

Supplementary Table 1. Patient Details for Cases Used in Double Immunofluorescence Study

Diagnosis	Age (years)	Gender	PMD (h:min)
Control 1	79	F	240:00
Control 2	68	F	69:05
Control 3	68	F	78:15
Control 4	57	M	15:30
Control 5	73	F	24:00
MSA SND 1	67	M	49:40
MSA SND 2	70	M	62:50
MSA SND 3	70	M	87:46
MSA SND 4	67	F	80:05
MSA SND 5	68	F	50:10
MSA OPCA 1	61	M	24:00
MSA OPCA 2	68	M	99:30
MSA OPCA 3	66	F	75:20
MSA OPCA 4	64	F	15:30
MSA OPCA 5	51	M	125:25

Supplementary Table 2. Patient Details of Cases Used in NanoString (NS), Cytokine Array (CA) and Western Immunoblotting (WB) Studies

Diagnosis	Age	Gender	PMD	Technique
Control 6	80	F	51:10	NS, CA, WB
Control 7	93	F	43:07	NS, CA, WB
Control 8	87	M	38:50	NS, CA
Control 9	88	M	16:25	NS, CA
Control 10	81	M	52:05	NS
Control 11	73	F	26:00	NS
Control 12	38	M	82:35	CA
Control 13	89	F	38:29	CA
Control 14	82	F	99:20	WB
Control 15	93	F	89:25	WB
Control 16	79	F	89:50	WB
Control 17	86	F	120:45	WB
Control 18	69	M	168:00	WB
Mixed MSA 1	66	F	23:20	NS, CA, WB
Mixed MSA 2	50	M	30:15	NS, CA
Mixed MSA 3	63	M	20:40	NS, CA
Mixed MSA 4	60	F	35:30	NS, CA

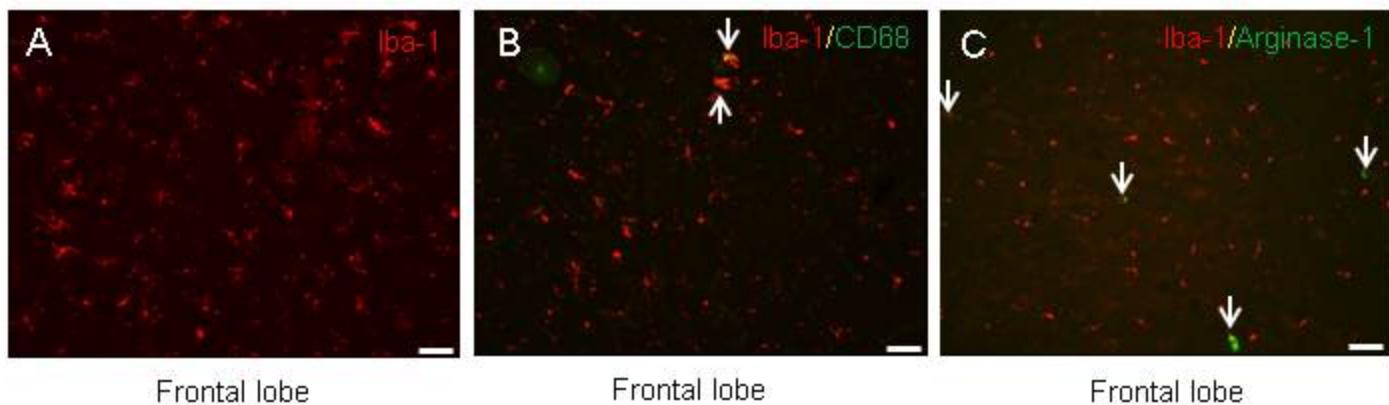
Mixed MSA 5	70	M	32:30	NS
Mixed MSA 6	65	F	34:25	NS
Mixed MSA 7	85	F	89:00	CA
Mixed MSA 8	67	F	108:00	CA
Mixed MSA 9	68	F	36:35	WB
Mixed MSA 10	63	M	20:40	WB
Mixed MSA 11	59	F	48:35	WB
Mixed MSA 12	69	M	53;15	WB
Mixed MSA 13	70	M	32:30	WB
Mixed MSA 14	68	F	107:00	WB

Supplementary Table 3. List of Genes Identified as Having Significantly Altered Expression in MSA Compared to Control

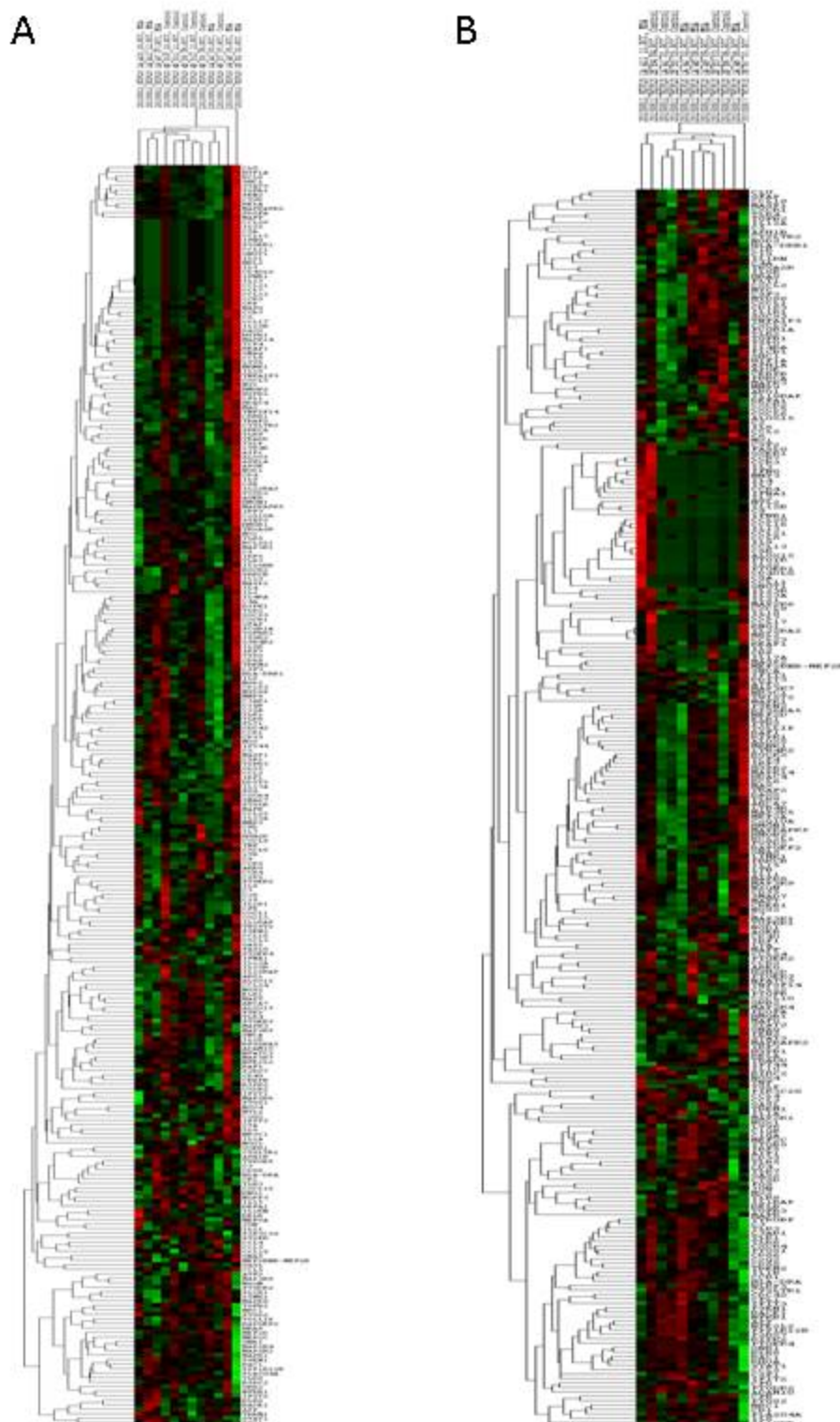
Gene name	Upregulation in MSA	Downregulation in MSA	Significance (p value)	Fold Change	Protein Encoded and Function
Frontal lobe					
<i>ABCA7</i>	-	Y	0.0144	1.96	ATP-binding cassette transporter A7: unknown, possibly lipid homeostasis [61]
<i>ARG1</i>	-	Y	0.0215	3.64	Arginase-1: Anti-inflammatory [58]
<i>DDIT3/CHOP</i>	Y	-	0.0379	1.68	DNA-damage inducible transcript 3: Induces cells cycle arrest in response to endoplasmic reticulum stress and DNA damage [62]
<i>IL15</i>	Y	-	0.0443	2.16	Interleukin 15: Natural killer cell development and function and CD8+ T-cell homeostasis

					[63]
<i>IL1A</i>	Y	-	0.0255	2.75	Interleukin 1A: Induces apoptosis and response to cell injury [64]
<i>MASP1</i>	Y	-	0.0437	3.64	Mannan-binding lectin serine protease 1; Pro-inflammatory [59]
<i>NOX4</i>	Y	-	0.0472	3.28	NADPH oxidase 4: Pro-inflammatory [55]
<i>PTGDR2</i>	-	Y	0.0186	3.10	Prostaglandin D2 Receptor 2: Pro-inflammatory [60]
<i>SMAD7</i>	-	Y	0.0276	1.36	SMAD family member 7: Negative regulator of transforming growth factor β (TGF- β) [6565]
Cerebellar white matter					

C6	Y	-	0.0436	2.88	Complement component 6: Pro- inflammatory
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Supplementary fig 1. Representative images of fields of view used to acquire multi-immunofluorescence microglial counts. Total microglial count, Iba-1 (red) (A), CD68+ cells (B) and Arginase-1+ cells (C). Scale = 50 μ m.



Supplementary fig 2. Heat map diagram using hierarchical clustering of differential gene expression in control and MSA frontal lobe (A) and cerebellar white matter (B) as determined by NanoString nCounter.