

Description of Additional Supplementary Files

Supplementary Data 1. Genes expressed with q values less than 0.05 when comparing NMOSD on Rituximab therapy vs Healthy controls. A Wald test was used for calculating p value and Benjamini-Hochberg procedure was used for q value (FDR) calculation.

Supplementary Data 2. Genes expressed with q values less than 0.05 when comparing NMOSD on Other therapies vs Healthy controls. A Wald test was used for calculating p value and Benjamini-Hochberg procedure was used for q value (FDR) calculation.

Supplementary Data 3. Genes expressed with q values less than 0.05 when comparing Untreated NMOSD vs Healthy controls. A Wald test was used for calculating p value and Benjamini-Hochberg procedure was used for q value (FDR) calculation.

Supplementary Data 4. Protein analytes with p values less than 0.05 when comparing IFN-high and IFN-low NMOSD patients to Healthy controls. A two-way ANOVA with Dunnett's multiple comparisons test was used to determine significance.

Supplementary Data 5. Genes expressed with q values less than 0.05 when comparing NMOSD patients on Rituximab therapy vs patients not on Rituximab therapy. Genes are grouped according to the respective gene cluster. A Wald test was used for calculating p value and Benjamini-Hochberg procedure was used for q value (FDR) calculation.

Supplementary Data 6. Protein analytes with p values less than 0.05 when comparing IFN-high and IFN-low NMOSD patients in B cell-deficient and B cell-sufficient groups vs Healthy controls. A two-way ANOVA with Dunnett's multiple comparisons test was used to determine significance.