Neural Progenitor Cells for Treatment of Spinal Cord Injury

Gene expression of pro-inflammatory cytokines/chemokines

Pro-inflammation over time

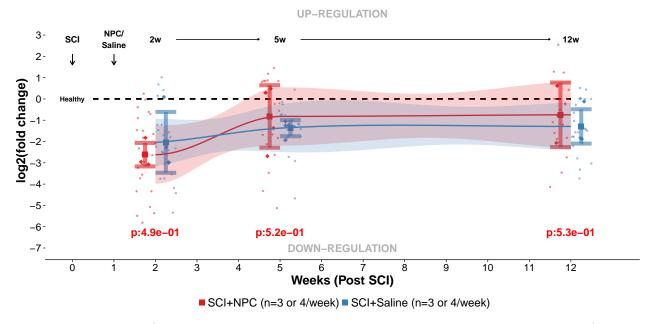


Figure 1. Figure log2(fold change in expression in relation to mean expression in healthy control) of proinflammatory cytokines/chemokines (GM-CSF, IL12p35, IL1a, IL1b, MIP1a, TNFa) over time for each treatment group. P-values for independent two group comparison is presented at each time point. Color of p-value is green if p-value < 0.05, orange if p-value > 0.05 & p-value < 0.1 and red if p-value > 0.1. Test is selected based on evaluation of assumptions.

Individual cytokines/chemokines over time

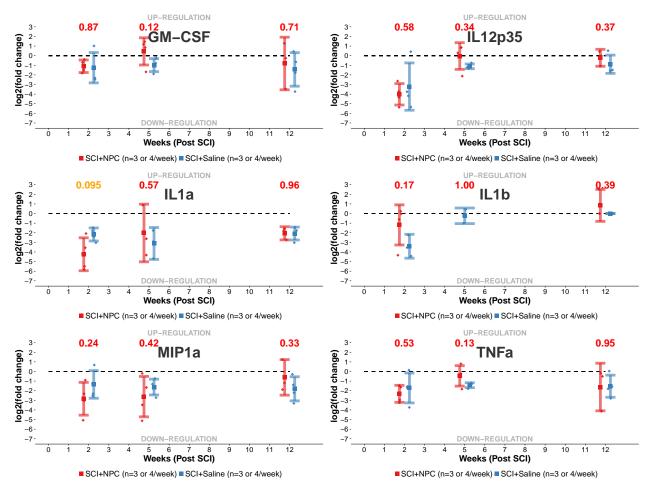
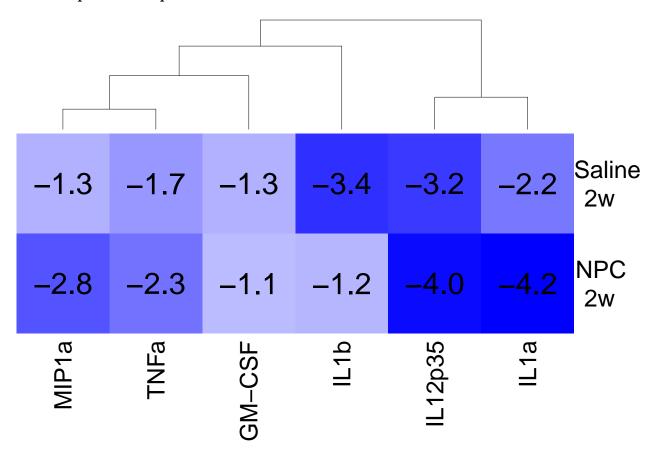
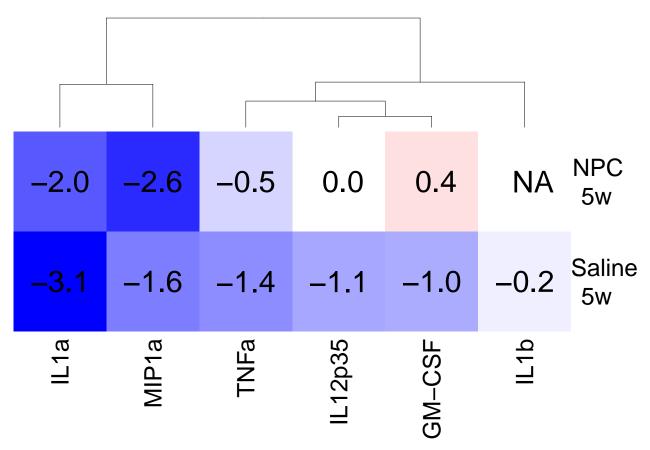


Figure 2: Each plot reports $\log 2$ (fold change in expression in relation to mean expression in healthy control) of one cytokine. P-values for comparison of the two independent groups are presented at each time point. Color of p-value is green if p-value < 0.05, orange if p-value > 0.05 & p-value < and red if p-value > 0.1.

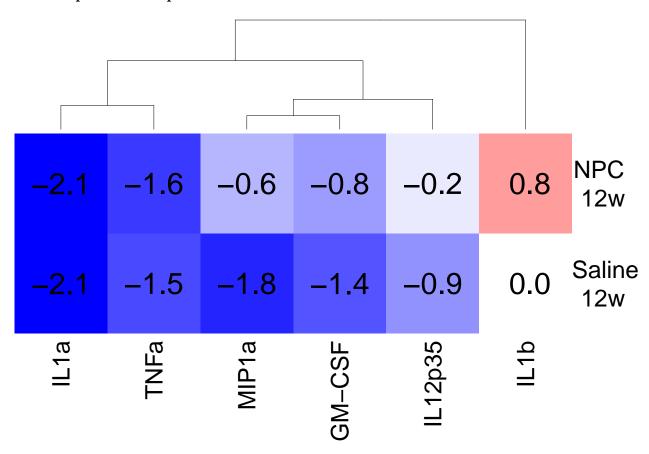
Heatmap 2 weeks post SCI



Heatmap 5 weeks post SCI



Heatmap 12 weeks post SCI



Heatmap 2, 5 and 12 weeks post SCI

| -0.5 | 0.4 | 0.0 | NA | -2.0 | -2.6 | NPC 5w |
|------|--------|---------|------|------|-------|---------------|
| -1.6 | -0.8 | -0.2 | 0.8 | -2.1 | -0.6 | NPC 12w |
| -1.5 | -1.4 | -0.9 | 0.0 | -2.1 | -1.8 | Saline 12w |
| -1.4 | -1.0 | -1.1 | -0.2 | -3.1 | -1.6 | Saline 5w |
| -1.7 | -1.3 | -3.2 | -3.4 | -2.2 | -1.3 | Saline 2w |
| -2.3 | -1.1 | -4.0 | -1.2 | -4.2 | -2.8 | NPC 2w |
| TNFa | GM-CSF | IL12p35 | IL1b | IL1a | MIP1a | _ |

| Week | P-value |
|------|---------|
| 2 | 0.487 |
| 5 | 0.523 |
| 12 | 0.531 |

Table 1. P-values for comparison of pro-inflammation between treatments within week.

| Treatment | P-value |
|-----------|---------|
| NPC | 0.105 |
| saline | 0.528 |

Table 2. P-values for comparison of pro-inflammation within treatment between weeks.

| Target | 2 | 5 | 12 |
|---------|-------|-------|-------|
| GM-CSF | 0.871 | 0.124 | 0.711 |
| IL12p35 | 0.582 | 0.343 | 0.373 |
| IL1a | 0.095 | 0.567 | 0.961 |
| IL1b | 0.166 | 1.000 | 0.386 |
| MIP1a | 0.237 | 0.420 | 0.326 |
| TNFa | 0.527 | 0.133 | 0.950 |

Table 3. P-values for difference in expression of cytokine/chemokine between treatments within week.

sessionInfo()

```
## R version 3.4.1 (2017-06-30)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 16.04.3 LTS
##
## Matrix products: default
## BLAS: /usr/lib/libblas/libblas.so.3.6.0
## LAPACK: /usr/lib/lapack/liblapack.so.3.6.0
## locale:
## [1] LC_CTYPE=en_US.UTF-8
                                   LC NUMERIC=C
## [3] LC TIME=sv SE.UTF-8
                                   LC COLLATE=en US.UTF-8
## [5] LC_MONETARY=sv_SE.UTF-8
                                   LC_MESSAGES=en_US.UTF-8
   [7] LC_PAPER=sv_SE.UTF-8
                                   LC NAME=C
## [9] LC_ADDRESS=C
                                   LC_TELEPHONE=C
## [11] LC_MEASUREMENT=sv_SE.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] grid
                           graphics grDevices utils
                                                         datasets methods
                 stats
## [8] base
##
## other attached packages:
## [1] gplots_3.0.1
                           gridExtra_2.3
                                               knitr_1.17
## [4] cowplot_0.9.1
                           RColorBrewer_1.1-2 data.table_1.10.4-3
## [7] ggplot2_2.2.1
##
## loaded via a namespace (and not attached):
## [1] Rcpp_0.12.13
                           magrittr_1.5
                                              munsell_0.4.3
   [4] colorspace_1.3-2
                           rlang_0.1.2
                                              highr 0.6
## [7] stringr_1.2.0
                           plyr_1.8.4
                                              caTools_1.17.1
## [10] tools_3.4.1
                           gtable_0.2.0
                                              KernSmooth_2.23-15
## [13] gtools_3.5.0
                           htmltools_0.3.6
                                              yaml_2.1.14
## [16] lazyeval_0.2.0
                           rprojroot_1.2
                                              digest_0.6.12
## [19] tibble_1.3.4
                                              evaluate_0.10.1
                           bitops_1.0-6
## [22] rmarkdown_1.6
                           labeling_0.3
                                              gdata_2.18.0
## [25] stringi_1.1.5
                           compiler_3.4.1
                                              scales_0.5.0
## [28] backports_1.1.1
```