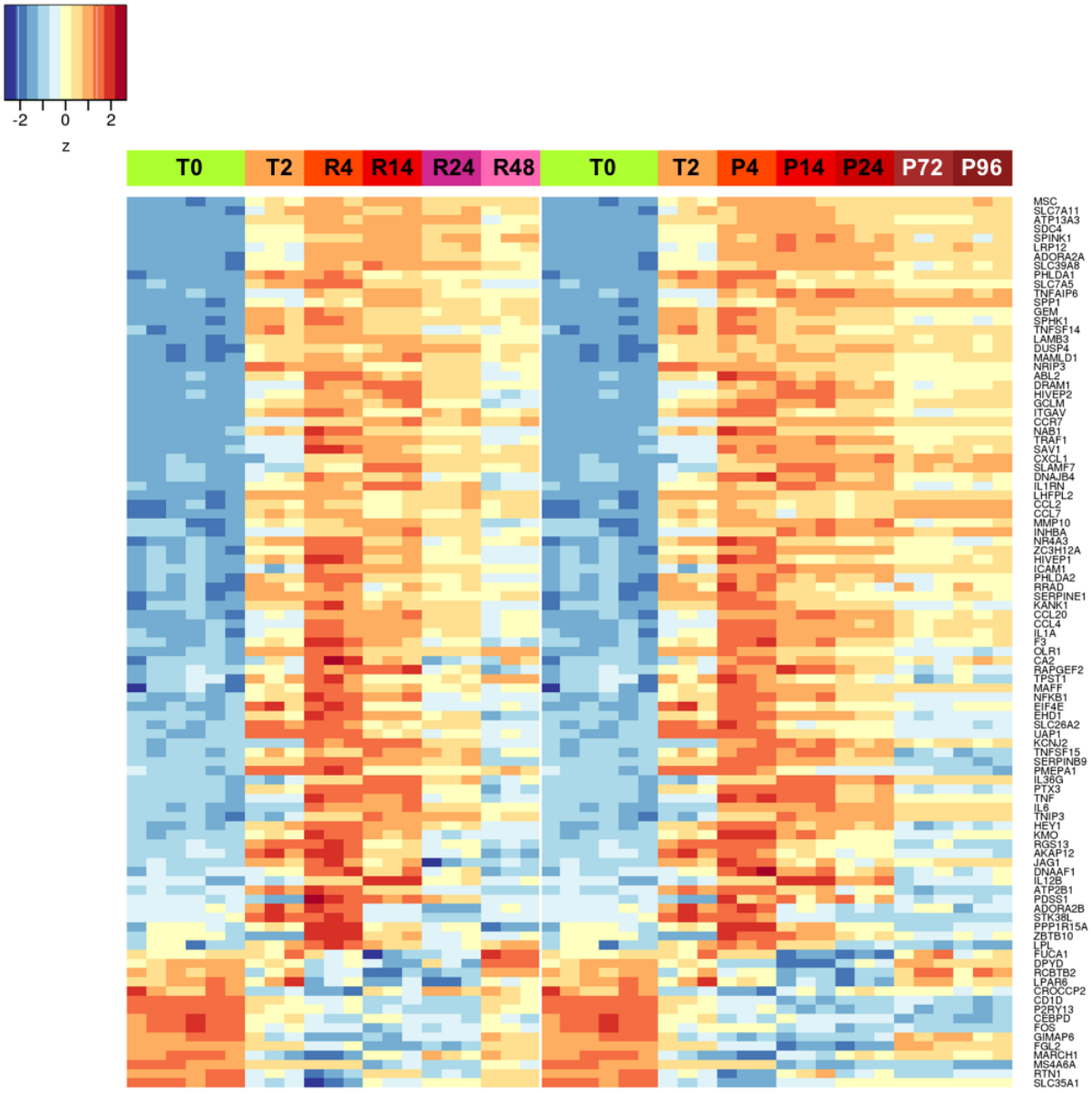


**Figure S1. Differentially expressed genes in M1 macrophages *vs.* fresh monocytes.**
The gene list originates from a meta-database with genes identified by SAM as statistically down-regulated (blue) or up-regulated (red) in M1 samples compared to fresh unstimulated monocytes, excluding genes that are modulated in M2 *vs.* fresh monocytes (45). This list was used to cluster samples of the two kinetic models of resolving and persistent inflammation. Heat-maps represent fold-expression levels of the monocyte-to-M1 genes assessed in the *in vitro* models of resolving inflammation (left) and persistent inflammation (right). Time points are indicated as T0 (fresh monocytes), T2 (after 2 h with CCL2, common to both models), R4 and P4 (4 h of resolving and persistent models), R14 and P14 (14 h both models), R24 and P24 (24 h both models), R48 (48 h resolving model only), P72 and P96 (72 and 96 h persistent model only).

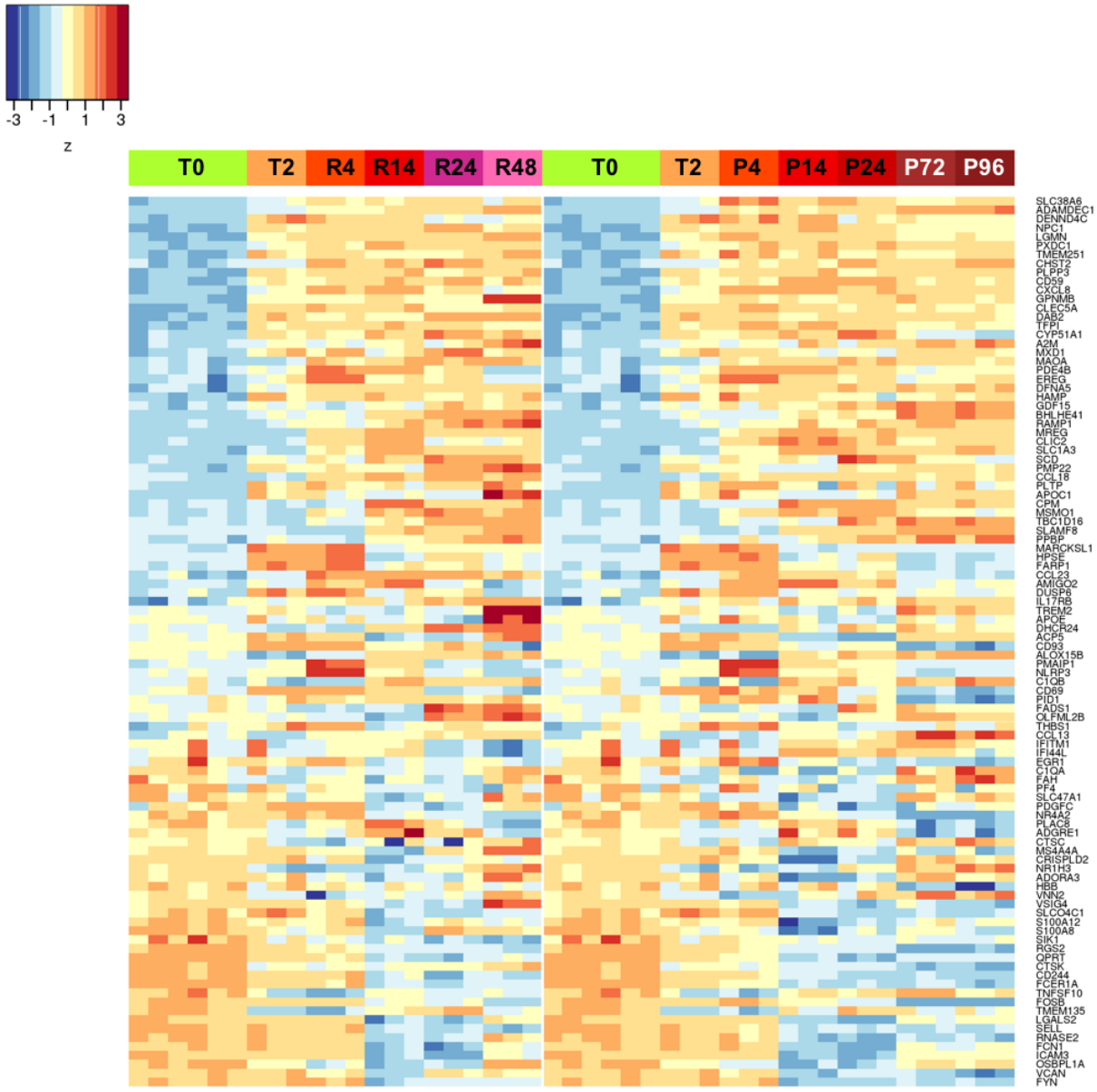


**Figure S2. Differentially expressed genes in M2 macrophages *vs.* fresh monocytes.**
The gene list originates from a meta-database with genes identified by SAM as statistically down-regulated (blue) or up-regulated (red) in M2 samples compared to fresh unstimulated monocytes, excluding genes that are modulated in M1 *vs.* fresh monocytes (45). This list was used to cluster samples of the two kinetic models of resolving and persistent inflammation. Heat-maps represent fold-expression levels of the monocyte-to-M2 genes assessed in the *in vitro* models of resolving inflammation (left) and persistent inflammation (right). Time points are indicated as described in the legend to Supplementary Figure S1.

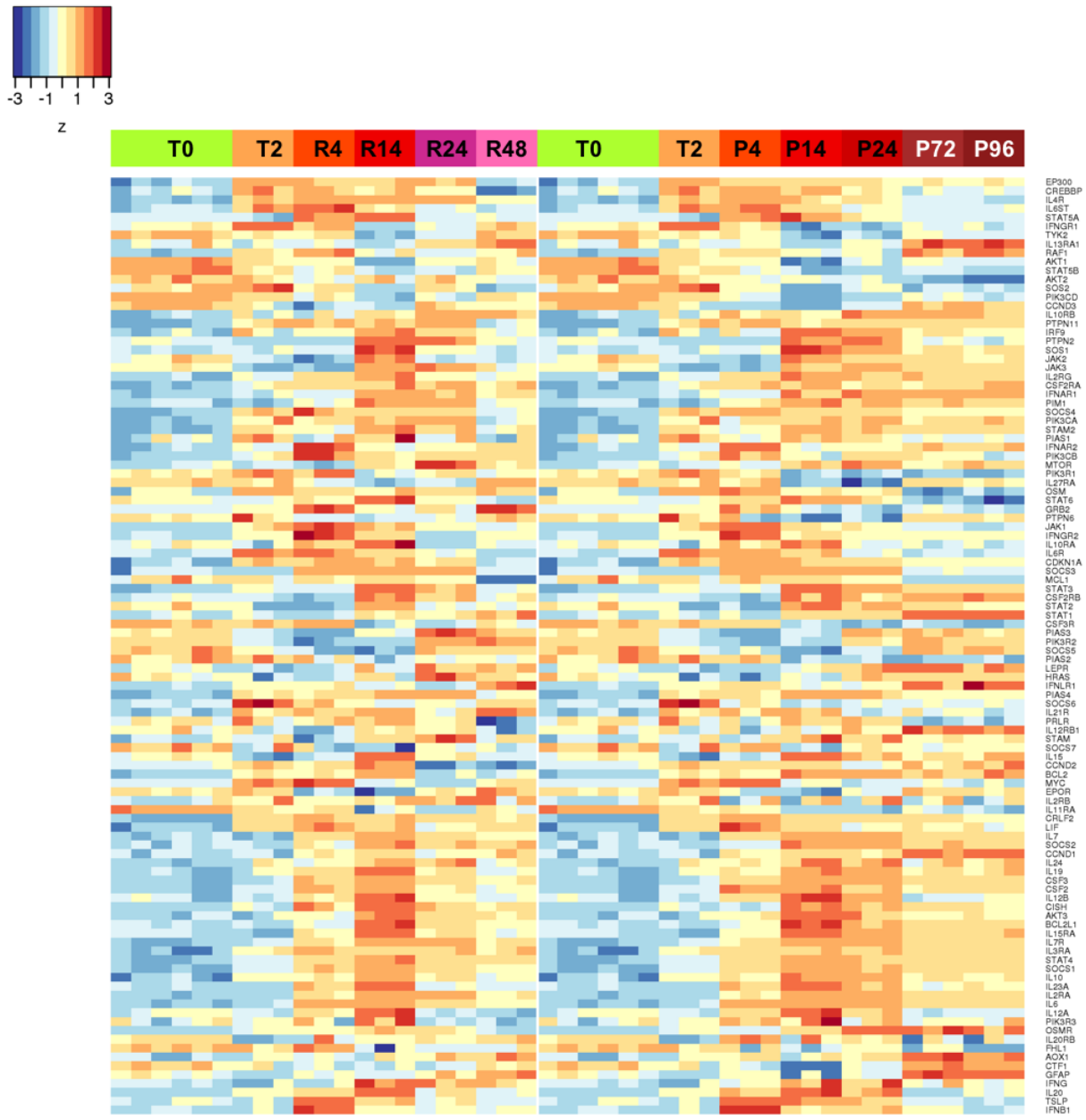


**Figure S3. Differentially expressed genes of the JAK/STAT pathway during the different phases of in vitro resolving and persistent inflammation.**
Heat-maps represent fold-expression levels of the genes involved in the JAK/STAT signalling pathway, assessed in the *in vitro* models of resolving (left) and persistent inflammation (right). The list of genes examined for JAK/STAT signalling is contained in https://www.ncbi.nlm.nih.gov/biosystems/?term=83077 . Time points are indicated as described in the legend to Supplementary Figure S1.

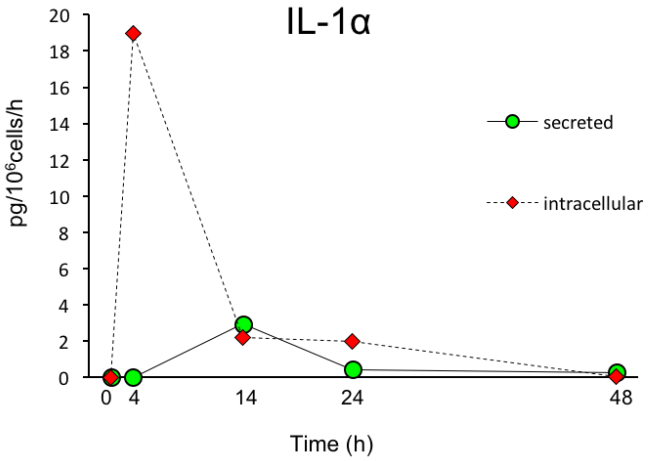


**Figure S4. Intracellular and secreted IL-1α levels during an *in vitro* resolving inflammatory reaction.**

Production of intracellular (green circles, continuous line) and secreted (red diamonds, dashed line) IL-1α during the resolving *in vitro* inflammatory reaction. The levels of the protein released in the supernatant or present in the cell lysate is reported in terms of rate of production, *i.e.*, the amount of protein produced per million viable cells per hour. The average values of one representative donor are reported. SD are not visible in the figure.

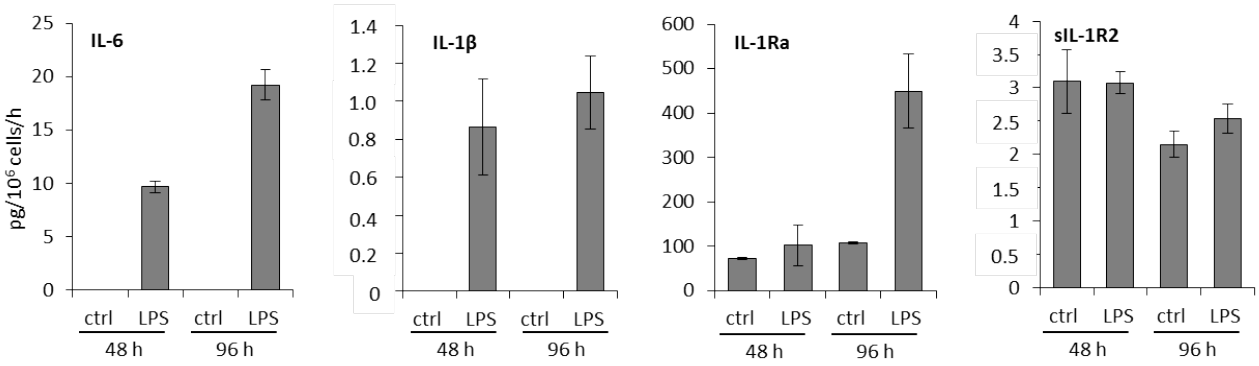


**Figure S5. Reactivity to inflammatory stimulation of monocytes kept in culture for 48 and 96 h.**

Freshly isolated human blood monocytes were kept in culture for 48 h and 96 h and then stimulated with LPS (10 ng/ml) for 24 h. The production of IL-6 and IL-1 family cytokines released in the supernatant is reported in terms of rate of production, *i.e.*, the amount of protein produced per million viable cells per hour. The mean values of triplicate determination from cells of one donor are reported. Statistical significance was calculated with one-way ANOVA followed by Tukey's multiple comparisons test. A $P$ value <0.05 was considered statistically significant. IL-6 ctrl *vs*. LPS (at 48 and 96 h) $P<.0001$; IL-6 LPS 48 *vs*. 96 h $P<.0001$; IL-1β ctrl *vs*. LPS (at 48 and 96 h) $P<.001$; IL-1Ra ctrl *vs*. LPS (at 96 h) $P<.0001$; IL-1Ra LPS 48 *vs*. 96 h $P<.0001$; sIL-1R2 ctrl 48 *vs*. 96 h $P<.05$; sIL-1R2 LPS 48 *vs.* 96 h $P<.05$.