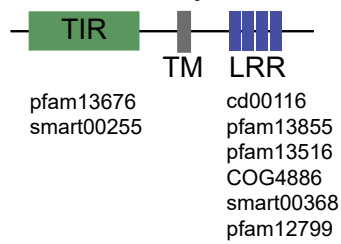
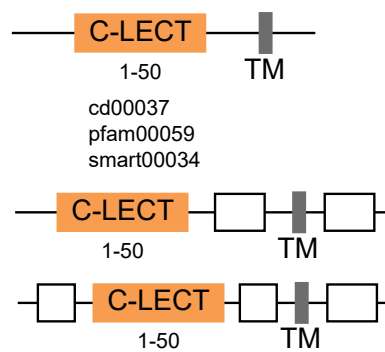


A. Pattern Recognition Receptors

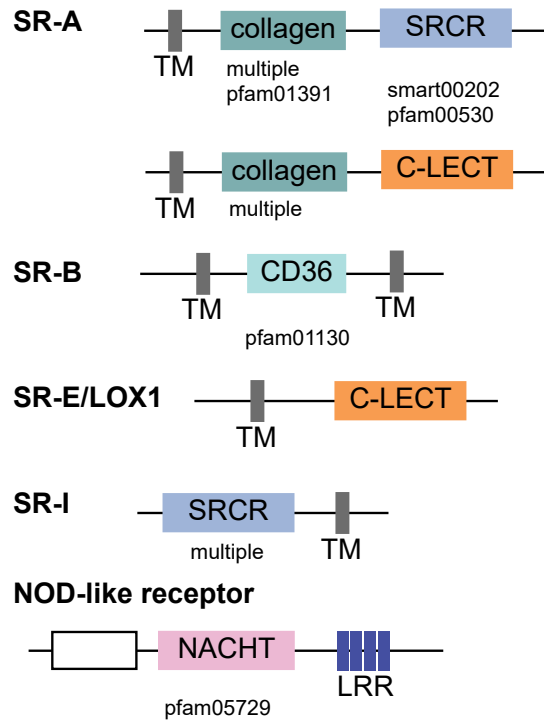
TOLL-like receptor



C-type lectins



Scavenger Receptors

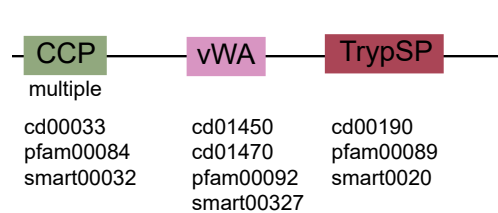


B. Complement System

C3



Factor B

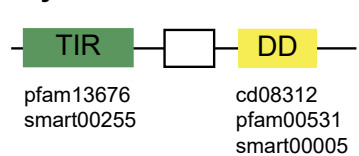


Complement Receptor 1/2

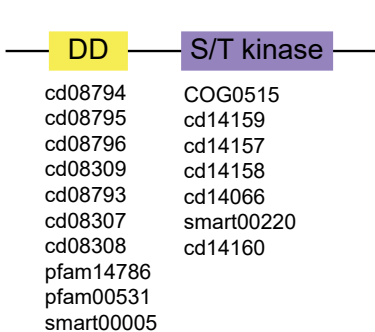


C. Toll Pathway

MyD88



IRAK



Rel/NF-kB

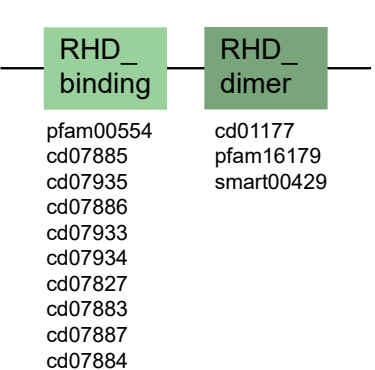


Fig. S1 – Gene domain structures searched in xenacoelomorph predicted proteomes

Schematic domain structure of the genes searched in xenacoelomorph genomes and transcriptomes: **A** Pattern Recognition Receptors, **B** Toll Pathway, **C** Complement system. Under each domain name, the number of times they can be repeated (if higher than one) and the accession numbers from NCBI Conserved Domain Database used to build the hmm profiles and to filter results.

A2M = α 2-macroglobulin domain; AM-R = alpha-macroglobulin binding domain; ANATO = anaphylatoxin domain; C345C = C-terminal domain specific to C3, C4, and C5; CCP = complement control protein domain; CD36 = cluster of differentiation 36; CLECT = C-type lectin domain; DD = Death Domain; IRAK = Interleukin-1 receptor-associated kinases; LRR = Leucine-rich repeat; MG = macroglobulin domain; MyD88 = Myeloid differentiation factor 88; NF- κ B = Nuclear Factor- κ B; RHD_bind = Rel homology DNA-binding domain; RHD_dimer = Rel homology dimerization domain (immunoglobulin-plexin-transcription domain); SR = Scavenger Receptor; SRCR = scavenger receptor cysteine rich domain; TIR = Toll/IL-1 receptor domain; TM = transmembrane region; TrypSP = trypsin-like serine protease domain; vWA = von Willebrand factor type A domain

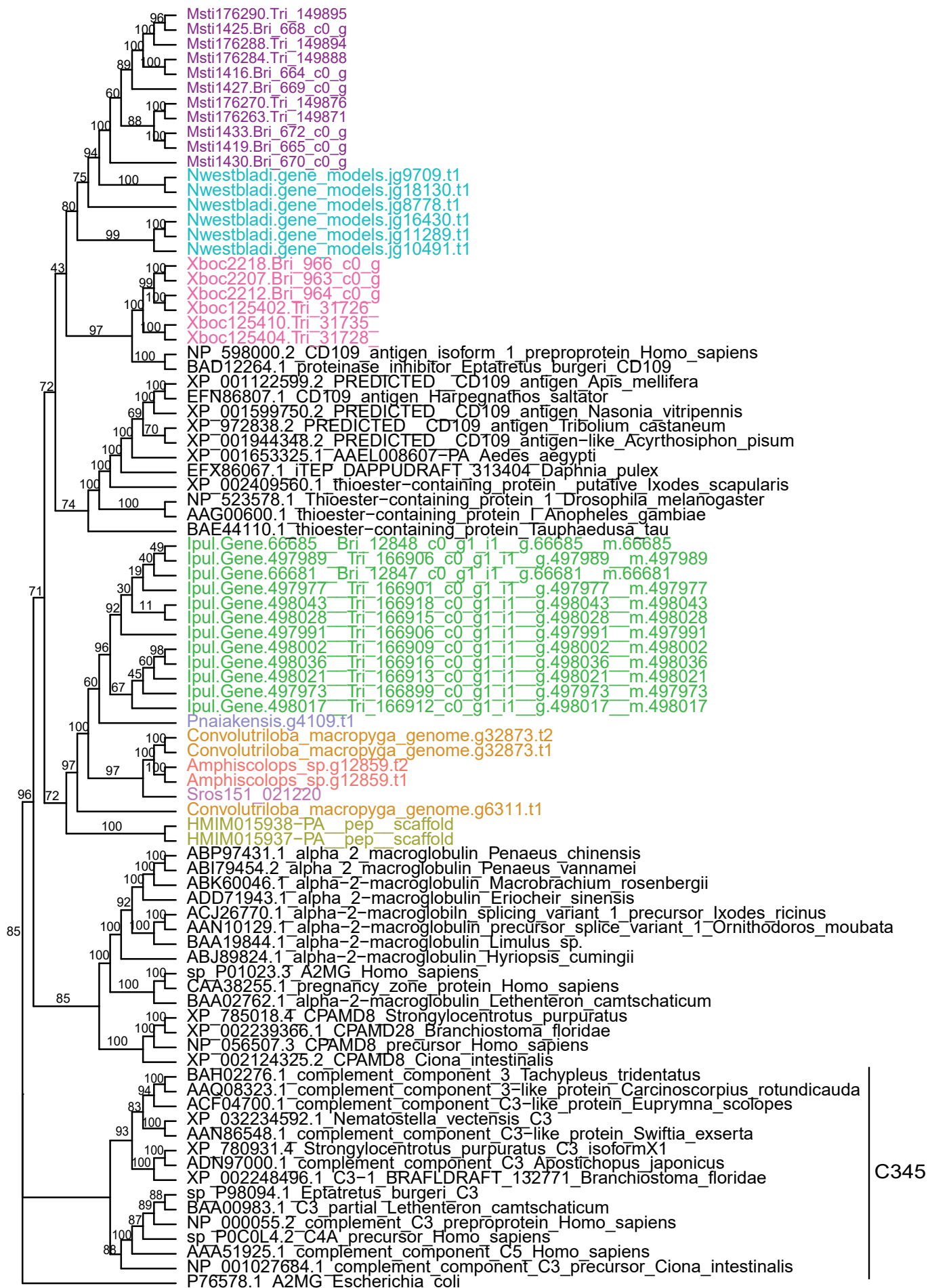


Fig. S2 – C3 phylogeny

Maximum likelihood phylogeny of domains in C3 and related proteins. UltraFast Bootstrap support values are shown.

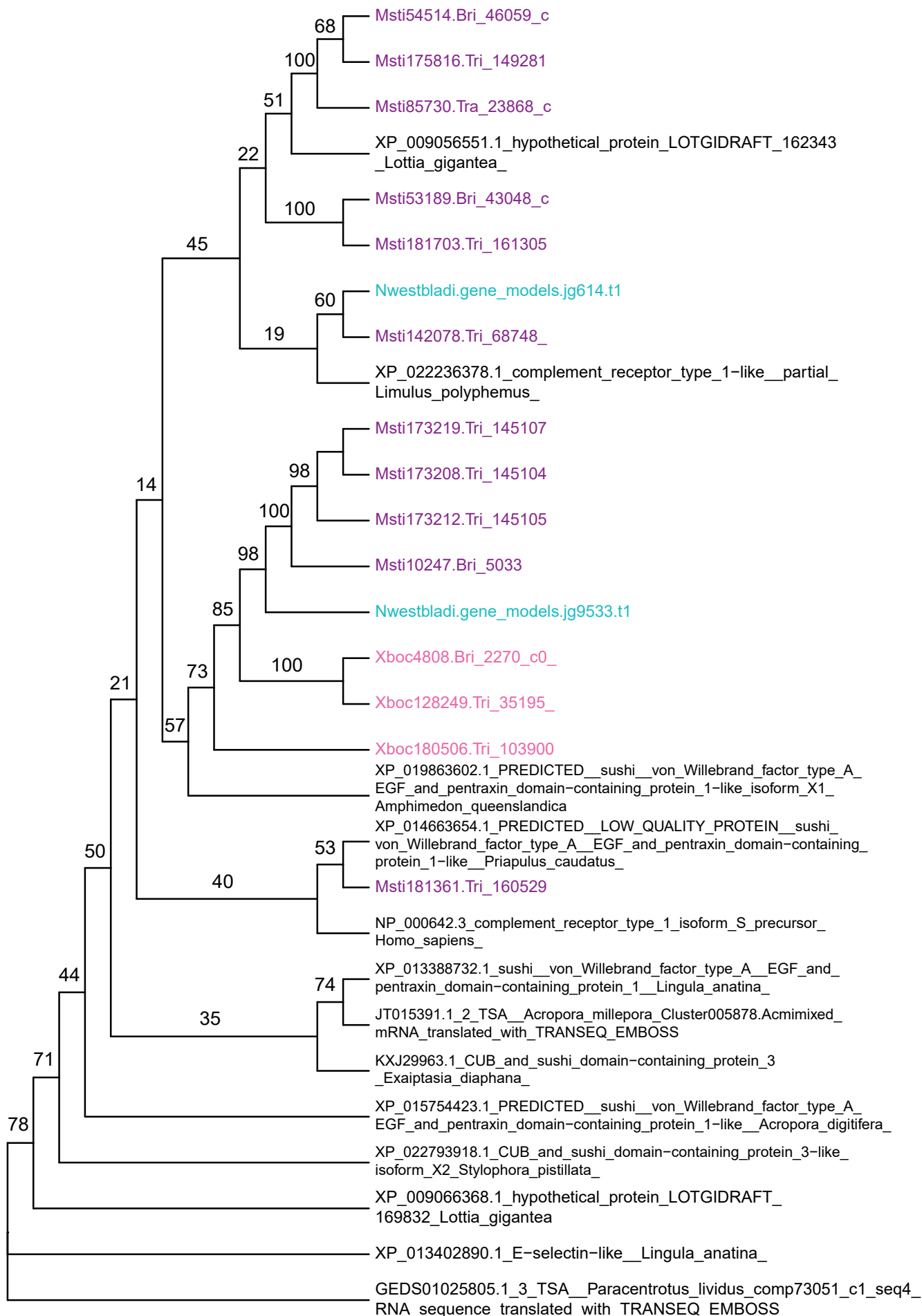


Fig. S3 – CR1/2 phylogeny

Maximum likelihood phylogeny of domains in Complement receptors 1/2 and related proteins. Ultra-Fast Bootstrap support values are shown.

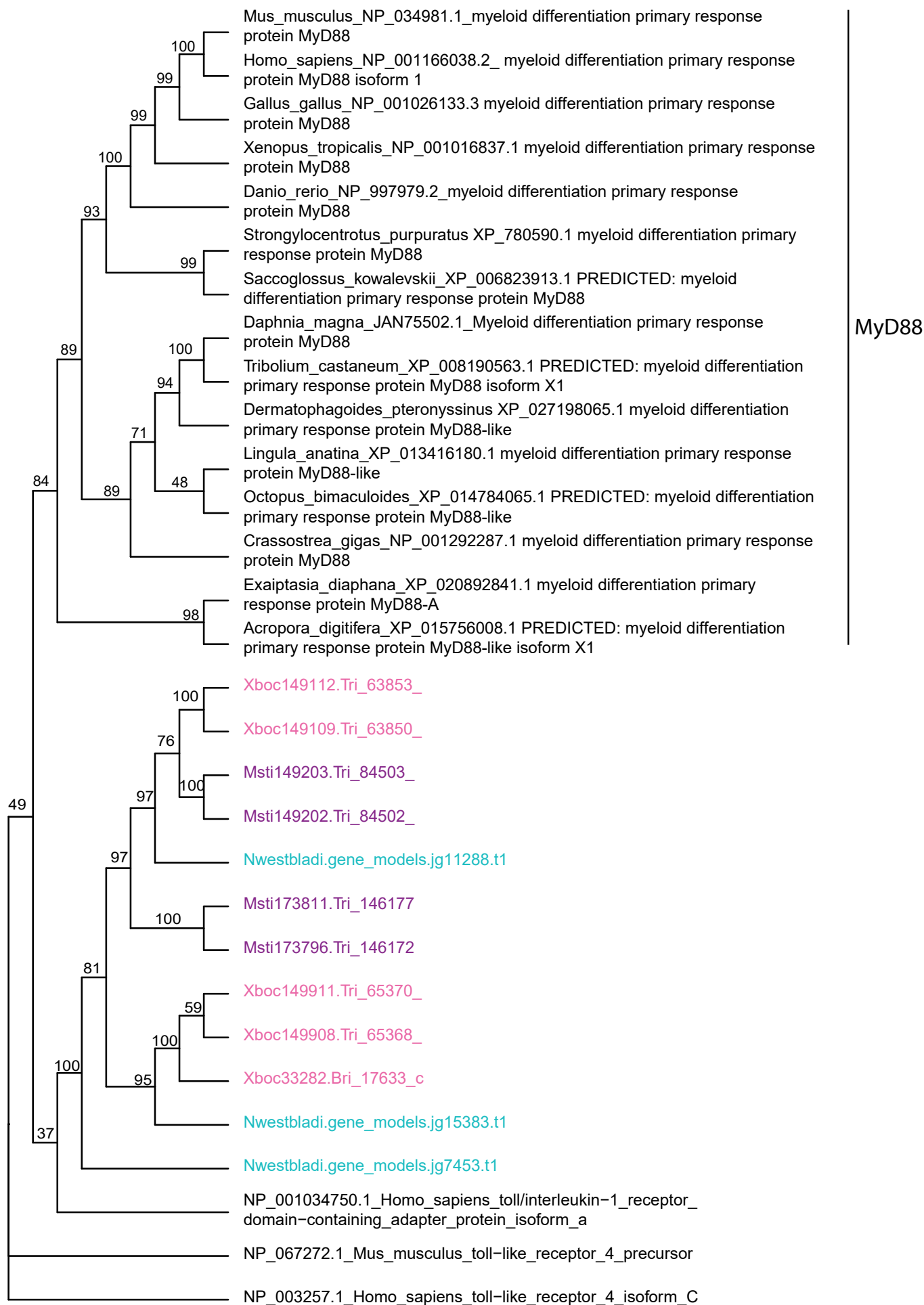
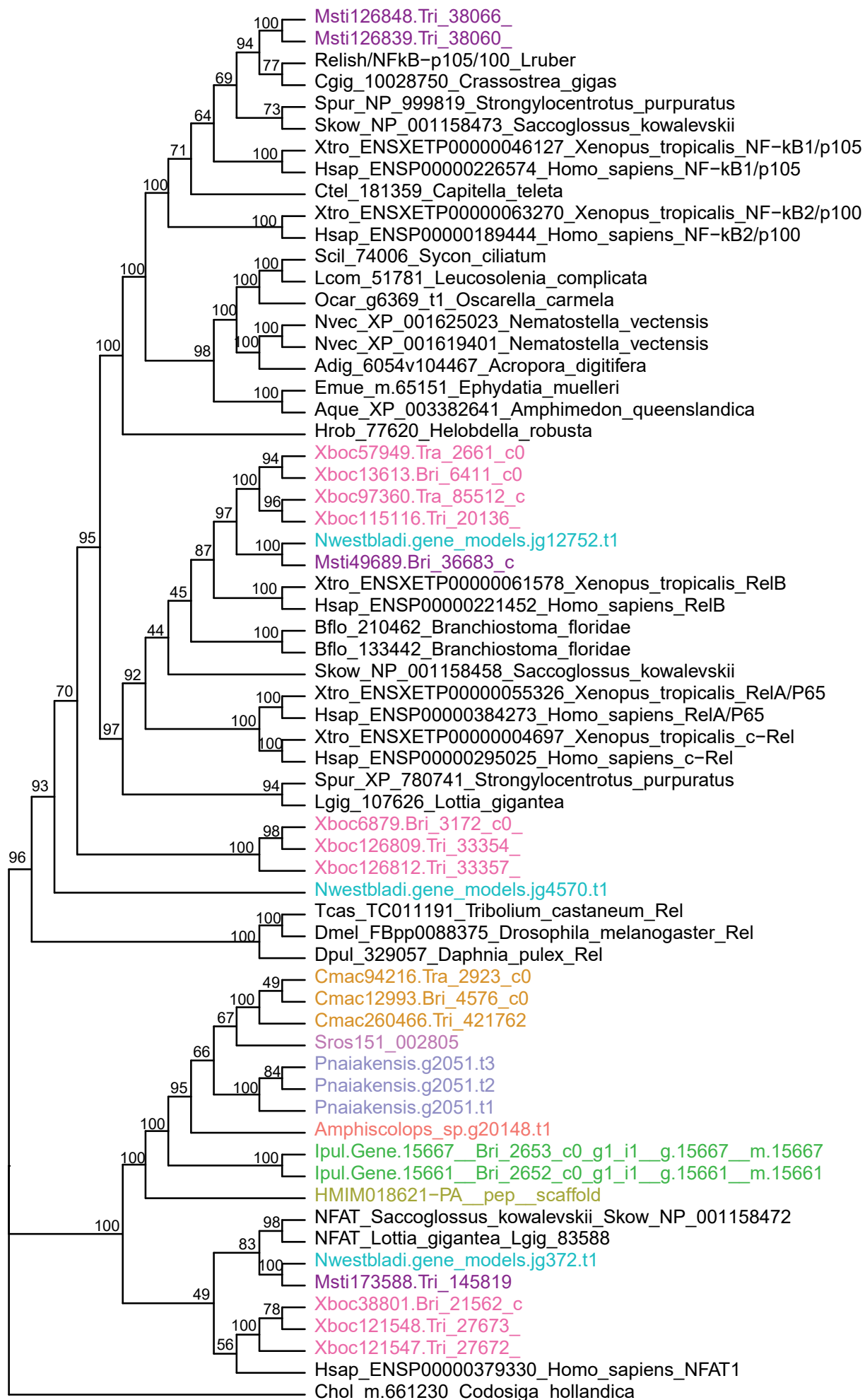


Fig. – S4 MyD88 phylogeny

Maximum likelihood phylogeny of domains in MyD88 and TIR-containing proteins as outgroup. UltraFast Bootstrap support values are shown.

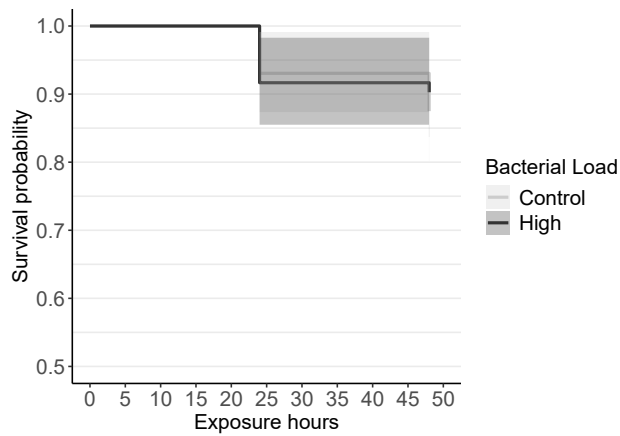


NF-kB

Fig. S5 – NF- κ B phylogeny

Maximum likelihood phylogeny of domains in NF κ B and related proteins. UltraFast Bootstrap support values are shown.

A *C. macropyga* exposed to heat-inactivated *V. coralliilyticus*



B *C. macropyga* exposed to *P. megaterium*

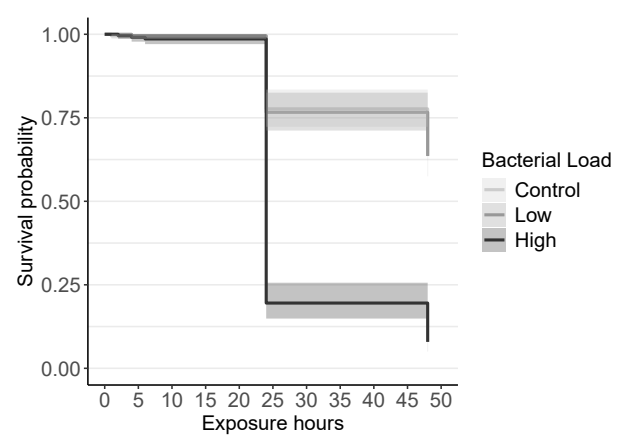


Fig. S6 – *C. macropyga* survival upon exposure to heat-inactivated *Vibrio coralliilyticus* and to *Priestia megaterium*

Survival curves with 95% confidence intervals for *C. macropyga* adults immune challenged with: **A** heat-inactivated *V. coralliilyticus* (minimal adequate Cox proportional hazards model $\text{Surv}(\text{last. obs, censored}) \sim 1$, $n = 145$) or **B** *P. megaterium* (minimal adequate Cox proportional hazards model $\text{Surv}(\text{last. obs, censored}) \sim \text{Bacterial.Load} + (1 | \text{batch})$, $X^2=252.3$, $p = 2.2\text{e-}16$, $n= 644$). Full statistics in Additional File 4: Table S2.

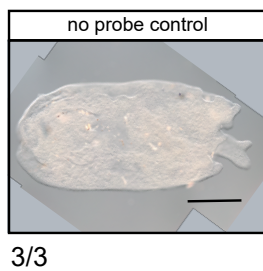
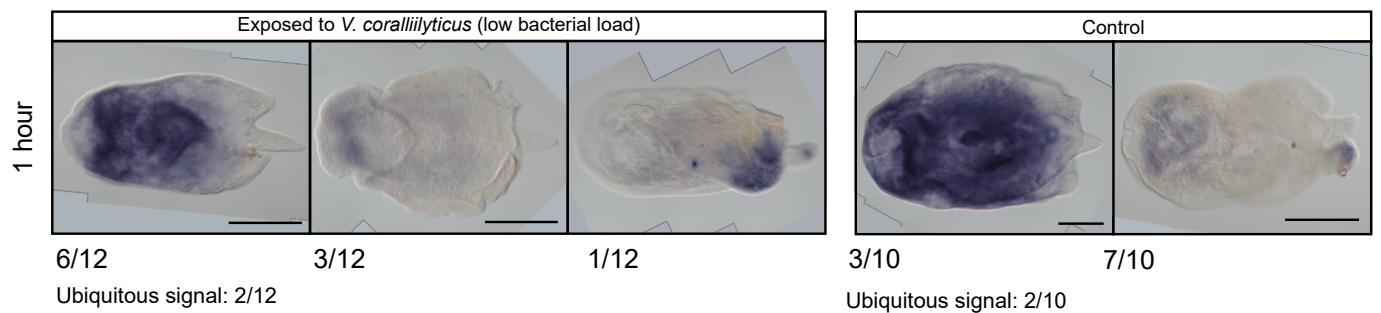
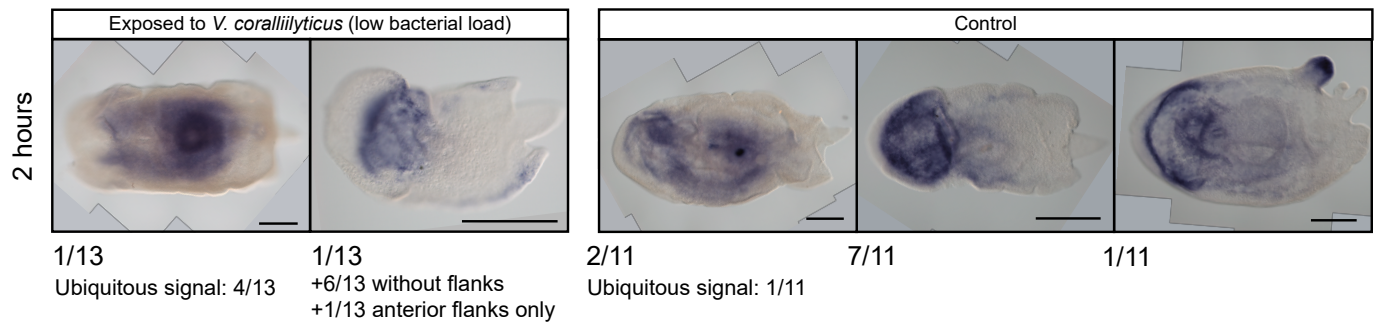
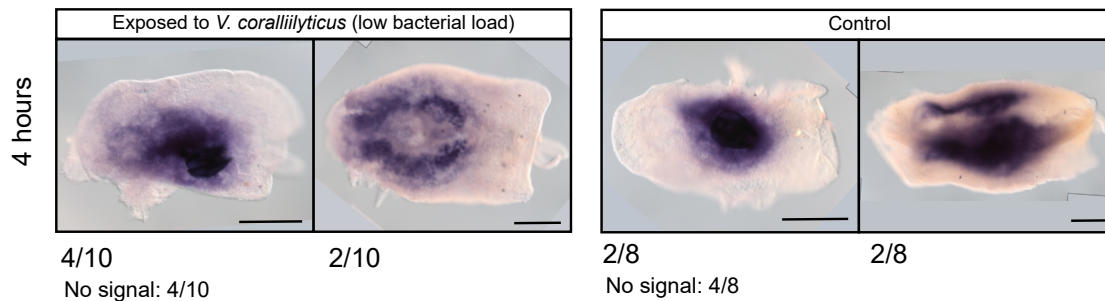
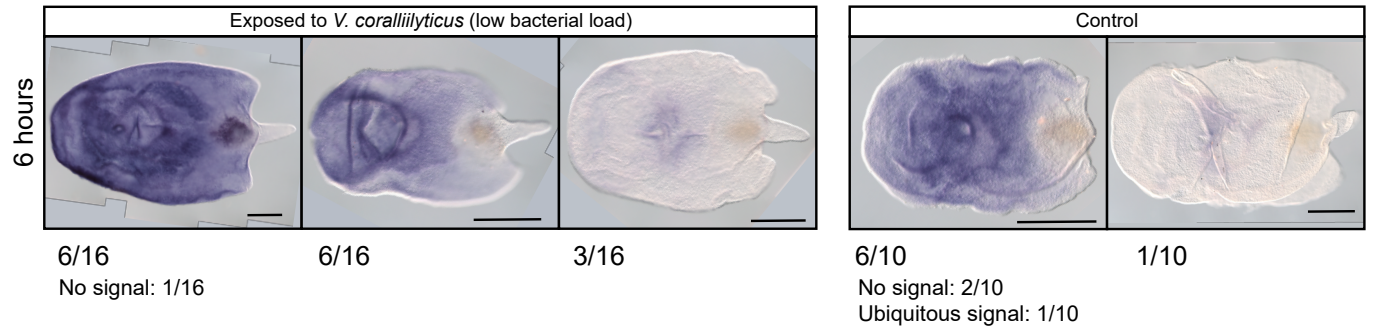
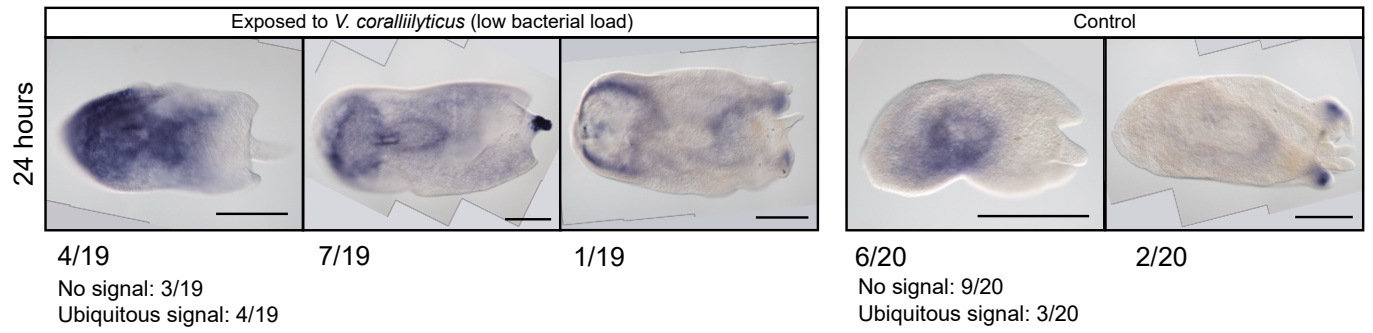


Fig. S7 – In situ hybridisation against *Vibrio coralliilyticus* 16S rRNA in *C. macropyga* at various times of bacterial exposure

RNA in situ hybridisation against *V. coralliilyticus* 16S in *C. macropyga* exposed to a low load of *V. coralliilyticus* or control medium for 1, 2, 4, 6, or 24 hours. Numbers indicate the ratios of individuals with the pattern shown above; dorsal view, anterior is facing left. Scale bars are 0.5 mm.

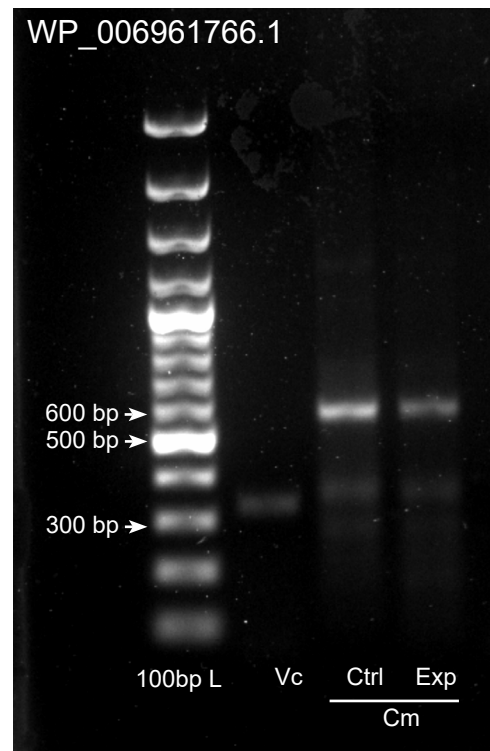
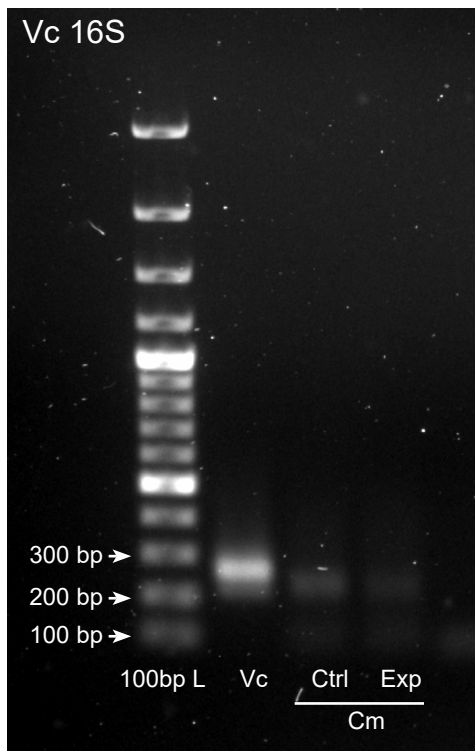
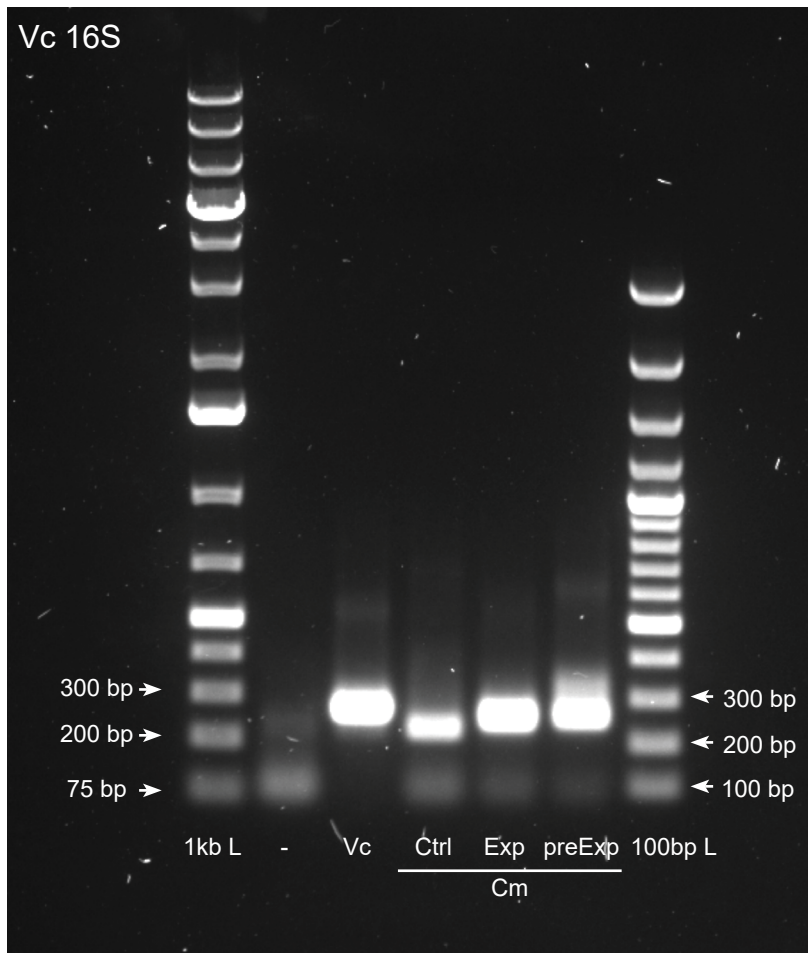


Fig. S8 – PCR for *V. coralliilyticus* 16S rRNA and virulence factor WP_006961766.1

Gel electrophoresis for PCR amplification with primers for *V. coralliilyticus* 16S and *V. coralliilyticus* virulence factor WP_006961766.1 from *V. coralliilyticus* and *C. macropyga* cDNA. As template: DNase and RNase free water as negative control (-), *V. coralliilyticus* cDNA as positive control (Vc), cDNA from unexposed *C. macropyga* (Ctrl), from *C. macropyga* exposed to a low dose of *V. coralliilyticus* (Exp), and *C. macropyga* cDNA synthesized before acquiring the bacterial cultures (preExp). The ladders are GeneRuler 1kb Plus DNA ladder (1kb L) and GeneRuler 100 bp Plus DNA ladder (100bp L) from Thermo Fisher Scientific (Waltham, MA, USA).

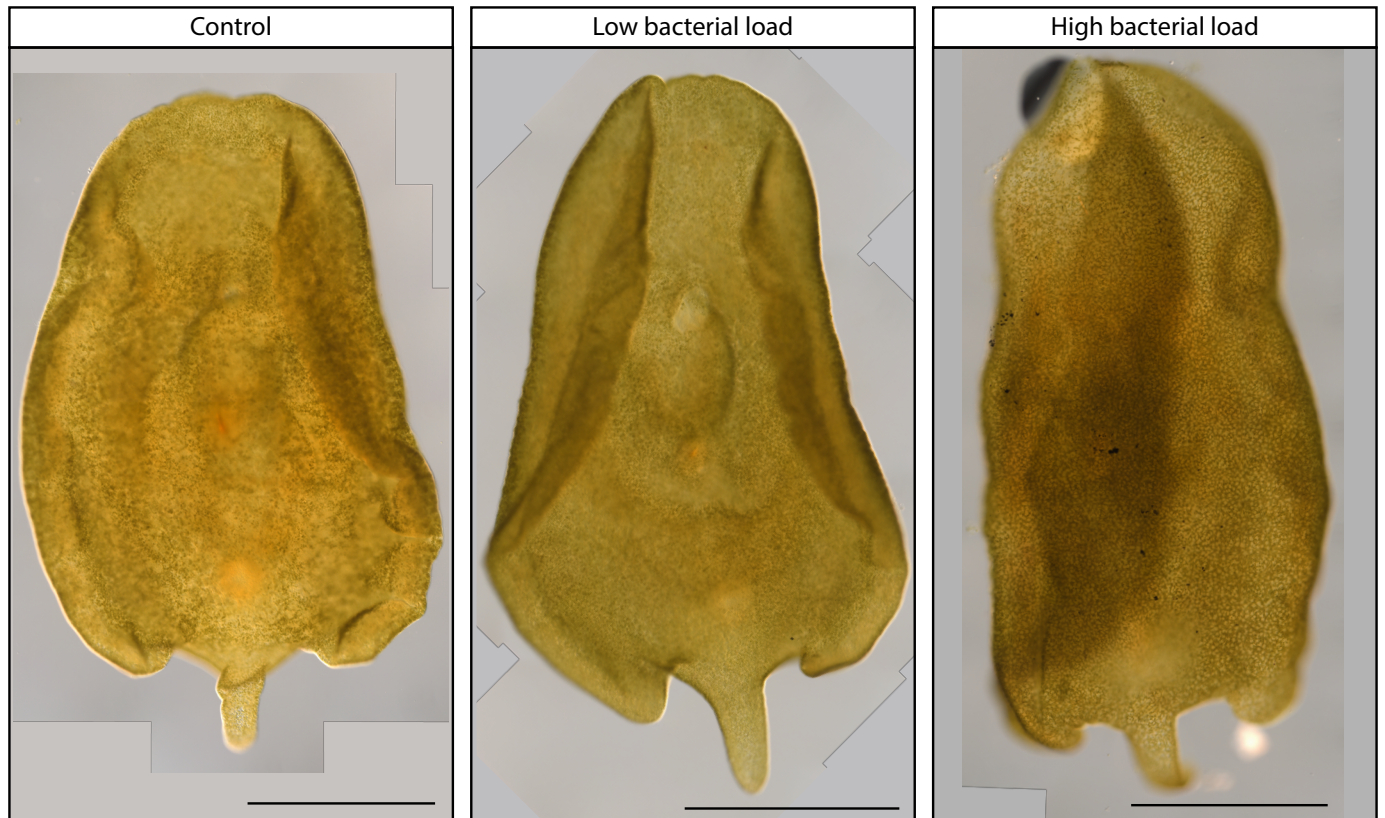


Fig. S9 – *Convolutriloba macropyga* exposed for 14 days to *Vibrio coralliilyticus*

C. macropyga after 14-days immune challenges with *V. coralliilyticus* (low dose, high dose, and control), imaged with DIC after fixation and mounting. Anterior facing upwards, ventral view.

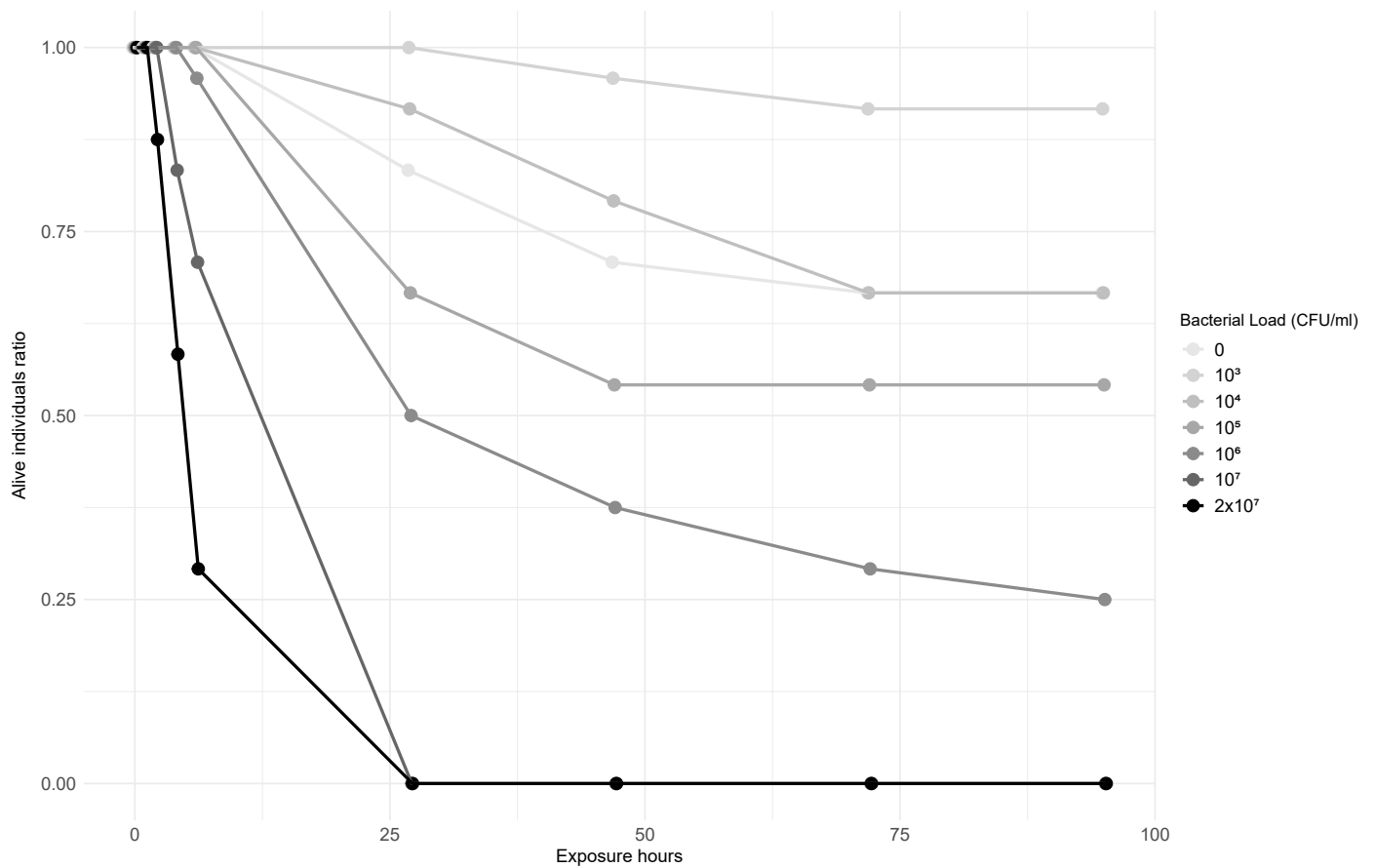


Fig. S10 – *Convolutriloba macropyga* exposed to different bacterial loads of *Vibrio coralliilyticus*

Survival curves of *C. macropyga* exposed to various loads of *V. coralliilyticus* for 96 hours. 24 individuals were immune challenged at each bacterial load.