

Transcriptomes of dendritic cells encountering commensal and pathogenic fungi highlight different response mechanisms and timing

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Supplementary Tables

Table S1: Fungal strains used in this study and references to sequence data deposited in ArrayExpress Archive.

Table S2 ("Table2_DEGs_GOs_pathways.xls"): Transcriptional profiles (DEGs, Gos, and pathways) of dendritic cells (DCs) exposed to four fungal species compared to unchallenged DCs.

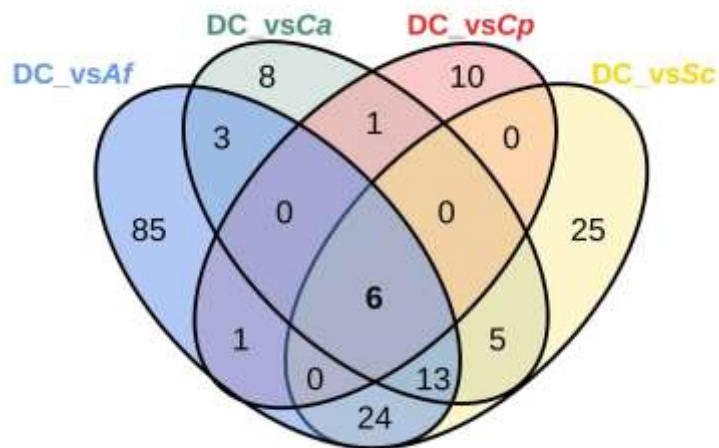
Table S3 ("Table3_shared_DEGs_GOs_pathways.xls"): Common features among transcriptional profiles of DCs challenged with *A. fumigatus*, *C. albicans*, *C. parapsilosis*, and *S. cerevisiae*.

Table S4 (“Table4_species-specific_DEGs_GOs_pathways.xls”): Features characterizing transcriptional profiles of DCs challenged with *A. fumigatus*, *C. albicans*, *C. parapsilosis*, or *S. cerevisiae*.

Figures

Figure S1

Venn diagrams comparing pathways differentially represented in DC treated with the tested fungal species. Differentially represented pathways were identified for every challenge, then the resulting lists were compared. Differentially represented pathways are listed in **Table S2**, the lists of shared and species specific pathways are in **Table S3** and **S4** respectively.



Expression levels of genes involved in the cytokine-cytokine receptor interaction pathway. This pathway was found to be differentially represented in DCs treated with any tested fungal species. Pathway enrichment analysis was carried out with David (Huang et al. 2009); the pathway map was obtained from the KEGG database (Kanehisa et al. 2017) and drawn with pathview (Luo et al. 2017).



TNF signaling pathway and expression of the involved genes. This pathway was found to be differentially represented in DCs treated with any tested fungal species. Pathway enrichment analysis was carried out with David (Huanget al. 2009); the pathway map was obtained from the KEGG database (Kanehisa et al. 2017) and drawn with pathview (Luo et al. 2017).



Figure S4:

MAPK-signaling pathway and expression of the involved genes. This pathway was found to be differentially represented in DCs treated with any tested fungal species. Pathway enrichment analysis was carried out with David (Huanget al. 2009); the pathway map was obtained from the KEGG database (Kanehisa et al. 2017) and drawn with pathway (Luo et al. 2017).

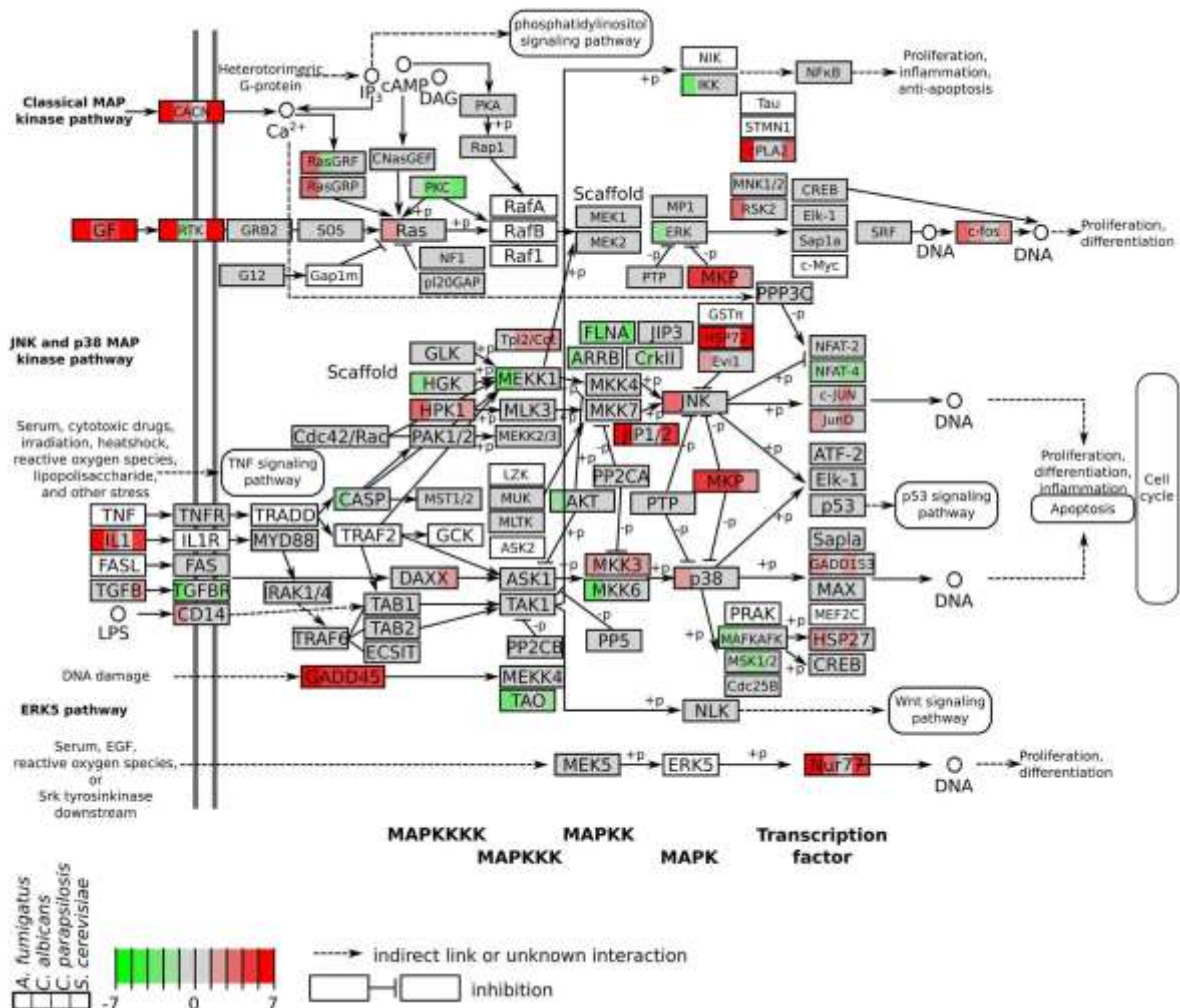
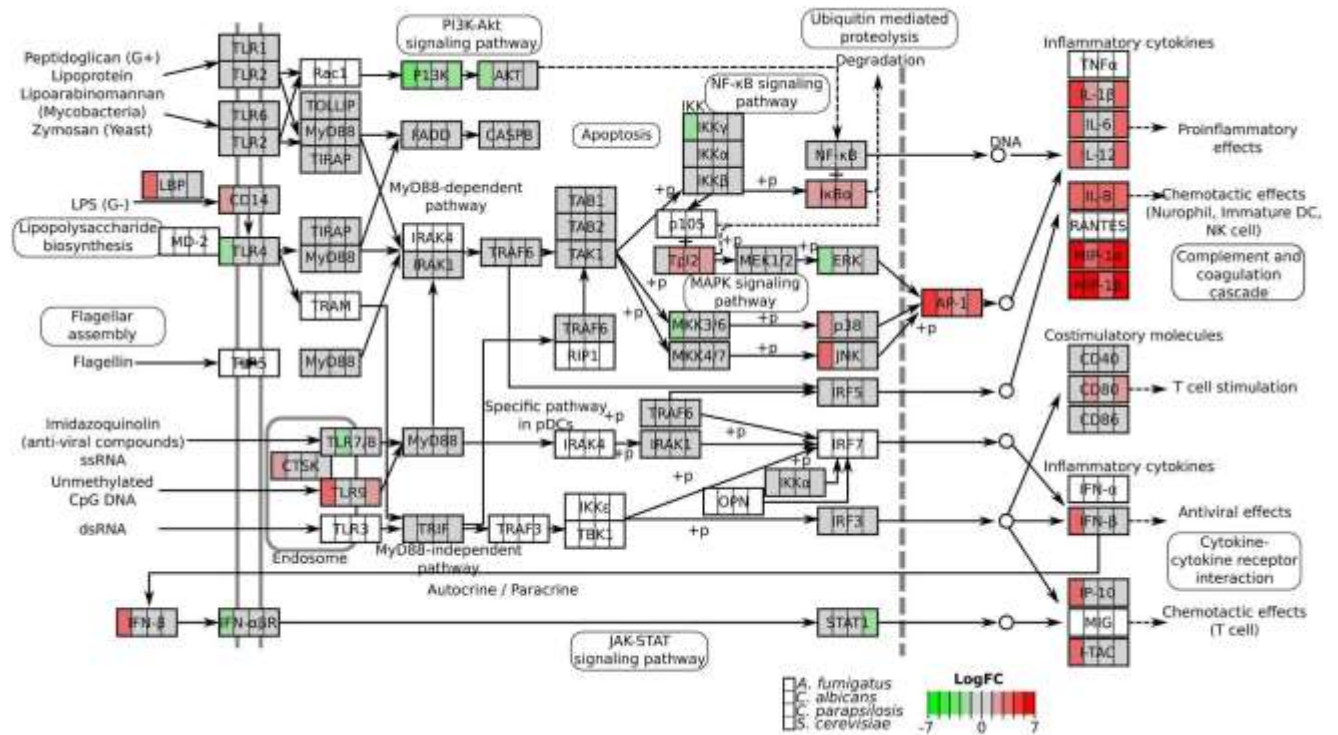


Figure S5

TOLL-like receptor signaling pathway and expression of the involved genes. This pathway was found to be differentially represented in DCs treated with *A. fumigatus* and *C. parapsilosis* strains. Pathway enrichment analysis was carried out with David (Huanget al. 2009); the pathway map was obtained from the KEGG database (Kanehisa et al. 2017) and drawn with pathview (Luo et al. 2017).



Cell adhesion molecules pathway and expression of the involved genes. This pathway was found to be differentially represented in DCs treated with *A. fumigatus* and *C. albicans* strains. Pathway enrichment analysis was carried out with David (Huanget al. 2009); the pathway map was obtained from the KEGG database (Kanehisa et al. 2017) and drawn with pathview (Luo et al. 2017).



Inflammatory bowel disease pathway and expression of the involved genes. This pathway was found to be differentially represented in DCs challenged with *A. fumigatus* and *S. cerevisiae* strains. Pathway enrichment analysis was carried out with David (Huang et al. 2009); the pathway map was obtained from the KEGG database (Kanehisa et al. 2017) and drawn with pathview (Luo et al. 2017).



Chemokine signaling pathway and expression of the involved genes. This pathway was found to be differentially represented in DCs challenged with *A. fumigatus* strains. Pathway enrichment analysis was carried out with David (Huanget al. 2009); the pathway map was obtained from the KEGG database (Kanehisa et al. 2017) and drawn with pathview (Luo et al. 2017).



Figure S9

Heatmap of genes involved in IL-6 signaling pathway.

The IL-6 signaling pathway was found to be differentially represented in DC_vs*Af* (Dendritic Cells exposed to *A. fumigatus* strains). The heatmap shows the genes belonging to this pathway and differentially represented in DC_vs*Af*.

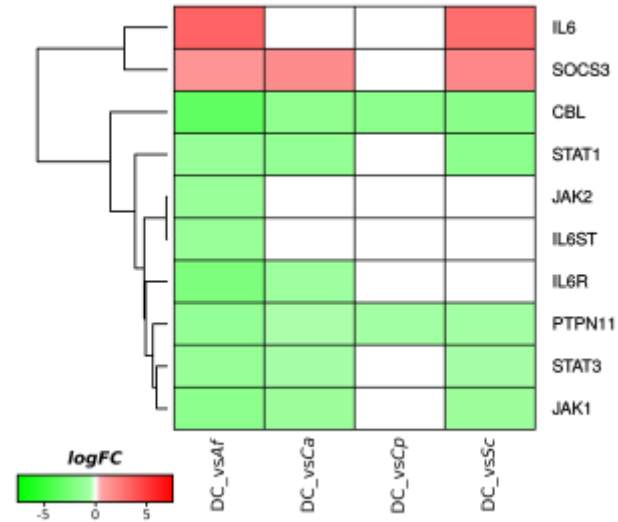
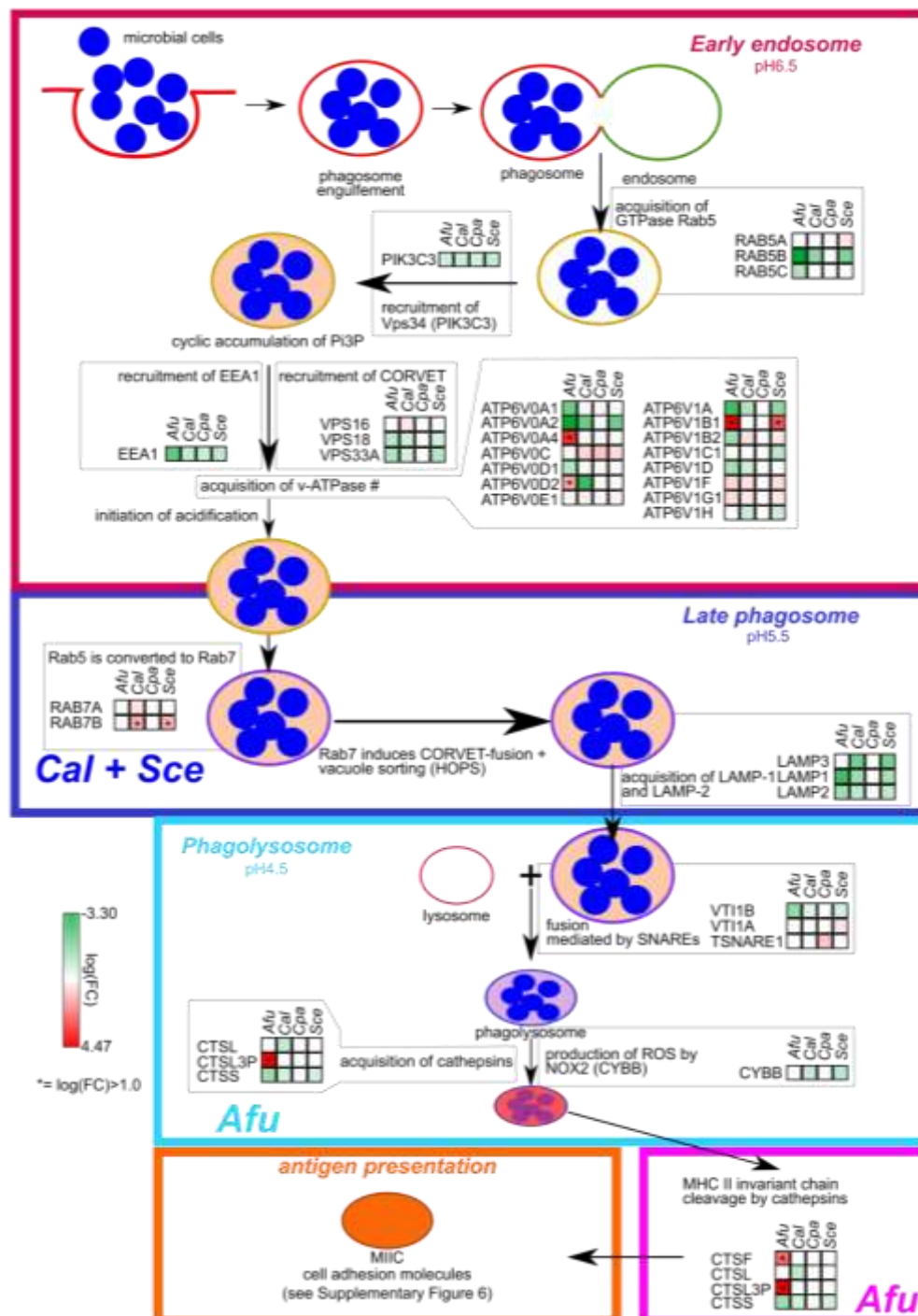


Figure S10

Phagolysosome maturation pathway and expression of the involved genes. The pathway was drawn according to Pauwels et al. 2017, and, for each step involving known genes, it was annotated with the DCs DEGs data gathered over this study. *=DEGs with $\text{Log}(\text{FC}) > 1$, $\text{FDR} < 0.05$. #: to have an impact on v-ATPase functions, the expression of coupled V0 and V1 moieties has to be concerted, hence, the observation of the over- or under-expression of these genes does not provide information on the functional consequences.



Intestinal immune network for IgA production pathway and expression of the involved genes. This pathway was found to be differentially represented in DCs challenged with *C. albicans* strains. Pathway enrichment analysis was carried out with David (Huanget al. 2009); the pathway map was obtained from the KEGG database (Kanehisa et al. 2017) and drawn with pathview (Luo et al. 2017).



Figure S12

Heatmap of genes involved in IFN alpha/beta signaling.

The IFN alpha/beta signaling pathways was found to be differentially represented in DC_vsCa (Dendritic Cells exposed to *C. albicans* strains).

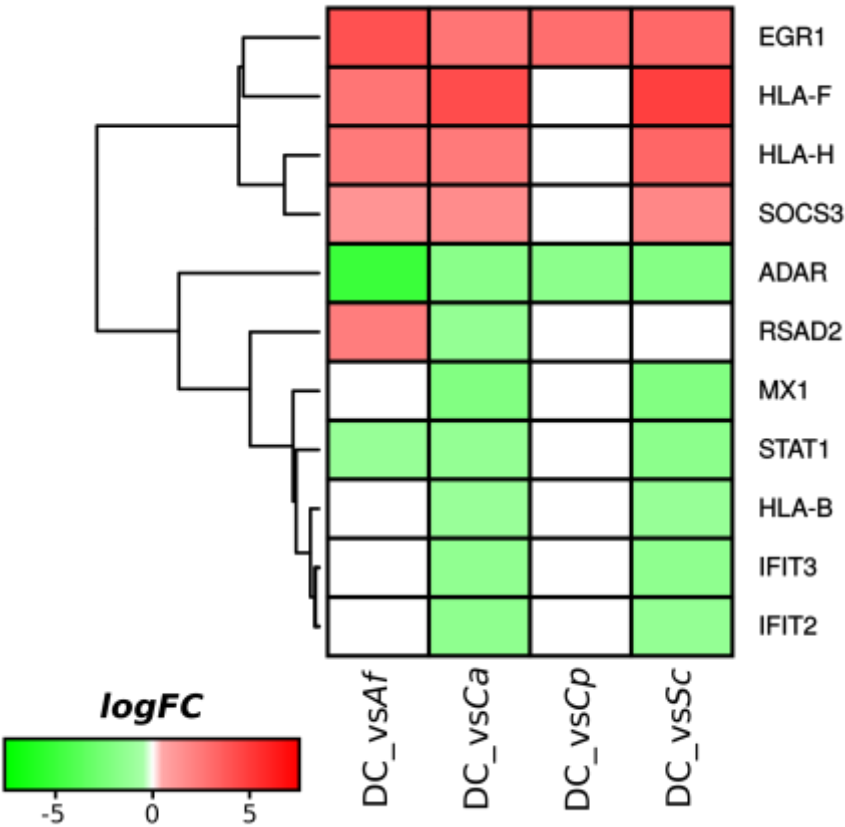


Figure S13

NOD-like receptor signaling pathway and expression of the involved genes. This pathway was found to be differentially represented in DCs challenged with *C. parapsilosis* strains. Pathway enrichment analysis was carried out with David (Huanget al. 2009); the pathway map was obtained from the KEGG database (Kanehisa et al. 2017) and drawn with pathview (Luo et al. 2017).

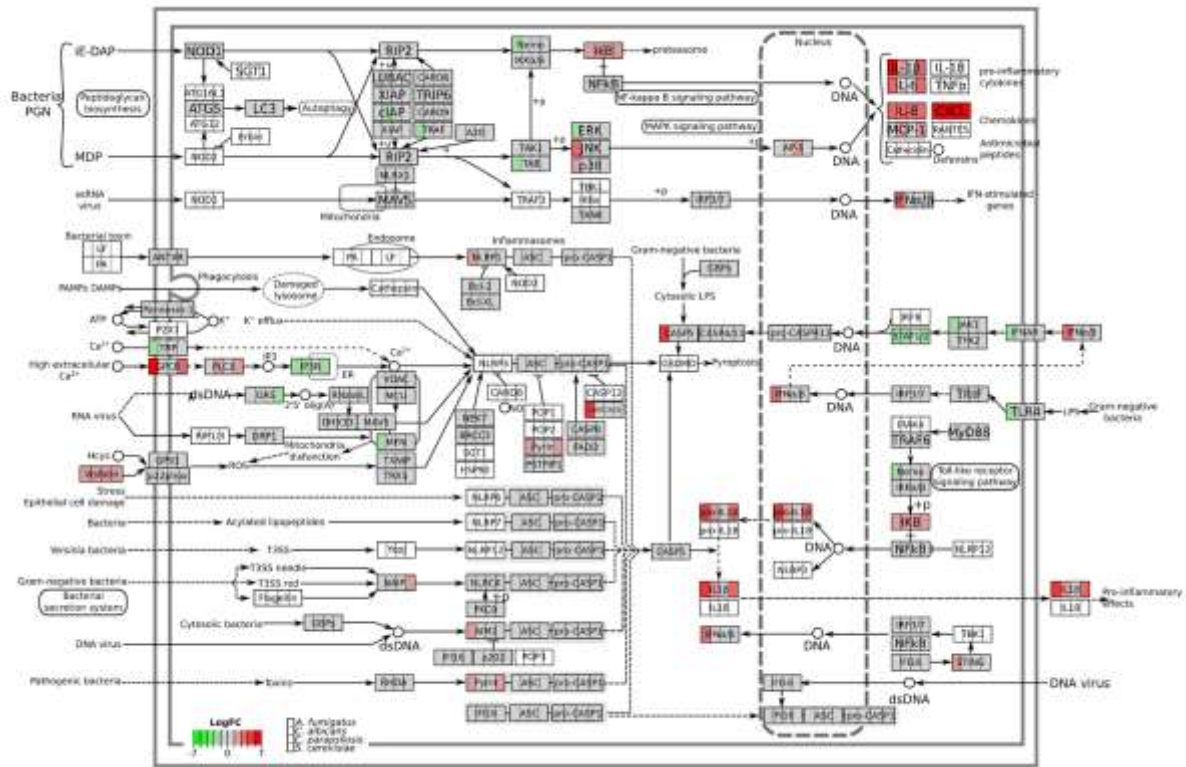


Figure S14

MyD88-MAL(TIRAP) cascade initiated on plasma membrane. This pathway was found to be differentially represented in DCs challenged with *C. parapsilosis* strains. Pathway enrichment analysis was carried out with David (Huanget al. 2009); the pathway map was obtained from the KEGG database (Kanehisa et al. 2017) and drawn with pathview (Luo et al. 2017).

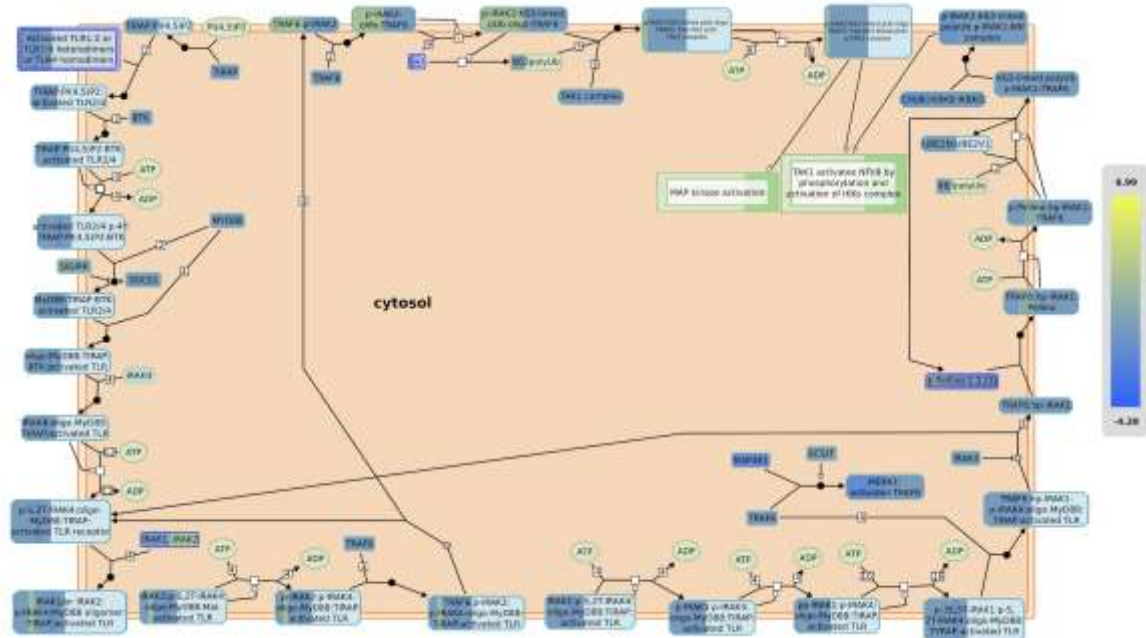


Figure S15

Interferon gamma signaling pathway and expression of the involved genes. This pathway was found to be differentially represented in DCs challenged with *S. cerevisiae* strains. Pathway enrichment analysis was carried out with David (Huanget al. 2009); the pathway map was obtained from the KEGG database (Kanehisa et al. 2017) and drawn with pathview (Luo et al. 2017).

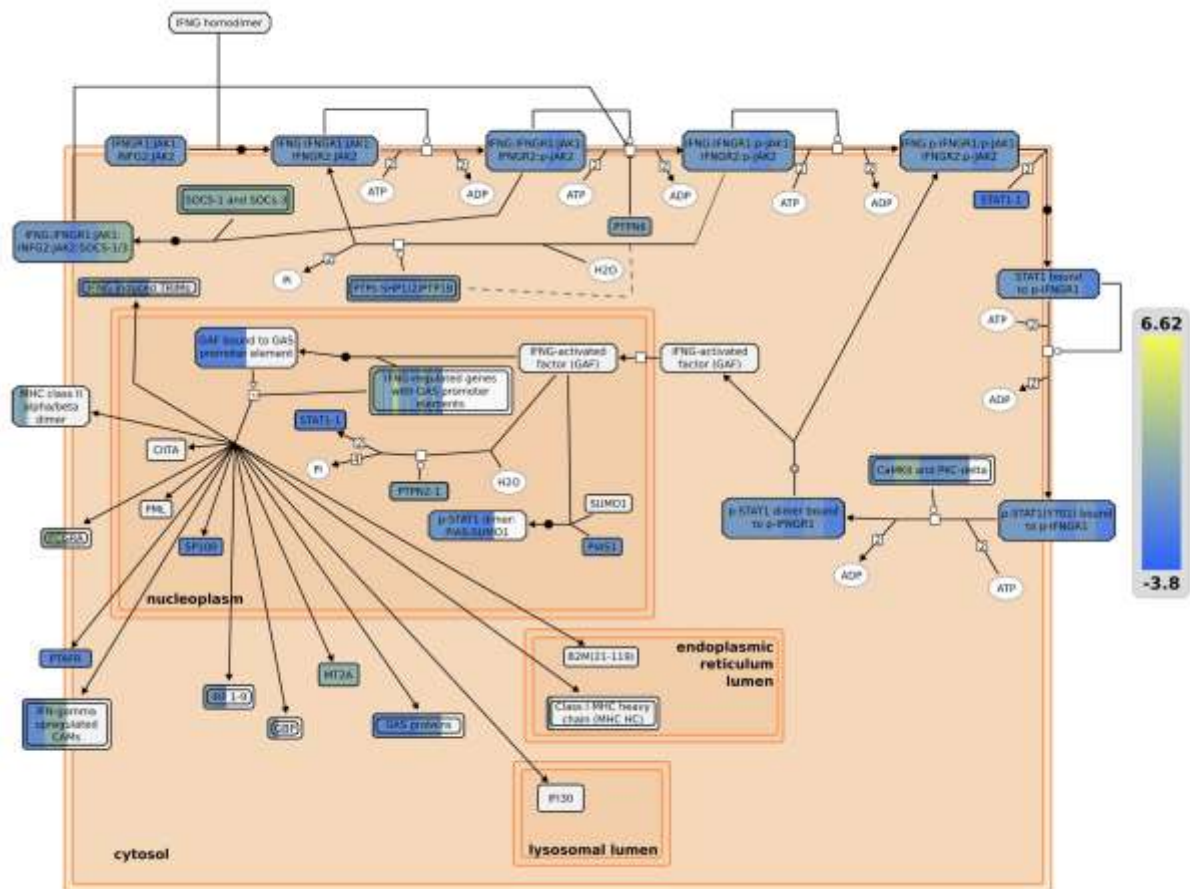


Figure S16

TRAF6 mediated induction of NFkB and MAP kinases upon TLR7-8 or 9 activation pathway and expression of the involved genes. This pathway was found to be differentially represented in DCs challenged with *S. cerevisiae* strains. Pathway enrichment analysis was carried out with David (Huanget al. 2009); the pathway map was obtained from the KEGG database (Kanehisa et al. 2017) and drawn with pathview (Luo et al. 2017).

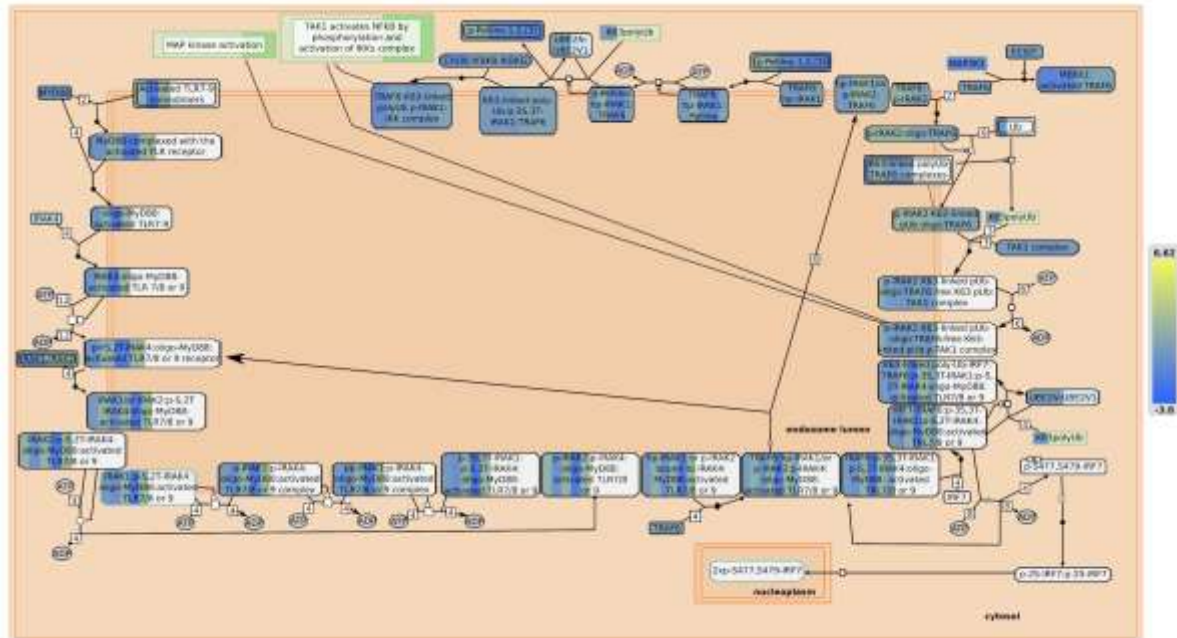


Figure S17

Known pathways involved in the DCs antifungal response to fungi triggered by surface receptors. The figure has been inspired by the schemes proposed by Ramirez-Ortiz and Means (Virulence 2012, 3:1-12) and Romani (Nature 2011, 11:275-288).

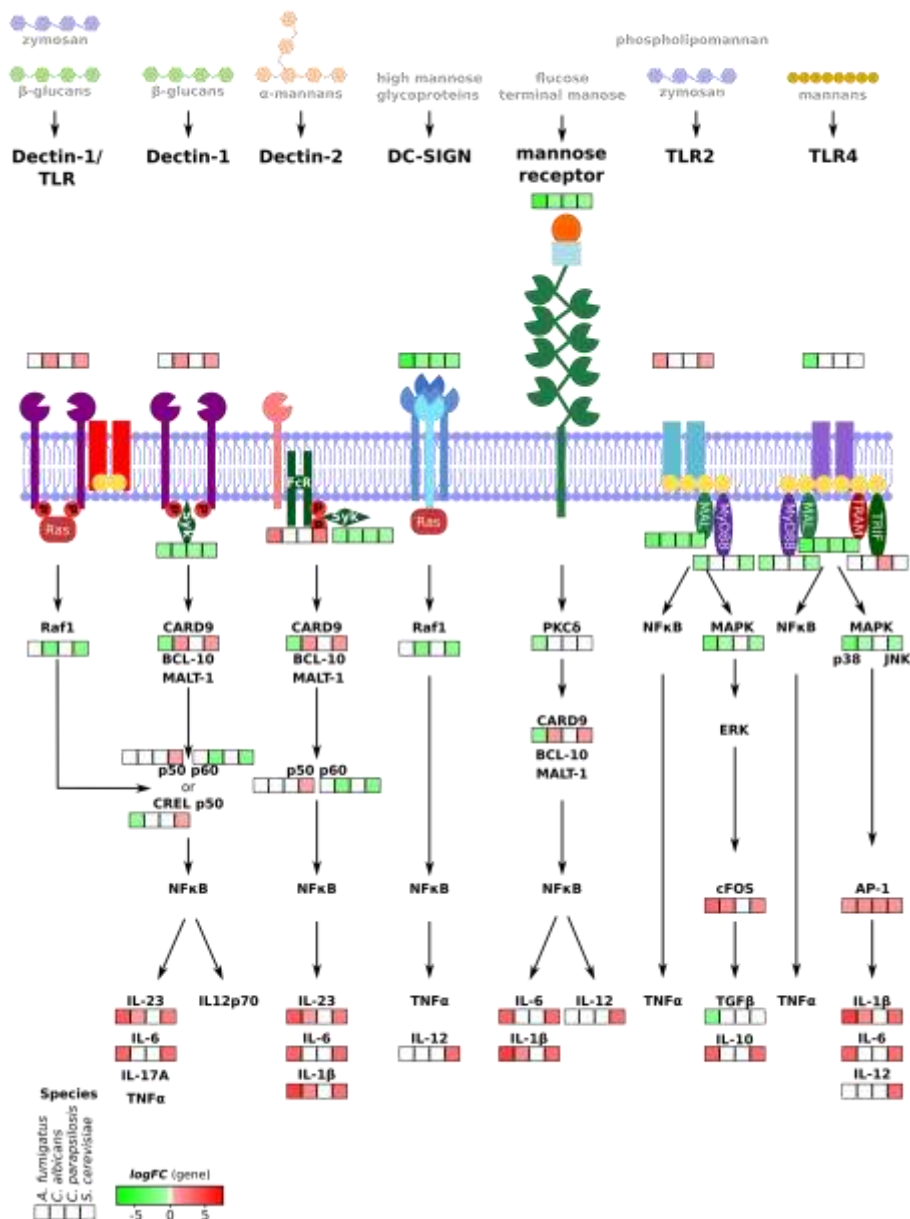


Figure S18

Known pathways involved in the DCs antifungal response to fungi triggered by endosomal receptors. The figure has been inspired by the schemes proposed by Ramirez-Ortiz and Means (Virulence 2012, 3:1-12) and Romani (Nature 2011, 11:275-288)

