vesicles	2.44E-05	hypertrophy of heart	1.31E-05	transport of carboxylic acid	1.67E-05
recurrent squamous cell cancer of the supraglottis	3.74E-05	scattering	2.47E-05	processing of RNA	1.35E-05	congenital aplastic anemia	1.84E-05
unresectable occult primary cancer of head and neck	3.74E-05	cell death of cortical neurons	2.56E-05	fatty acid oxidation disorder	1.35E-05	synaptic transmission of cerebral cortex cells	1.84E-05
unresectable squamous cell cancer of the ethmoid sinus	3.74E-05	metabolism of amino acids	2.60E-05	long-term potentiation of brain cells	1.42E-05	mental retardation	1.89E-05
unresectable squamous cell cancer of the lip	3.74E-05	aciduria	2.83E-05	elongation of cells	1.45E-05	abnormal morphology of cells	1.92E-05
unresectable squamous cell cancer of the maxillary sinus	3.74E-05	fusion of cells	2.84E-05	apoptosis of pheochromocytoma cell lines	1.51E-05	blebbing	1.94E-05
unresectable squamous cell cancer of the oropharynx	3.74E-05	invasion of carcinoma cell lines	2.93E-05	release of amino acids	1.52E-05	low-grade lymphoma	1.94E-05
unresectable squamous cell cancer of the supraglottis	3.74E-05	reorganization of cytoskeleton	2.95E-05	apoptosis of fibroblast cell lines	1.54E-05	hypertrophy of heart	1.96E-05
neurodegeneration of brain	3.78E-05	quantity of cellular inclusion bodies	2.98E-05	glioblastoma cancer	1.60E-05	export of protein	1.96E-05
progressive encephalopathy	3.78E-05	transport of L-glutamic acid	2.98E-05	morphology of tumor cell lines	1.63E-05	inborn error of lipid metabolism	1.96E-05
binding of microtubules	3.78E-05	homo-oligomerization of protein	3.12E-05	inborn error of lipid metabolism	1.65E-05	development of central nervous system	2.00E-05
aciduria	3.91E-05	adult-onset amyotrophic lateral sclerosis	3.18E-05	long-term potentiation of hippocampal cells	1.71E-05	development of cerebral cortex	2.01E-05
chronic kidney disease	4.17E-05	formation of clathrin-coated vesicles	3.18E-05	cell movement of kidney cell lines	1.81E-05	cell movement of fibrosarcoma cell lines	2.02E-05
degeneration of cerebral cortex	4.24E-05	development of muscle	3.22E-05	polarity of cells	1.82E-05	aplastic anemia	2.07E-05
exchange of GDP	4.33E-05	long term depression of brain cells	3.24E-05	metabolism of L-glutamic acid	1.84E-05	concentration of phosphatidylinositol	2.13E-05
formation of endosomes	4.33E-05	abnormal morphology of white matter	3.26E-05	refolding of protein	1.84E-05	exchange of GDP	2.15E-05
spherocytosis	4.33E-05	phagocytosis by macrophage cancer cell lines	3.26E-05	cell polarity formation	1.87E-05	size of intercellular junctions	2.15E-05
synthesis of acetyl-coenzyme A	4.33E-05	quantity of lamellipodia	3.26E-05	morphology of synapse	1.87E-05	synthesis of acetyl-coenzyme A	2.15E-05
cell death of pheochromocytoma cell lines	4.40E-05	startle response	3.32E-05	phagocytosis of tumor cell lines	1.87E-05	large-cell lymphoma	2.15E-05
reorganization of actin cytoskeleton	4.40E-05	cell death of cardiomyocytes	3.44E-05	Clathrin mediated endocytosis	1.90E-05	abnormal morphology of hippocampus	2.15E-05
formation of cytoplasmic aggregates	4.42E-05	cell spreading of fibroblast cell lines	3.72E-05	migration of breast cancer cell lines	1.91E-05	Rac protein signal transduction	2.24E-05
phagocytosis	4.44E-05	cell-cell adhesion	3.76E-05	fusion of early endosomes	1.96E-05	autoimmune pancreatitis	2.24E-05
contextual conditioning	4.56E-05	nuclear export	3.76E-05	priming of vesicles	1.96E-05	fatty acid oxidation disorder	2.24E-05

Supp. Table 4

Symbol	Cluster	WT, w11	WT, w12	Eif2b5^{M}, w11	Eif2b5^{M}, w12
Eif1	cluster 1	0.9869	0.3002	0.9573	0.9525
Mx1	cluster 1	1.6331	1.111	0.9046	
Mpp2	cluster 1	1.586		0.9409	1.1224
Ngef	cluster 1	1.4572		0.9422	1.0044
Cryz	cluster 1	2.0832		1.0492	1.0534
Nd1	cluster 1	1.5391	0.7	0.983	0.9751
Vps26a	cluster 1	3.48		1.1656	1.0198
Dctn6	cluster 1	2.0639		1.0814	0.9802
Arpp19	cluster 1	0.9895	1.7989		0.9189
Twf2	cluster 1	1.1482	1.8332	1.0394	1.0277
Tardbp	cluster 1	1.5822	2.2572	1.1906	1.1351
Kars	cluster 1	0.9678	1.3	0.8487	0.7789
Ppp1r9b	cluster 1	0.9836	1.4415	0.8869	0.9117
Serbp1	cluster 1	0.8996	2.8593	1.2805	0.9726
Hip1r	cluster 1	1.199	1.9369	1.2064	1.0507
Basp1	cluster 1	1.1091	1.8254	1.0568	1.0098
Rpl15	cluster 1	0.9967	1.5822	1.0242	0.9844
Fam162a	cluster 1	0.9043	1.5061	0.8678	0.9027
Timm44	cluster 2	1.4388		0.7327	1.1062
Sh3bgrl2	cluster 2	1.7025	1.2804	0.7788	1.0385
Serpina1	cluster 2	1.7074	0.5829	0.7725	
Fam195b	cluster 2	1.1366	0.2624	0.6111	0.8766
Ranbp1	cluster 2	0.9133	4.3206	0.5545	1.034
Copa	cluster 2	1.2143	1.1425	0.6988	0.9571
Dbnl	cluster 2	1.0981	1.3268	0.5793	1.0631
Lars	cluster 2	1.0746	1.277	0.276	0.7969
Rab39b	cluster 2	2.275	1.2697		2.1503
Hebp1	cluster 2	4.2693		1.2656	4.1985
Dlst	cluster 2		0.07944	0.08862	0.9444
Slc32a1	cluster 2	0.7802	0.7519	1.035	1.3085
Syncrip (Sy	cluster 2	1.3571	1.0181	1.1353	1.8607
Krt76	cluster 2	8.8684		14.0087	26.1712
Ncs1	cluster 2	0.9614	0.8842	0.9348	1.4403
Ptp4a1	cluster 2	1.5361	1.1596		2.1906
Map7d1	cluster 3	0.7443		4.0583	0.8853
Appl1	cluster 3	1.09		1.8417	0.8933
Lasp1	cluster 3	1.1542	0.2097	1.8354	1.029
Rph3a	cluster 3	1.1079	0.2646	3.0742	0.9065
Myh14	cluster 3	0.8277	0.9385	1.5713	
Vat1l	cluster 3	0.4977	0.7553	1.2486	0.8535
Hepacam	cluster 3	0.8391	1.0298	1.5732	1.3336
Kiaa1244	cluster 3	1.2158	1.524	2.0074	0.9531
Madd	cluster 3	1.3051	1.5026	2.1596	1.0569
Unc13a	cluster 3	1.4059	1.4753	2.0381	1.1164
Tceal3	cluster 3	1.0793	1.196	2.4192	0.9979
Mthfd1l	cluster 3	1.1206	1.1744	1.8739	1.0294
Sec22b	cluster 3	1.2025	1.2023	1.8382	1.1711
Rab24	cluster 3	1.0799	1.0956	1.6738	0.9312
Kif1a	cluster 3	0.9746	1.1094	1.7927	1.1089

Supp. Table 4 (cont.)

Symbol	Cluster	WT, w11	WT, w12	Eif2b5^M, w11	Eif2b5^M, w12
Rtn4	cluster 3	1.088	1.0861	1.7196	1.1579
Aldh2	cluster 3	0.9503	0.8995	1.5596	0.973
Mink1	cluster 3	1.4154	1.4903	2.0813	1.6012
Gpr158	cluster 3	1.3873	1.4854	2.2507	1.6882
Map7d2	cluster 3	0.6445	0.8577	1.5097	0.7407
Gnb2L1	cluster 3	1.0427	1.1792	1.6423	1.084
Mobp	cluster 3	0.7639		1.3002	0.7729
Rpl23a	cluster 3	0.9493	1.2536	1.4723	0.9661
Ap1b1	cluster 3	0.9785	1.3159	1.5434	1.0062
Add2	cluster 3	1.0382	1.5214	1.8016	1.0451
Slc9a3r1	cluster 3	1.1246	1.7276	2.0271	1.1483
Nefh	cluster 3	0.6173	1.0875	1.3842	0.6921
Marcks	cluster 3	0.9011	1.3544	1.698	0.9864
Akap12	cluster 3	0.8389	2.4796	3.6256	1.1242
Hint3	cluster 3	0.7685	1.0992	1.3015	0.8728
Mapre1	cluster 3	1.0043	1.5125	1.5809	1.0669
Hspa4	cluster 3	0.9122	1.7793	1.9262	1.0321
Sparcl1	cluster 3	0.8885	1.371	1.5089	0.9743
Eif4g1	cluster 3	1.0577	1.5343	1.7026	1.1003
Ubqln2	cluster 3	0.9689	1.4164	1.5541	1.0233
Hnrnpu	cluster 3	0.9661	1.7736	1.9666	1.0434
Dlat	cluster 3	0.9108	1.7793	2.1662	1.0363
Fxyd6	cluster 3	1.022	1.6182	1.6399	1.2246
Ddx6	cluster 3	1.1432	2.0525	1.8325	
Ociad1	cluster 3	0.9128		2.4933	1.2387
Kiaa1217	cluster 3	1.0023		1.728	1.1871
Htt	cluster 3	0.9693	1.7591	1.5057	1.101
Gap43	cluster 3	0.8803	1.6775	1.431	1.0088
Trim2	cluster 3	1.0323	1.8782	1.6637	1.1838
Fau	cluster 3	0.9767	1.8237	1.6806	1.0926
Rplp1	cluster 3	0.9629		3.4208	1.0121
Map1b	cluster 3	0.9687	4.0174	2.9148	1.0084
Rtn1	cluster 3	0.9993	2.1534	1.9969	0.9468
Tceal5	cluster 3	1.0594	2.2366	2.0265	1.0636
Bsn	cluster 3	1.2793	2.1781	2.0326	1.3044
Mrps36	cluster 3	0.9705	1.8966	1.733	0.9941
Itsn1	cluster 3	0.9295	1.833	1.6839	0.9839
Pdcd6Ip	cluster 3	0.849	2.5632	2.1889	0.9313
H1F0	cluster 3	1.4272		18.5333	1.3875
Syn1	cluster 3	1.1524	1.4539	3.0546	1.046
Nt5C	cluster 3	1.0383		3.8124	0.9788
Lmnb1	cluster 3	1.0946	1.5392	1.8202	1.0798
Actr3b	cluster 3	1.1442	1.4156	1.7403	1.1101
Srcin1	cluster 3	1.1438	1.3535	1.6773	1.1792
Caskin1	cluster 3	1.1179	2.0156	3.3604	1.1229
Macrod2	cluster 3	1.0255		1.9736	0.8887
Camkv	cluster 3	1.1529	1.9035	1.8706	1.0369
Map4	cluster 3	1.088		1.6595	1.027
Hp1Bp3	cluster 3	1.196		2.8006	1.0787

Supp. Table 4 (cont.)

Symbol	Cluster	WT, w11	WT, w12	Eif2b5^{M}, w11	Eif2b5^{M}, w12
Plcb1	cluster 3	1.0562	1.4599	1.5963	1.0203
Ncan	cluster 3	1.1438	1.9413	2.0945	1.0655
Dnaja2	cluster 3	1.0103	1.4257	1.521	1.0063
Gprin1	cluster 3	1.2259	3.5204	4.0445	1.1057
Bin1	cluster 3	1.0444	3.4427	4.1375	1.0442
Ckap5	cluster 3	0.9948	1.6228	1.7182	0.9978
Map1a	cluster 3	0.9903	1.9551	2.0901	0.9599
Cap1	cluster 3	1.1353	3.1236	3.3868	1.0199
Aak1	cluster 3	1.1758	3.4613	3.649	1.1367
Ncl	cluster 3	1.0416	5.4843	5.9165	1.0429
Hnrpll	cluster 3	1.0142	1.6207	1.6294	1.0945
Ap3d1	cluster 3	1.0448	1.5573	1.5672	1.0913
Rplp2	cluster 3	1.0036	1.8336	1.8418	1.0688
Amph	cluster 3	1.0247	2.1034	2.1219	1.0793
Syn2	cluster 3	1.1113	1.7667	1.7456	1.1062
Wasf1	cluster 3	1.2478	1.6894	1.7506	1.0926
Dync1li2	cluster 3	1.0424	1.4452	1.3415	0.8618
Palm	cluster 3	1.1728		1.9548	0.8929
Acot9	cluster 3	1.4059		2.475	1.0359
Mapt	cluster 3	0.9877	1.9968	1.5855	0.7849
Cttn	cluster 3	1.1775	1.6698	1.47	1.0652
Dbn1	cluster 3	1.2286	1.7195	1.5192	1.0976
Fam120a	cluster 3	1.235	1.8588	1.5722	0.9968
Fubp1	cluster 3	1.119		2.1344	0.8838
Sept8	cluster 3	1.0146	1.527	1.1547	0.98
Map6	cluster 3	1.0164	2.2648	1.3816	0.9981
Pdap1	cluster 3	1.0153	1.7723	1.4247	1.0848
Trim3	cluster 3	0.9555	1.8696	1.3452	1.0484
Tln2	cluster 3	1.1061	1.7719	1.3991	1.1657
Vps13c	cluster 3	1.2936	1.6546	1.3957	0.9045
Kiaa1967	Other	0.9758	1.9478		1.4239
Eif4g3	Other	1.0172	2.546		1.1081
Klc1	Other	0.8657	1.9566		0.986
Brp44l	Other	0.9483	1.9232		1.0718
Sgsm1	Other	0.9557	1.6033		1.0645
Ppp1r2	Other	0.9099	1.4497		0.877
Fam136a	Other	0.9228	2.0469		0.8614
Mllt4	Other	1.2207	1.9241		1.1819
Cdc42bpb	Other	1.3086	1.9957		1.0976
Nras	Other	1.3941	2.0484		1.3878
Npm1	Other	1.0426	3.1137		1.0513

Supp. Table 5

	Funcional category	**P-value**	**Number of genes**	**Gene symbols**
Nervous System Development and Function	axonal transport	1.E-07	6	Dync1li2, Htt, Kif1a, Kcl1, Mapt, Nefh
	recycling of synaptic vesicles	4.E-07	5	Amph, Dbnl, Gap43, Itsn1, Syn1
	synaptogenesis	6.E-07	10	Bsn, Htt, Kif1a, Ncan, Palm, Rtn4, Sparcl1, Syn1, Syn2, Unc13a
	posttetanic potentiation	4.E-06	4	Add2, Htt, Syn1, Syn2
	seizures	6.E-06	14	Amph, Bsn, Dbnl, Gap43, Htt, Map1b, Mapt, Plcb1, Ppp1r9b, Ptp4a1, Slc32a1, Syn1, Syn2, Trim3
	outgrowth of axons	9.E-06	7	Gap43, Map1b, Mapt, Neph, Ngef, Rtn4, Syn1
	length of dendritic spines	6.E-06	4	Dbn1, Htt, Itsn1, Mapt
Cellular assembly and organization	assembly of cell-cell contacts	1.E-07	12	Bsn, Gnb2l1, Htt, Kif1a, Ncan, Palm, Rtn4, Sparcl1, Syn1, Syn2, Tln2, Unc13a
	assembly of intercellular junctions	9.E-07	11	Bsn, Htt, Kif1a, Ncan, Palm, Rtn4, Sparcl1, Syn1, Syn2, Tln2, Unc13a
	microtubule dynamics	2.E-10	32	Akap12, Basp1, Bsn, Cap1, Cdc42bpb, Ckap5, Cttn, Dbn1, Dync1li2, Eif4g3, Gap43, Gprin1, Htt, Itsn1, Klc1, Lasp1, Map1a, Map1b, Map4, Map6, Mapre1, Mapt, Marcks, Nefh, Palm, Ppp1r9b, Ranbp1, Rtn4, Slc9a3r1, Syn1, Twf2, Wasf1
	stabilization of filaments	7.E-08	9	Cttn, Gap43, Htt, Map1a, Map1b, Map4, Map6, Mapre1, Mapt
	quantity of filaments	4.E-06	8	Gnb2l1, Htt, Map1b, Map4, Mapt, Marcks, Nefh, Nras
mRNA translation	Translation machinery	1.E-05	8	Eif1, Eif4g1, Eif4g3, Fau, Rpl15,Rpl23a,Rplp1,Rplp2