Supplementary Figure 3. Upstream pathways in fibroblasts. A. and B. Image quantification of the depth of dermal invasion by *C. albicans* 48 h post infection. A. shows models with or without the addition of 25 ng/ml hIL-17A or 333 ng/ml hIL-22 2 h prior to infection. B. shows models with in the presence or absence of CD4$^+$ T cells with or without 5 µg/ml anti-IL-17RA added to the medium 2 h prior to infection. P-values (two tailed Wilcoxon-Mann-Whitney U-test) in A. and B. are indicated as n.s. (not significant) and *** (p < 0.001). C. Quantification by ELISA of CXCL9, CXCL10 and CXCL11 in the culture medium of infected skin models in the absence or presence of CD4$^+$ T cells with or without 5 µg/ml anti-IL-17RA added to the medium 2 h prior to infection. Bars represent the mean and standard deviation of three independent skin models. Significant differences (two tailed student t-test): ** (p < 0.01), *** (p < 0.001) and **** (p < 0.0001) D. Image quantification of the depth of dermal invasion by *C. albicans* 48 h post infection of models without immune cells and models supplemented with CD4$^+$ T cells. Fibroblasts were either transfected with psiRNA plasmids for TLR2 or TLR9. P-values (two tailed Wilcoxon-Mann-Whitney U-test) are indicated. E. Expression levels of inflammasome-related genes in fibroblasts from non-infected or infected skin models as determined by RNA-seq (mean and standard deviation of triplicate samples).