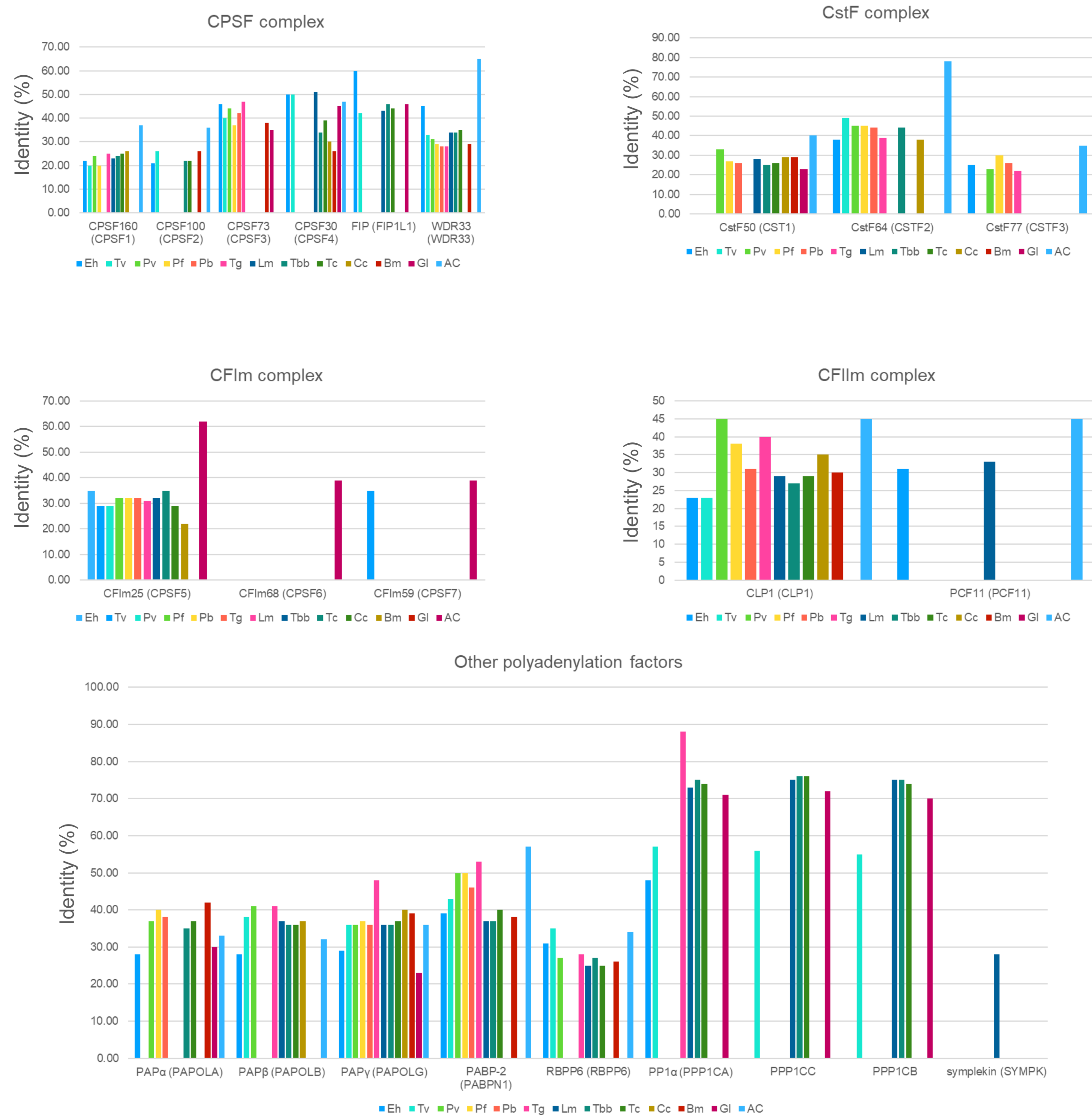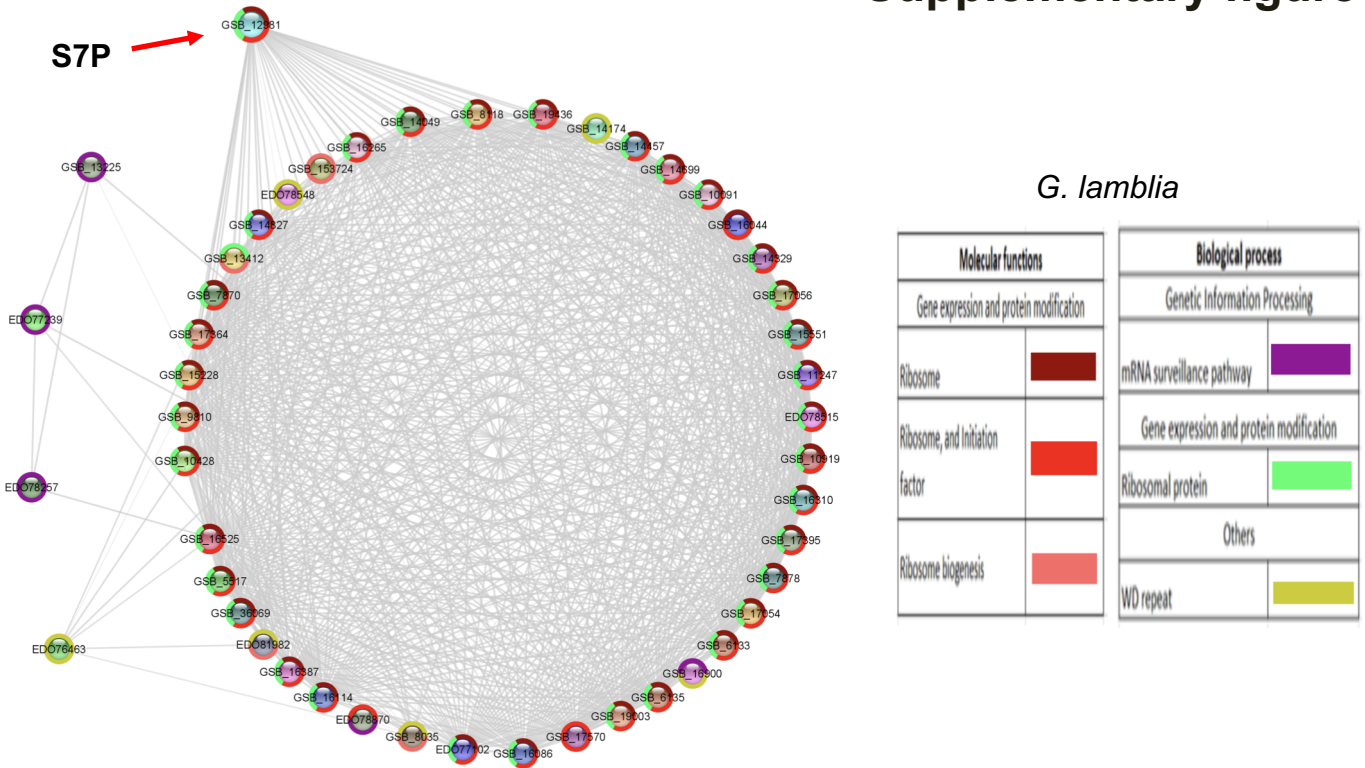**Supplementary Figure 1.** Polyadenylation factors length (gene name is in parenthesis) in protozoan parasites and their human host. Each species corresponds to a specific color. H. sapiens (Hs), Entamoeba histolytica (Eh), Acanthamoeba castellani (Ac), Trichomonas vaginalis (Tv), Leishmania mexicana (Lm), Trypanosoma brucei brucei (Tbb), T. cruzi (Tc). Tozoplasma gondi (Tg), Plasmodium vivax (Pv), P. falciparum (Pf), Babesia microti (Bm), P. berghei (Pb), Cyclospora cayatenesis (Cc), and Giardia lamblia (Gl).

**Supplementary Figure 2.** Conservation of protein sequences in polyadenylation factors (gene name is in parenthesis). The protein sequence for each parasite factor was compared to the homologous human factor by BLAST analysis to obtain the percentage of identity. Each species corresponds to a specific color. H. sapiens (Hs), Entamoeba histolytica (Eh), Acanthamoeba castellani (Ac), Trichomonas vaginalis (Tv), Leishmania mexicana (Lm), Trypanosoma brucei brucei (Tbb), T. cruzi (Tc). Tozoplasma gondi (Tg), Plasmodium vivax (Pv), P. falciparum (Pf), Babesia microti (Bm), P. berghei (Pb), Cyclospora cayatenesis (Cc), and Giardia lamblia (Gl).
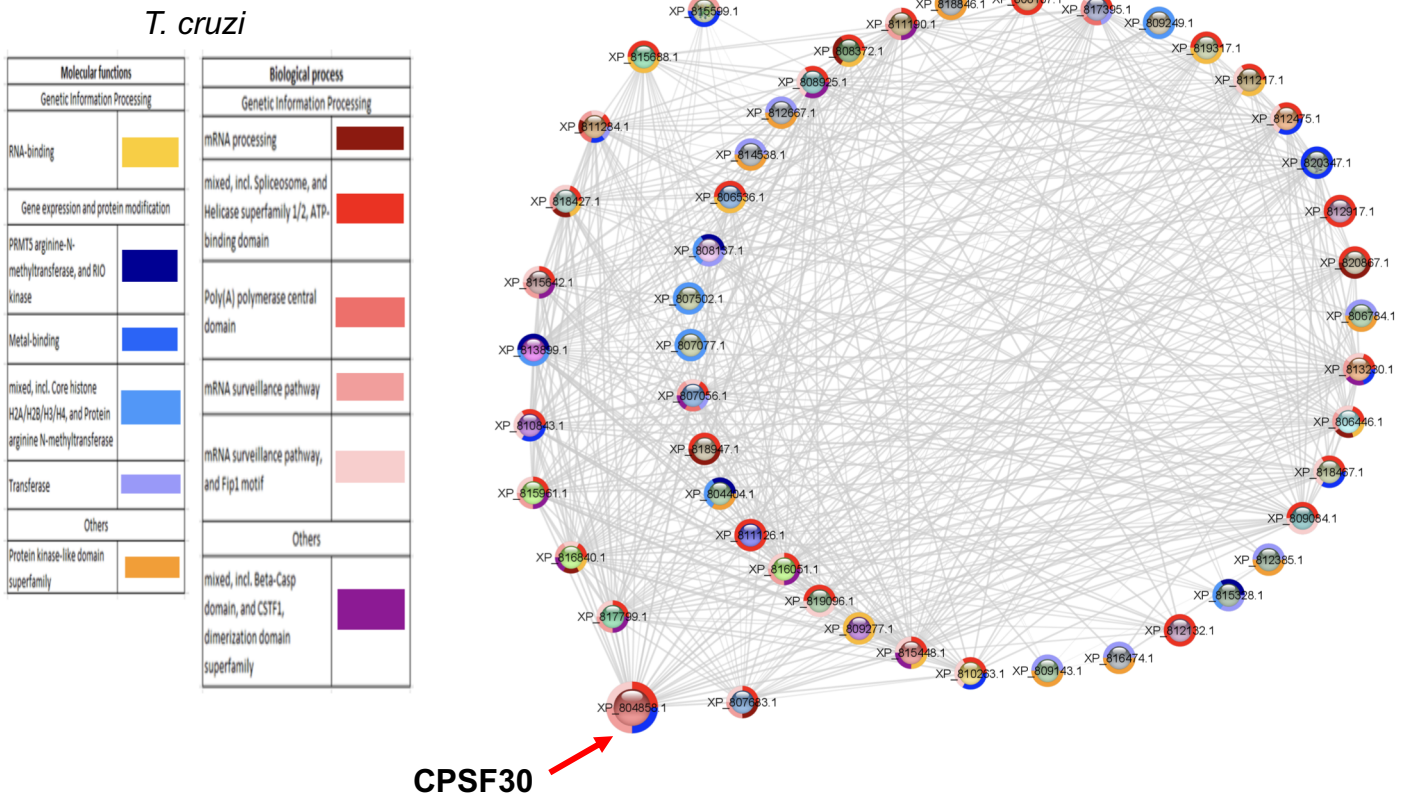
**Supplementary figure 3.** Analysis of polyadenylation factors interactions in other protozoan pathogens. Data were obtained from STRING database and EuPathDB Bioinformatics Resource Center with the corresponding parasite genome database including (A) *Giardia lamblia*, (B) *Trypanosoma cruzi*, (C) *Plasmodium berghei*, (D) *P. falciparum*, and (E) *Toxoplasma gondii*. The networks were visualized using the Cytoscape tool, principal proteins corresponding to polyadenylation factors were represented in the external network. Internal interactions represent proteins associate with polyadenylation process. Central hubs proteins are indicated with red arrows. GO terms including Molecular functions and biological process were carried out using KEGG Pathways, STRING clusters and Interior domains. Proteins were marked with the corresponding GO term color.

**C**

*P. falciparum*

RNA helicase → PFF0100w

| Molecular functions | |
|---|---|
| **Gene expression and protein modification** | |
| mixed, incl. Ribosome biogenesis in eukaryotes, and K homology RNA-binding domain | |
| mixed, incl. PNPase/RNase PH domain superfamily, and KH domain | |
| **Others** | |
| WD40/YVTN repeat-like-containing domain superfamily | |

| Biological process | |
|---|---|
| **Genetic Information Processing** | |
| mixed, incl. mRNA surveillance pathway, and Beta-Casp domain | |
| mRNA surveillance pathway | |
| RNA degradation | |
| **Gene expression and protein modification** | |
| mixed, incl. Ribosome biogenesis in eukaryotes, and rRNA processing | |
| mixed, incl. Ribosome biogenesis in eukaryotes, and DEAD/DEAH box helicase domain | |

**D**

Nucleic acid binding protein → PBANKA_093980

*P. berghei*

| Molecular functions | |
|---|---|
| **Genetic Information Processing** | |
| RNA binding | |
| **Gene expression and protein modification** | |
| mixed, incl. Ribosome biogenesis in eukaryotes, and Helicase, C-terminal | |
| **Others** | |
| WD repeat | |

| Biological process | |
|---|---|
| **Genetic Information Processing** | |
| mixed, incl. mRNA surveillance pathway, and YTH domain | |
| mRNA processing | |
| mRNA surveillance pathway | |
| RNA degradation | |
| **Gene expression and protein modification** | |
| mixed, incl. Ribosome biogenesis in eukaryotes, and DEAD/DEAH box helicase domain | |
| **Others** | |
| WD40 repeats | |

**Supplementary figure 3.** Part 3

E

mago nashi
protein 2



*T. gondii*

| Molecular functions | |
| --- | --- |
| Genetic Information Processing | |
| mixed, incl. Spliceosome, and RNA recognition motif | ■ (dark green) |
| RNA-binding | ■ (light green) |
| Others | |
| Nucleus | ■ (orange) |

| Biological process | |
| --- | --- |
| Genetic Information Processing | |
| mRNA surveillance pathway | ■ (dark navy) |
| mixed, incl. mRNA surveillance pathway, and YTH domain | ■ (dark blue) |
| RNA transport | ■ (medium blue) |
| mRNA surveillance pathway, and Partial cleavage stimulation factor domain | ■ (light blue) |
| mRNA processing | ■ (blue) |
| mixed, incl. DNA-directed RNA polymerase, and Basal transcription factors | ■ (pale blue) |

**Supplementary figure 3.** Part 3
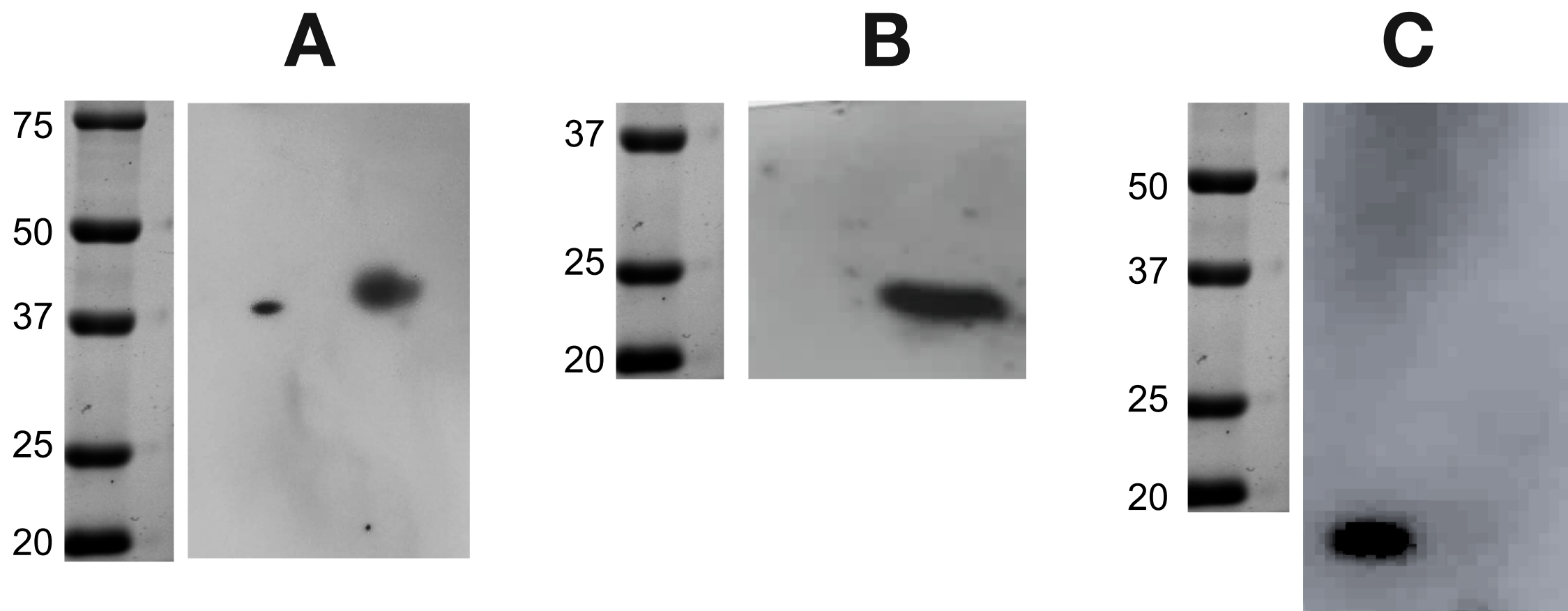
Uncropped figure of raw Western blot experiments shown in figure 8 using anti-HsCFIm25 (A), anti-EhPC4 (B) and anti-EhPSP (C) antibodies that confirm the recognition of parasite CFIm25 protein by heterologous antibody and the absence of cross contamination between CE (left) and NE (right).