Additional figures for the manuscript

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| **Figure** 1: Cytokine expression. Recreated from the original data. |

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| **Figure** 2: mRNA expression for selected genes. Expression is normalized and log2-transformed using the rlog function from DESeq2 package. |

Table 1: Results of differential expression analysis for pre-selected genes. FDR control was performed using the Benjamini-Hochberg method within the pre-selected data set. pvalue, raw p-value with no correction; padj, p-value corrected for false discovery rate for the whole data set; FDR, p-value corrected for false discovery rate for the set of selected genes.

| Contrast | SYMBOL | ENSEMBL | log2FoldChange | pvalue | padj | FDR |
| --- | --- | --- | --- | --- | --- | --- |
| Sp\_HEPES\_vs\_Ctr\_HEPES | CSF2 | ENSG00000164400 | 3.985 | < 2e-16 | 4.0e-16 | < 2e-16 |
|  | CXCL8 | ENSG00000169429 | 2.943 | < 2e-16 | 2.9e-14 | < 2e-16 |
|  | IL10 | ENSG00000136634 | 3.325 | < 2e-16 | 8.9e-15 | < 2e-16 |
|  | IL1B | ENSG00000125538 | 4.427 | < 2e-16 | < 2e-16 | < 2e-16 |
|  | IL6 | ENSG00000136244 | 1.871 | 1.6e-05 | 0.00037 | 2.4e-05 |
|  | PTGS2 | ENSG00000073756 | 2.814 | 2.4e-13 | 1.1e-10 | 7.1e-13 |
|  | TNF | ENSG00000232810 | 4.418 | < 2e-16 | < 2e-16 | < 2e-16 |
| Sp\_HEPES\_vs\_Sp\_no\_HEPES | CSF2 | ENSG00000164400 | -0.02694 | 0.94879 | 0.99944 | 0.94879 |
|  | CXCL8 | ENSG00000169429 | 0.3784 | 0.27696 | 0.93899 | 0.32312 |
|  | IL10 | ENSG00000136634 | 1.169 | 0.00084 | 0.23379 | 0.00104 |
|  | IL1B | ENSG00000125538 | 2.024 | 4.2e-08 | 0.00026 | 8.0e-08 |
|  | IL6 | ENSG00000136244 | -0.1338 | 0.75757 | 0.99944 | 0.79588 |
|  | PTGS2 | ENSG00000073756 | 0.1183 | 0.75798 | 0.99944 | 0.79588 |
|  | TNF | ENSG00000232810 | 1.605 | 0.00030 | 0.15967 | 0.00039 |
| Sp\_no\_HEPES\_vs\_Ctr\_no\_HEPES | CSF2 | ENSG00000164400 | 3.402 | 6.8e-15 | 1.3e-11 | 2.4e-14 |
|  | CXCL8 | ENSG00000169429 | 2.226 | 1.6e-10 | 4.0e-08 | 3.7e-10 |
|  | IL10 | ENSG00000136634 | 1.443 | 0.00017 | 0.00253 | 0.00023 |
|  | IL1B | ENSG00000125538 | 1.668 | 7.3e-06 | 0.00023 | 1.2e-05 |
|  | IL6 | ENSG00000136244 | 1.979 | 5.1e-06 | 0.00017 | 8.9e-06 |
|  | PTGS2 | ENSG00000073756 | 2.493 | 8.5e-11 | 2.6e-08 | 2.2e-10 |
|  | TNF | ENSG00000232810 | 2.622 | 2.2e-08 | 2.2e-06 | 4.6e-08 |

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| **Figure** 3: Cytokine and RNA-seq data for the same genes. The RNA-seq data is relative and log-normalized. The cytokine data is shown on the log10 scale. Points correspond to group median values. Squares show the corresponding interquartile ranges and whiskers show the range of the data. |

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| **Figure** 4: Cytokine and RNA-seq data for the same genes. The RNA-seq data is relative and log-normalized. The cytokine data is shown on the log10 scale. Points correspond to group median values. Squares show the corresponding interquartile ranges and whiskers show the range of the data. |

# 1. New figures

Figures:

* heatmap with genes from the selected gene set (X)
* heatmap with top genes from the interesting comparisons (X)
* disco plot of Sp\_no\_HEPES\_vs\_Ctrl\_no\_HEPES VS ph6\_vs\_Ctrl\_no\_HEPES (X)
* heatmap of logFC for the various comparisons and genes from the pathway
* boxplot with eigengenes for the selected gene set (X)

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| **Figure** 5: Heatmap of the normalized expression values for the selected genes in the cell junction pathway (GO:0007043). The genes are ordered by hierarchical clustering. The expression values are scaled for each gene. |

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| **Figure** 6: Heatmap of the normalized expression values for the selected 75 genes that are most differentially expressed between the two comparisons of interest (Sp\_no\_HEPES\_vs\_Ctrl\_no\_HEPES and pH6\_vs\_Ctr\_no\_HEPES). The genes are ordered by hierarchical clustering. The expression values are scaled for each gene. |

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| **Figure** 7: Disco plot of the two comparisons of interest (Sp\_no\_HEPES\_vs\_Ctrl\_no\_HEPES and pH6\_vs\_Ctr\_no\_HEPES). The genes are colored by the disco score. Labels are shown for the genes in the selected gene set (GO:0007043). |

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| **Figure** 8: Boxplot of the eigengene values for the selected gene set (GO:0007043). |

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| **Figure** 9: Boxplot of the eigengene values for the gene set “myeloid, dendritic cell activation via NFkB (I)” (tmod ID LI.M43.0). |