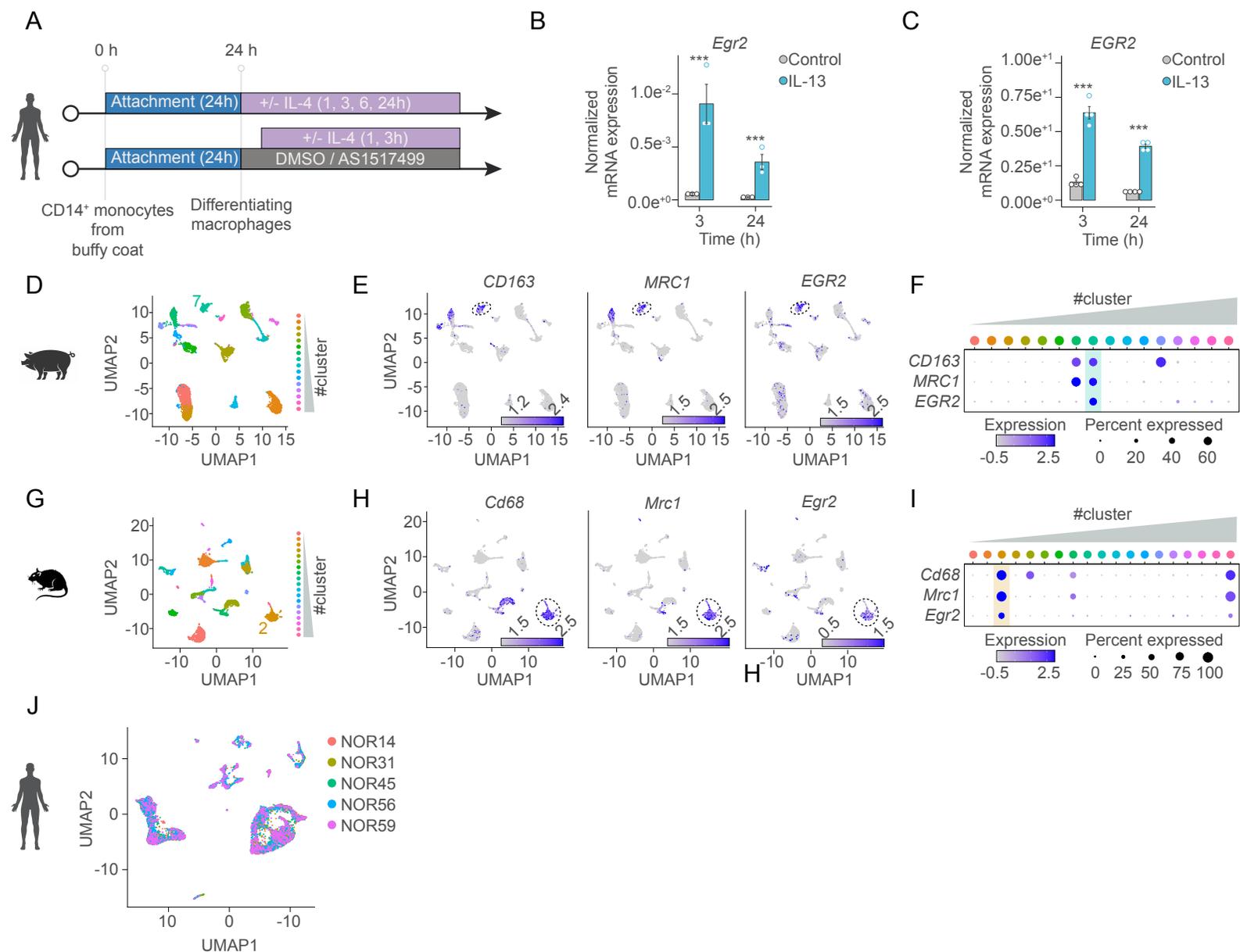


# Supplemental Fig. S7



## Supplemental Fig. S7. The IL-4/STAT6-mediated induction and lung-resident macrophage expression of *Egr2* is evolutionarily conserved. Related to Fig. 7.

**A**, Experimental scheme for studying the IL-4/STAT6-mediated induction of *EGR2* in human CD14<sup>+</sup> monocyte-derived macrophages. CD14<sup>+</sup> monocytes were isolated from buffy coat and plated for 24 hours to adhere followed by IL-4 treatments for the indicated periods of time in the presence and absence (DMSO – solvent control) of the STAT6 inhibitor (AS1517499).

**B**, RT-qPCR measurements of *Egr2* mRNA levels in control and IL-13 polarized mouse bone marrow-derived macrophages over the indicated time course. The level of mRNA is normalized to the expression of *Ppia*. Experiments were repeated four times, and significant changes between groups were calculated by two-way analysis of variance (ANOVA).

**C**, RT-qPCR measurements of *EGR2* mRNA levels in control and IL-13 polarized human differentiating macrophages over the indicated time course. The level of mRNA is normalized to the expression of *PPIA*. Experiments were repeated four times, and significant changes between groups were calculated by two-way analysis of variance (ANOVA).

**D**, UMAP depicting the different cell clusters of the pig lung defined by single cell RNA-seq (GSE133747). Cluster 7 is highlighted which corresponds to the macrophage cluster having high *CD163* and *MRC1* expression.

**E**, Feature plots depicting the expression of *CD163*, *MRC1* and *EGR2* expression in the pig data set. Cluster 7 is encircled to highlight the macrophage population. Log normalized expression values are plotted.

### Supplementary Fig. S7 continued

**F**, Dot plot representation of the average expression and percentage wise expression of *CD163*, *MRC1* and *EGR2* in the different cell clusters of the pig data set.

**G**, UMAP depicting the different cell clusters of the rat lung defined by single cell RNA-seq (GSE133747). Cluster 2 is highlighted which correspond to the macrophage cluster having high *Cd68* and *Mrc1* expression.

**H**, Feature plots depicting the expression of *Cd68*, *Mrc1* and *Egr2* expression in the rat data set. Clusters 2 is encircled to highlight the macrophage population. Log normalized expression values are plotted.

**I**, Dot plot representation of the average expression and percentage wise expression of *Cd68*, *Mrc1* and *Egr2* in the different cell clusters of the rat data set.

**J**, UMAP depicting the different cell clusters of the human lung data set defined by single cell RNA-seq and colored by the five samples (donors) from where the cells originate from. Each sample is derived from a healthy donor and data sets can be found under GSE128033.