

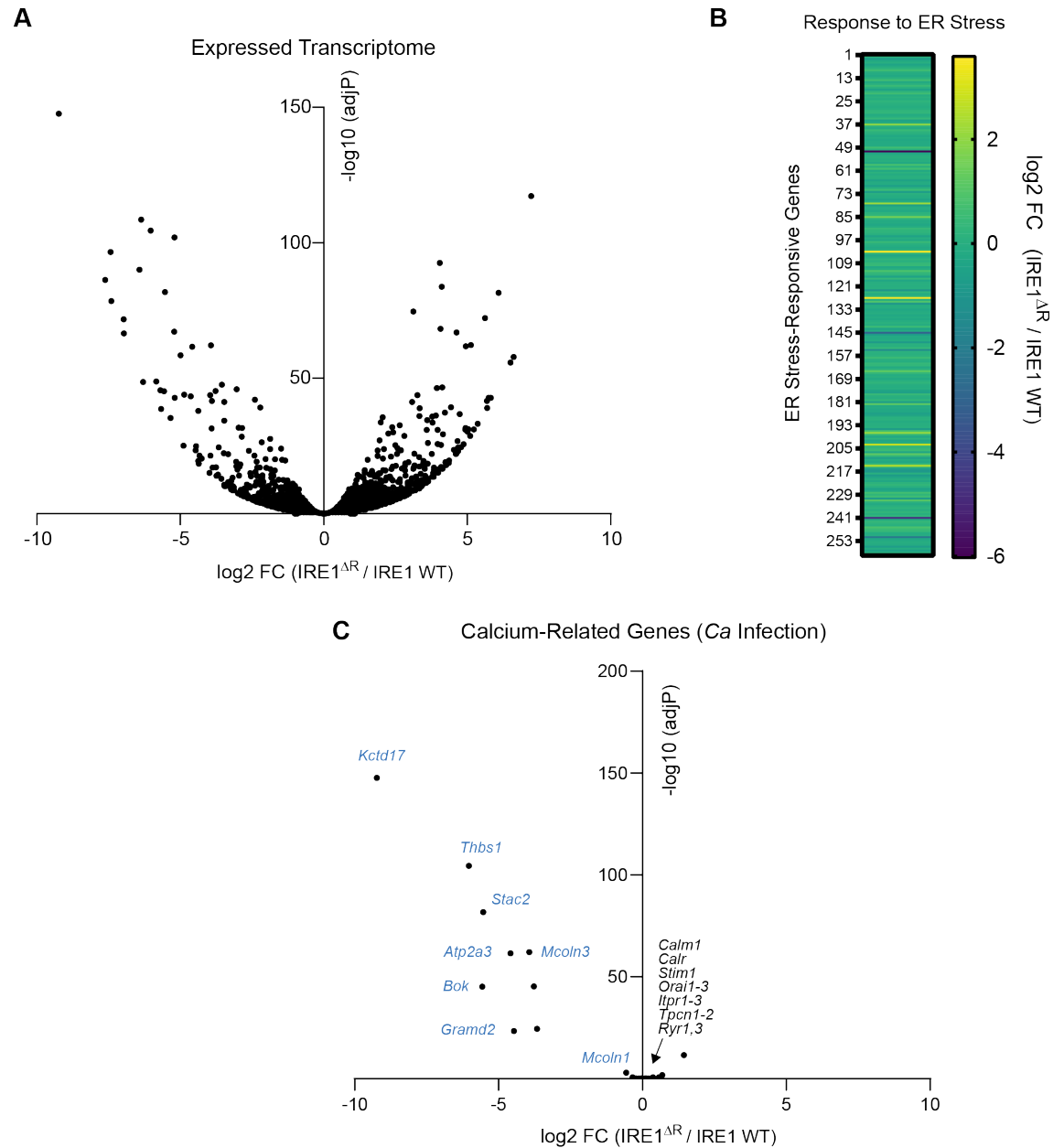
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**Figure S1: Related to Figure 1. (A)** Immunoblot analysis of XBP1S and XBP1U expression from WT iBMDM lysates following infection with *C. albicans* (MOI=1), or treatment with positive controls

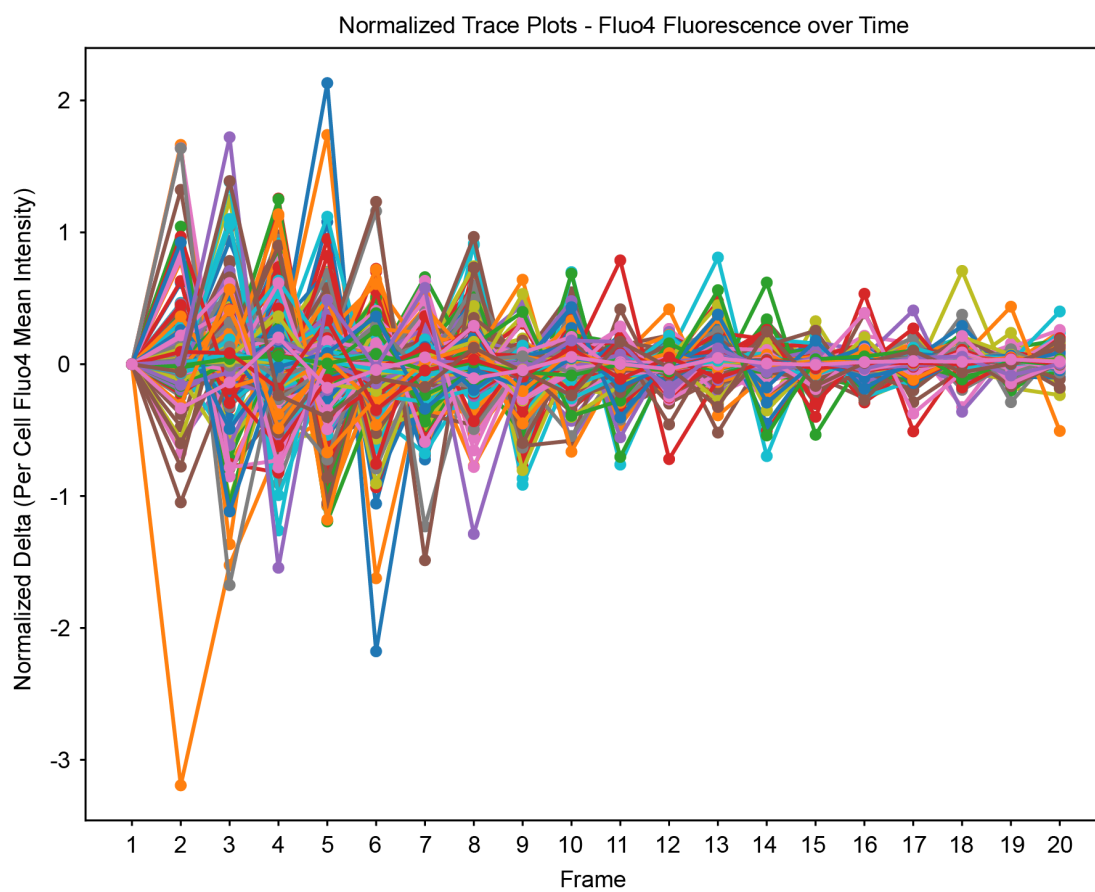
204 LPS (100 ng/mL) or thapsigargin (5  $\mu$ M). **(B)** Quantification of 3 independent experiments, as  
205 shown in (A). **(C)** Immunoblotting validation of clonal TRAF6 WT controls (WT-1 and WT-2) and  
206 TRAF6 knockout iBMDM (KO-1 and KO-2).



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347 **Supplemental Figure 2: IRE1 $\alpha$  regulates macrophage gene expression. (A)** Volcano plot of  
 348 the effect of IRE1 $\alpha$  activity ablation on the expressed transcriptome (IRE1 $\Delta$ R / IRE1 WT) of  
 349 iBMDM, revealed by RNA-seq. **(B)** Heatmap of differential gene expression in IRE1 $\Delta$ R iBMDM of  
 350 genes in the GO category "Response to ER stress", showing that IRE1 $\Delta$ R macrophages do not  
 351 have a chronic ER stress signature. **(C)** Heatmap of downregulated genes involved in organelle  
 352 calcium homeostasis (blue text) in IRE1 $\Delta$ R iBMDM, and major calcium homeostasis regulators  
 353 (black text) whose expression is not impacted.

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375 **Supplemental Figure 3: Related to Figure 4.** Representative trace plots of cellular Fluo4  
376 intensity in individual cells tracked over time for quantification of cellular calcium flux, as shown in  
377 Figure 4C-D.