

Calprotectin modulates inflammatory collateral tissue damage during intraperitoneal origin systemic candidiasis

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15 Abstract

16 Peritonitis is a leading cause of severe sepsis in surgical intensive care units, as
 17 over 70% of patients diagnosed with peritonitis develop septic shock. A critical role of
 18 the immune system is to return to homeostasis after combating infection. S100A8/A9
 19 (calprotectin) is an antimicrobial, pro-inflammatory protein used as a marker for
 20 diagnosis of inflammatory diseases. Here we describe the role of calprotectin on
 21 inflammatory collateral tissue damage (ICTD). WT and calprotectin-deficient *in vivo*
 22 *Candida albicans* disseminated peritonitis mice model, and primary macrophages were
 23 treated with recombinant calprotectin and the anti-inflammatory compound,
 24 paquinimod. The effects on ICTD and fungal clearance were investigated. Calprotectin-
 25 deficient mice developed less ICTD than wildtype mice. Injection of recombinant
 26 calprotectin resulted in increased ICTD and fungal clearance comparable to wildtype
 27 levels. Treatment with paquinimod, a specific inhibitor of calprotectin, abolished ICTD.
 28 The data indicated that calprotectin controls ICTD levels and host antimicrobial
 29 modulation at a systemic level during intra-abdominal candidiasis (ICA).

30 **IMPORTANCE:** Fungal pathogens like *C. albicans* pose a significant burden on health
 31 at a global level comparable to malaria and tuberculosis. Despite the increasing
 32 antifungal drug resistance, fungi remain underestimated as pathogens. Fungal
 33 dissemination to organs during severe fungal systemic inflammation is often lethal for
 34 immunocompromised patients, particularly during intraabdominal surgeries where
 35 disseminating infections in patients can become life-threatening conditions with a
 36 matter of hours. This study utilizes *in vivo* techniques for recombinant protein therapy
 37 and pharmacological inhibition (paquinimod) to modulate activity of a systemic

38 antimicrobial protein demonstrating that calprotectin controls the severity of fungal

39 sepsis and hence provides an option for pharmacological intervention.

40

41 Introduction

42 Peritonitis frequently results in severe sepsis in surgical patients, especially in
 43 the intensive care unit (ICU),(1), as more than 70% of patients often succumb to death
 44 within 72h,(2). Hence, we require treatments that extend life expectancy to allow proper
 45 treatment.(3). Peritonitis is characterized by inflammation of the membrane in the
 46 abdominal cavity, the peritoneum. Peritonitis often occurs upon disruption of physical
 47 barriers or can become spontaneous in severe organ failure, causing alterations of the
 48 physiologic flora residing in the gastrointestinal tract (GIT),(1, 4). These alterations
 49 prompt an inflammatory response that targets the removal of contaminants from the
 50 peritoneal cavity into circulation. There, pathogens prompt activation of host immune
 51 responses and the release of pro-inflammatory mediators including Interleukin-6 (IL6),
 52 macrophage inflammatory protein -1 α (MIP-1 α) and tumor necrosis factor - α (TNF α) to
 53 recruit phagocytes to the peritoneum,(5). The attempt to restrict infection promotes
 54 abscess development through production of fibrinous exudate. Failure to confine
 55 peritonitis may lead to organ failure, coma and death,(6).

56 Interestingly, inflammation can be described as a spectrum degrees of deviation
 57 from homeostasis, characterized by outcomes that are either intentional (pathogen
 58 clearance) or collateral (pathological side effect, called inflammatory collateral tissue
 59 damage -ICTD),(7). The focus of most studies on detection and elimination of
 60 pathogens has neglected host tolerance to disease through the resolution of collateral
 61 outcomes of inflammation in an attempt to establish homeostasis, (8).

62 Acute or systemic inflammatory pathological states are often associated with
 63 intra-abdominal surgery,(9). Surgical intervention disrupting the natural barriers of the
 64 gastrointestinal tract (GIT) lead to deep-seated microbial infection by gut colonizing

organisms and frequently *Candida albicans* infection. As a result, the most common non-mucosal fungal diseases among hospitalized patients in the developed world are *Candida* peritonitis, also referred to as intra-abdominal candidiasis (IAC). IAC is challenging to diagnose and hence results in high mortality rates ranging from 25% - 60%, (9).

The resolution of infection is an active process involving reprogramming of cells and modulation of mediators,(10). Included among these mediators are multifunctional proteins, such as the S100A8/A9 heterodimeric complex (calprotectin). Here, we used an experimental model for IAC to study the contribution of calprotectin to ICTD.

Participating as a signaling molecule that binds toll-like receptor-4 (TLR4) to induce pro-inflammatory chemokines and cytokines, the heterodimer calprotectin is the physiologically relevant and is the bioactive form that is secreted by activated, stressed or necrotic cells. Under high calcium conditions, such as present in the extracellular milieu and culture medium, S100A8/A9 heterodimers quickly tetramerize, thereby losing TLR4 signaling capacity,(11). Thus, S100A8 homodimers, which cannot tetramerize, are widely accepted experimental stimuli to mimic heterodimer activity.

Furthermore, calprotectin binds micronutrients including zinc, manganese, and calcium, and is often deployed by leukocytes as a mechanism to either deprive microbes of the nutrients or poison the microbes in high quantities,(12). Neutrophils deploy the heterodimer against *C. albicans* during the formation of neutrophil extracellular traps,(13). In addition to the antimicrobial benefit, calprotectin is used in diagnostics to monitor neutrophil elevation in various inflammatory diseases, though the exact

88 mechanisms on calprotectin modulation to resolve inflammatory homeostasis remains
89 elusive,(14).

90 One treatment currently under clinical trials is paquinimod, an
91 immunomodulatory compound that prevents the binding of S100A9 to TLR4, designed
92 to target chronic inflammatory diseases,(15–20). Using a murine peritonitis model with
93 *C. albicans*, we show that inflammatory responses failed to contain the pathogen in the
94 peritoneum, which in turn led to detrimental ICTD dependent on the presence of
95 calprotectin. Interestingly, treatment of mice with paquinimod abrogated calprotectin-
96 induced ICTD suggesting paquinimod as promising adjunct therapy option during
97 severe ICA.

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Results

A disseminated fungal peritonitis model to determine roles of S100A8/A9

During ICA, fungal cells dissemination reach the liver and other organs via lymphatics or bloodstream,(6). Liver tissue damage and leukocytosis are hallmarks of deep-seated and systemic *C. albicans* infection,(21). To establish a fungal ICA model and determine the role of calprotectin in systemic inflammation, we obtained the previously characterized *S100A9*-deficient mouse (*S100A9*^{-/-}) that can induce the *S100A8* transcripts but lacks the S100A8 protein,(22). S100A8 in *S100A9*^{-/-} mice is rapidly degraded in the proteasome, avoiding systemic overwhelming immune responses. However, under chronic TNF conditions, this degradation process is insufficient leading to severe phenotypes in artificial mouse strains (*TTP*^{-/-}/*S100A9*^{-/-} or *itghTNF*/*S100A9*^{-/-}) indicating that heterodimer activity must be regulated tightly to restrict operating range,(23).

Using wildtype (WT) and *S100A9*^{-/-} mice, *C. albicans* intraperitoneal injections were administered, liver tissues collected after 24 hours of infection and indicators of sepsis were measured. The infection was determined to be systemic using phenotypic analysis of mice and histopathological analysis from hematoxylin-eosin stained (H & E stain) liver sections after 24 hours. The development of eye exudates (Figure 1a) was an indication of fungal dissemination from the peritoneal cavity to other loci in the mouse. WT liver sections indicated higher numbers of leukocytic infiltration zones compared to *S100A9*^{-/-} sections (Figure 1b, top panel). Conversely, there was visual evidence of more fungal cells in the *S100A9*^{-/-} livers compared to WT (Figure 1b, bottom panel). The inflammatory score (Figure 1c). showed a large number of inflammatory cell infiltrates

(level 3) in WT *C. albicans* infected samples compared to lack of inflammation (level 1) observed in *S100A9*^{-/-} mice.

Blood alanine aminotransferase (ALT) levels in the blood are an indicator of liver damage,(1, 24). *C. albicans* infected WT mice (101.6U/L) showed elevated levels compared to *S100A9*^{-/-} mice (37.2U/L) which showed similar ALT levels to uninfected mice, suggesting lack of systemic tissue damage in the calprotectin-deficient animals (Figure 2a). The ability of the host to clear the infection or organ microbial load is related to the colony-forming units (CFUs),(25). *S100A9*^{-/-} mice had a significantly higher fungal load (2.5 fold of average levels) compared to WT mice (Figure 2b).

Macrophages are sentinels for immune signaling that leads to leukocytosis but may cause problems when uncontrolled,(26). The pro-inflammatory cytokine response of WT and *S100A9*^{-/-} was determined using bone marrow-derived macrophages (BMDMs) to monitor the ability of primary macrophages to induce TNF α (Figure 2c). Higher levels of TNF α (3.1 fold of average levels measured) were induced by WT BMDMs (570.7 pg/ml) compared to *S100A9*^{-/-} BMDMs (185.5 pg/ml), suggesting a defect in TNF α induction in cells lacking calprotectin.

S100A8/A9 is responsible for ICTD during disseminated peritonitis

The active role of calprotectin on systemic candidiasis is currently unknown. Further, the implications on the use of calprotectin in recombinant protein therapy is also unknown. A recombinant therapy approach was employed to determine the role calprotectin in sepsis,(27). Murine *S100A8* was expressed in *E. coli*, purified and verified by mass spectrometry to obtain functional and structurally stable homodimers

as previously reported,(28). For completion, we also purified *S100A9*, as a control, although purified protein dimerization does not occur and renders the protein inactive,(23). To determine the effects of recombinant S100A9 and S100A8 proteins (rS100A8 and rS100A9) on disseminated *C. albicans* infection Purified calprotectin monomers (Figure 3a) of predicted sizes (S100A8 (~10 kDa) and S100A9 (~14 kDa)) were purified and injected (100µl (100 µg/ml) protein per WT or *S100A9*^{-/-} in *C. albicans* infected mice. We did not use the recombinant heterodimer (S100A8/A9) in our experiments as these quickly form tetramers with predominantly anti-inflammatory effects *in vivo*,(23).

S100A9^{-/-} mice showed no difference when treated with rS100A9 (Figure 3b). Treatment of *S100A9*^{-/-} mice with rS100A8 showed a higher level of ALT (5.9 fold of average levels measured) compared to untreated with levels not significantly different to WT suggesting that constitutively active S100A8 homodimers mimic heterodimers to cause WT levels of liver damage (Figure 3b) and that the calprotectin-mediated effect on ICTD is direct rather than indirect. calprotectin is an antimicrobial protein against *C. albicans*,(13). In this context, the fungal clearance defect observed in *C. albicans* infected *S100A9*^{-/-} mice was remedied, reducing fungal load after treatment with rS100A8 (Figure 3c). To determine whether the S100A8 activity would aid the *S100A9*^{-/-} mutant in eliciting an appropriate cytokine response, BMDMs infected with *C. albicans* were treated with rS100A8. Induction (7.5 fold of average levels) of TNFα levels was obtained in *S100A9*^{-/-} BMDMs treated with rS100A8 (Figure 3d) comparable to WT levels upon *C. albicans* infection (Figure 2c). *In vivo*, *S100A9*^{-/-} BMDMs infected with *C. albicans* showed higher levels of various cytokines compared to rS100A8 treated BMDMs (Figure 3e-3j). Furthermore, the macrophage chemoattractant

MIPI α (*CCL3*) and *MIPI β* (*CCL4*), crucial for the recruitment of various leukocytes and expression of inflammatory cytokines including IL6 and TNF α , (29), were both significantly elevated (3.9 and 3.4 fold respectively) upon rS100A8 treatment (Figure 3g and 3h). In agreement, *C. albicans* infected *S100A9^{-/-}* BMDMs treated with rS100A8 produced higher levels of IL6 and TNF α than untreated BMDMs (Figure 3e and 3f). Also monitored was the induction of the anti-inflammatory cytokine IL10, which showed low but significant levels induced when mice were treated with rS100A8, while CXCL-1 levels declined (Figure 3i and 3j). Induction of pro-inflammatory cytokines and modulation of tissue damage by rS100A8 suggest that calprotectin heterodimers are main contributors of inflammatory responses during *C. albicans* infection. The induction of lower levels of the anti-inflammatory IL-10 suggests that calprotectin also affects anti-inflammatory cytokines.

Paquinimod therapy nullifies ICTD induced by rS100A8

Targeted deletion of *S100A9* improves survival in mouse models of bacterial-induced sepsis, (30). Higher lethality of a systemic infection is often due to the inability to contain sepsis-induced organ and tissue damage by the host, (1). There are no specific therapies against sepsis, and often management focuses on containing the infection through source control and antibiotics or antifungals plus organ function support, (31). We hypothesized that using an anti-inflammatory drug in WT mice may mimic the beneficial aspect (lack of tissue damage) observed in the *S100A9^{-/-}* mutant might extend host survival from fungal sepsis.

The activity of paquinimod, a novel anti-inflammatory compound initially developed against systemic Lupus Erythematosus (SLE) that targets liver, lung, heart and skin *S100A9*, (32), was tested *in vitro* and *in vivo*. Supplementary figure 1 shows the

percentage of dead cells (propidium iodide positive cells) using flow cytometry analysis (FACS) on treatments of WT BMDMs with various drug concentrations of paquinimod. Among the concentrations used, no significant toxic effects were observed (Supplementary figure 1). However, there was significant TNF α , and CCL-3/MIP-1 α reduction at 300 μ g/ml and 930 μ g/ml paquinimod concentrations compared to untreated *C. albicans* infected BMDMs (Figure 4a and 4c). The anti-inflammatory cytokine IL10 (Figure 4b), was also reduced albeit, initial levels (BMDMs + Ca) were too low to discern systemic effects compared to levels observed under rS100A8 treatment (Figure 3i). Treatment of mice with the drug had a higher fungal burden in infected WT mice, while and the higher levels of the fungal load was consistently high in *S100A9*^{-/-} mice compared to treated *S100A9*^{-/-} mice (Figure 4d). Paquinimod did not have significant effects on fungal clearance in *S100A9*^{-/-} mice (Figure 4e), and complete elimination of liver tissue damage was observed in *C. albicans* infected *S100A9*^{-/-} mice with rS100A8 upon treatment with paquinimod (Figure 4f).

To determine whether paquinimod could be used to alleviate sepsis derived from fungal peritonitis, infected wildtype mice were treated with paquinimod every 24 hours with paquinimod (Figure 5a). Although the drug did not prevent mice from succumbing to systemic infection, treated mice survived longer compared to untreated mice, particularly between 24 and 48 hours (Figure 5b). Despite the similar weight loss observed between treated and untreated mice (figure 5c), treated mice presented an inability to clear fungal exudates in the eyes (Figure 5d), consistent the observed decreased fungal clearance in the liver by *S100A9* mutant mice (Figure 2b). In addition to this, treated mice were generally more active during *C. albicans* infection, despite the higher fungal burden.

Discussion

This work establishes the first study to characterize the role of immune-modulating calprotectin on host resolution of inflammation from a peritoneal-derived disseminated fungal infection. The gastrointestinal commensal nature of *C. albicans* requires that mucosal damage and neutropenia are achieved for *C. albicans* dissemination,(33). Unfortunately, most experimental models studying systemic fungal diseases use intravenous (IV) injection of fungal cells even though this route primarily bypasses mucosal host defenses that require breach before the development of sepsis,(34). This study utilized an IAC model to induce systemic inflammation mimicking a severe clinical concern of postoperative *Candida* peritonitis,(35). Similar to IV, IP-induced infection allows rapid blood dissemination of pathogens with exposure to an active population of phagocytes, complement cascade and the potential for abscess formation in the peritoneal cavity,(35). The peritonitis infection model presented here aimed to breach the immune barriers in the peritoneal cavity, and this was phenotypically clear in the dissemination of *C. albicans* in murine eyes (figure 1a). This method was superior in that; it is more representative of a systemic fungal infection that occurs in peritonitis, compared to the standard blood IV infection route that efficient to bypass many absorption barriers and metabolic mechanisms,(36). The IP injection route allows pathogen exposure to active phagocyte populations in the peritoneum and the potential for the host to contain the infection through the formation of abscesses,(6).

WT liver fungal clearance was ~3 times more efficient when compared to the calprotectin mutant (Fig 2b). Notably, the *S100A9*^{-/-} mutant used, lacks the S100A8 protein as well, despite the presence of S100A8 transcripts as previously reported,(23,

37). The various leucocyte infiltration zones observed in WT liver tissues compared to *S100A9*^{-/-} mice (Fig 1b, c) indicated that the recruitment of higher levels of leukocytes coincides with fungal clearance in WT mice. These findings suggested that the presence of calprotectin is required for fungal clearance during disseminated infection, and supports our previous findings that implicated antimicrobial properties of calprotectin during candidiasis,(13). Notably, presence of calprotectin subjected WT mice to nearly ~3 times more TNFα levels and tissue damage compared to *S100A9*^{-/-} mice as indicated by ALT levels (Fig 2 b, c), implicating that the induction of S100A8/A9 inflammatory responses modulates processes which contribute to tissue damage. These findings support the association of the S100 family of proteins with inflammatory disorders,(23), and our data indicates that calprotectin activity depends on strict modulation of both antimicrobial and inflammatory activity. These insights would especially be critical in the case of immunocompromised patients.

Despite constitutive expression (6.5% of transcriptome) and abundance (~ 45% of cytosol) of S100A9 and S100A8 in neutrophils Elgazzar, 2015; Niemiec et al., 2017, these proteins are additionally induced through appropriate stimulants and are often strongly expressed in acute and chronic inflammatory lesions and degenerative disorders such as Alzheimer disease,(38), suggesting potentially systemic roles by calprotectin. Indeed, the IP treatment of *C. albicans* *S100A9*^{-/-} with rS100A8 resulted in *S100A9*^{-/-} fungal clearance similar to WT. Depending on the Ca²⁺ and Zn²⁺-binding properties of calprotectin, various protein conformation and oligomerization states are obtained, including self-assembly into tetramers and possibly larger oligomers,(38). Experimental limitation did not allow us to determine the exact site of recombinant

protein activity if either direct *C. albicans* targeting in the peritoneal cavity, intra-organ
fungal clearance or both.

Since rS100A8 showed significant *in vivo* activity, we used *in vivo* *S100A9*^{-/-} and
the *S100A9*^{-/-} primary macrophages in a *C. albicans* *ex vivo* infection assay, and showed
that rS100A8 mediates macrophage activation as indicated by the higher levels of the
chemokines Cxcl-1, CCL-3 and CCL-4 (Fig 2e), pro-inflammatory cytokines as well as
the anti-inflammatory cytokine IL10. The induction of IL10 by rS100A8 is consistent
with homeostatic management of systemic inflammation,(39). Balancing of pro- and
anti-inflammatory cytokines is a common theme of host factors with local and system-
wide effects as exemplified by interferon signaling pathways during viral infections,
(40). Though rS100A8 showed efficient fungal clearance, in circumstances where the
immune system is compromised, the activity of S100A8 has the potential to induce dire
effects on host-mediated tissue damage.

Our data not only demonstrate the potential of recombinant protein therapy of
calprotectin but also showed a new therapeutic potential for paquinimod. The chemical
inhibition of S100A9 by paquinimod is used to treat chronic inflammatory diseases,(15,
18). As a specific binder for S100A9, we found paquinimod targeting the inflammatory
effects of S100A8, potentially indirectly affecting the active dimer site. Paquinimod
alleviated the tissue-damaging effects of rS100A8 (Fig 3d, e). No toxicity was observed
against bone marrow-derived macrophages (BMDMs) at the concentration used on mice
trials and paquinimod activity affected the inflammatory modulators as observed in the
reduction of CCL-3 and IL-10. Hence, paquinimod represents a potential adjuvant
therapeutic option that targets the host responses instead of the pathogen, in particular,
since the compound had no adverse effect on fungal clearance. Although only 12 hours

were added to the survival time of paquinimod treated mice between 24 and 48 hours, the rate of drug metabolism and therefore depletion in mice are unknown, and this information would be required to fine-tune treatment. However, an extra 12 hours to a patient with a 72-hour survival/diagnostic window might be valuable.

This study showed the dilemma of the protective and harmful roles of calprotectin in *Candida albicans*-induced fungal peritonitis (Figure 6). Fungal peritonitis that is not contained by host defenses leads to pathogen infiltration of host organs (Figure 6.1). Fungal-host interaction induces the systemic release of calprotectin,(13) for fungal clearance and ALTs into the systemic circulation (Figure 6.2-6.3). Local innate immune cells (represented in this study as primary macrophages respond with a cytokine ‘storm’ of pro-inflammatory cytokines (Figure 6.4- 6.5), that leads to increased leukocyte infiltrates systemically (Figure 6.6), and promote increased tissue damage in the effort of fungal clearance (Figure 6.7). To our knowledge, this is the first study to present both the potential for a systemically functional protein, evidence for potential antimicrobial recombinant protein therapy, and adjuvant treatment as paquinimod-mediated inhibition of calprotectin showed reduction of ICTD (Figure 6.vi).

The significant improvement of ICTD in mice with experimental IAC upon paquinimod treatment supports the idea that the detrimental effects of inflammation may indeed influence the increased mortality associated with invasive fungal infections,(41). Therefore, more insights in the activity of this compound will provide options that might be utilized to increase the time required for proper diagnosis of infection related to systemic inflammation. Considering the high mortality (>50%) due

312 to do fungal sepsis,(1), future adjuvant therapies similar to paquinimod could be the key

313 against peritonitis and other severe inflammatory malignancies.

314

Materials and Methods

Ethical statement. Animal experiments and isolation of cells were carried out

following the recommendations in the Guide for the Care and Use of Laboratory Animals, conformed to Swedish animal protection laws and applicable guidelines (djurskyddslagen 1988:534; djurskyddsförordningen 1988:539; djurskyddsmyndigheten DFS 2004:4) in a protocol approved by the local Ethical Committee (Umeå djurförsöksetiska nämnd, Permit Number A79-14).

Statistical analysis. Statistical analysis was conducted using Graphpad Prism 6

software and *P* values less than 0.5 were considered significant. All two-group comparisons in *Candida* CFU data, inflammatory score, ALT data, and ELISA data were conducted using the unpaired, two-tailed student's *t*-test. Comparisons of WT and *SI00A9*^{-/-} mice data were performed using One-way ANOVA multiple comparisons analysis as specified in figure legends. In all comparisons, the sample size is specified in figure legends, and a *P*<0.05 was considered significant. **p*<0.05; ***p*<0.01; ****p*<0.001; *****p*<0.0001.

Yeast strains and growth conditions. *C. albicans* clinical isolate strain -

SC5314 was cultured overnight in YPD (1% yeast extract, 2% bacto-peptone and 2% glucose) at 30°C. The *Candida* cells were washed three times in PBS prior use in all assays. Cell numbers were calculated using Vi-CELL Cell Viability Analyzer (Beckman Coulter AB).

Animal infections and isolation of bone marrow-derived macrophages, and

tissue analyses. All mice were maintained according to a previous report,(42) at Umeå Centre for Comparative Biology (UCCB), Umeå University, Umeå, Sweden.

Primary macrophages (BMDMs) cells and differentiated as described in a previous report,(43). BMDMs flow cell cytometry (FACs) was conducted using BD LSR II flow cytometer (BD Biosciences, San Jose, CA), using propidium iodide,(43), on paquinimod treated cells at indicated concentrations.

For tissue damage and fungal load, analyses were conducted according to a previous report,(44), with 3×10^6 *C. albicans* cells intraperitoneal injection per g of mouse after 24 hours of infection,(11). Blood ALT levels were measured using vetscan VS2™ (SCIL animal care company) as previously reported,(24, 45, 46).

Histological preparations and inflammatory score analyses were conducted as in previous reports, (13, 47), For the inflammatory score, Whole sections were analyzed for inflammation and scored under the supervision of a specialized animal pathologist. The sections from each animal were scored as zero if they had no inflammatory cells present in the tissue, one for a few inflammatory cells (1–20 cells), two for moderate cell infiltration (21–40 cells), three for a large number of inflammatory cells (41–60 cells), and four if inflammation was spread all over in the tissue (61 cells),(47).

Cytokine and chemokine quantification. BMDMs were seeded at 1×10^5 cells per well in 96-well microplates and then infected with *C. albicans* at an MOI of 1 for 24 hours. Cell-free culture supernatants were harvested after *C. albicans* infection. Supernatants were analyzed for indicated cytokines of chemokines by ELISA (Biolegend-ELISA MAX™ 9727 Pacific Heights Blvd, San Diego, CA, USA), or Pro-Mouse cytokine BioPlex® 200 multiplex (Bio-Rad Laboratories) according to the manufacturer's instructions.

Generation of recombinant S100A8 and S100A9. The S100A8 and S100A9

gene encoding for monomers of the mouse dimer calprotectin (UniProt P27005, P31725) were codon-optimized and synthesized using DNA2.0, GST tagged and cloned in *E. coli* BL2. Proteins were fractionated and purified using Superdex 75 16/600 column (GE Healthcare Life Sciences, UK) The primary sequence, the intact mass and the presence of product were confirmed by mass spectrometry using an ABI 4800 MALDI tandem time-of-flight mass spectrometry. Recombinant proteins were screened for endotoxin and LPS contamination and levels were below 0.1EU/ mL, as previously recommended,(48).

Acknowledgements

The authors thank José Pedro Lopes and Sujana Yellagunda for support with animal experiments. We acknowledge essential advice and the kind gift of paquinimod by from Active Biotech. We acknowledge support for heterologous protein expression of the Protein Expertise Platform (PEP) at Umeå University.

Author contributions

CFU provided funding and together with MS and NU designed the study, MS and NU collected and analyzed the data. TV and JR contributed to the conceptualization of the study. Manuscript drafting by NU, MS and CFU. SH contributed preparation of histological sections. All authors contributed to data analysis, drafting and critically revising the paper, gave final approval of the version to be published, and agree to be accountable for all aspects of the work

Funding

Furthermore, we are grateful for funding provided to CFU by the Swedish research council VR-M 2014-02281 and VR-M 2017-01681, the Kempe Foundation SMK-1453, the Åke Wiberg Foundation M14-0076 and M15-0108, and the Medical Faculty of Umeå University 316-886-10. NU and MS held a postdoctoral fellowship received in competition from UCMR. The funders had no role in study design nor analysis and interpretation of the results.

Competing interests, none declared.

Ethics approval

Animals, conformed to Swedish animal protection laws and applicable guidelines (djurskyddslagen 1988:534; djurskyddsförordningen 1988:539;

393 djurskyddsmyndigheten DFS 2004:4) in a protocol approved by the local Ethical
394 Committee (Umeå djurförsöksetiska nämnd, Permit Number A79-14.
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Figure Legends

Figure 1. Intraperitoneal fungal peritonitis mouse model depicting the necessity of

calprotectin in inflammation and fungal clearance. A) Fungal eye exudate (pus) as

evidence for peritoneal cavity failure to contain *C. albicans* infection after 24 hours

intraperitoneal (IP) infection in a calprotectin inhibited mouse (more details in figure 5).

Shown is the clear eye of uninfected (PBS) compared to the white pus and loss of vision

in infected wild type (WT) mice. **B)** Representative photomicrographs of hematoxylin-

eosin (H&E) stained liver sections of uninfected and infected wildtype and s100A9

mutant used in quantifications in **C**. Zoomed images show one of many observed

increased inflammatory cell infiltrates in WT infected cells (top panel) and arrows

indicate yeast or hyphal cells (bottom panel) at 20x magnification. CV: central vein,

PV: portal vein. **C)** An inflammatory score of H&E-stained liver sections of uninfected

and infected WT and *S100A9*^{-/-} mutant mice (hence, also S100A8 protein-deficient). A

score of 2 = moderate cell infiltration, >3 = large number of infiltrates, 4 = full tissue

inflammatory infiltration. Error bars indicate standard deviation and ****p< 0.0001

Figure 2. Calprotectin is required for liver inflammatory induced collateral tissue damage (CTD) and fungal clearance. A) *Alanine transferase levels (ALTs) used as an indicator of liver tissue damage as a result of C. albicans infection.* Plasma ALT levels were analyzed from 100µl of plasma in a vetscan rotor 24 h post-infection. WT and *S100A9*^{-/-} mice were infected with 3 x 10⁶ cells per g of mice. n = 7 (WT and *S100A9*^{-/-}), and n= 10 (WT and *S100A9*^{-/-} + Ca) total mice. **** *p*-value =<0.0001. **B)** *Organ levels of colony-forming units (CFUs) as a measure of host fungal burden. C. albicans* CFUs in homogenized infected livers of indicated mice were quantified. **A-B)** Box- and whisker plots show the smallest observation, lower quartile, mean, upper quartile and largest observation. **** *p*-value =<0.0001. **C)** *C. albicans* infection induces the production of less pro-inflammatory cytokines in *S100A9*^{-/-} mice. WT and *S100A9*^{-/-} bone marrow-derived macrophages (BMDMs) were infected with *C. albicans* (1 *C. albicans*: 1 macrophage). *TNFα* levels were measured from supernatants at 24-hour post-infection. ** *p*-value =<0.01, n = 3.

Figure 3. The calprotectin S100A8 monomer is required to induce pro-inflammatory cytokines and liver tissue damage. A) *The purity of murine recombinant S100A8 and S100A9 proteins expressed in E. coli used in B - I.* Shown is a representative blot of each fractionated protein using size exclusion chromatography, confirmed by mass spectrometry. **B).** *Effect of calprotectin monomers on C. albicans induced collateral tissue damage.* S100A8 (r S100A8) and S100A9 (r S100A9) murine recombinant soluble proteins were intraperitoneally administered (100µg/ml) to WT and *S100A9*^{-/-} mice and shown are plasma ALT levels. **C)** *Effect of calprotectin on host*

fungus clearance. Shown are CFUs in homogenized infected livers of indicated mice **B-C**) Data are presented as a box- and whisker plots showing the smallest observation, lower quartile, mean, upper quartile and largest observation, statistical significance was analyzed by one-way Anova (n = 5 mice per group in 3 separate experiments), **** p -value ≤ 0.0001 . **(D-I)** Recombinant calprotectin can restore WT levels of pro-inflammatory cytokines in *S100A9*^{-/-} mice. *In vitro* cytokine levels in bone marrow-derived macrophages (BMDMs) infected with *C. albicans* (1 *C. albicans*: 1 macrophage) were measured from supernatants, 24-hour post-infection. a Pro-Mouse cytokine BioPlex[®] 200 multiplex array (Bio-Rad, Hercules, CA) was used to detect and quantify *S100A9*^{-/-} mouse cytokines infected with *C. albicans* and treated with rS100A8. n=3, * p -value ≤ 0.05 **** p -value ≤ 0.0001 .

Figure 4. Paquinimod reverses the tissue-damaging effects of S100A8. A-C) Effect of the anti-inflammatory drug paquinimod (Paq) on anti/pro-inflammatory cytokines in C. albicans infected BMDMs. A) BMDM infected with *C. albicans* (1 *C. albicans*: 1 macrophage) were treated with indicated concentrations of paquinimod. **B-C)** BMDM were infected and treated with Paq (930μg/ml). Cytokines were measured from supernatants 24 h post-infection. n=3. **D-F) In vivo effects of Paq on rS100A8 activity against fungal burden and tissue damage. D-E)** Shown are liver CFUs of *C. albicans* from infected, and then Paq (30mg/kg) treated WT and *S100A9*^{-/-} mice. Data are mean \pm SD from n =3. **E)** S100A8 murine recombinant soluble proteins were intraperitoneally administered (100μg/ml) to *C. albicans* infected WT and *S100A9*^{-/-} mice and treated with Paq. **F).** Effect of Paq on recombinant calprotectin induced collateral tissue damage during *C. albicans* infection. Note that **F** contains WT and *S100A9*^{-/-} controls

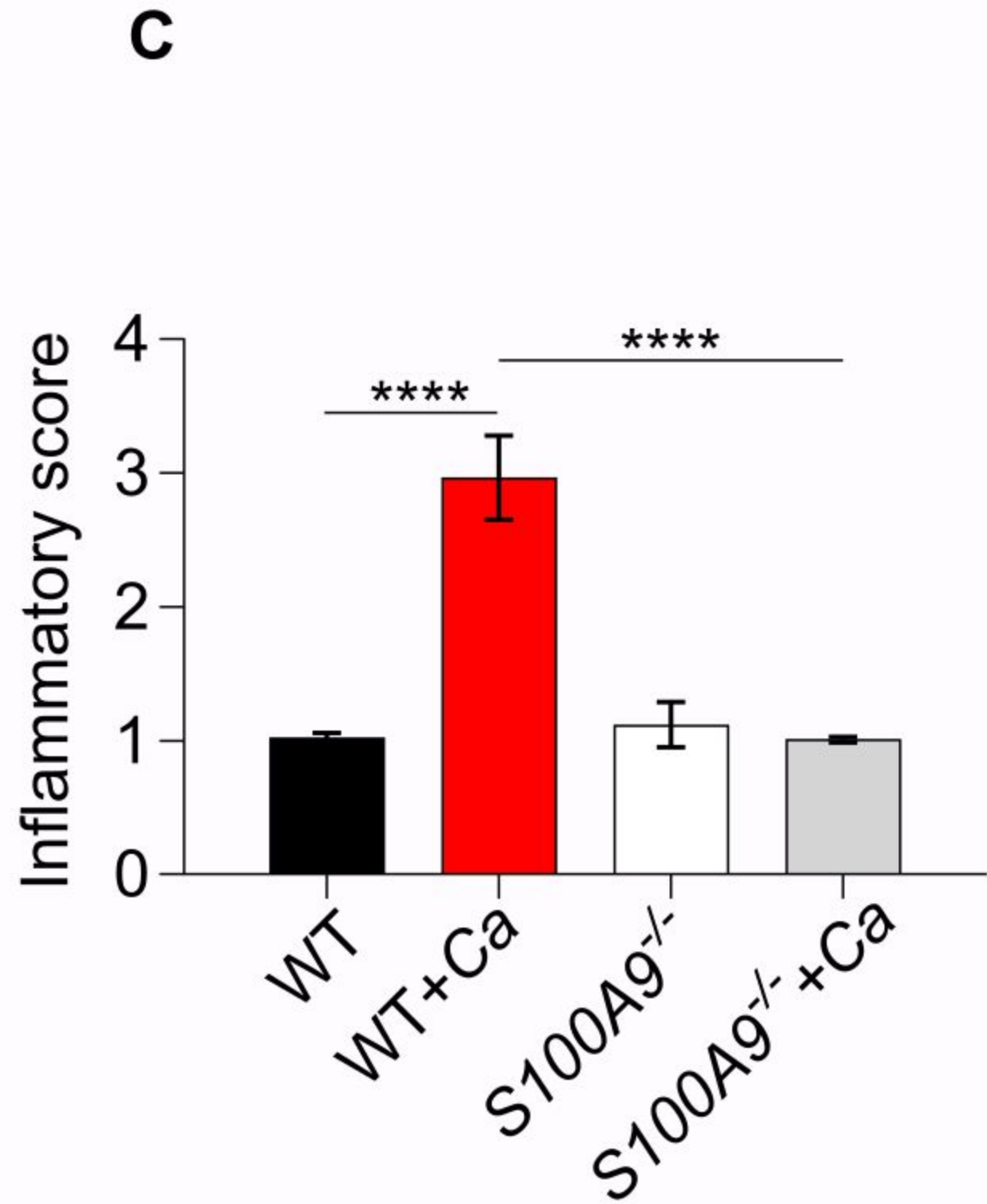
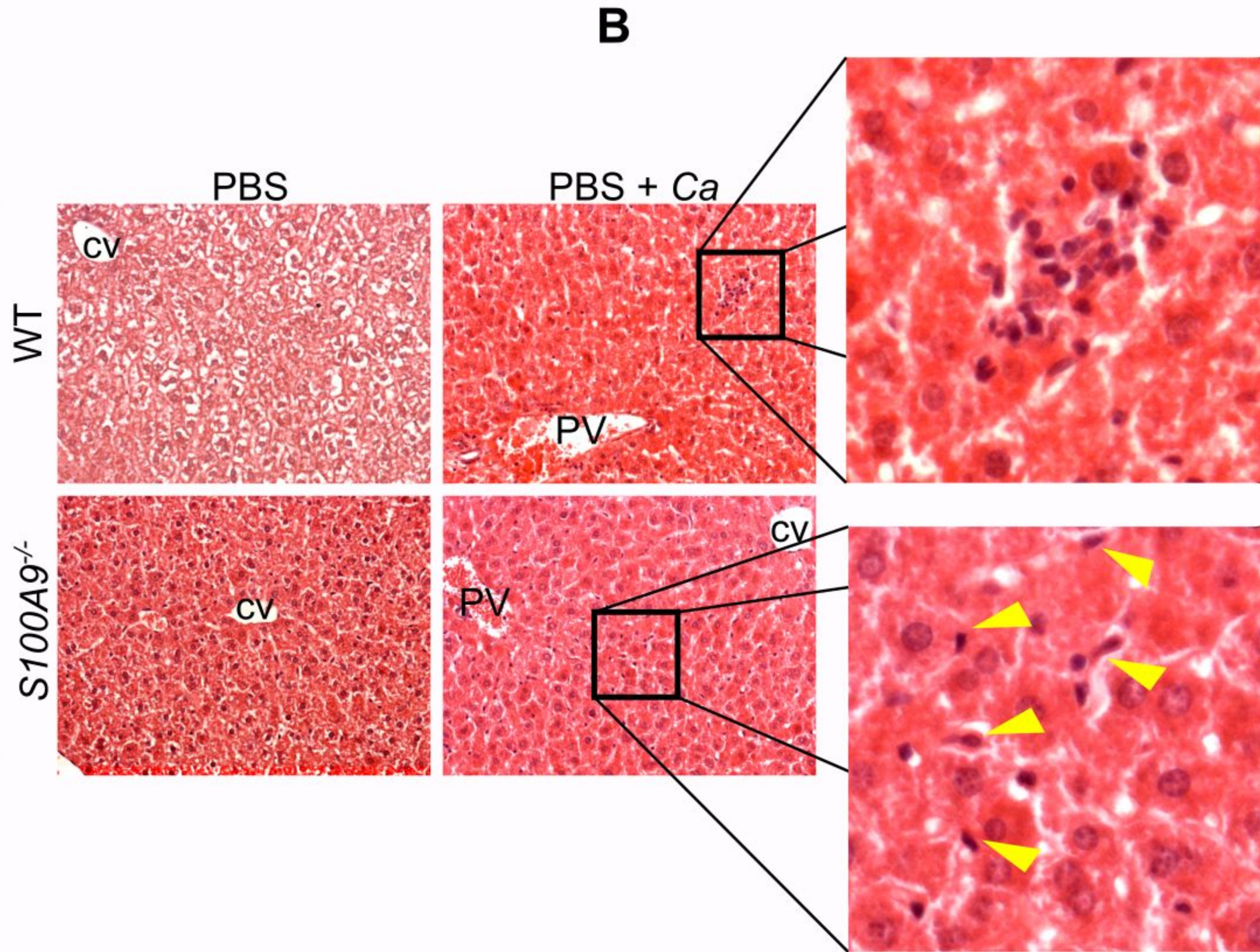
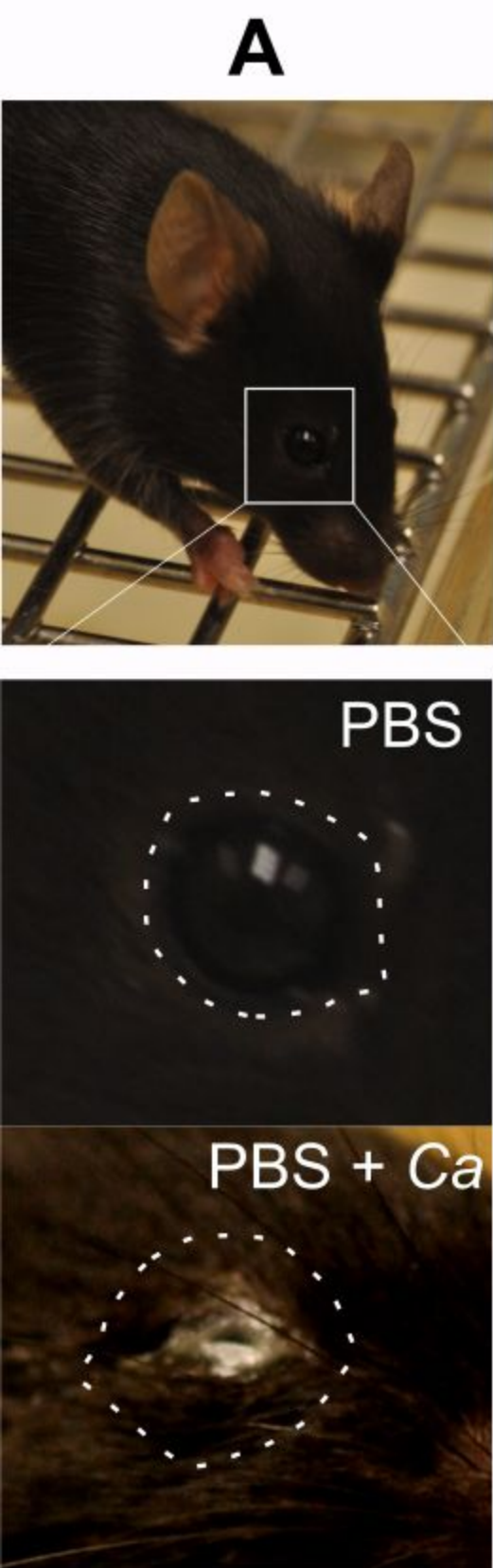
623 initially presented in figure **3B** as experiments were conducted together. Data are
 624 presented as a box- and whisker plots showing the smallest observation, lower quartile,
 625 mean, upper quartile and largest observation, statistical significance was analyzed by
 626 student t-test n = 5 mice per group, * p -value ≤ 0.05 , **** p -value ≤ 0.0001 .
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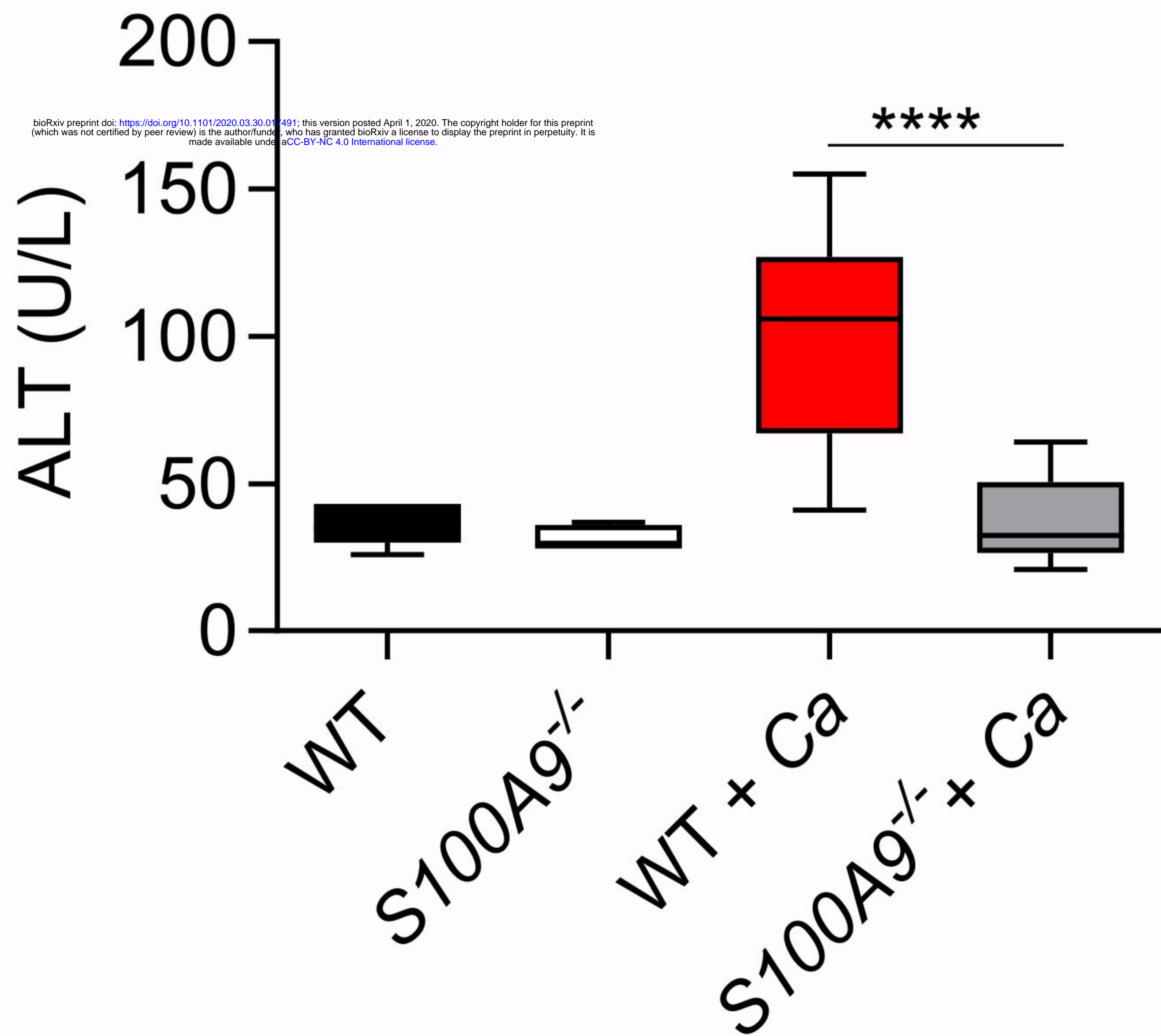
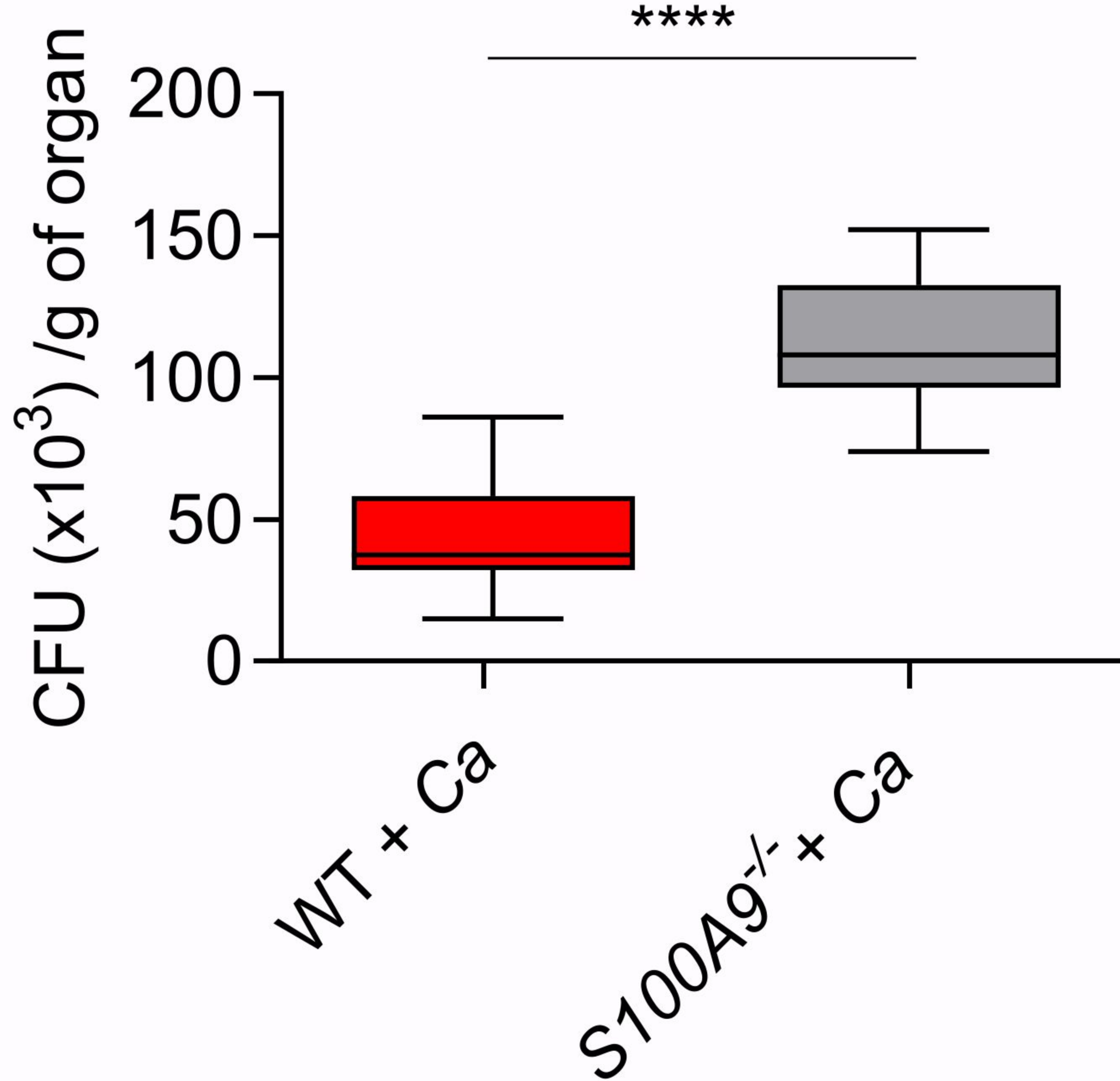
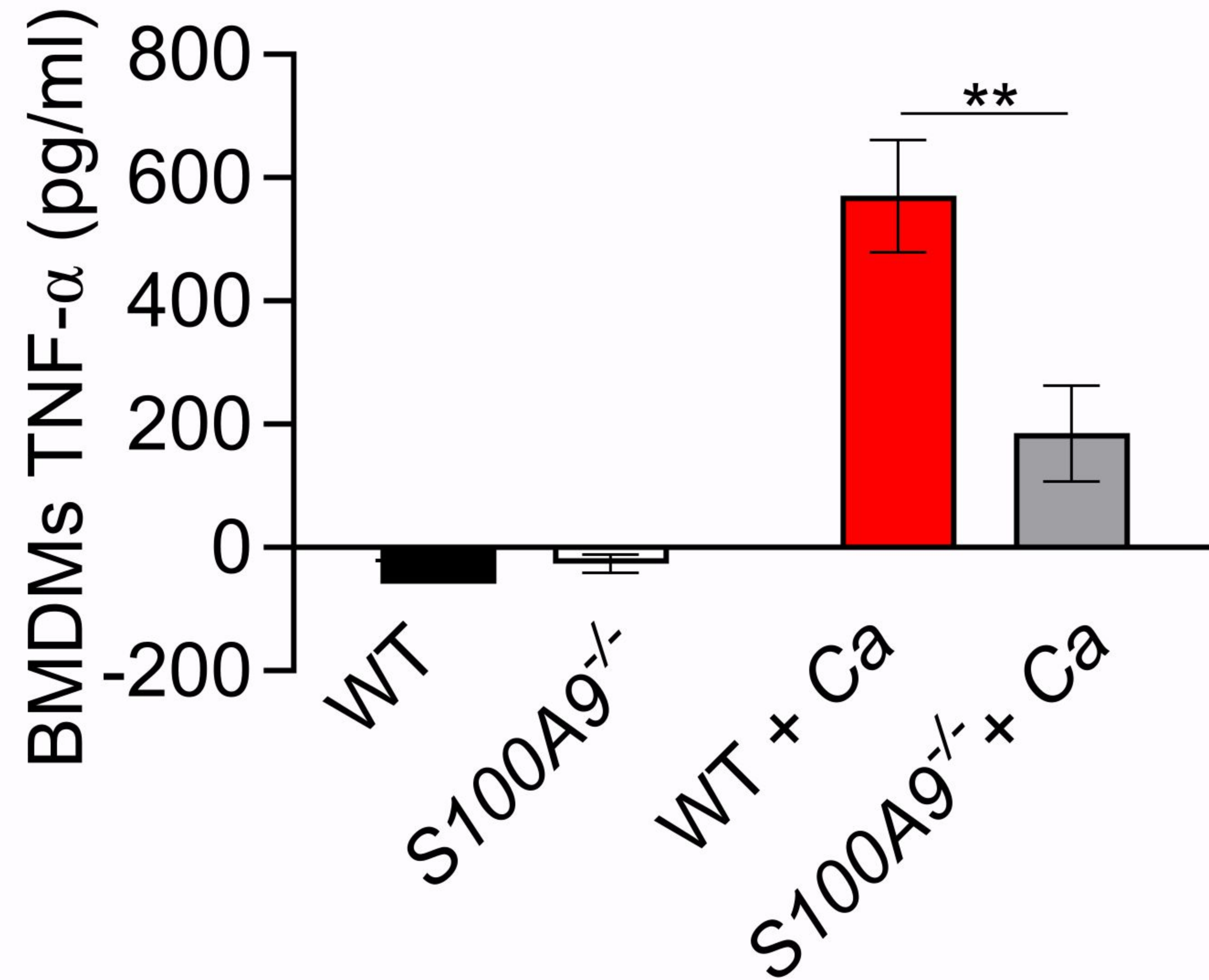
Figure 5. Inhibition of calprotectin by paquinimod significantly increases host survival from *C. albicans* infection **A-D)** WT mice infected with *C. albicans* were treated with Paq (30mg/kg) at 24-hour intervals up to 5 days, and mice weight and survival were monitored. **A)** Paq mice treatment strategy. **B-C)** Survival and sequential body weight of WT mice infected at the indicated timeline in **A**. **B).** *Paq treated infected mice survived 12 hours longer than untreated mice after 24 hours of C. albicans infection.* **C)** *Paq does not affect mice weight loss during C. albicans infection.* Shown are the grams lost over time. **p-value <0.01. Shown are mean and SD. **D)** *paquinimod-treated infected WT mice showing decreased eye fungal clearance.* Shown are the pictures of mice eyes. Healthy mice are black, open and clear of debris. Unhealthy mice have eye exudates/pus, squinty or shut due to *C. albicans* infiltration of the eyes.

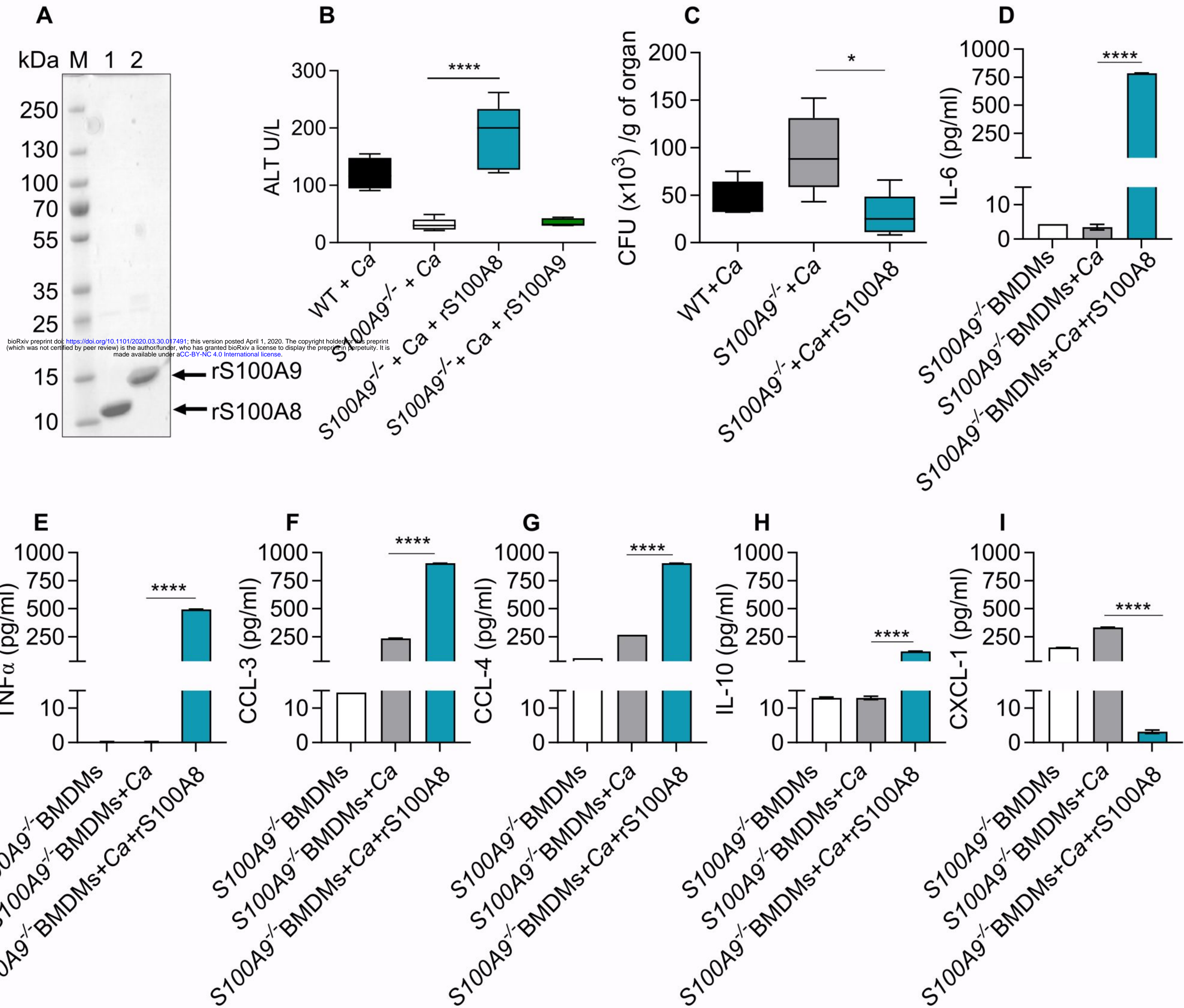
Figure 6. Study summary. Using a systemic fungal peritonitis mouse model **(1)**, findings implicate calprotectin as a systemically essential protein **(2-6, i-vi)** for the control of cytokine and chemokine modulation **(4-5)**, organ leukocytes recruitment **(6)**, host tissue damage **(7)** and fungal clearance **(vi)**. In systemic intra-abdominal originating candidiasis, the cost of fungal clearance (antimicrobial/active calprotectin signaling) a feedback-loop that increases tissue damage, while the cost of decreased tissue damage (anti-inflammatory/ inactive calprotectin signaling) is a high fungal burden (Figures 1-5). Both are lethal if not controlled (Figure 5b). Future studies should focus on fine-tuning recombinant therapy in cases where active calprotectin signaling is inadequate, and anti-inflammatory treatments like paquinimod, in conjunction with antifungal treatments to increase host survival time to aid treatment.

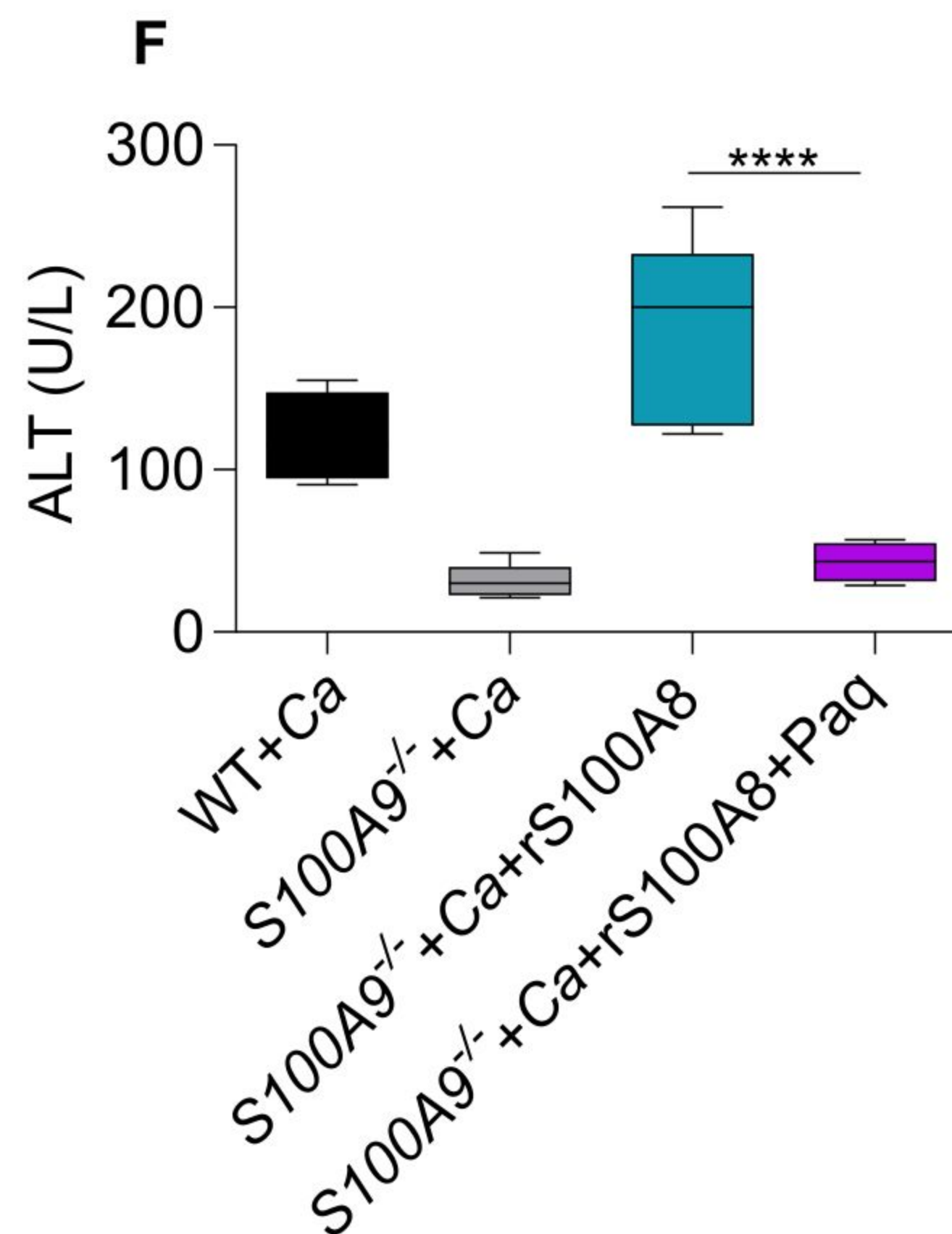
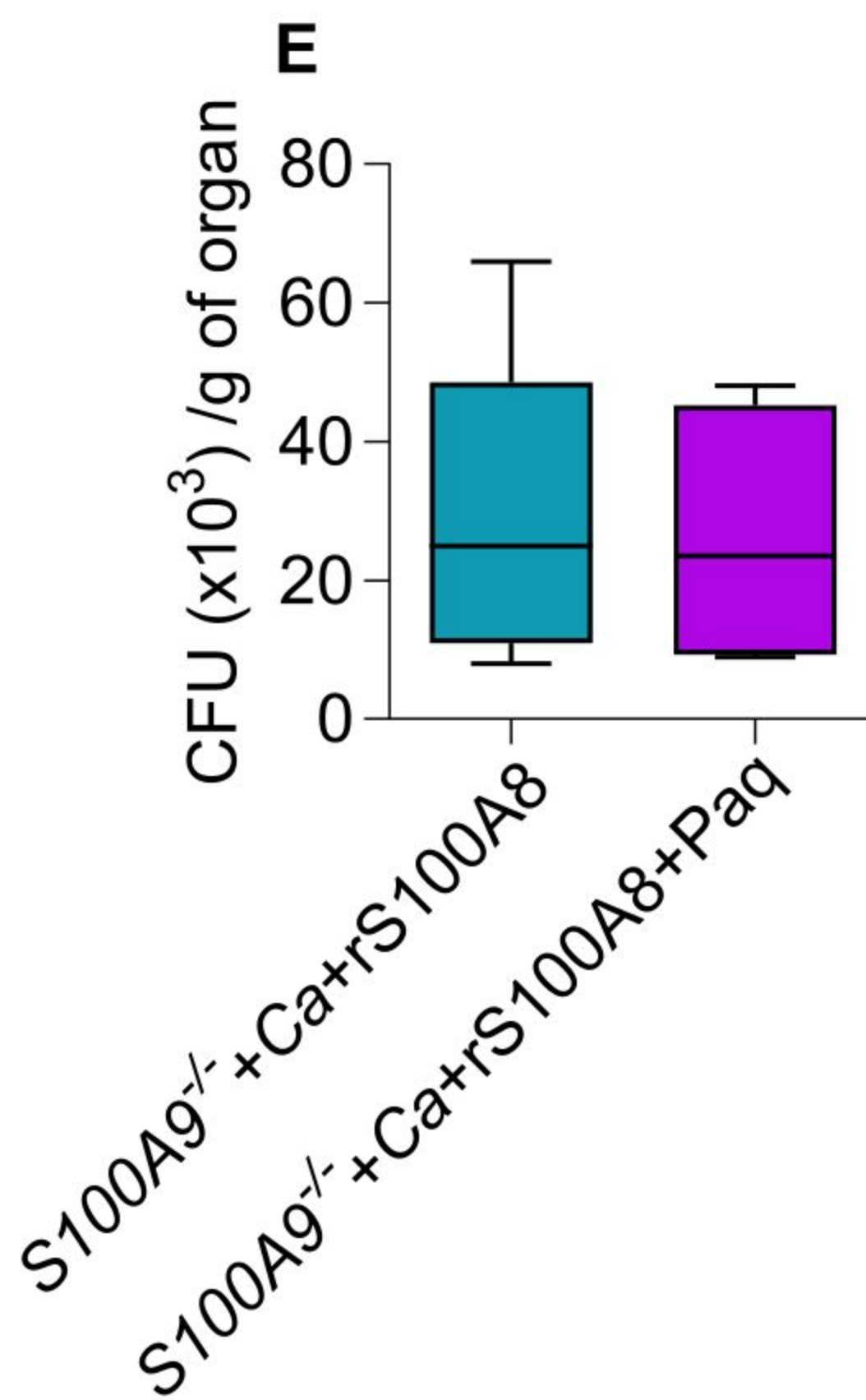
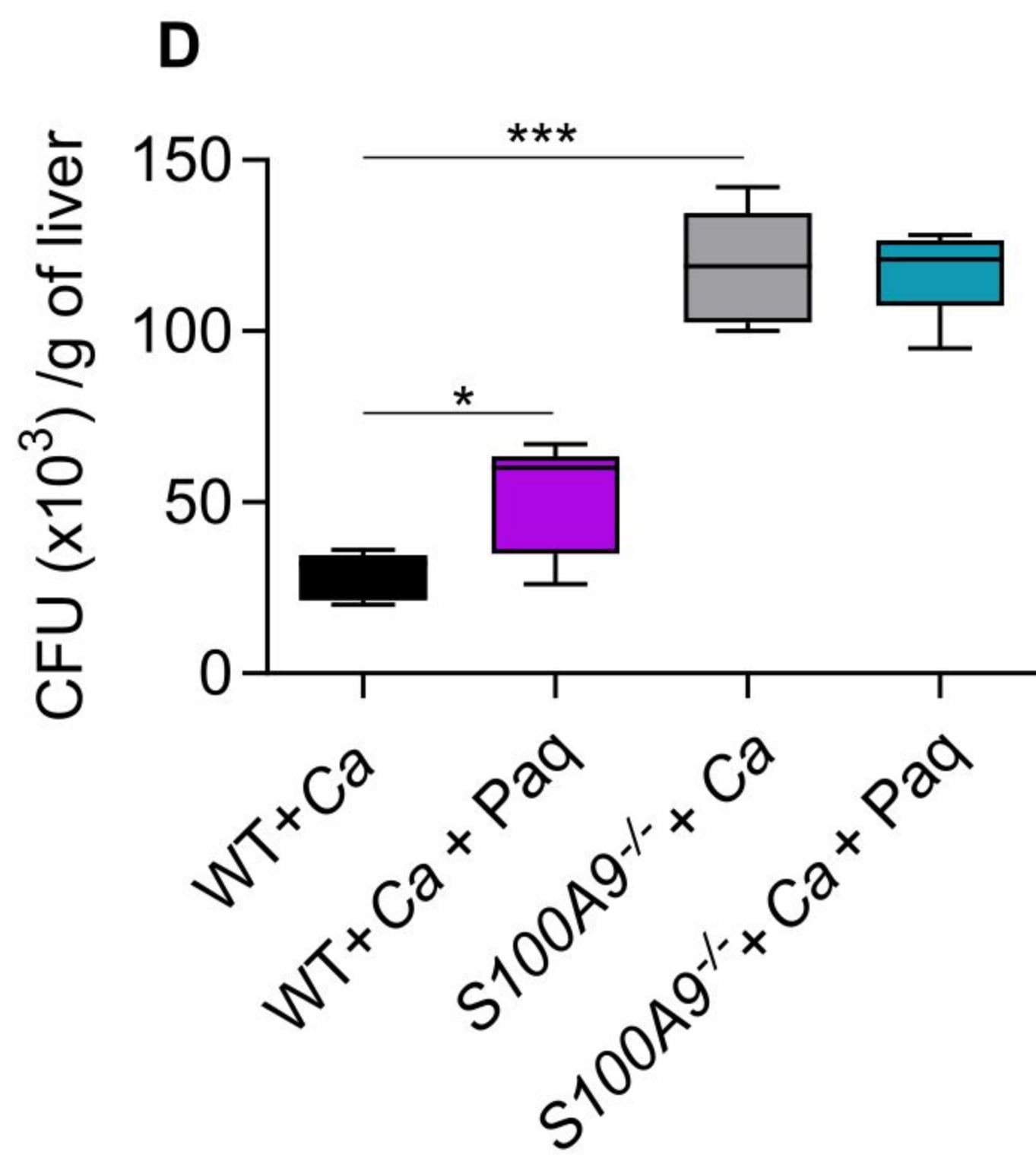
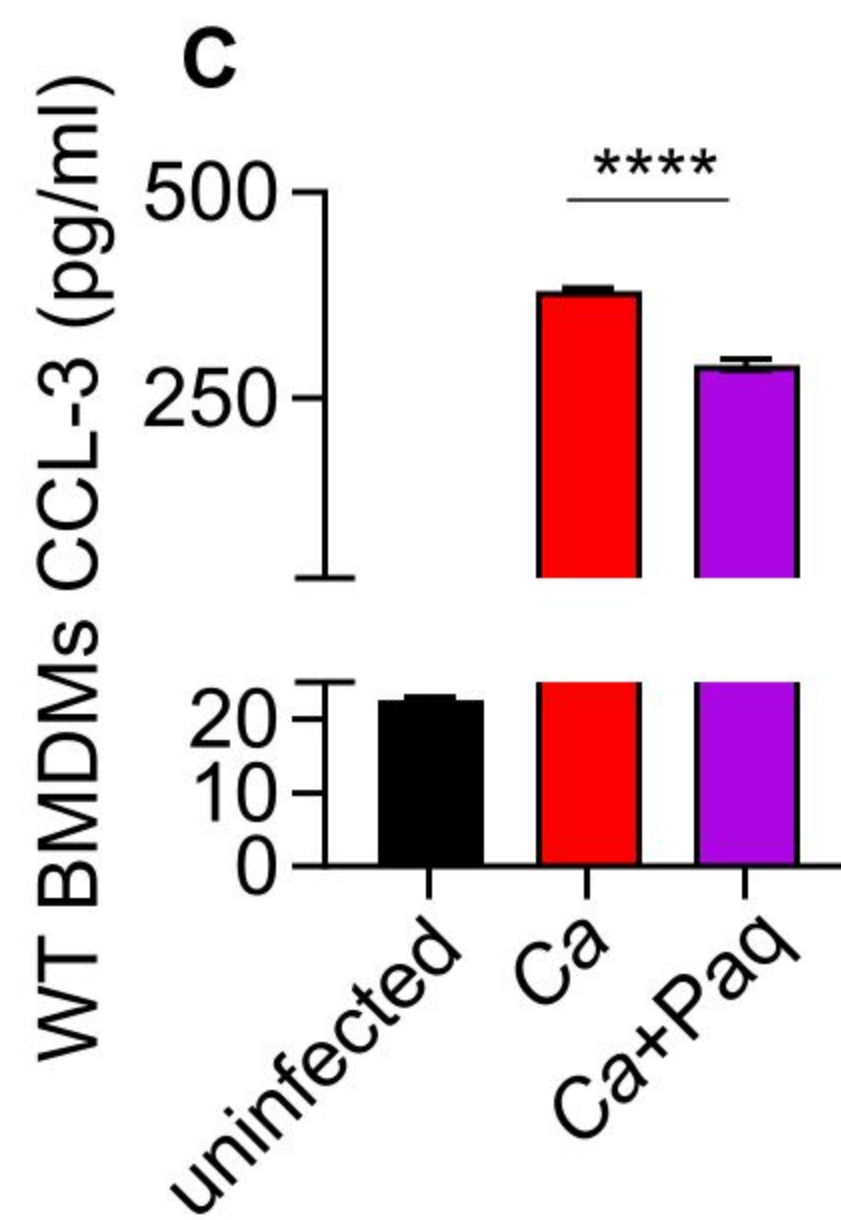
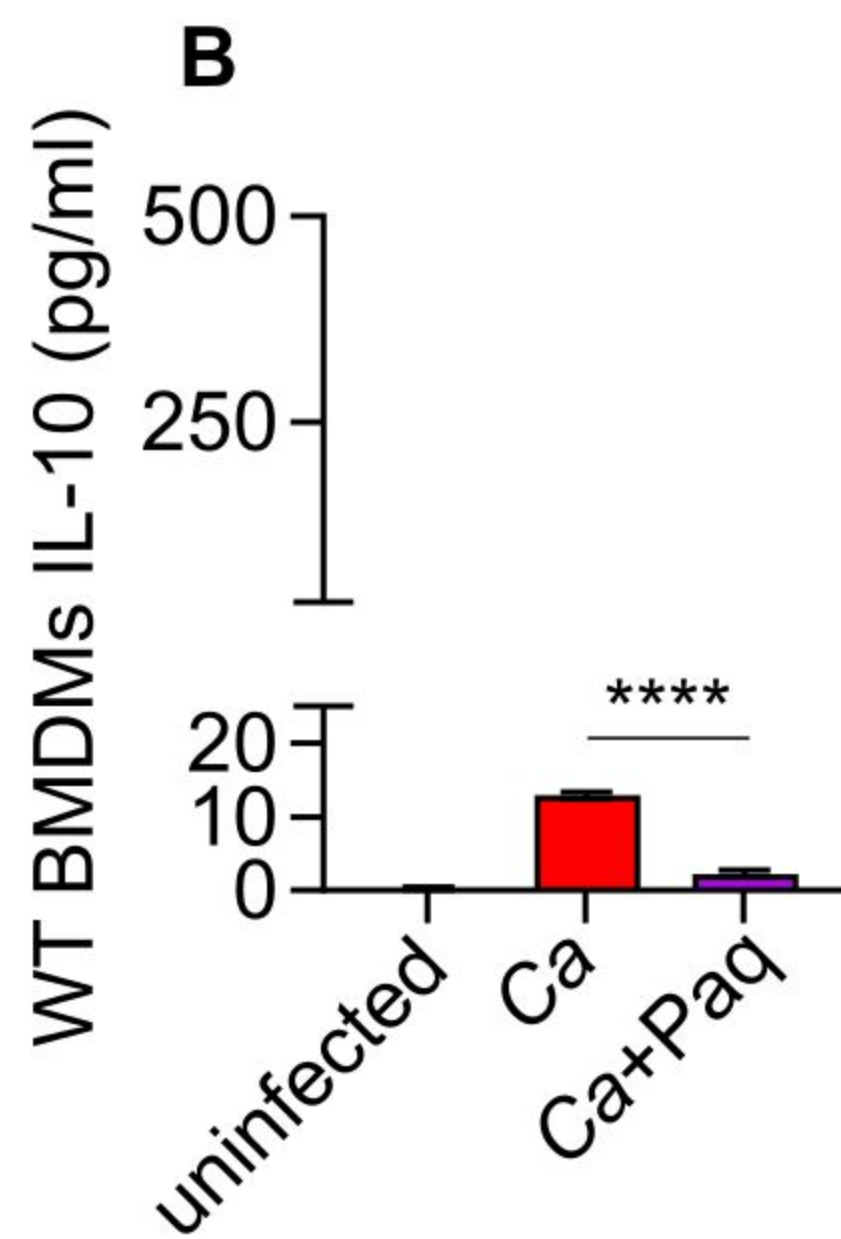
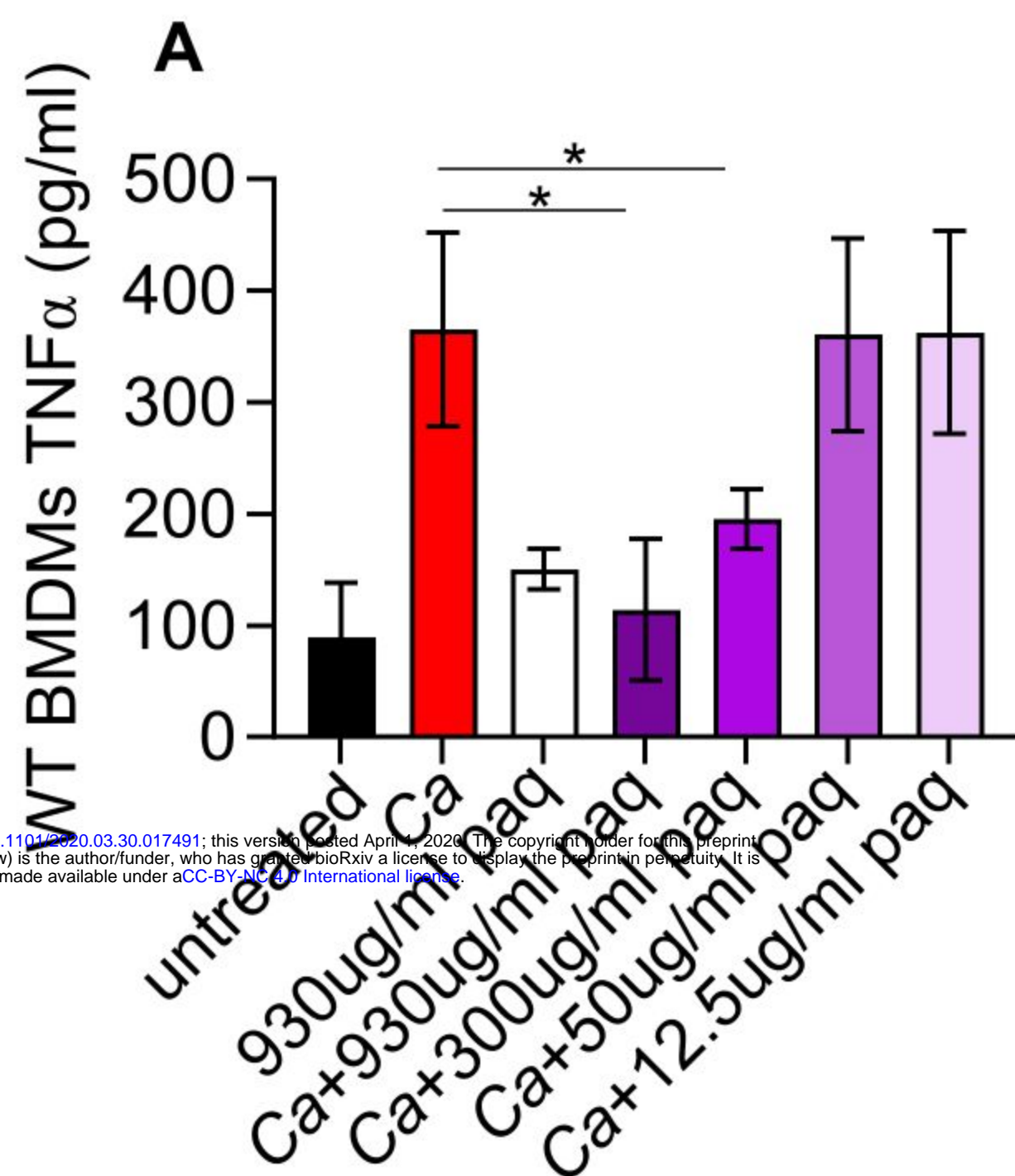
Supplementary figure 1. A) Paquinimod at tested concentrations was not cytotoxic.

Bone marrow-derived macrophages (BMDMs) were treated with indicated concentrations of paquinimod (Paq), stained with propidium iodide (pI) and analyzed using FACS live cell analysis. Shown are representative histograms and percent cell death due to paquinimod.



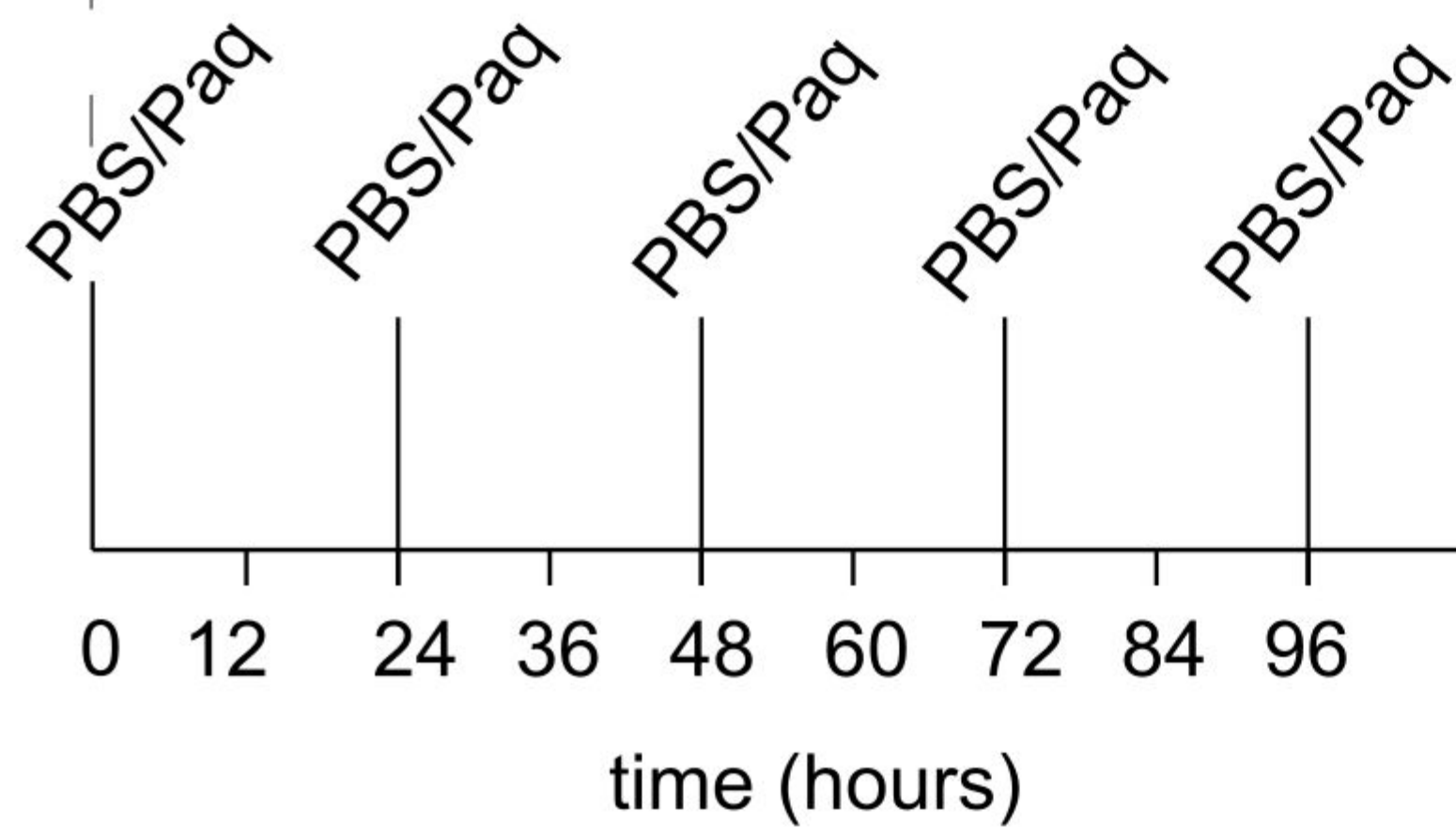
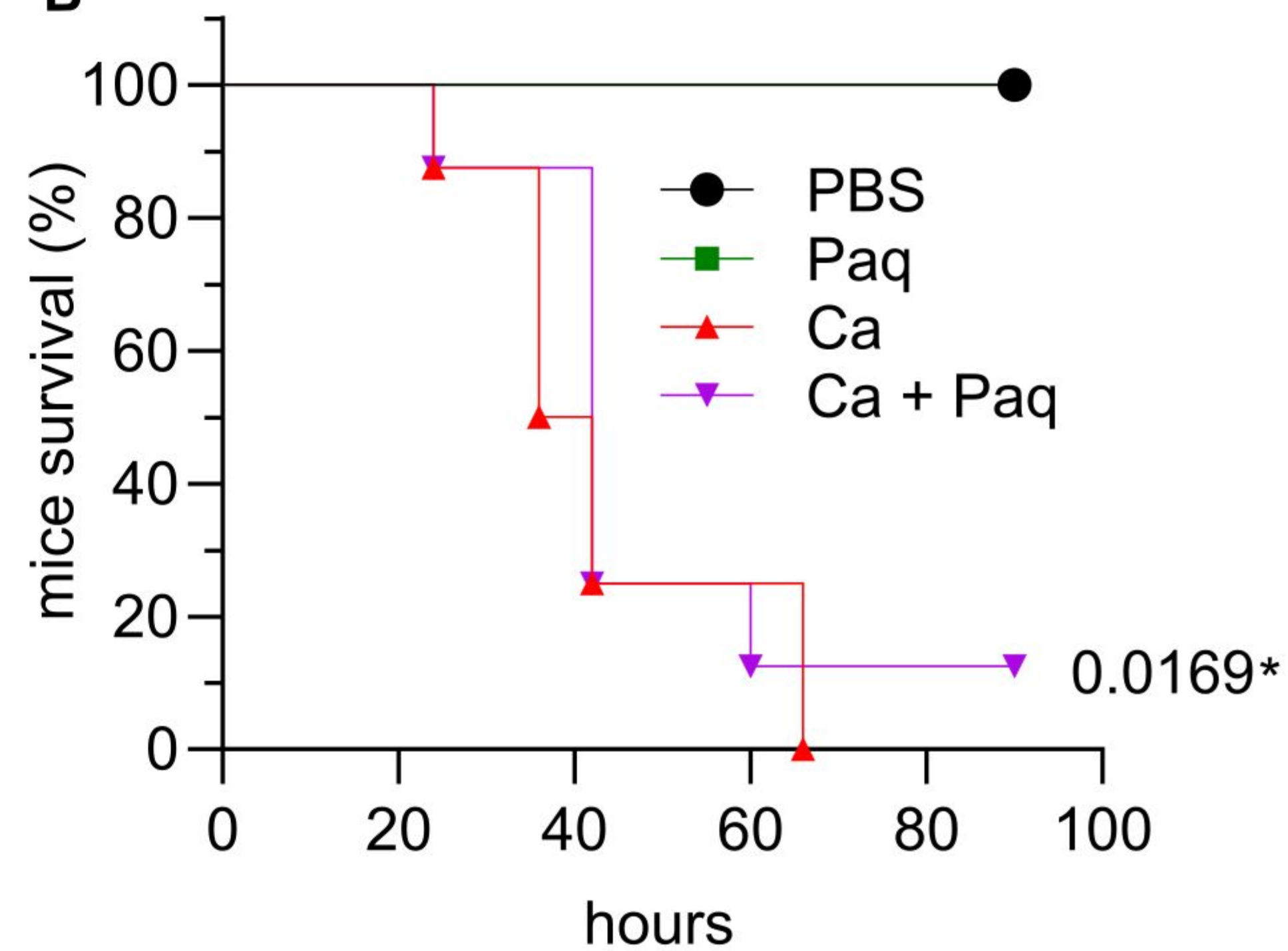
A**B****C**



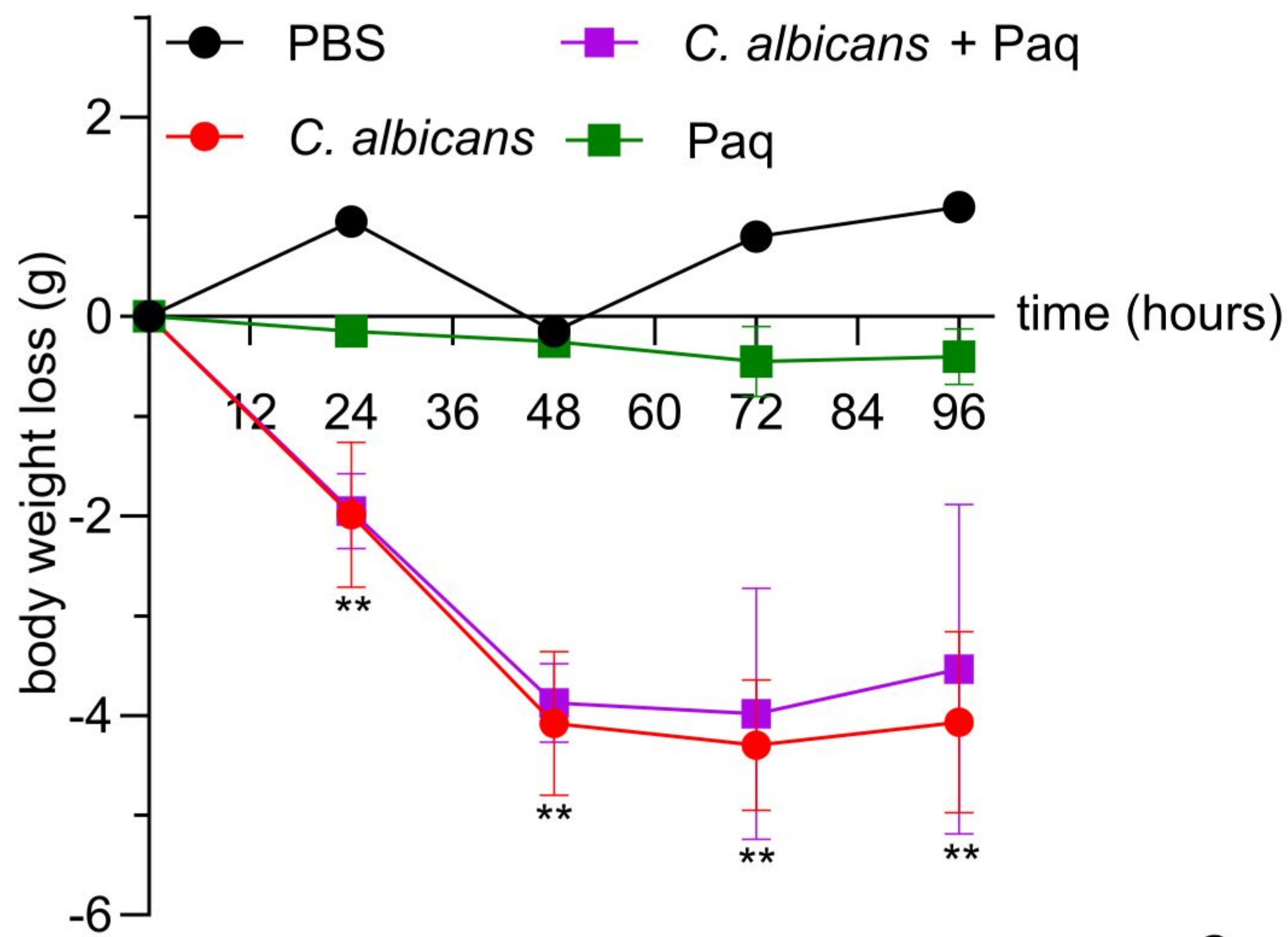
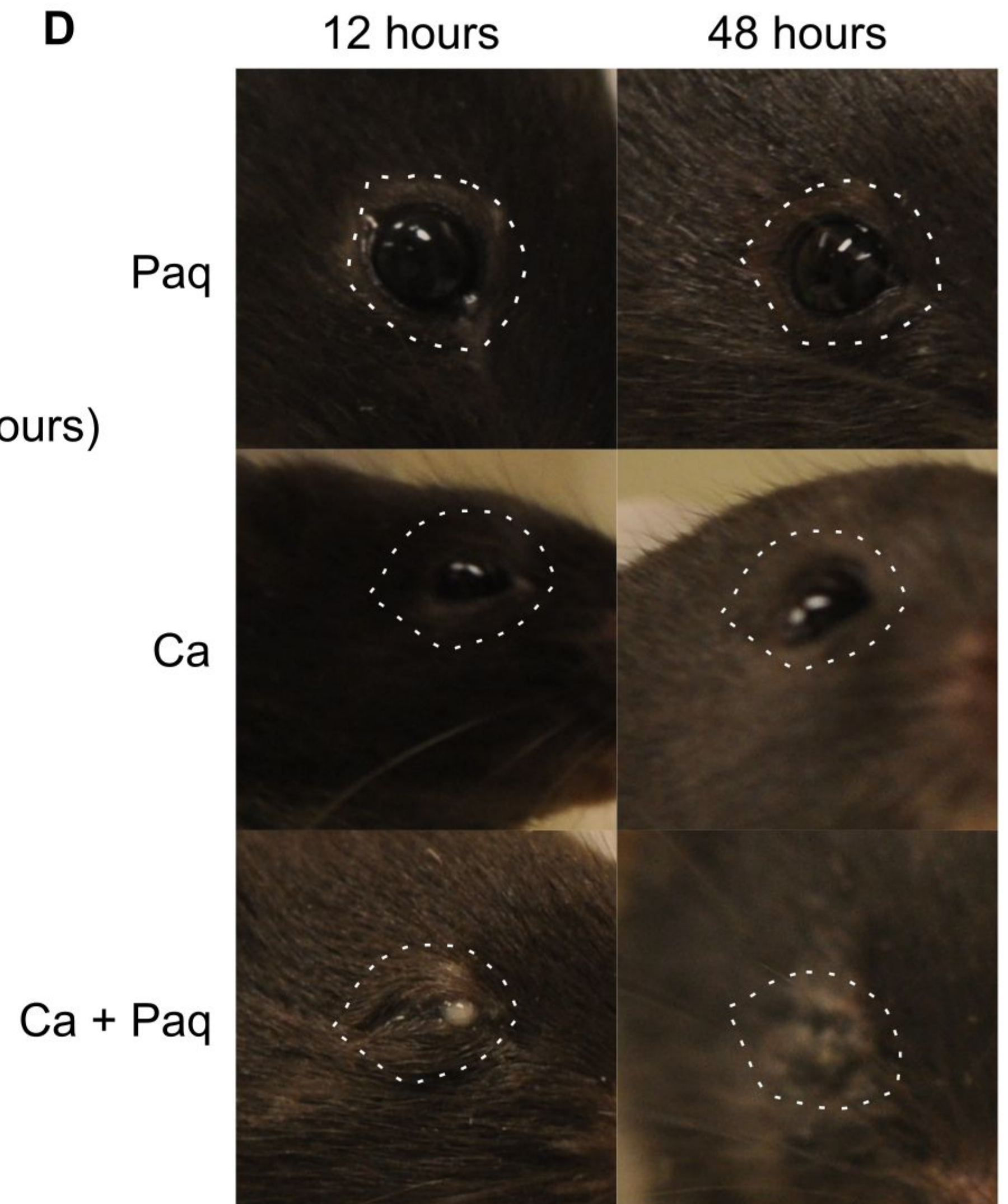


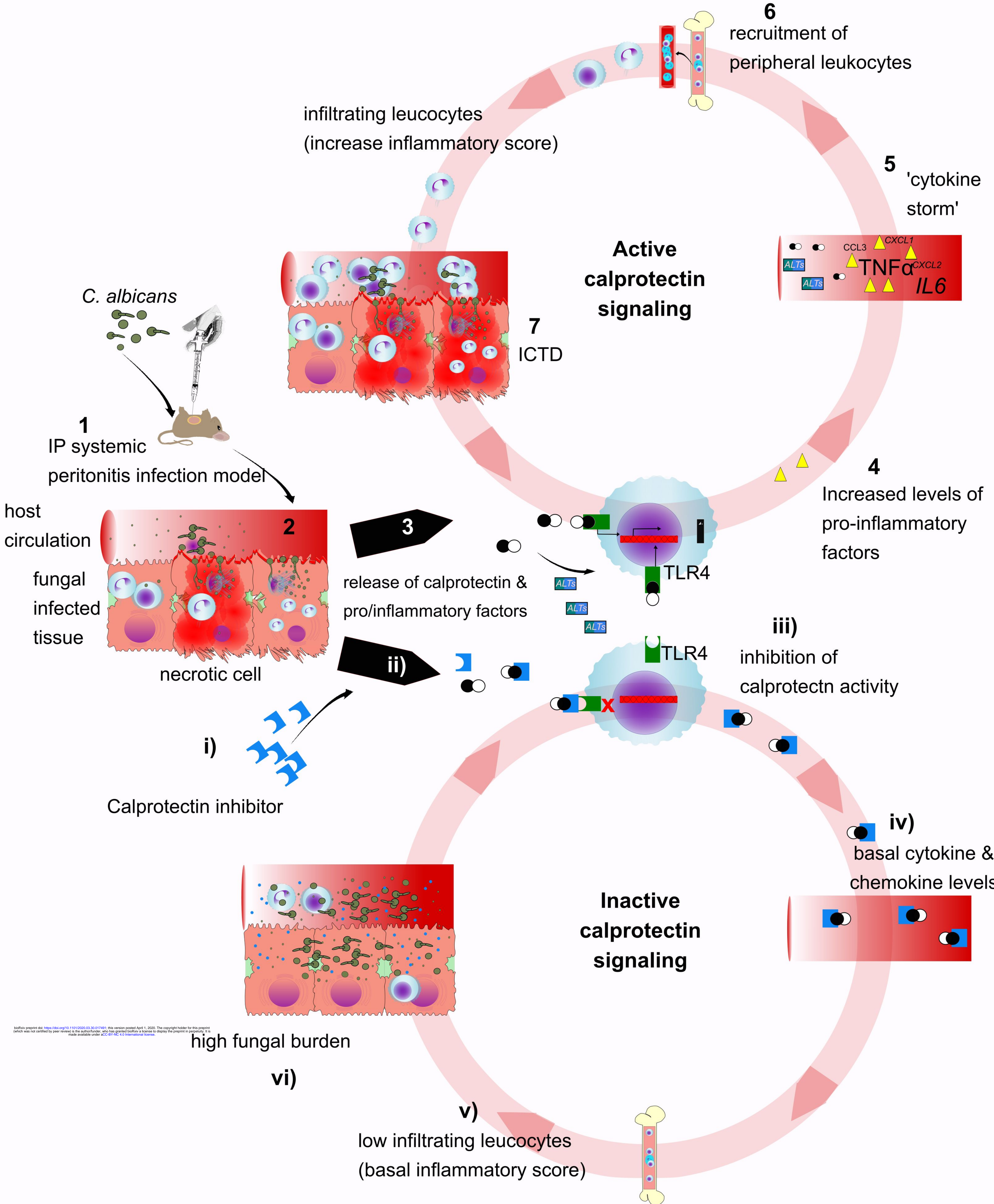
A

Single infection

C. albicans**B**

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C**D**



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