Transcriptome and proteome response of *Rhipicephalus annulatus* tick vector to *Babesia bigemina* infection

Sandra Antunes[1*], Joana Couto[1], Joana Ferrolho[1], Gustavo Seron Sanches[1], José Octavio Merino Charrez[2], Ned de la Cruz-Hernández[2], Monica Mazuz[3] Margarita Villar[4], Varda Shkap[3], José de la Fuente[4,5], Ana Domingos[1]

[1]GHMT - Global Health and Tropical Medicine, Instituto de Higiene e Medicina Tropical - IHMT, Universidade Nova de Lisboa – UNL, Rua da Junqueira 100, 1349-008 Lisboa, Portugal.
[2]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autónoma de Tamaulipas, Km. 5 carretera Victoria-Mante, CP 87000 Ciudad Victoria, Tamaulipas, Mexico.
[3]Kimron Veterinary Institute, P.O. Box 12, Bet Dagan, 50250, Israel.Instituto de.
[4] SaBio. Instituto de Investigación en Recursos Cinegéticos IREC, CSIC-UCLM-JCCM, Ronda de Toledo s/n, 13005 Ciudad Real, Spain.
[5]Department of Veterinary Pathobiology, Center for Veterinary Health Sciences, Oklahoma State University, Stillwater, OK 74078, USA.
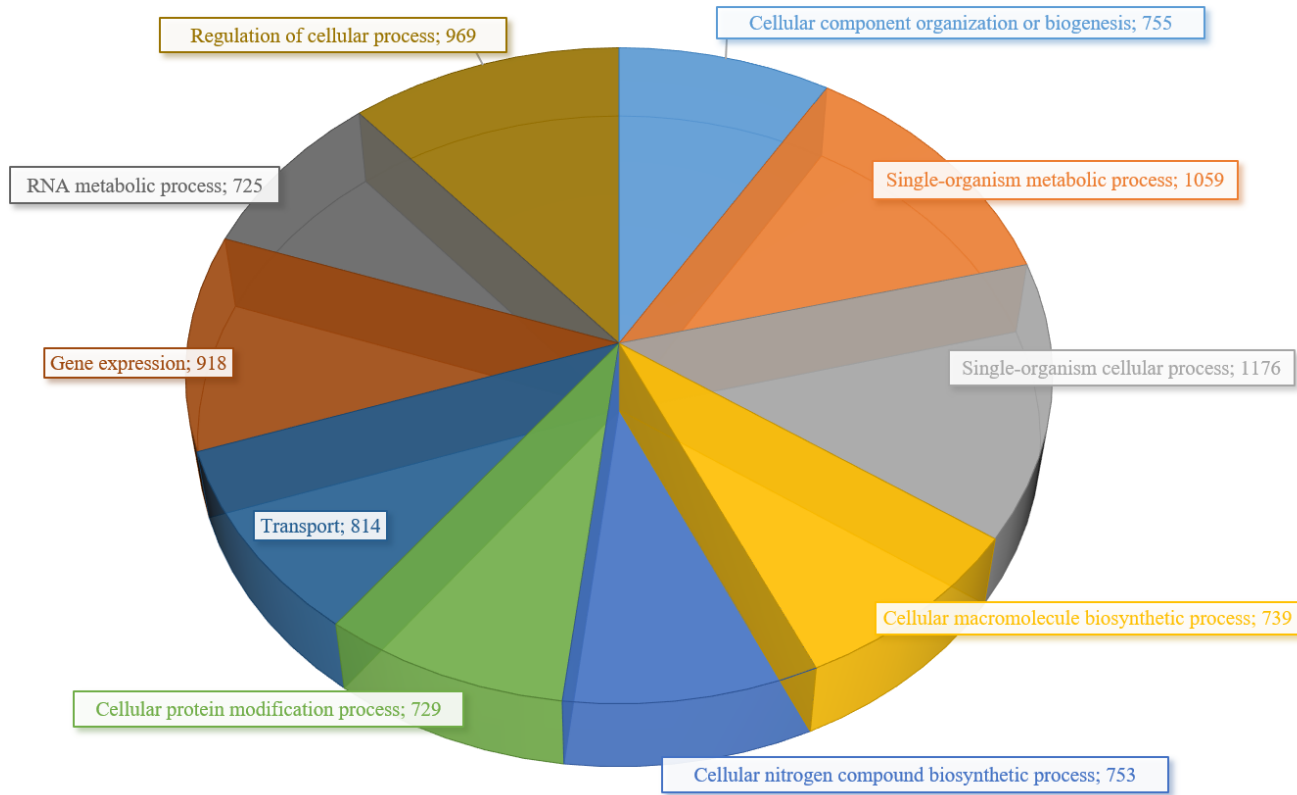
* Correspondence:
Sandra Antunes
santunes@ihmt.unl.pt

Supplementary figures S1 to S4.

A

BIOLOGICAL PROCESS

Regulation of cellular process; 969

Cellular component organization or biogenesis; 755

RNA metabolic process; 725

Single-organism metabolic process; 1059

Gene expression; 918

Single-organism cellular process; 1176

Transport; 814

Cellular macromolecule biosynthetic process; 739

Cellular protein modification process; 729

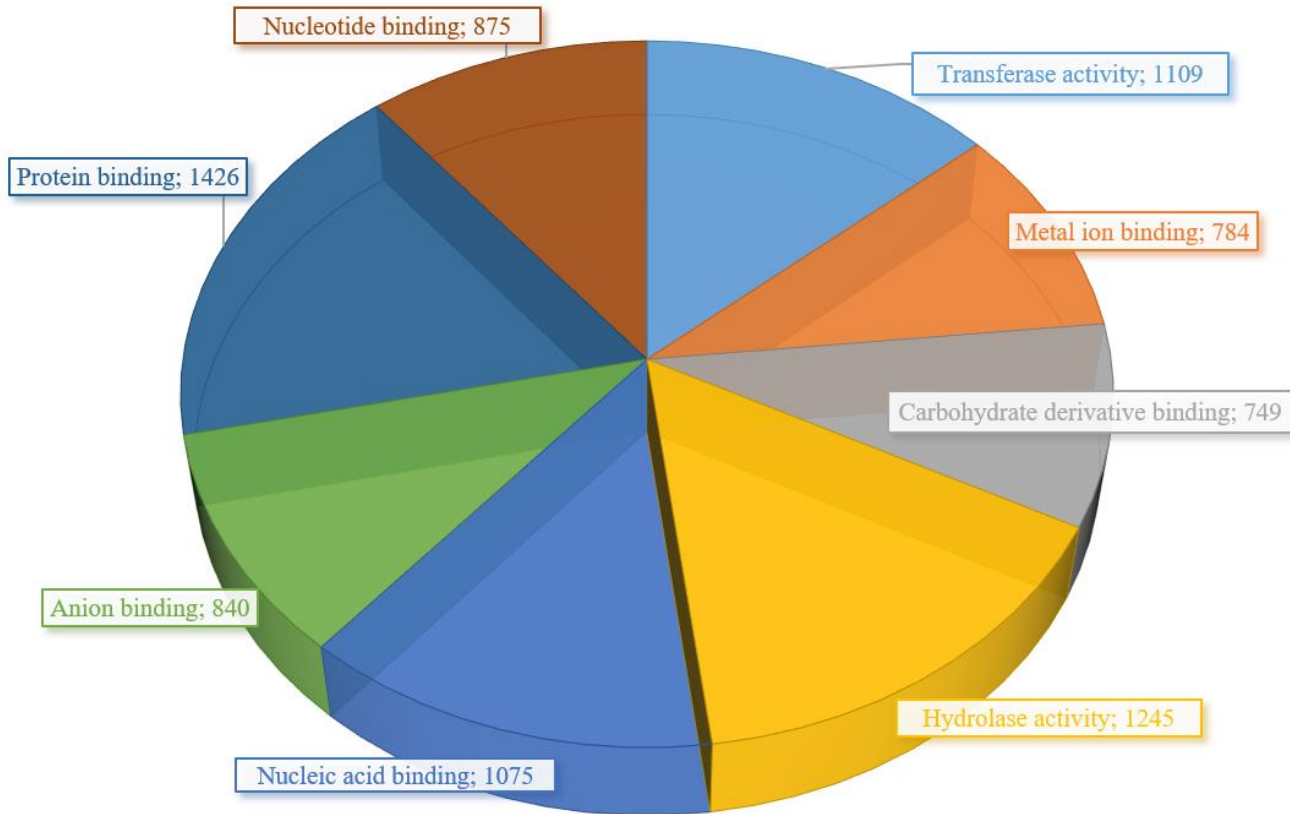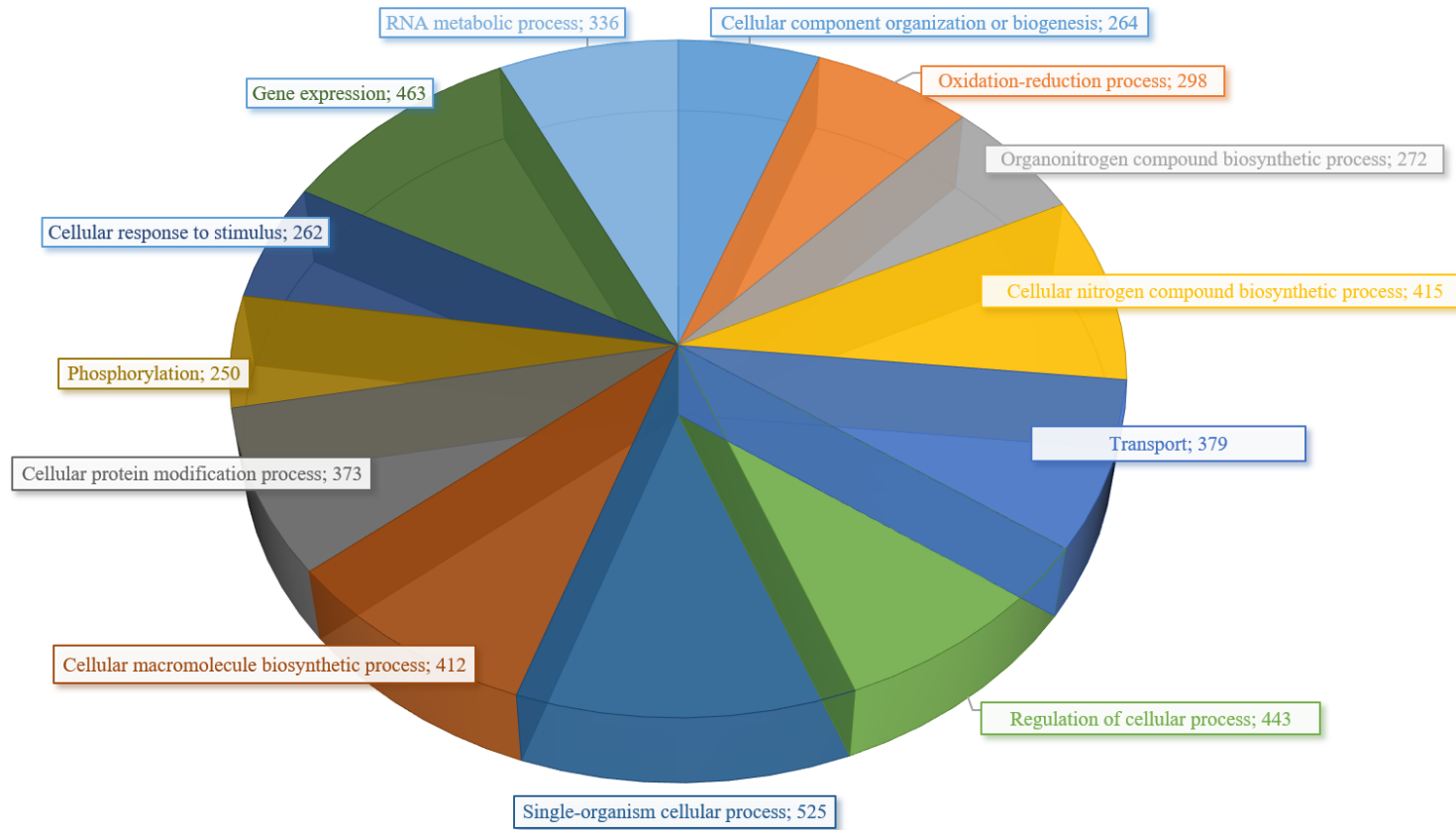Cellular nitrogen compound biosynthetic process; 753

B

Figure S1: **Multi-level chart of biological processes(A) and molecular functions (B) of the sialotranscriptome of *R. annulatus* female ticks based in Gene Ontology.** For each slice a biological process or a molecular function is shown and its representation in number of transcripts.

A

BIOLOGICAL PROCESS

RNA metabolic process; 336

Cellular component organization or biogenesis; 264

Gene expression; 463

Oxidation-reduction process; 298

Organonitrogen compound biosynthetic process; 272

Cellular response to stimulus; 262

Cellular nitrogen compound biosynthetic process; 415

Phosphorylation; 250

Transport; 379

Cellular protein modification process; 373

Cellular macromolecule biosynthetic process; 412

Regulation of cellular process; 443

Single-organism cellular process; 525

B MOLECULAR FUNCTION

- Transition metal ion binding; 290
- Transferase activity; 598
- Hydrolase activity; 675
- Nucleic acid binding; 592
- Oxidoreductase activity; 285
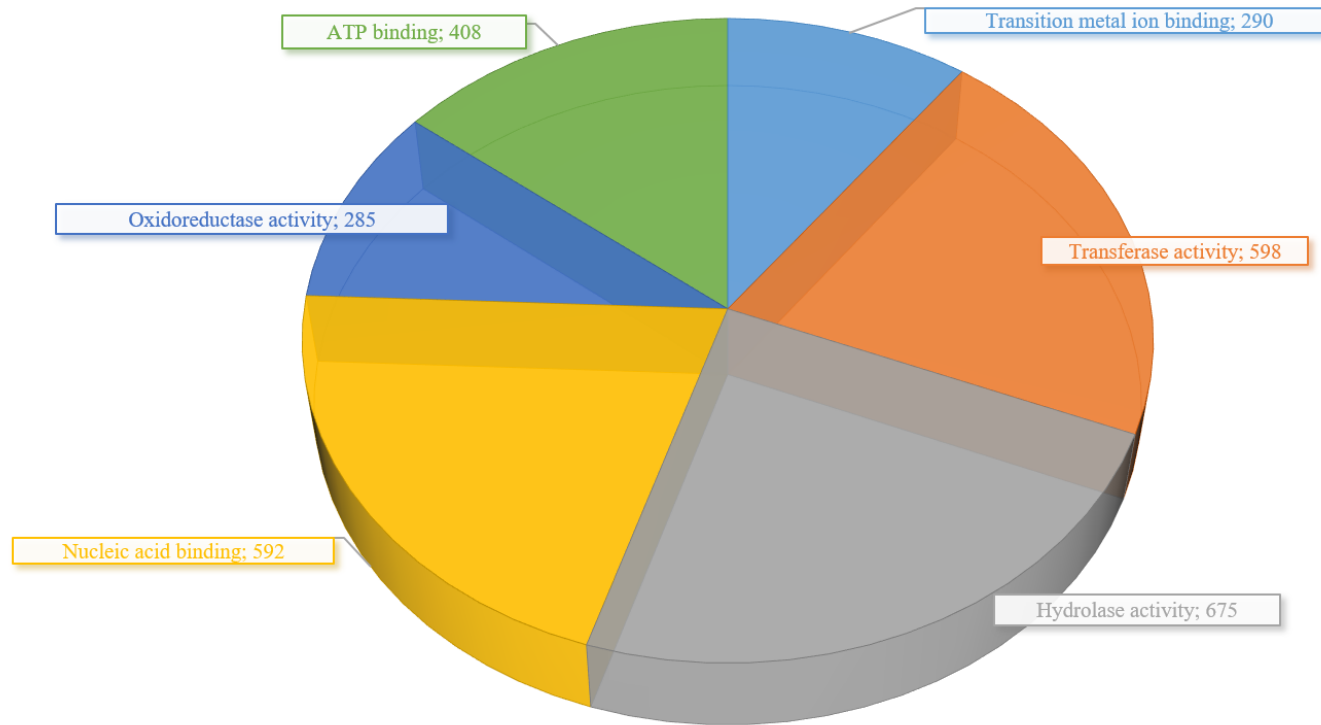- ATP binding; 408

Figure S2: **Multi-level chart of biological processes(A) and molecular functions (B) of the proteome of *R. annulatus* female ticks based in Gene Ontology.** For each slice a biological process or a molecular function is shown and its representation in number of transcripts.
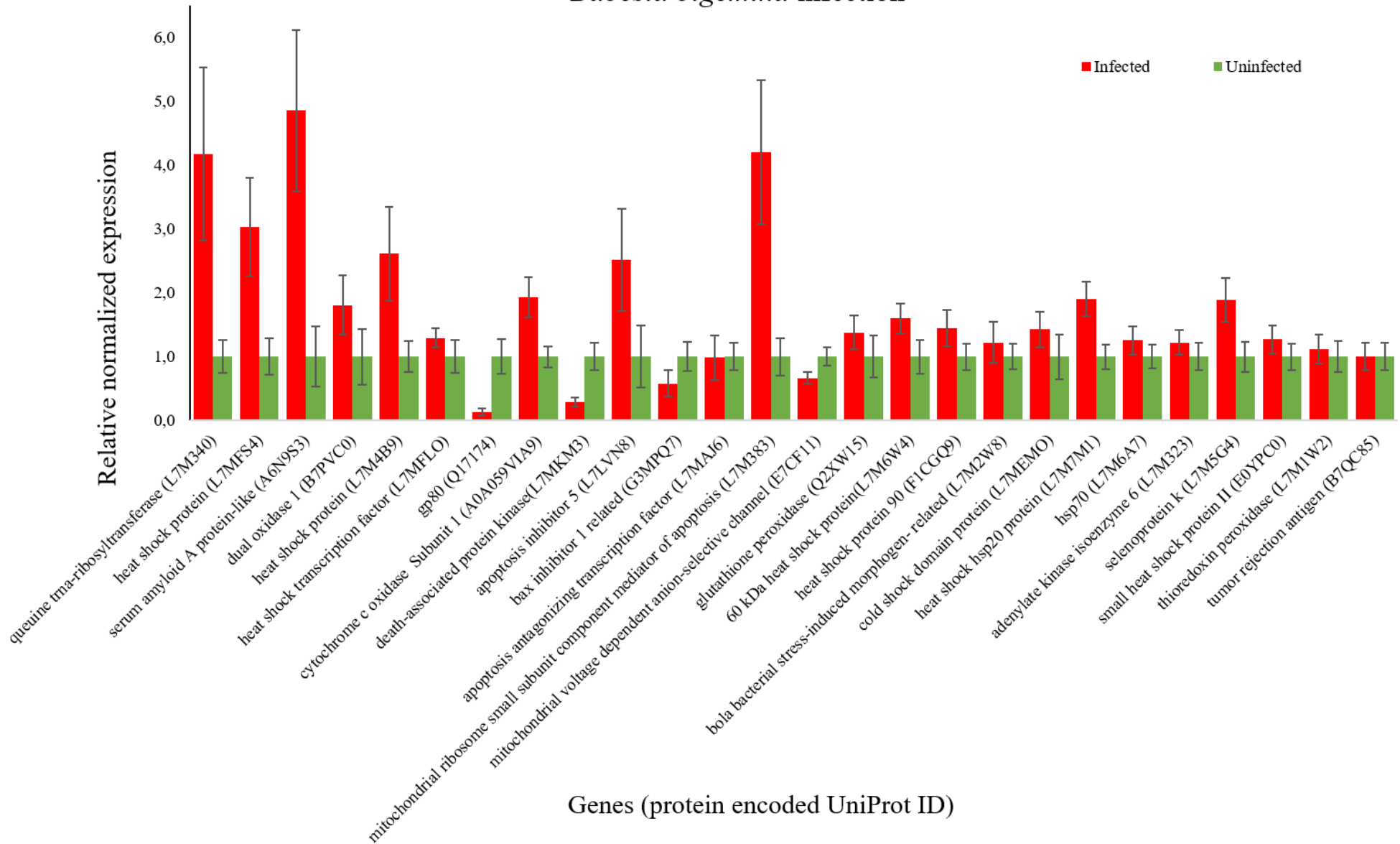
Figure S3: **Differentially gene expression of *R. annulatus* in response to *B. bigemina* infection evaluation by qPCR.** Red bars represent the *B. bigemina* infected SG and green bars represent the SG from uninfected *R. annulatus* female ticks. * P < 0.05
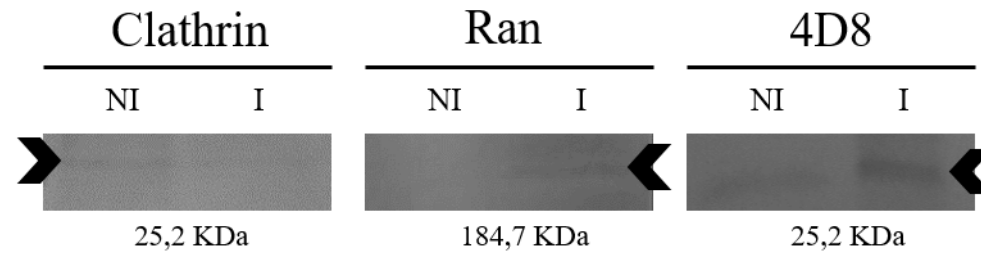
Figure S4: **Evaluation of differential representation of the proteins Clathrin, Ran and 4D8 in *R. annulatus* in response to *B. bigemina* infection by Western blot.** NI correspond to the uninfected sample; I correspond to the infected sample. The protein weight is referred below each panel.