

Description of Additional Supplementary Files

Supplementary Data 1: Classical monocyte gene expression variation between pre- and post-simulation in malaria-naïve children and adults. Gene expression data from FACS-isolated classical monocytes obtained from children and adults, both at baseline and following stimulation with *Plasmodium falciparum*-infected red blood cells, were analyzed using generalized linear mixed models implemented in the R package *glmmSeq*. Fold change due to stimulation was calculated by subtracting the log-transformed response term of unstimulated from stimulated samples. Fold change due to age was calculated by subtracting the log-transformed response term of children from adults for both stimulated and unstimulated samples. We corrected for multiple testing using Storey's q-value method, defining significance for q-values lower than 0.05 with the q-value R package. Code available at <https://github.com/Boyle-Lab-CRDV/Age-is-an-intrinsic-driver-of-inflammatory-responses-to-malaria/>.

Supplementary Data 2: V δ 2 T cell gene expression variation between pre- and post-simulation in malaria-naïve children and adults. Gene expression data from FACS-isolated V δ 2 T cells obtained from children and adults, both at baseline and following stimulation with *Plasmodium falciparum*-infected red blood cells, were analyzed using generalized linear mixed models implemented in the R package *glmmSeq*. Fold change due to stimulation was calculated by subtracting the log-transformed response term of unstimulated from stimulated samples. Fold change due to age was calculated by subtracting the log-transformed response term of children from adults for both stimulated and unstimulated samples. We corrected for multiple testing using Storey's q-value method, defining significance for q-values lower than 0.05 with the q-value R package. Code available at <https://github.com/Boyle-Lab-CRDV/Age-is-an-intrinsic-driver-of-inflammatory-responses-to-malaria/>.