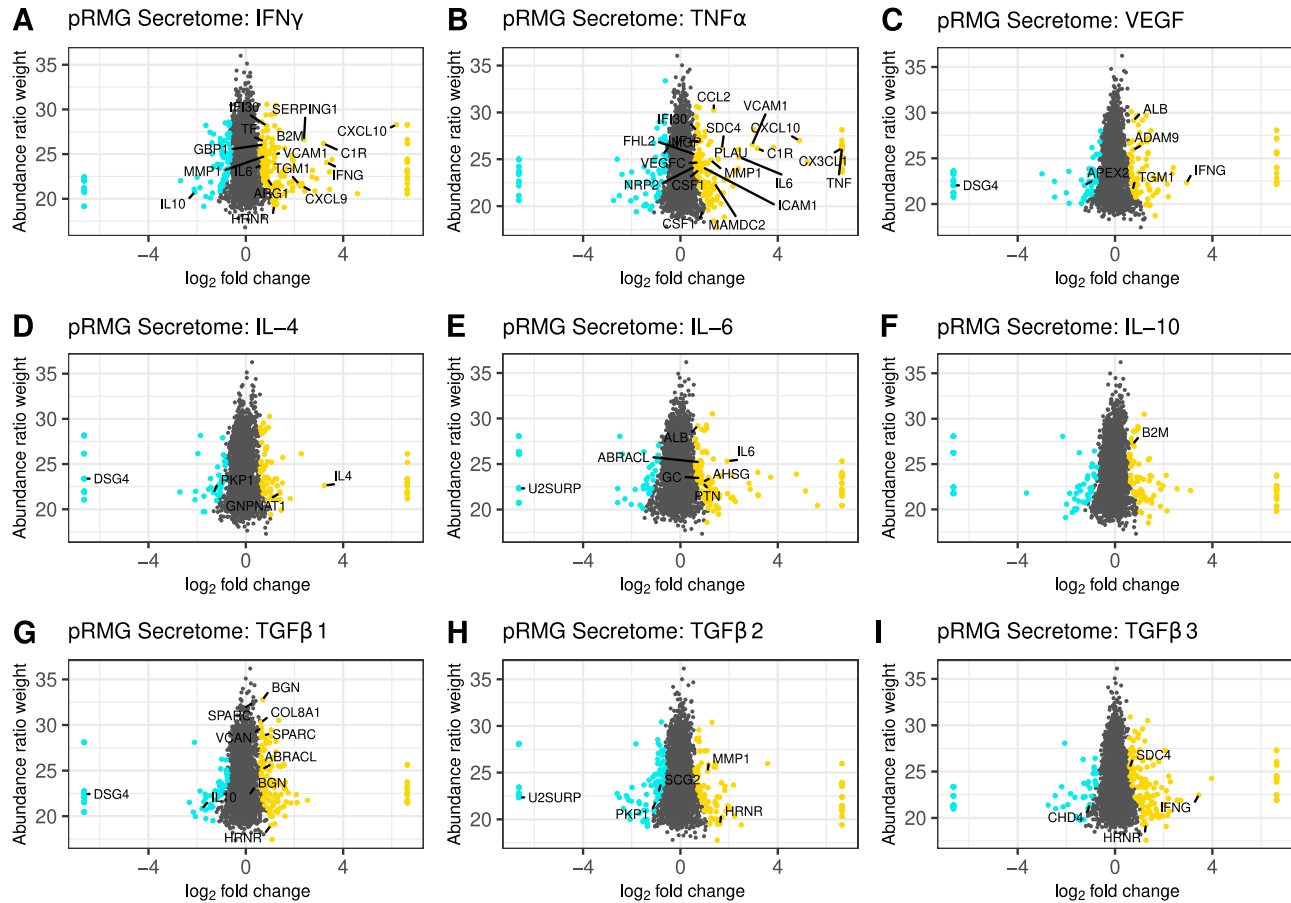
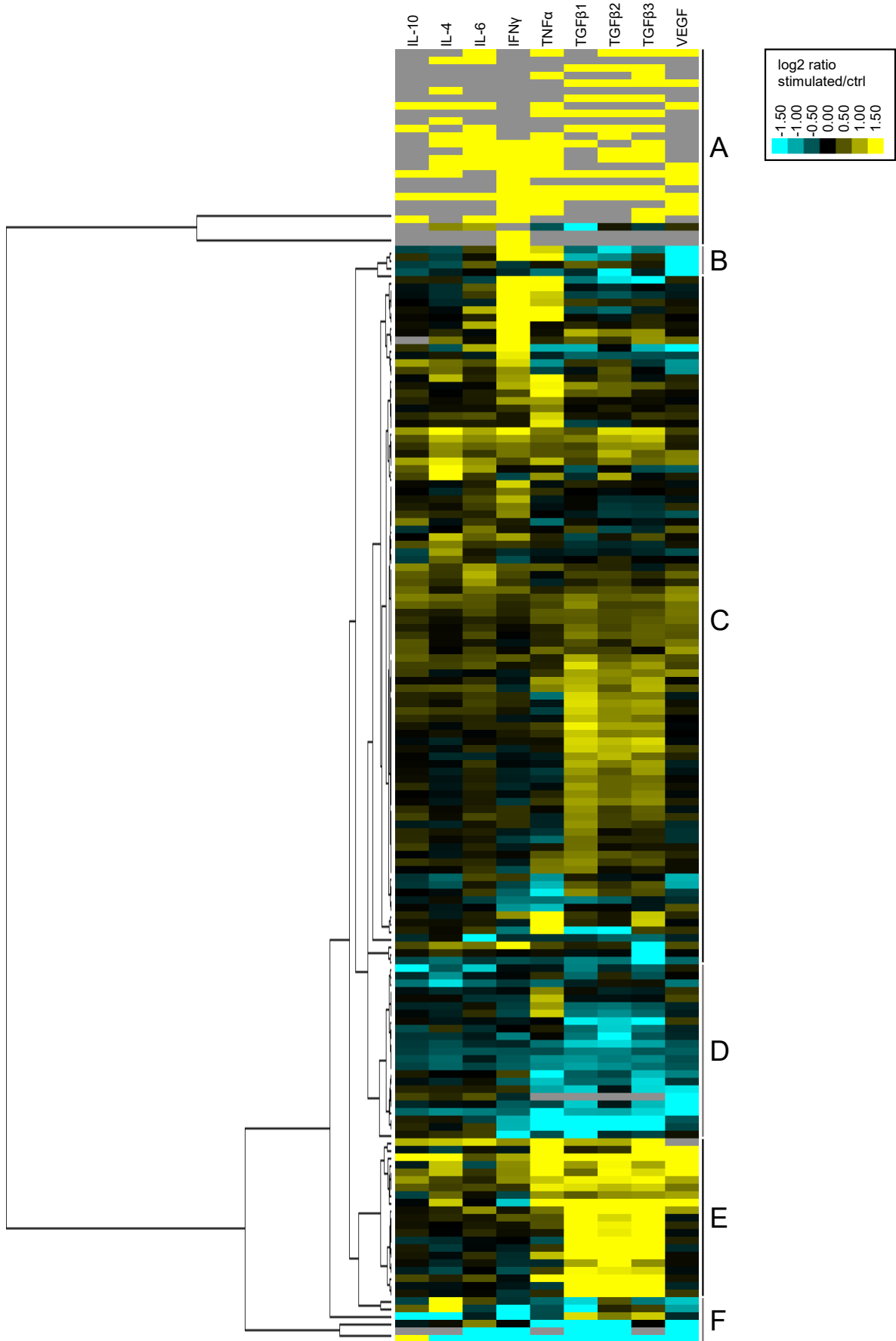


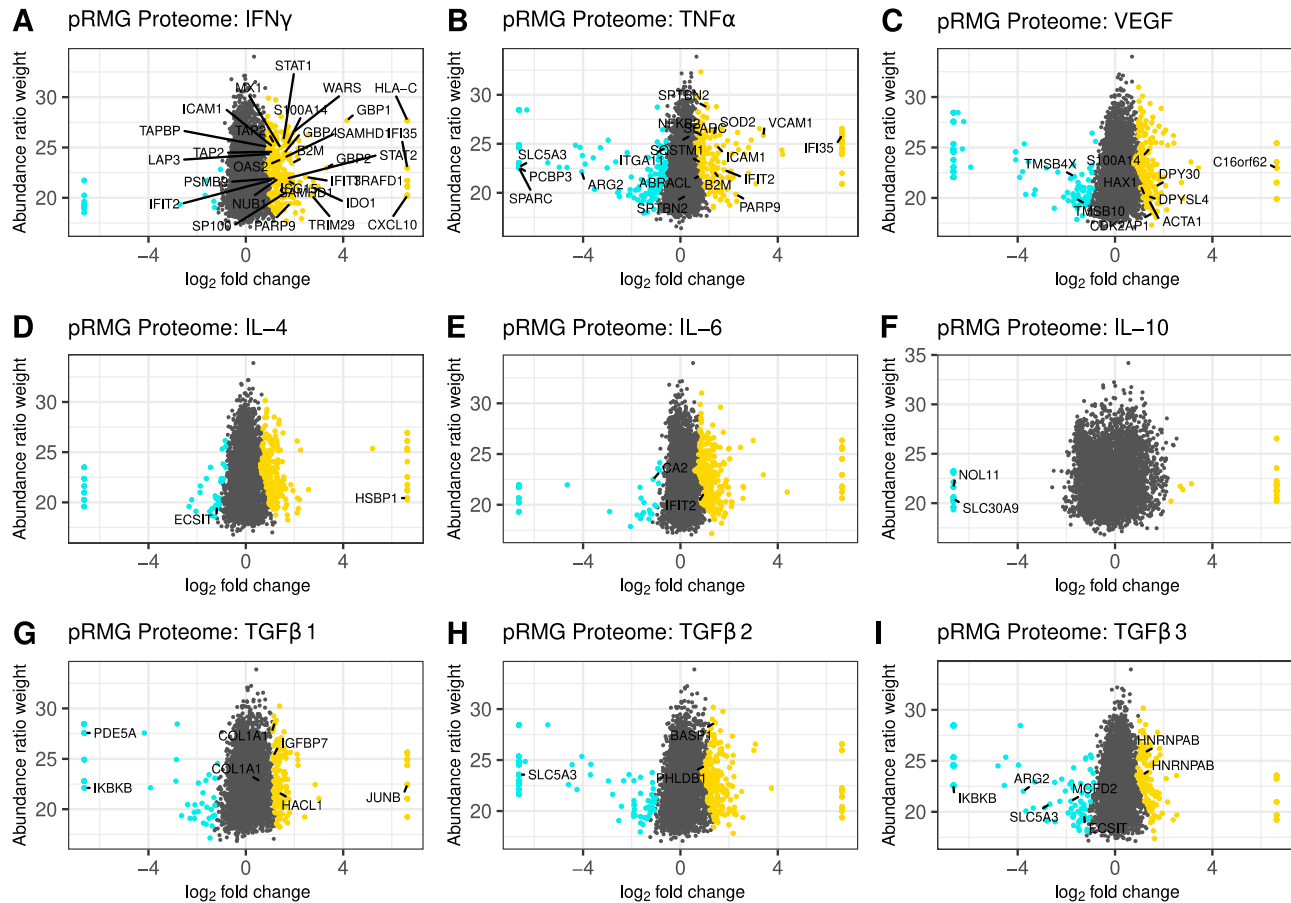
Supplementary Figures



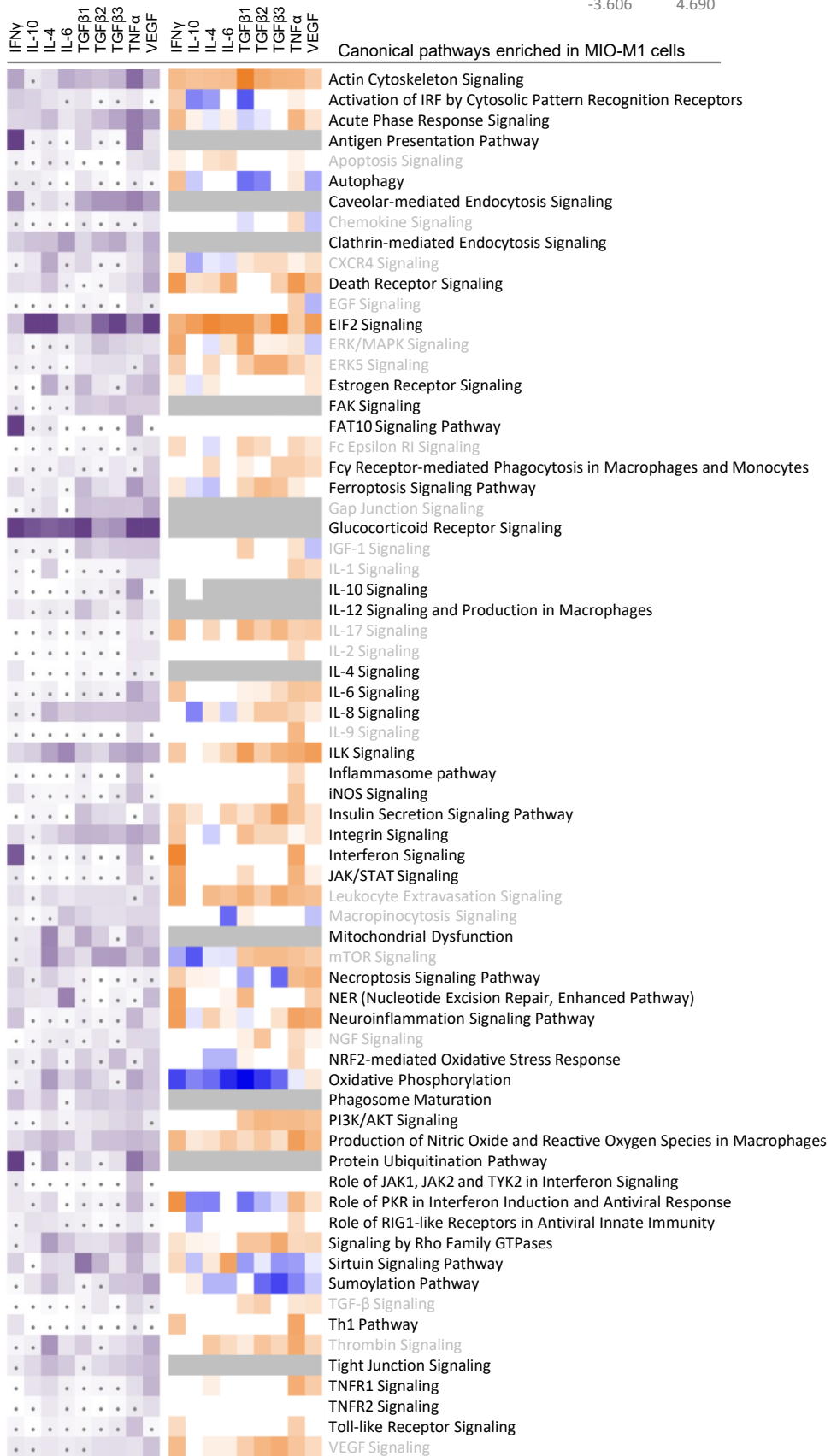
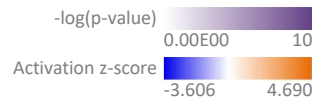
Supplementary Figure S1. Scatterplot of all identified proteins from the pRMG secretomes after treatment with the indicated cytokines for 24 h (A-I). Proteins with significant changes in their abundance ($\pm \log_2(1.5)$ fold expression, corrected p-value ≤ 0.05) were colored, with upregulated proteins being depicted as yellow dots, while down-regulated proteins are colored cyan. Proteins with significantly altered abundance in both, MIO-M1 and pRMG secretomes, are labeled with their gene symbol. Keratins were excluded.



Supplementary Figure S2. Heatmap of hierarchical cluster analysis with a dendrogram of proteins secreted by MIO-M1 cells after treatment with various cytokines. Identified proteins were filtered for extracellular proteins with significant changes in their expression ($\pm \log_2(1.5)$ fold expression, corrected p-value ≤ 0.05). Down-regulated proteins are presented in cyan, while up-regulated proteins are depicted yellow for the respective treatments. Gray squares represent proteins that were neither identified in the untreated control, nor in the respective treatment. The heatmap was generated on the basis of the log₂ fold change of the respective proteins. Clusters A-F were defined using the branches of the dendrogram.



Supplementary Figure S3. Scatterplot of all identified proteins from pRMG lysates after treatment with the indicated cytokines for 24 h (A-I). Proteins with significant changes in their abundance ($\pm \log_2(1.5)$ fold expression, corrected p -value ≤ 0.05) were colored, with upregulated proteins being depicted as yellow dots, while down-regulated proteins are colored cyan. Proteins with significantly altered abundance in both, MIO-M1 and pRMG lysates, are labeled with their gene symbol. Keratins were excluded.



Supplementary Figure S4. A comparative IPA analysis with the significantly regulated proteins identified in the MIO-M1 lysates after stimulation with the indicated cytokines was performed. Canonical pathways related to signaling, cell death, immune system processes and the cellular redox state were selected. Pathways with significant enrichment of genes after stimulation with at least one cytokine are presented. Significance of the gene enrichment for each pathway and treatment is indicated by purple squares in the left array. Treatments that did not meet the significance threshold ($p\text{-value} \leq 0.05$) are marked with a dot. The z-score is indicated on the right array and represents a prediction of activation (orange) or inhibition (blue) of the pathway. Gray squares mark treatments where the activation state of a pathway could not be calculated. Pathways with significant enrichment in MIO-M1 cells that are not enriched in pRMG cells are labeled gray.