



Figure S6: Transcriptional analysis of sLC vs. sCD14+ DC. **a.** Hierarchical clustering of the 466 transcripts (identified by post-hoc Tukey test) differentially expressed between sLC and sCD14+ DC. **b.** Bar chart representing the IPA canonical pathway enrichment for the 199 transcripts over-expressed in sLC and the 267 transcripts over-expressed sCD14+ DC. **c.** Network analysis of the 199 transcripts over-expressed in sLC. **d.** Network analysis of the 267 transcripts over-expressed in sCD14+ DC.