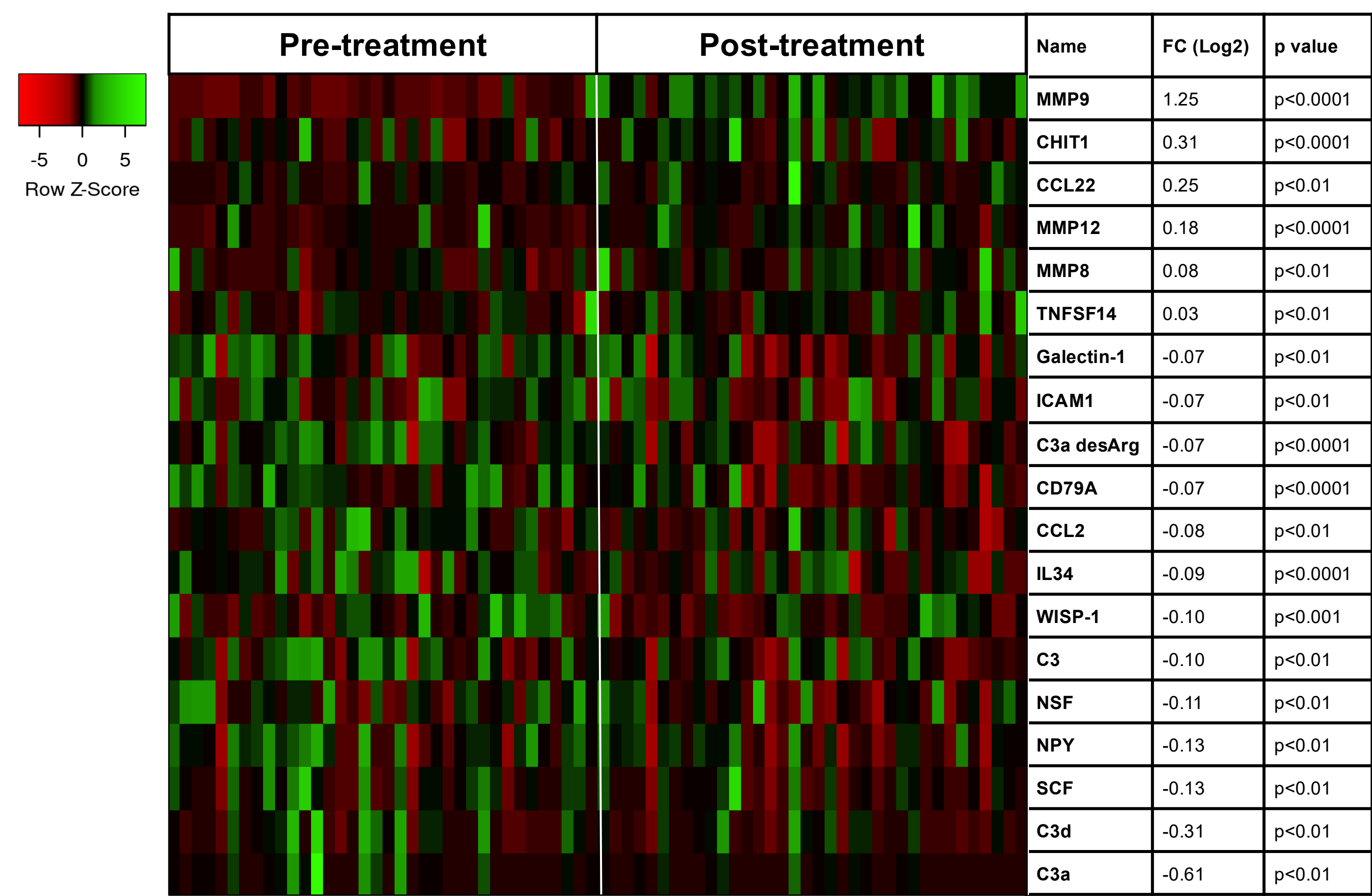
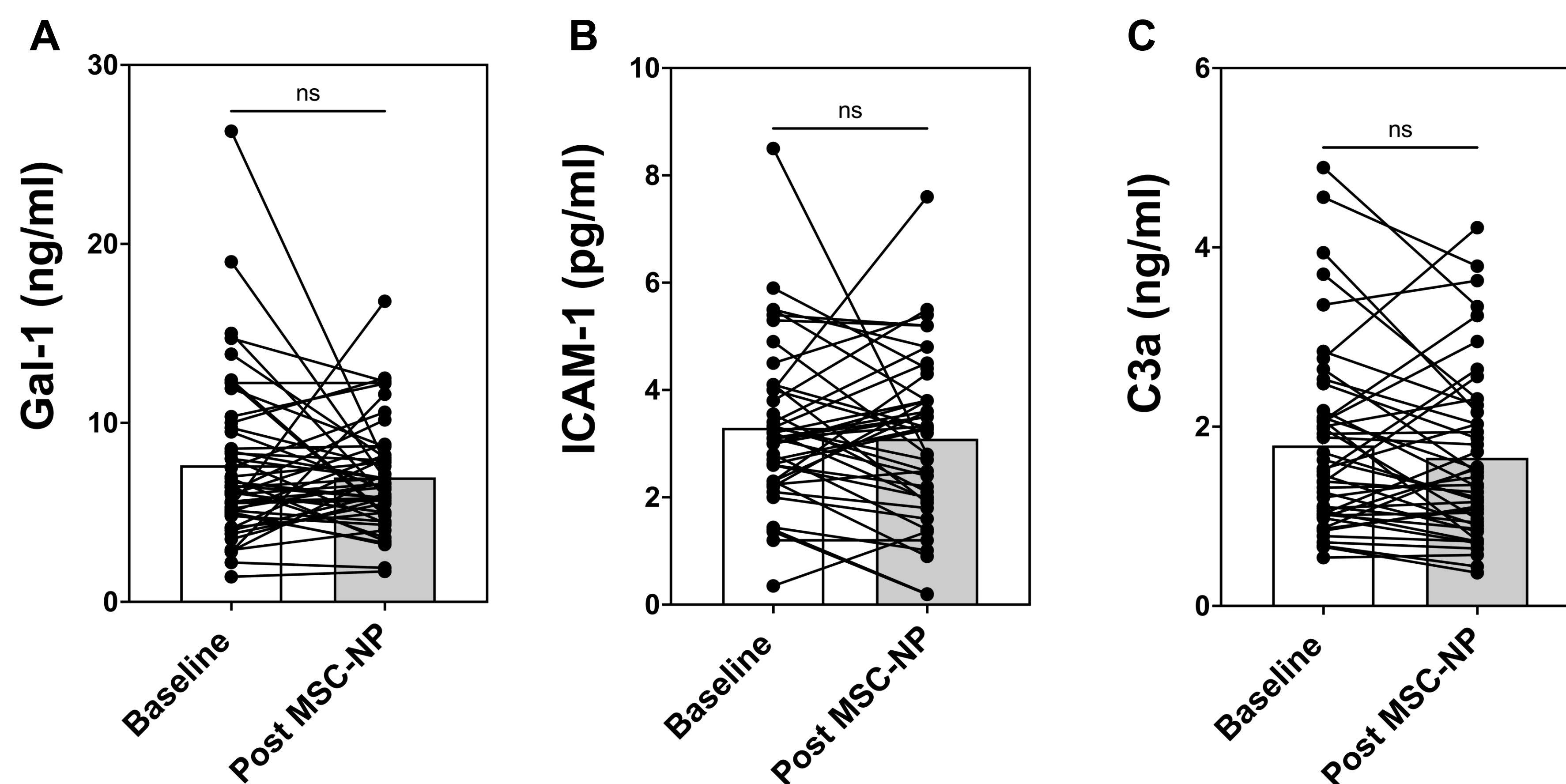


Supplemental Figure 1



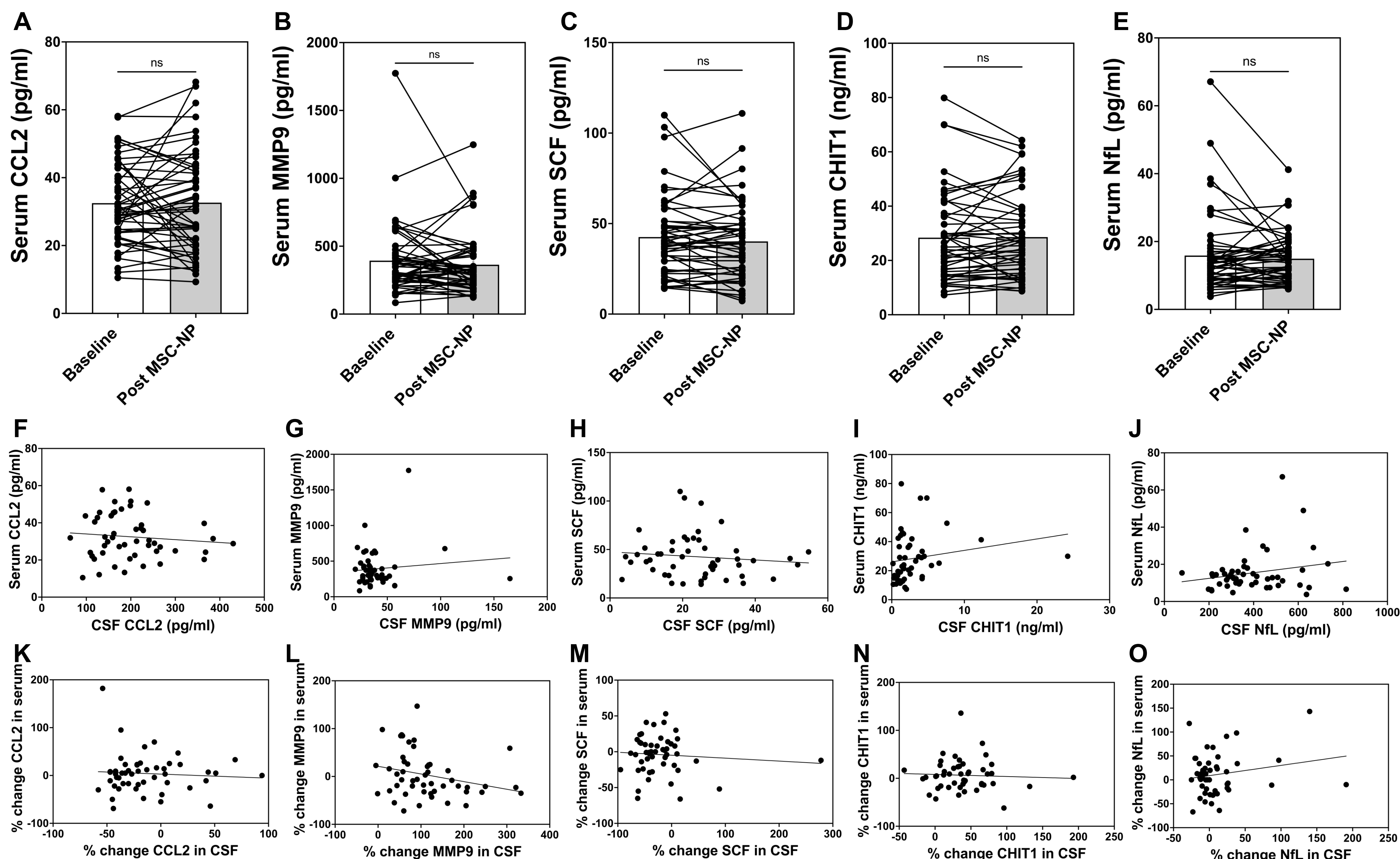
Supplemental Figure 1. Heatmap of candidate biomarkers following proteomic analysis of CSF. CSF was collected from 36 Phase 2 trial participants pre- and post-MSC-NP treatment. CSF supernatants (n=72) were analyzed using SOMAScan Assay. Heatmap shows relative fluorescent unit values for 19 selected differentially expressed proteins with p value <0.01, listed in order of fold change.

Supplemental Figure 2



Supplemental Figure 2. No change in Gal-1, ICAM-1, or C3a levels in CSF following MSC-NP treatment. (A) Gal-1, (B) ICAM-1, and (C) C3a levels in CSF pre- and post-MSC-NP treatment in the phase 2 cohort. Bars represent mean value. “ns”, not significant.

Supplemental Figure 3



Supplemental Figure 3. No change in serum levels of biomarkers following MSC-NP treatment. (A) CCL2, (B) MMP9, (C) SCF, (D) CHIT1, and (E) NfL levels in serum pre- and post-MSC-NP treatment in the phase 2 cohort were unchanged following treatment. (F-J) Baseline levels of all biomarkers in CSF did not correlate with levels in serum. All p values were >0.05 . (K-O) Percentage change of all biomarkers in CSF pre- vs. post-treatment did not correlate with percentage change in serum. All p values were >0.05 .