Introduction:
Sepsis, a leading cause of mortality among critically-ill patients in the ICU, recently recognized by the WHO as a global health burden. Patients that suffer from sepsis exhibit an early hyper-inflammatory immune response which can lead to organ failure and death. In our study, we assessed the immune modulations in the human in vivo endotoxemia model and compared it to ex vivo lipopolysaccharides (LPS) stimulation using 38 transcriptomic markers.

Methods:
Eight healthy volunteers were challenged with intravenous LPS in vivo. In parallel, blood from another 8 volunteers was challenged with LPS ex vivo. Blood was collected before and after 4 hours of LPS challenge and tested with the Immune Profiling Panel (IPP) prototype using the FilmArray® system.

Results:
The use of IPP showed that markers from the innate immunity dominated the response to LPS in vivo, mainly markers related to monocytes and neutrophils. Comparing the two models, in vivo and ex vivo, revealed that most of the markers were modulated in a similar pattern (68%). Some cytokine markers such as TNF, IFN-γ and IL-1β were under-expressed ex vivo compared to in vivo. T-cell markers were either unchanged or up-modulated ex vivo, compared to a down-modulation in vivo. Interestingly, markers related to neutrophils were expressed in opposite directions, which might be due to the presence of cell recruitment and feedback loops in vivo.

Conclusion:
The majority of IPP markers showed similar patterns of expression post-LPS challenge in both models, except for several markers related to neutrophils and T-cells. The IPP tool was able to capture the early immune response in the human in vivo endotoxemia model, which is a translational model mimicking immune host response in septic patients.