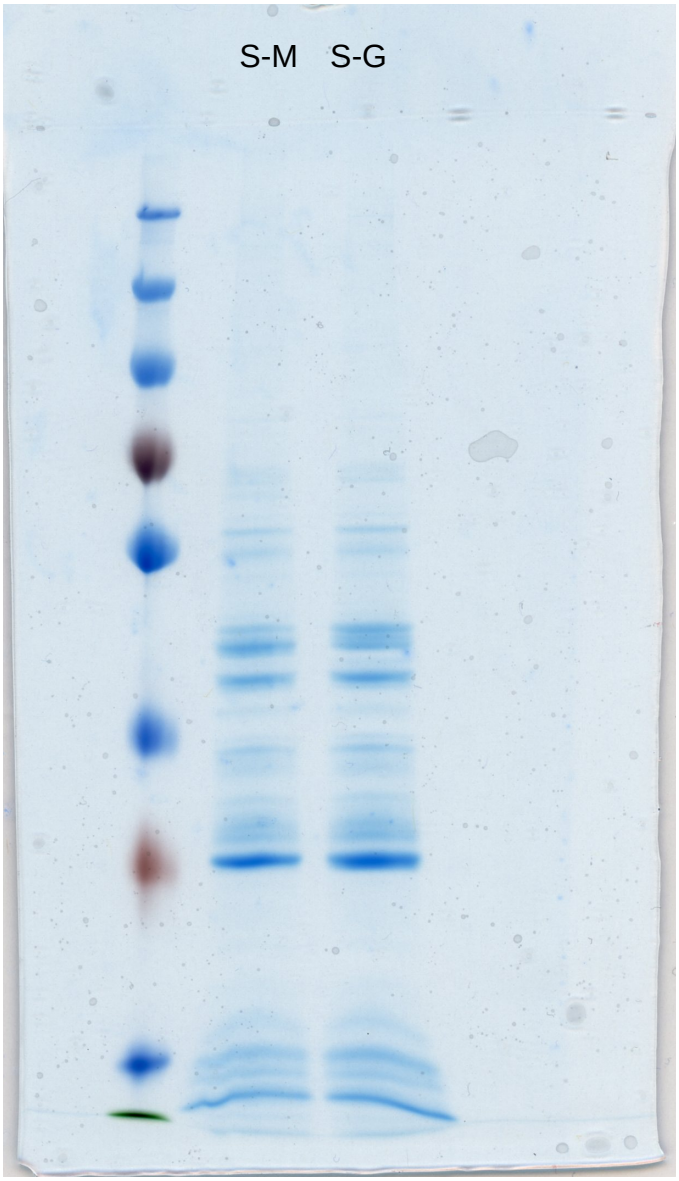
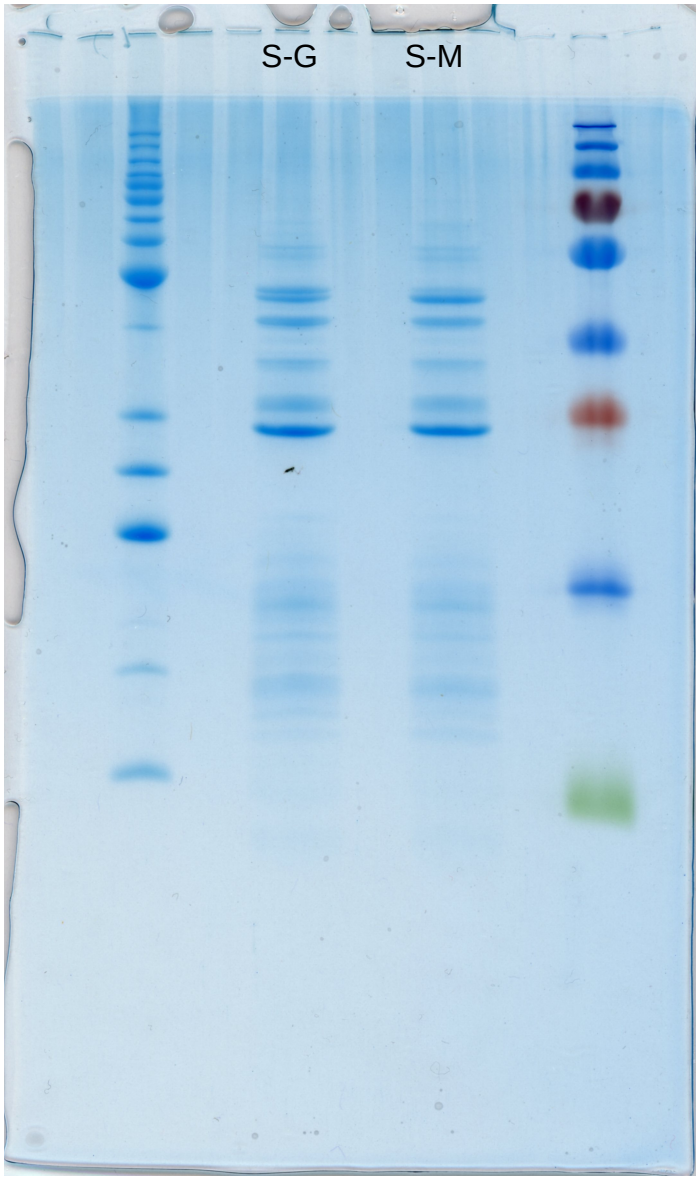
Raw SDS-PAGE gels visualized on figure 12

A) protein separation on 10% PAGE gel

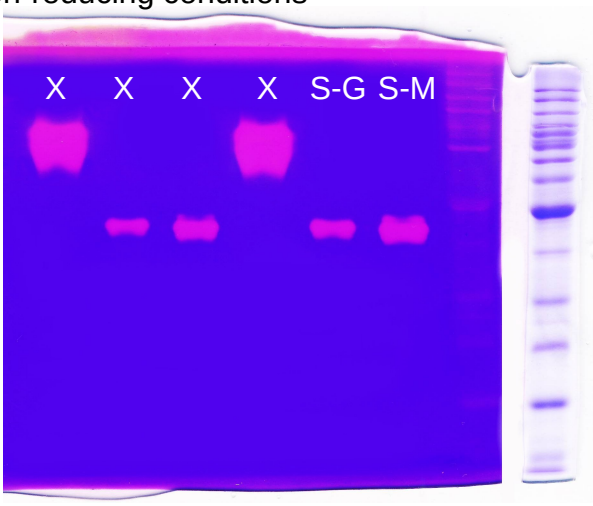


B) protein separation on 15% PAGE gel

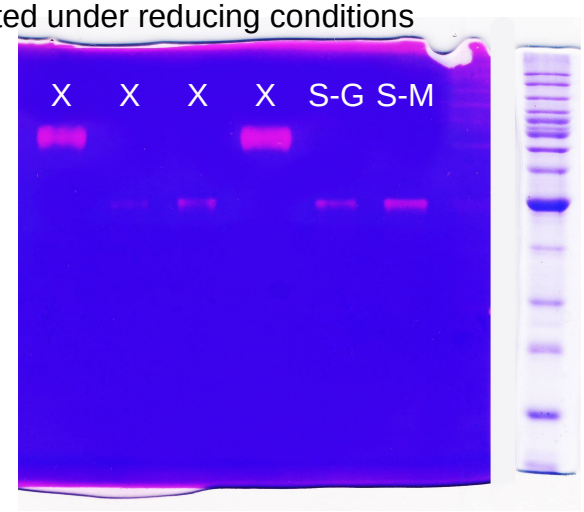


Raw SDS-PAGE zymography gels visualized on figure 13

A) Salivary gland homogenate tested on SDS PAGE zymography gel containing 10% polyacrylamide with 0.002% HA, tested under non-reducing conditions

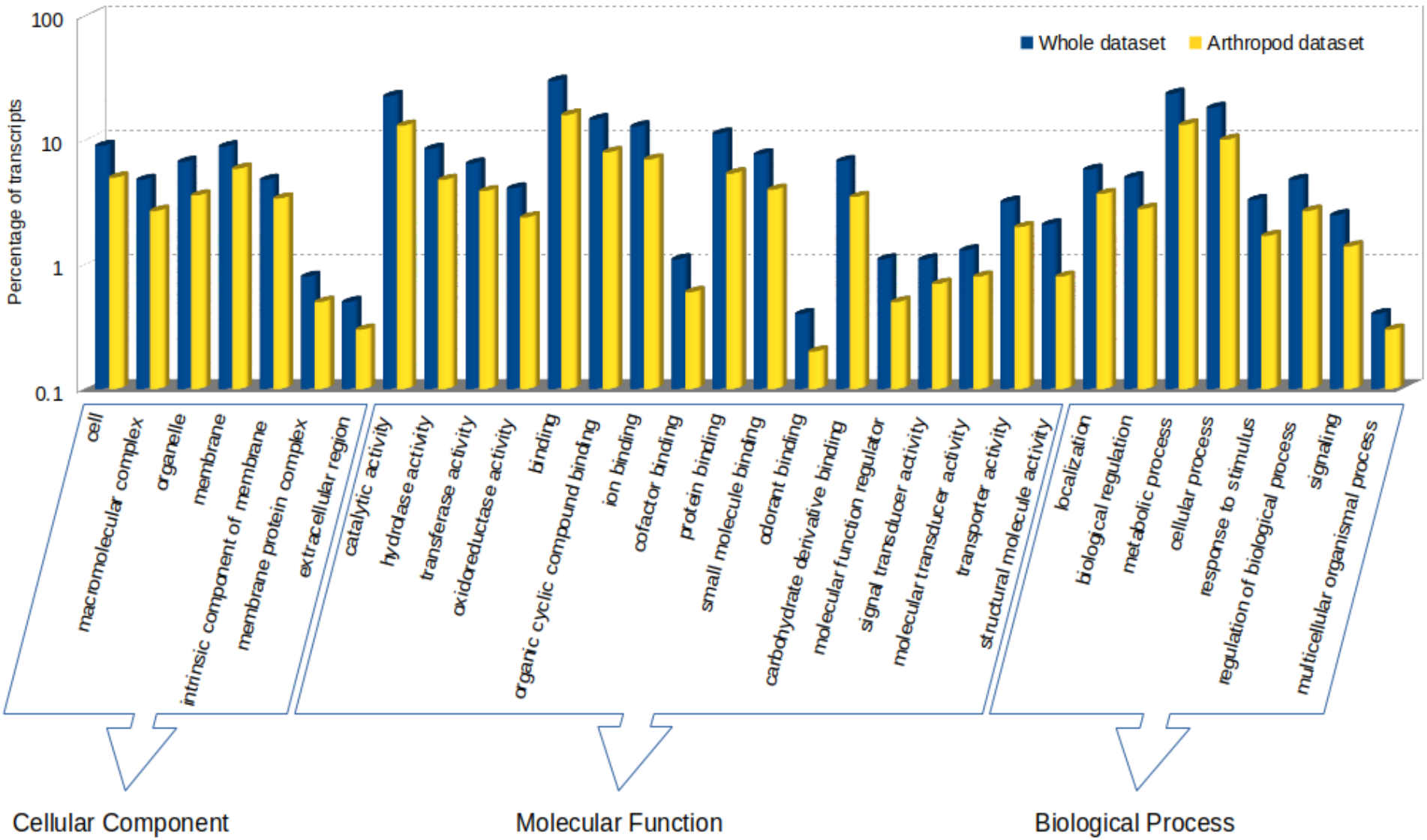


B) Salivary gland homogenate tested on SDS PAGE zymography gel containing 10% polyacrylamide with 0.002% HA, tested under reducing conditions



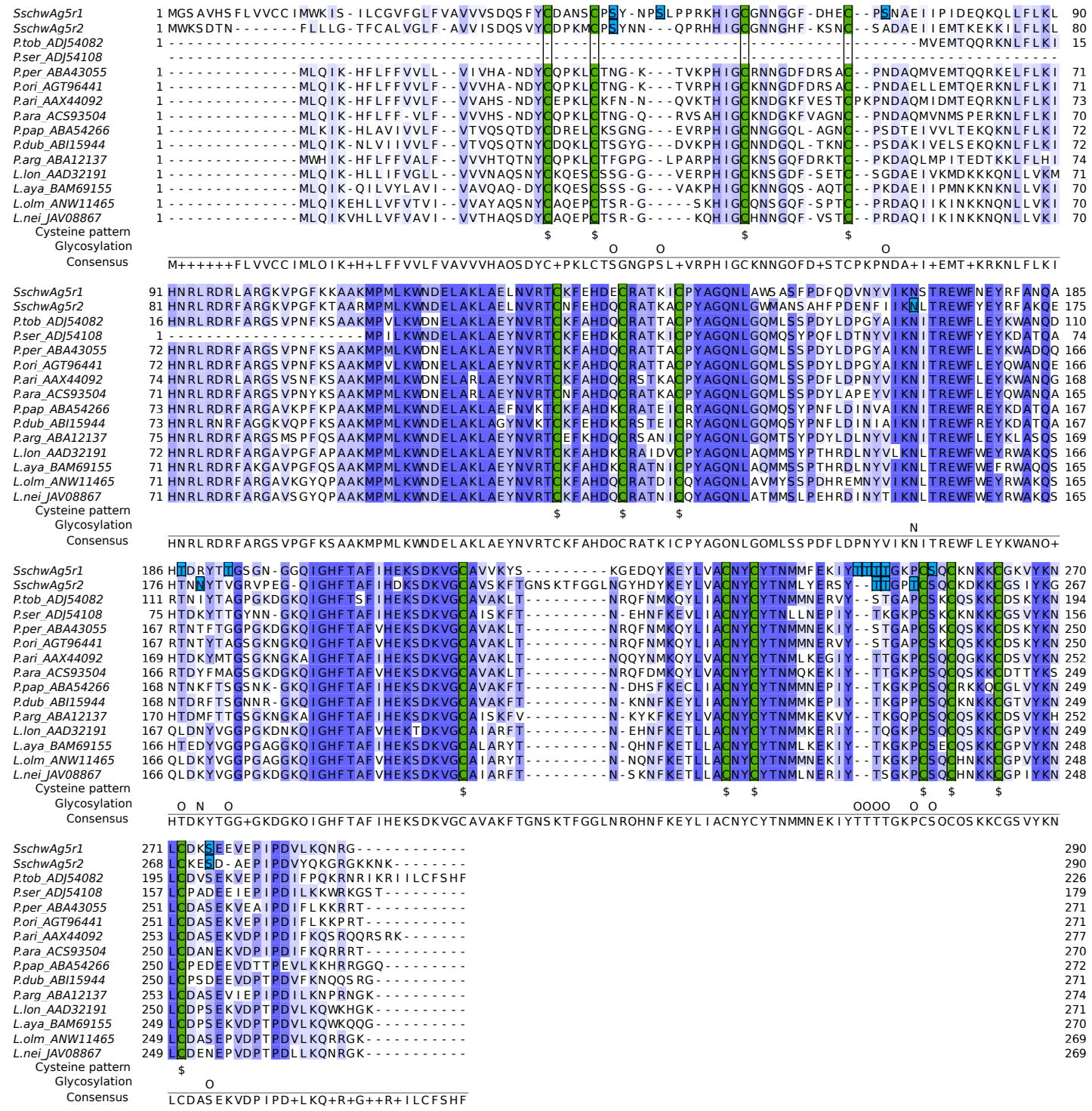
First three lines on both gels: concentration 0.5 salivary gland per line; second three lines: concentration 1 salivary gland per line, which was used for publication; samples order: positive control *Phlebotomus papatasi*, *Sergentomyia schwetzi* gecko lineage, *S. schwetzi* mouse lineage

S2 Fig. Functional gene ontology (GO) classification of the *S. schwetzi* salivary gland transcriptome



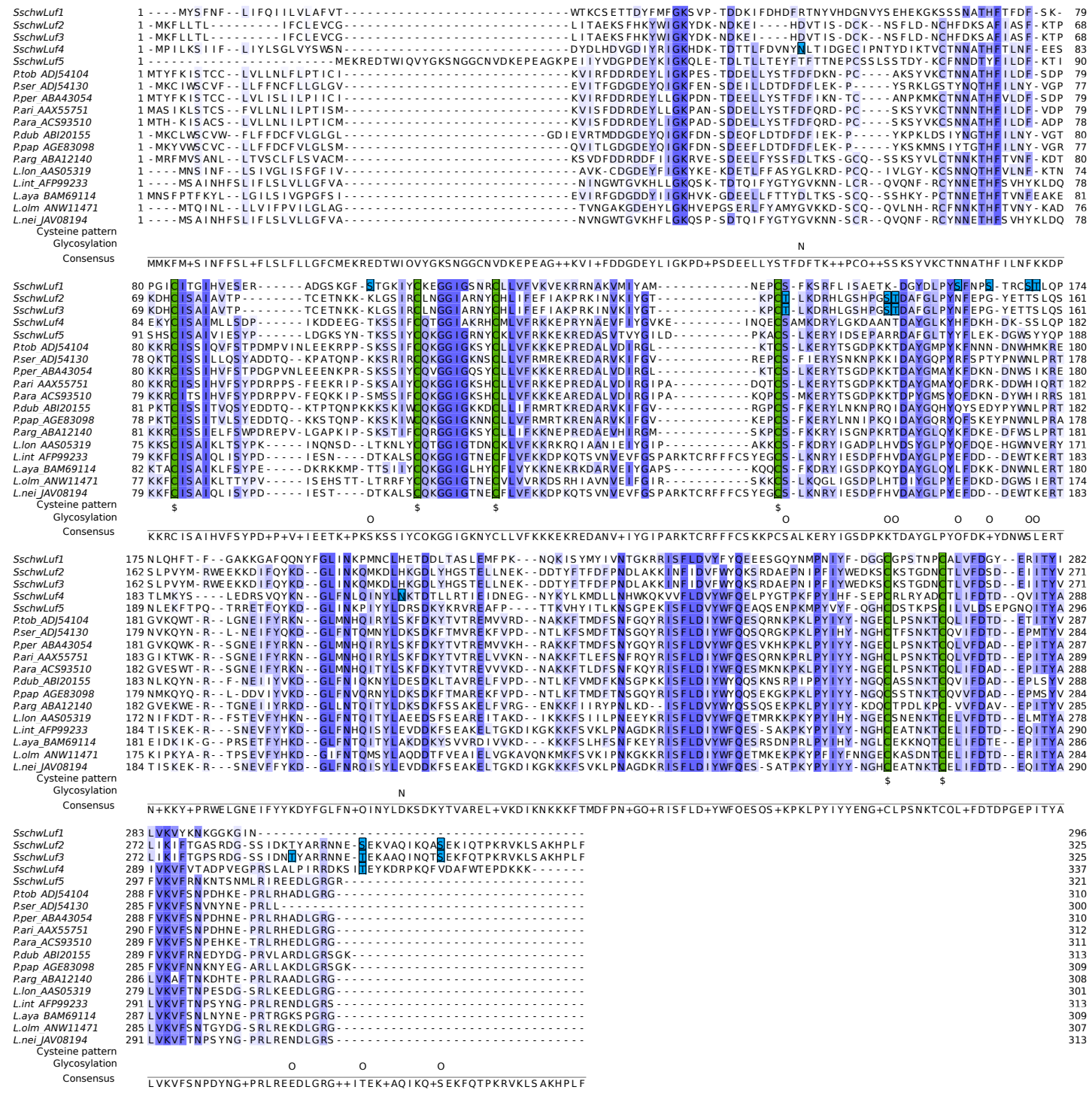
Functional gene ontology (GO) classification of the *S. schwetzi* salivary gland transcriptome. The percentage and distribution of top-level GO-terms are portrayed in the three categories: cellular component, molecular function and biological process. Transcripts annotated from whole transcriptome sequences dataset are indicated by blue bar (7,749 sequences) and transcripts annotated from arthropod sequences subset are in yellow (5,937 sequences).

S3 Fig. Multiple sequence alignment of sand flies' antigen 5-related proteins



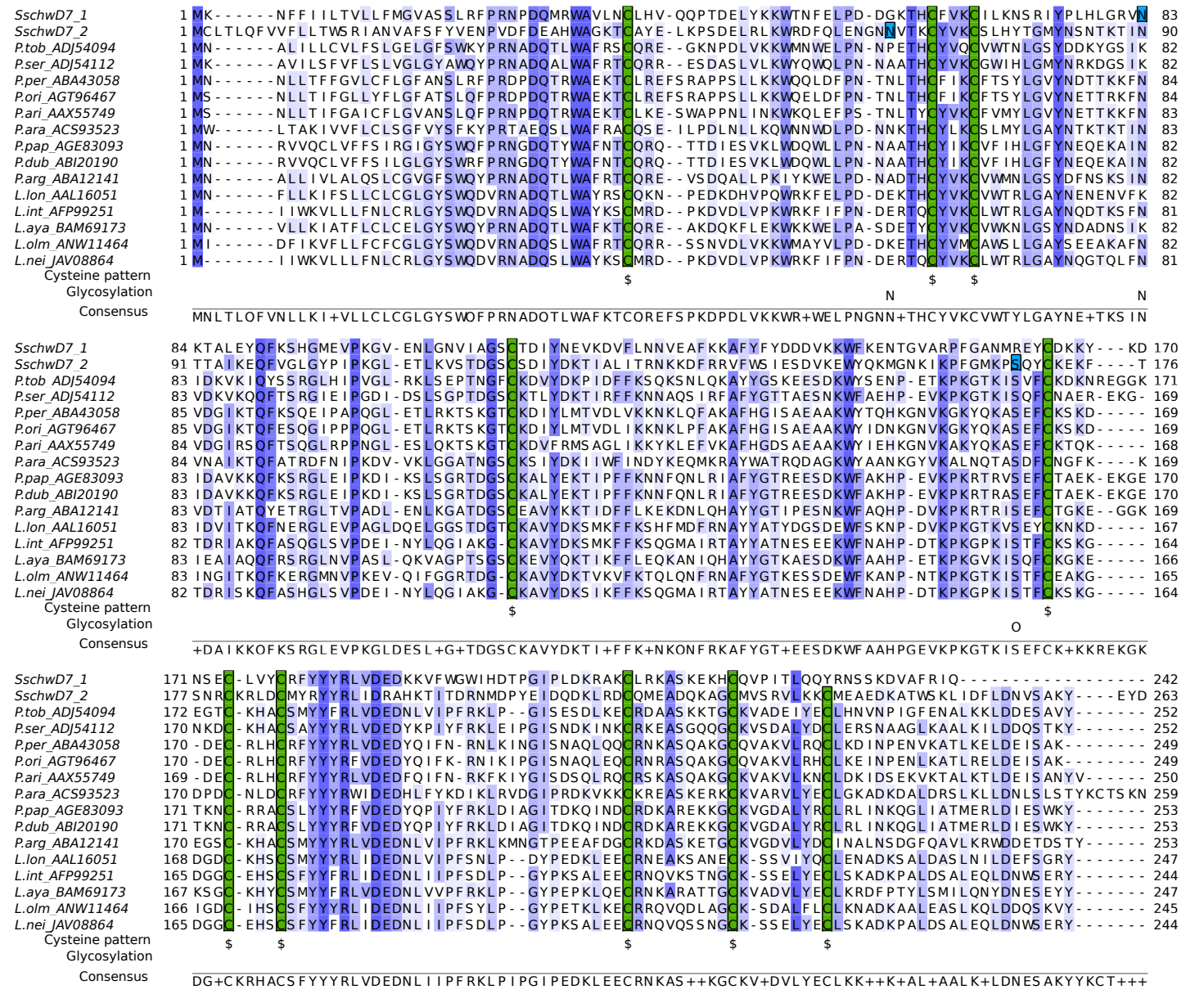
Multiple sequence alignment of *S. schwetzi* antigen 5-related proteins with chosen sand flies' antigen 5-related proteins. Name of sequence include sand fly species shortcut (P.tob – *P. tobbi*, P.ser – *P. sergenti*, P.per – *P. perniciosus*, P.ori – *P. orientalis*, P.ari – *P. ariasi*, P.ara – *P. arabicus*, P.pap – *P. papatasi*, P.dub – *P. duboscqi*, P.arg – *P. argentipes*, L.lon – *L. longipalpis*, L.aya – *L. ayacuchensis*, L.olm – *L. olmeca*, L.nei – *L. neivai*) and GenBank accession number. Sequence conservation is depicted by shading of purple color. Conserved cysteines residues are highlighted in green, putative glycosylation sites in SschwAg5r sequence are highlighted in blue. Lines below the alignment indicates conserved cysteines residues by "$", glycosylation by "N" for N-glycosylation and by "O" for O-glycosylation and consensus sequence. Alignment was made by MAFFT with L-INS-i method and visualized in Jalview.

S4 Fig. Multiple sequence alignment of sand flies' lufaxin proteins



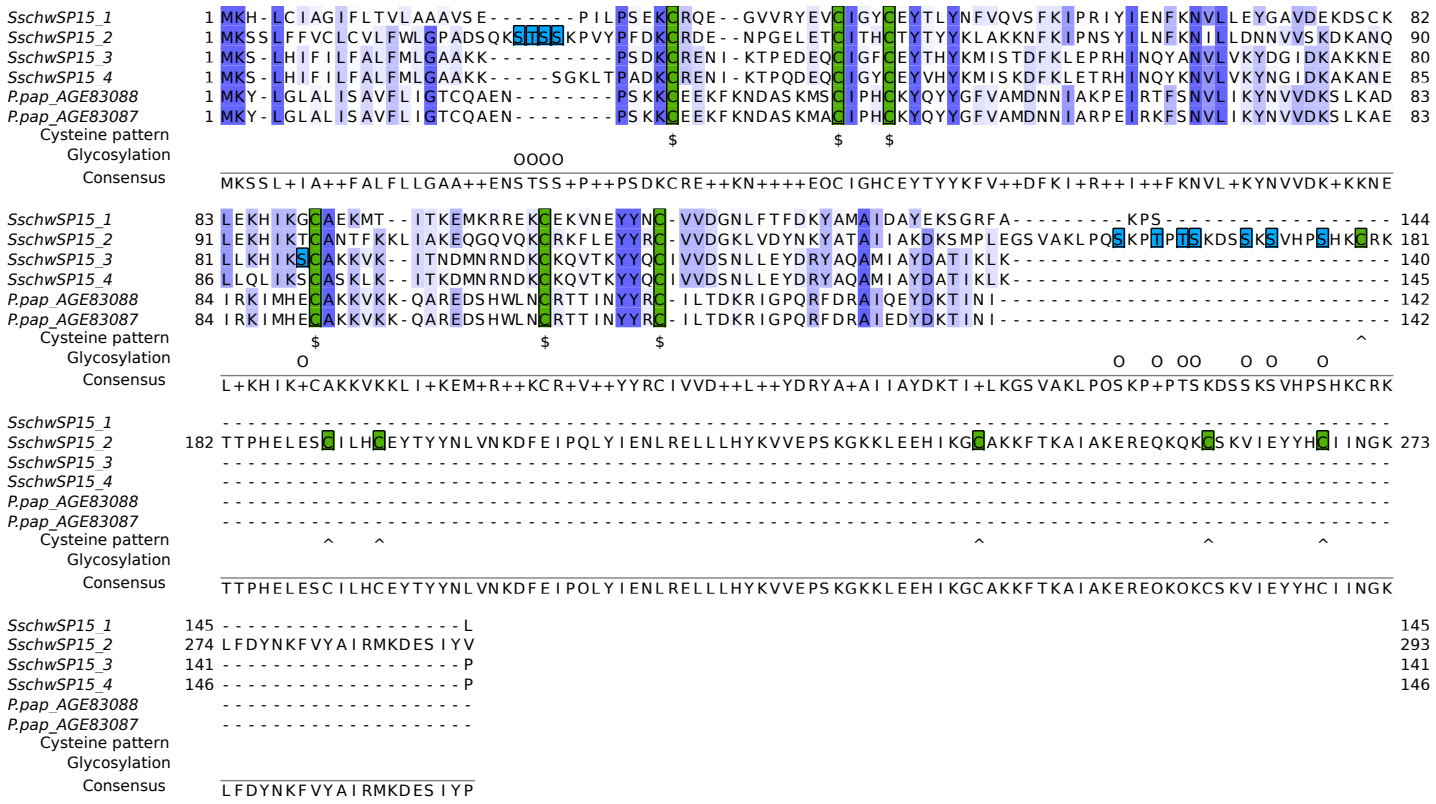
Multiple sequence alignment of *S. schwetzi* lufaxin proteins with chosen sand flies' lufaxin proteins. Name of sequence include sand fly species shortcut (P.tob – *P. tobbi*, P.ser – *P. sergenti*, P.per – *P. perniciosus*, P.ari – *P. ariasi*, P.ara – *P. arabicus*, P.pap – *P. papatasi*, P.dub – *P. duboscqi*, P.arg – *P. argentipes*, L.lon – *L. longipalpis*, L.int – *L. intermedia*, L.aya – *L. ayacuchensis*, L.olm – *L. olmeca*, L.nei – *L. neivai*) and GenBank accession number. Sequence conservation is depicted by shading of purple color. Conserved cysteines residues are highlighted in green, putative glycosylation sites in SschwLuf sequences are highlighted in blue. Lines below the alignment indicates conserved cysteines residues by "$", glycosylation by "N" for N-glycosylation and by "O" for O-glycosylation and consensus sequence. Alignment was made by MAFFT with L-INS-i method and visualized in Jalview.

S5 Fig. Multiple sequence alignment of sand flies' D7-related proteins



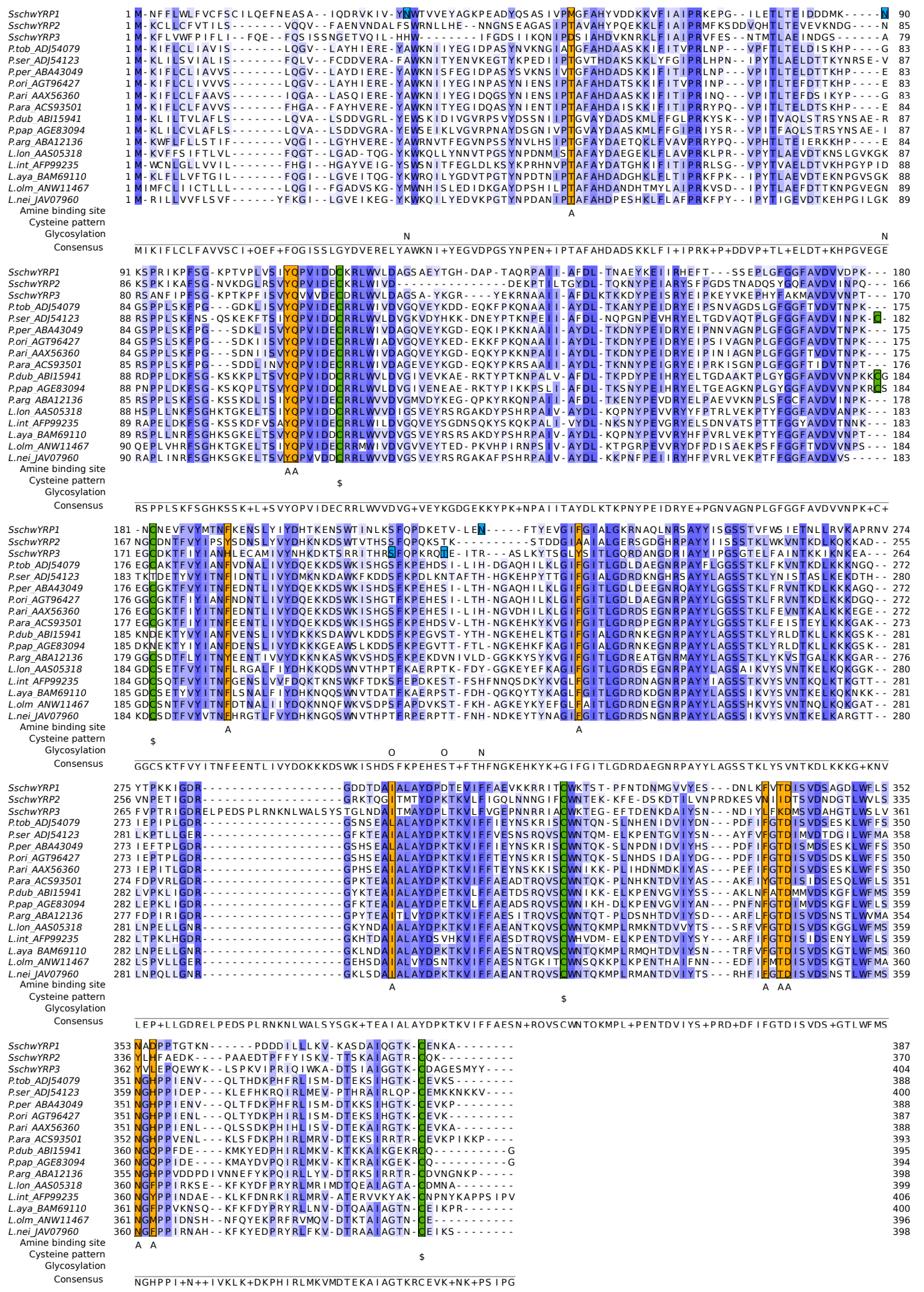
Multiple sequence alignment of *S. schwetzi* D7-related proteins with chosen sand flies' D7-related proteins. Name of sequence include sand fly species shortcut (P.tob – *P. tobbi*, P.ser – *P. sergenti*, P.per – *P. perniciosus*, P.ori – *P. orientalis*, P.ari – *P. ariasi*, P.ara – *P. arabicus*, P.pap – *P. papatasi*, P.dub – *P. duboscqi*, P.arg – *P. argentipes*, L.lon – *L. longipalpis*, L.int – *L. intermedia*, L.aya – *L. ayacuchensis*, L.olm – *L. olmeca*, L.nei – *L. neivai*) and GenBank accession number. Sequence conservation is depicted by shading of purple color. Conserved cysteines residues are highlighted in green, putative glycosylation sites in SschwD7 sequences are highlighted in blue. Lines below the alignment indicates conserved cysteines residues by "$", glycosylation by "N" for N-glycosylation and by "O" for O-glycosylation and consensus sequence. Alignment was made by MAFFT with L-INS-i method and visualized in Jalview.

S6 Fig. Multiple sequence alignment of *S. schwetzi* PpSP15-like proteins



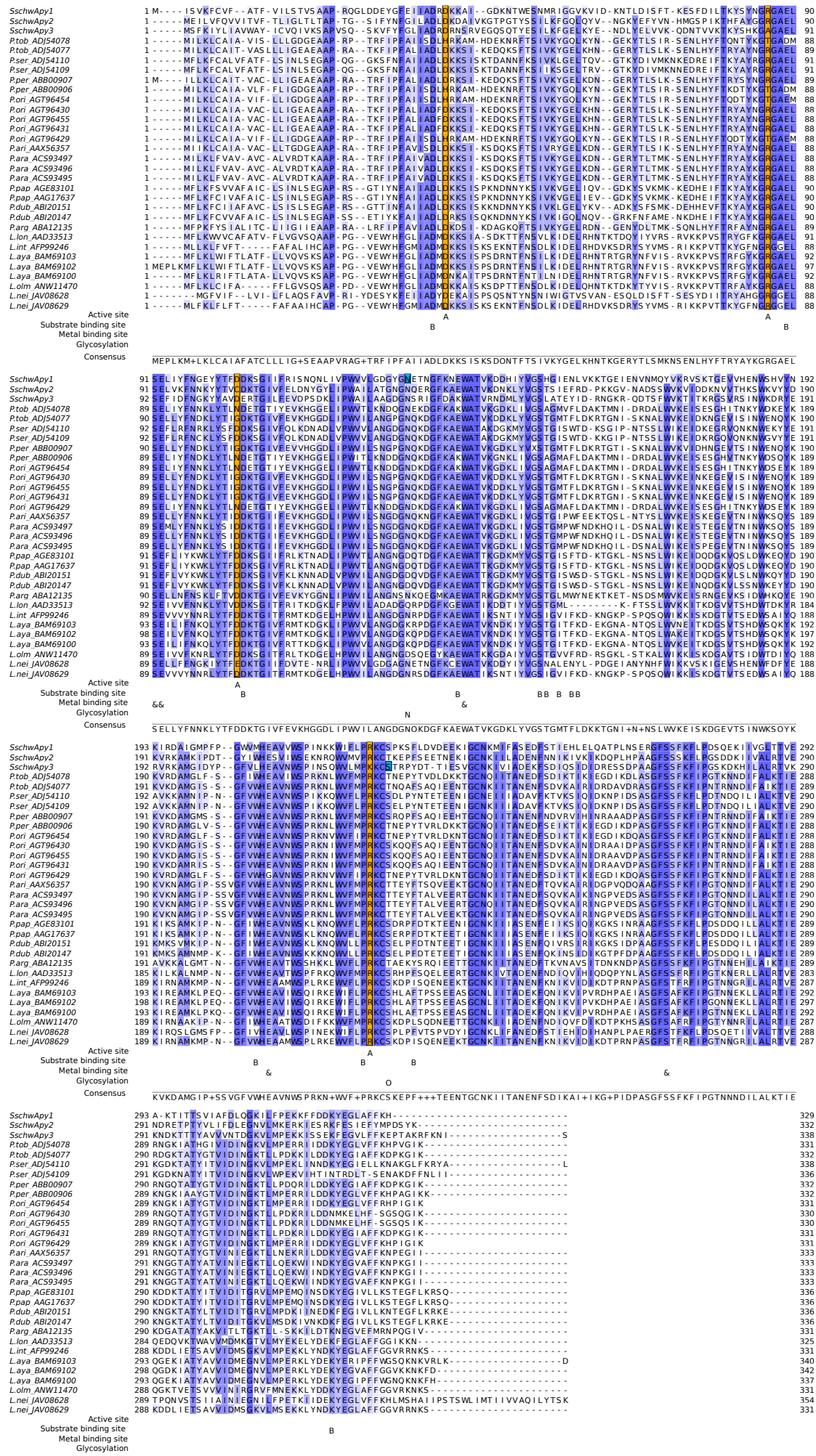
Multiple sequence alignment of *S. schwetzi* PpSP15-like proteins with two chosen *P. papatasi* SP15-like proteins. Name of sequence include sand fly species shortcut (P.pap – *P. papatasi*) and GenBank accession number. Sequence conservation is depicted by shading of purple color. Conserved cysteines residues are highlighted in green, putative glycosylation sites in SschwSP15 sequences are highlighted in blue. Lines below the alignment indicates conserved cysteines residues by “$” and for SschwSP15_2 the duplication of cysteines motive by “^”, glycosylation by “O” for O-glycosylation and consensus sequence. Alignment was made by MAFFT with L-INS-i method and visualized in Jalview.

S7 Fig. Multiple sequence alignment of sand flies' yellow-related proteins



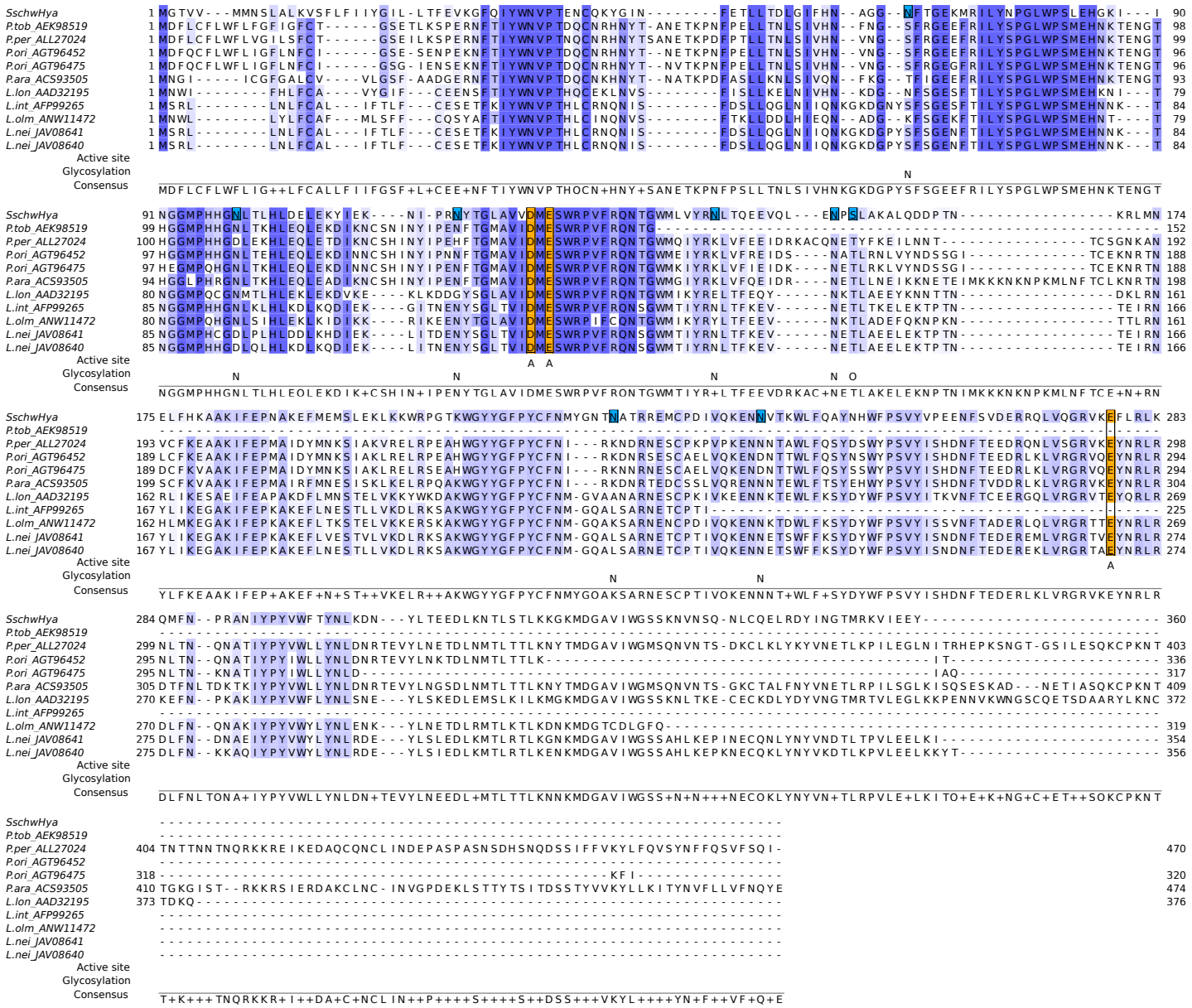
Multiple sequence alignment of *S. schwetzi* YRPs with chosen sand flies' YRPs. Name of sequence include sand fly species shortcut (P.tob – *P. tobbi*, P.ser – *P. sergenti*, P.per – *P. perniciosus*, P.ori – *P. orientalis*, P.ari – *P. ariasi*, P.ara – *P. arabicus*, P.pap – *P. papatasi*, P.dub – *P. duboscqi*, P.arg – *P. argentipes*, L.lon – *L. longipalpis*, L.int – *L. intermedia*, L.aya – *L. ayacuchensis*, L.olm – *L. olmeca*, L.nei – *L. neivai*) and GenBank accession number. Sequence conservation is depicted by shading of purple color. Conserved cysteines residues are highlighted in green, putative glycosylation sites in SschwYRPs sequences are highlighted in blue, putative amine binding residues are highlighted in orange. Lines below the alignment indicates amine binding site by "A", conserved cysteines residues by "$", glycosylation by "N" for N-glycosylation and by "O" for O-glycosylation and consensus sequence. Alignment was made by MAFFT with L-INS-i method and visualized in Jalview.

S8 Fig. Multiple sequence alignment of sand flies' apyrases



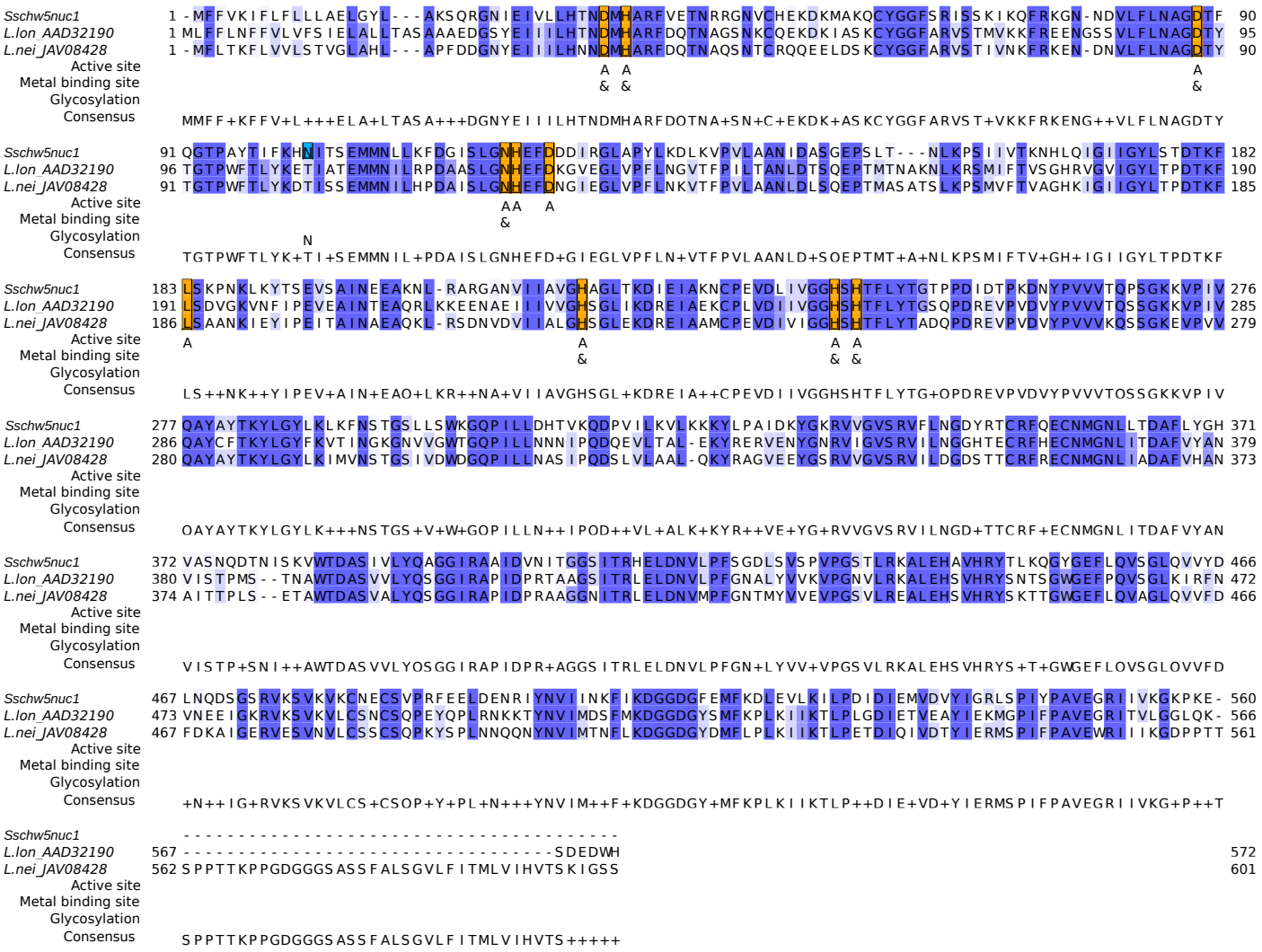
Multiple sequence alignment of *S. schwetzi* apyrases with chosen sand flies' apyrases. Name of sequence include sand fly species shortcut (P.tob – *P. tobbi*, P.ser – *P. sergenti*, P.per – *P. perniciosus*, P.ori – *P. orientalis*, P.ari – *P. ariasi*, P.ara – *P. arabicus*, P.pap – *P. papatasi*, P.dub – *P. duboscqi*, P.arg – *P. argentipes*, L.lon – *L. longipalpis*, L.int – *L. intermedia*, L.aya – *L. ayacuchensis*, L.olm – *L. olmeca*, L.nei – *L. neivai*) and GenBank accession number. Sequence conservation is depicted by shading of purple color. Active sites of enzyme are highlighted in orange, putative glycosylation sites in SschwApys sequence are highlighted in blue. Lines below the alignment indicates active site of enzyme by "A", metal binding site by "&", substrate binding site by "B", glycosylation by "N" for N-glycosylation and "O" for O-glycosylation and consensus sequence. Alignment was made by MAFFT with L-INS-i method and visualized in Jalview.

S9 Fig. Multiple sequence alignment of sand flies' hyaluronidases



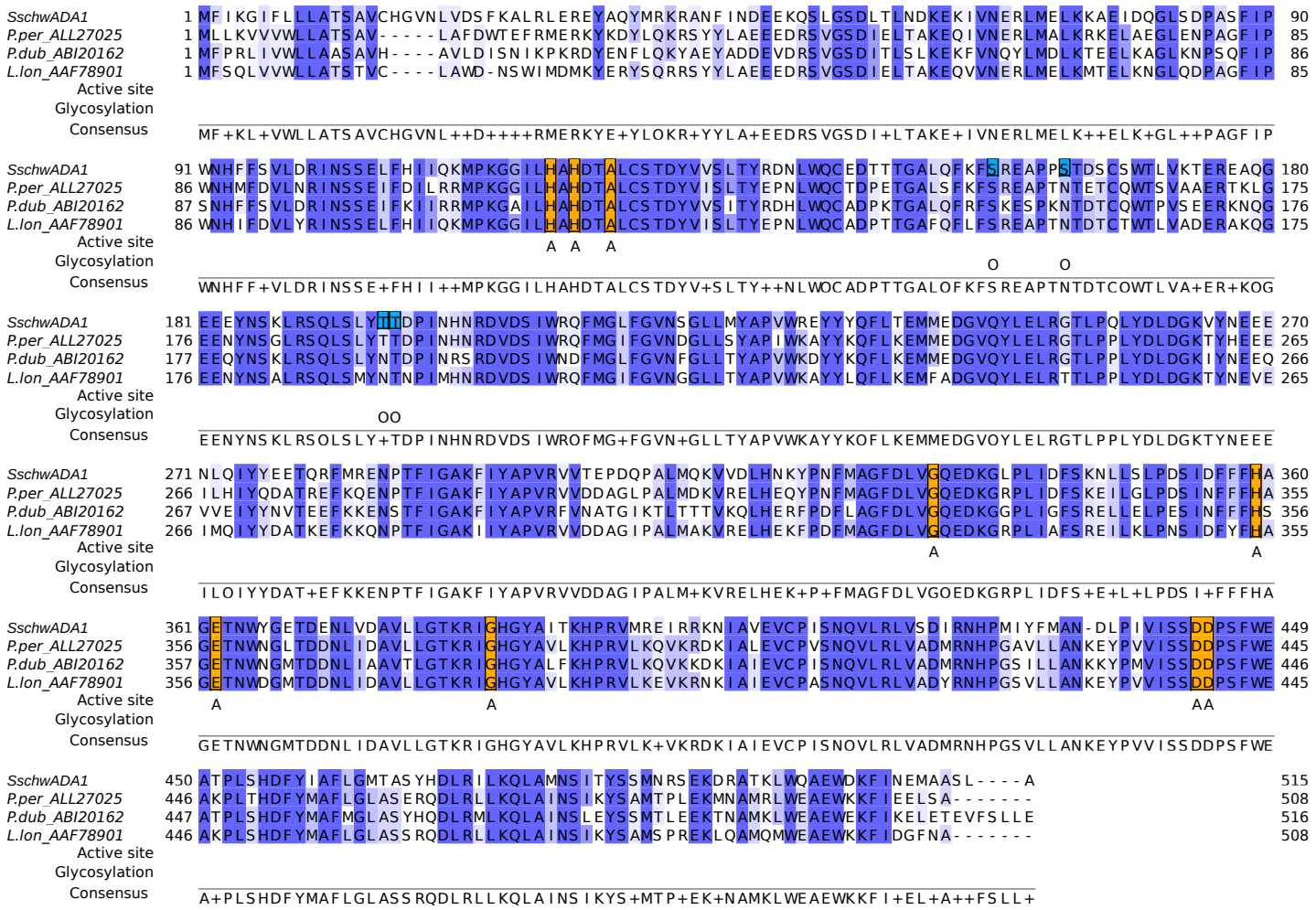
Multiple sequence alignment of *S. schwetzi* hyaluronidase with sand flies' hyaluronidases. Name of sequence include sand fly species shortcut (P.tob – *P. tobbi*, P.per – *P. perniciosus*, P.ori – *P. orientalis*, P.ara – *P. arabicus*, L.lon – *L. longipalpis*, L.int – *L. intermedia*, L.olm – *L. olmeca*, L.nei – *L. neivai*) and GenBank accession number. Sequence conservation is depicted by shading of purple color. Active sites of enzyme are highlighted in orange, putative glycosylation sites in SschwHya sequence are highlighted in blue. Lines below the alignment indicates active site of enzyme by "A", glycosylation by "N" for N-glycosylation and "O" for O-glycosylation and consensus sequence. Alignment was made by MAFFT with L-INS-i method and visualized in Jalview.

S10 Fig. Multiple sequence alignment of sand flies' 5'-nucleotidases



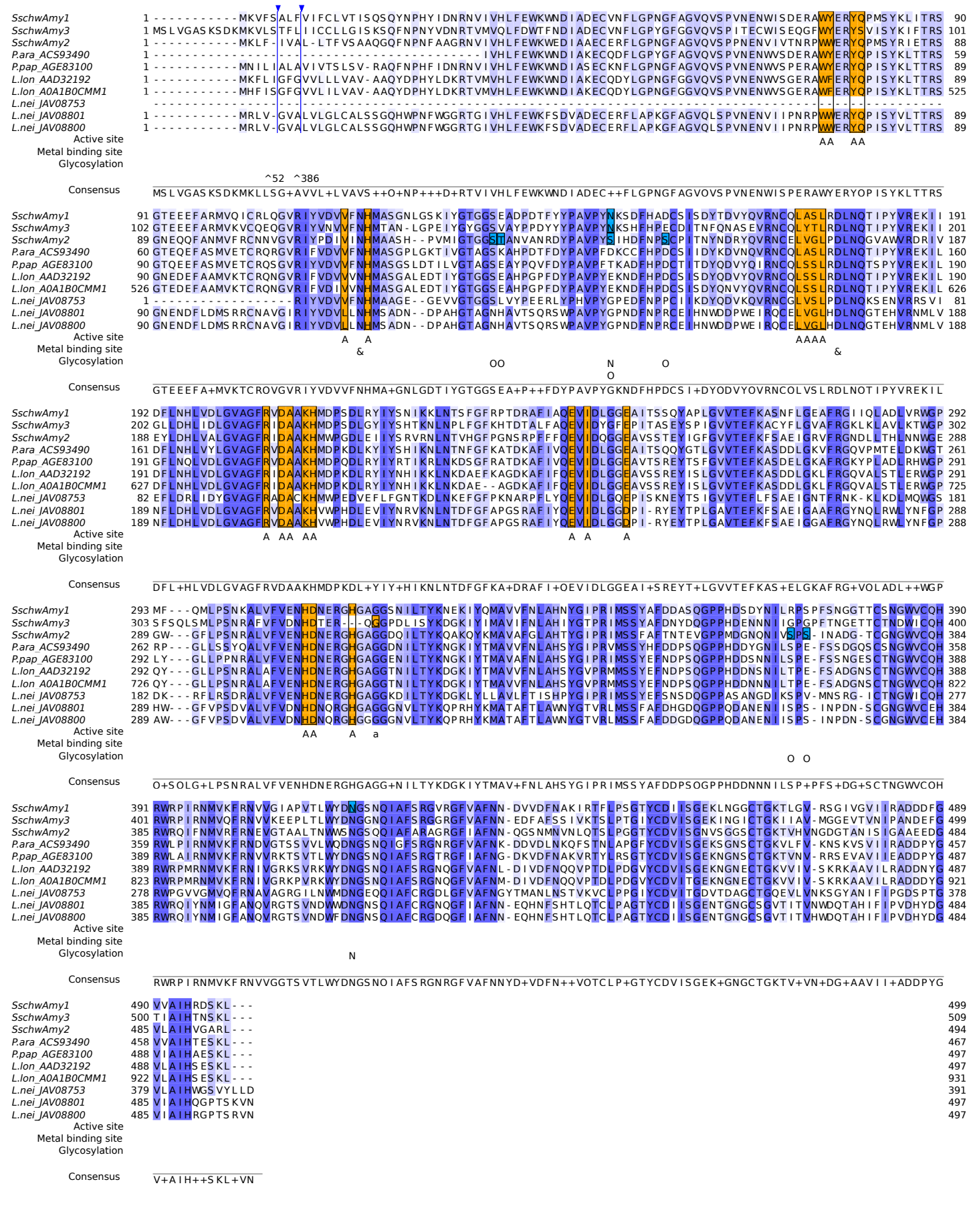
Multiple sequence alignment of *S. schwetzi* 5'-nucleotidase with other sand flies' 5'-nucleotidases. Name of sequence include sand fly species shortcut (L.lon – *L. longipalpis*, L.nei – *L. neivai*) and GenBank accession number. Sequence conservation is depicted by shading of purple color. Active sites of enzyme are highlighted in orange, putative glycosylation sites in Sschw5nuc sequence are highlighted in blue. Lines below the alignment indicates active site of enzyme by "A", metal binding site by "&", glycosylation by "N" for N-glycosylation and consensus sequence. Alignment was made by MAFFT with L-INS-i method and visualized in Jalview.

S11 Fig. Multiple sequence alignment of sand flies' adenosine deaminases



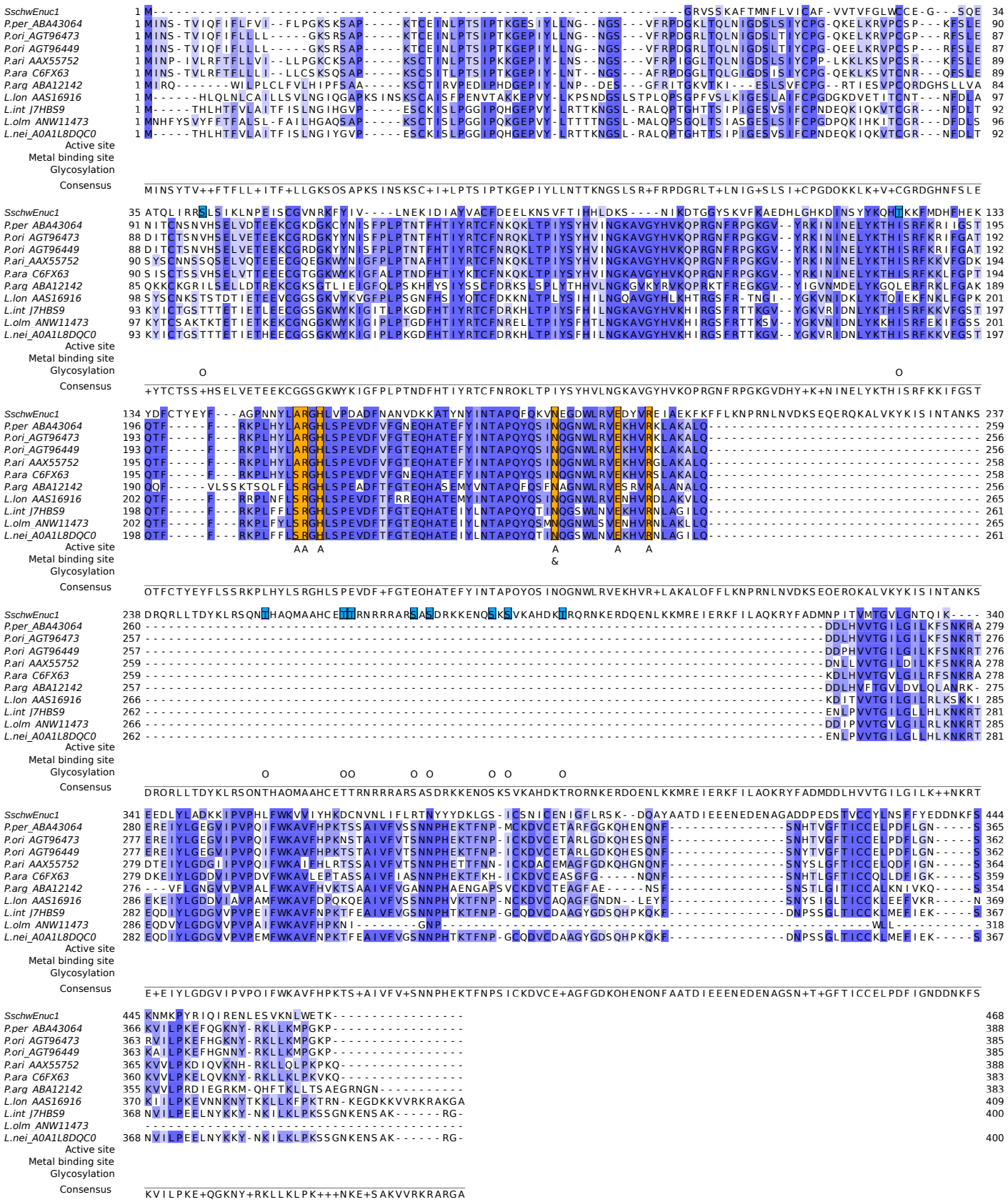
Multiple sequence alignment of *S. schwetzi* and other sand flies' adenosine deaminases. Name of sequence include sand fly species shortcut (P.per – *P. perniciosus*, P.dub – *P. duboscqi*, L.lon – *L. longipalpis*) and GenBank accession number. Sequence conservation is depicted by shading of purple color. Active sites of enzyme are highlighted in orange, putative glycosylation sites in SschwADA1 sequence are highlighted in blue. Lines below the alignment indicates active site of enzyme by "A", glycosylation by "O" for O-glycosylation and consensus sequence. Alignment was made by MAFFT with L-INS-i method and visualized in Jalview.

S12 Fig. Multiple sequence alignment of sand flies' amylases



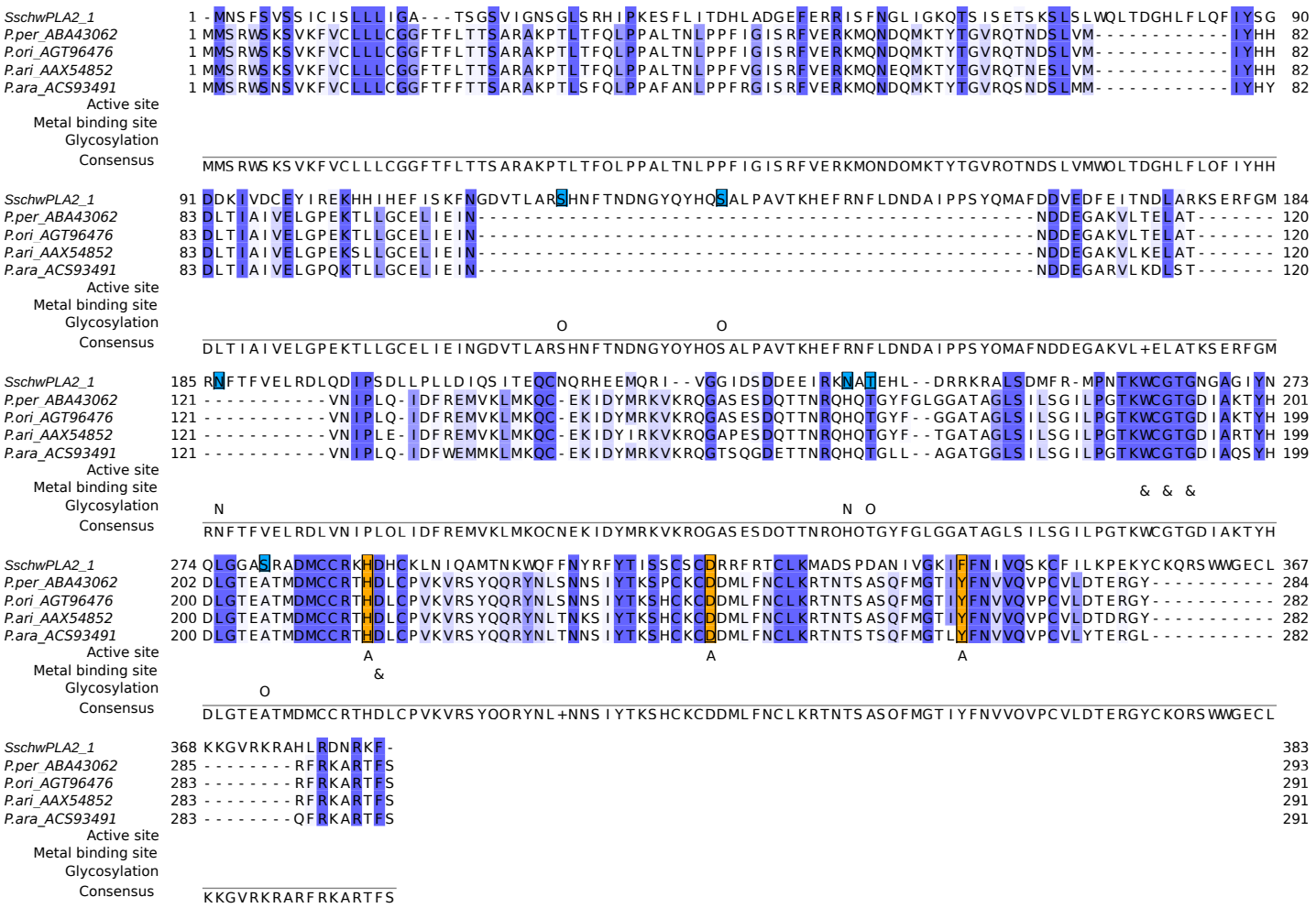
Multiple sequence alignment of *S. schwetzi* amylases and other sand flies' amylases. Name of sequence include sand fly species shortcut (P.ara – *P. arabicus*, P.pap – *P. papatasi*, L.lon – *L. longipalpis*, L.nei – *L. neivai*) and GenBank accession number or UniProtKB accession number. Sequence conservation is depicted by shading of purple color. Active sites of enzyme are highlighted in orange, putative glycosylation sites in SschwAmy sequences are highlighted in blue. Lines below the alignment indicates active site of enzyme by "A", metal binding site by "&", glycosylation by "N" for N-glycosylation and "O" for O-glycosylation and consensus sequence. For easier visualisation two parts of sequence *L. longipalpis* (A0A1B0CMM1) were hidden (highlighted by blue vertical lines with arrows, number of hidden aa is displayed below the alignment). Alignment was made by MAFFT with L-INS-i method and visualized in Jalview.

S13 Fig. Multiple sequence alignment of sand flies' endonucleases



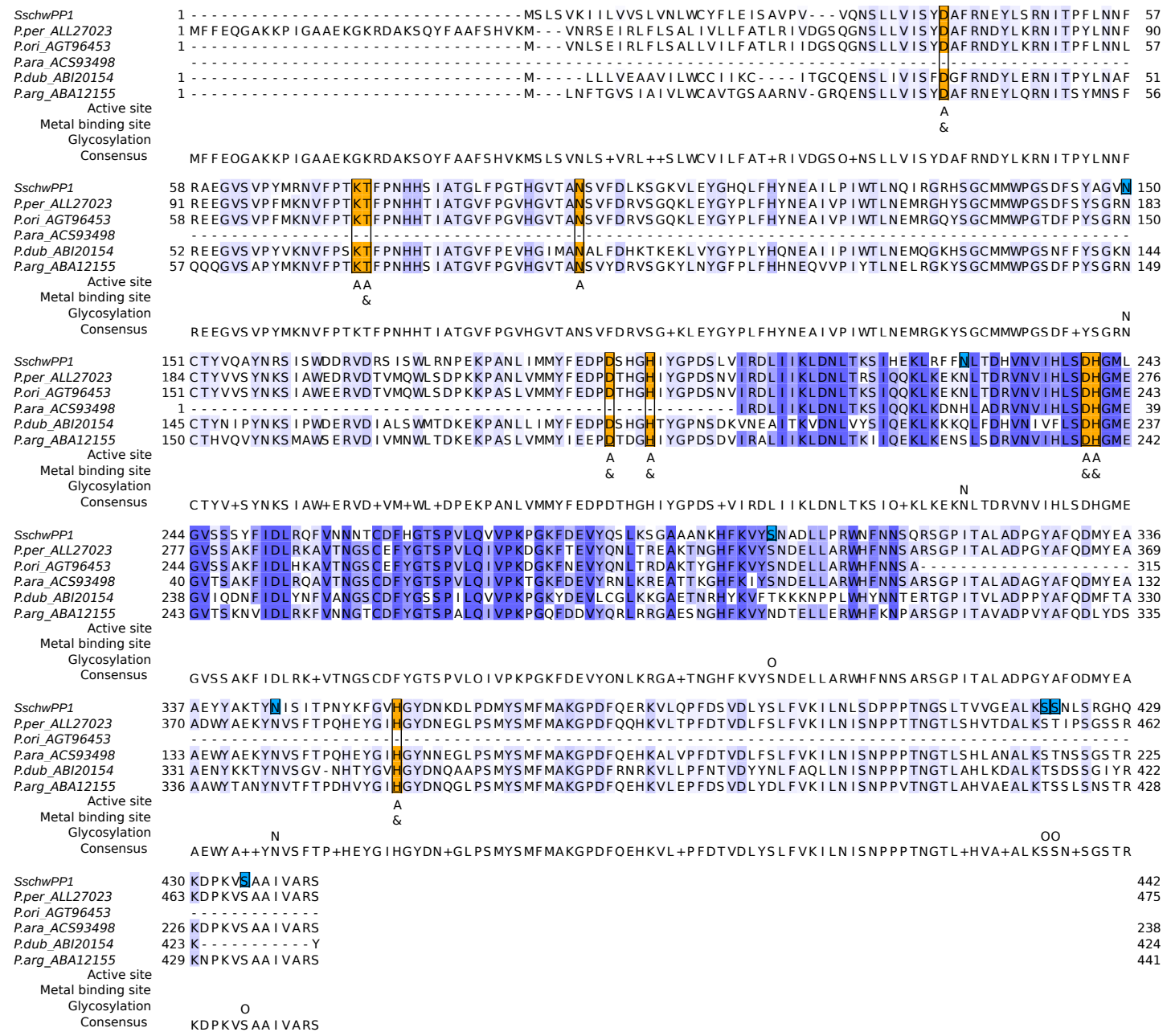
Multiple sequence alignment of *S. schwetzi* and other sand flies endonucleases. Name of sequence include sand fly species shortcut (P.per – *P. perniciosus*, P.ori – *P. orientalis*, P.ari – *P. ariasi*, P.ara – *P. arabicus*, P.arg – *P. argentipes*, L.lon – *L. longipalpis*, L.int – *L. intermedia*, L.olm – *L. olmeca*, L.nei – *L. neivai*) and GenBank accession number or UniProtKB accession number. Sequence conservation is depicted by shading of purple color. Active sites of enzyme are highlighted in orange, putative glycosylation sites in SschwEnuc1 sequence are highlighted in blue. Lines below the alignment indicates active site of enzyme by "A", metal binding site by "&", glycosylation by "O" for O-glycosylation and consensus sequence. Alignment was made by MAFFT with L-INS-i method and visualized in Jalview.

S14 Fig. Multiple sequence alignment of sand flies' phospholipases A2



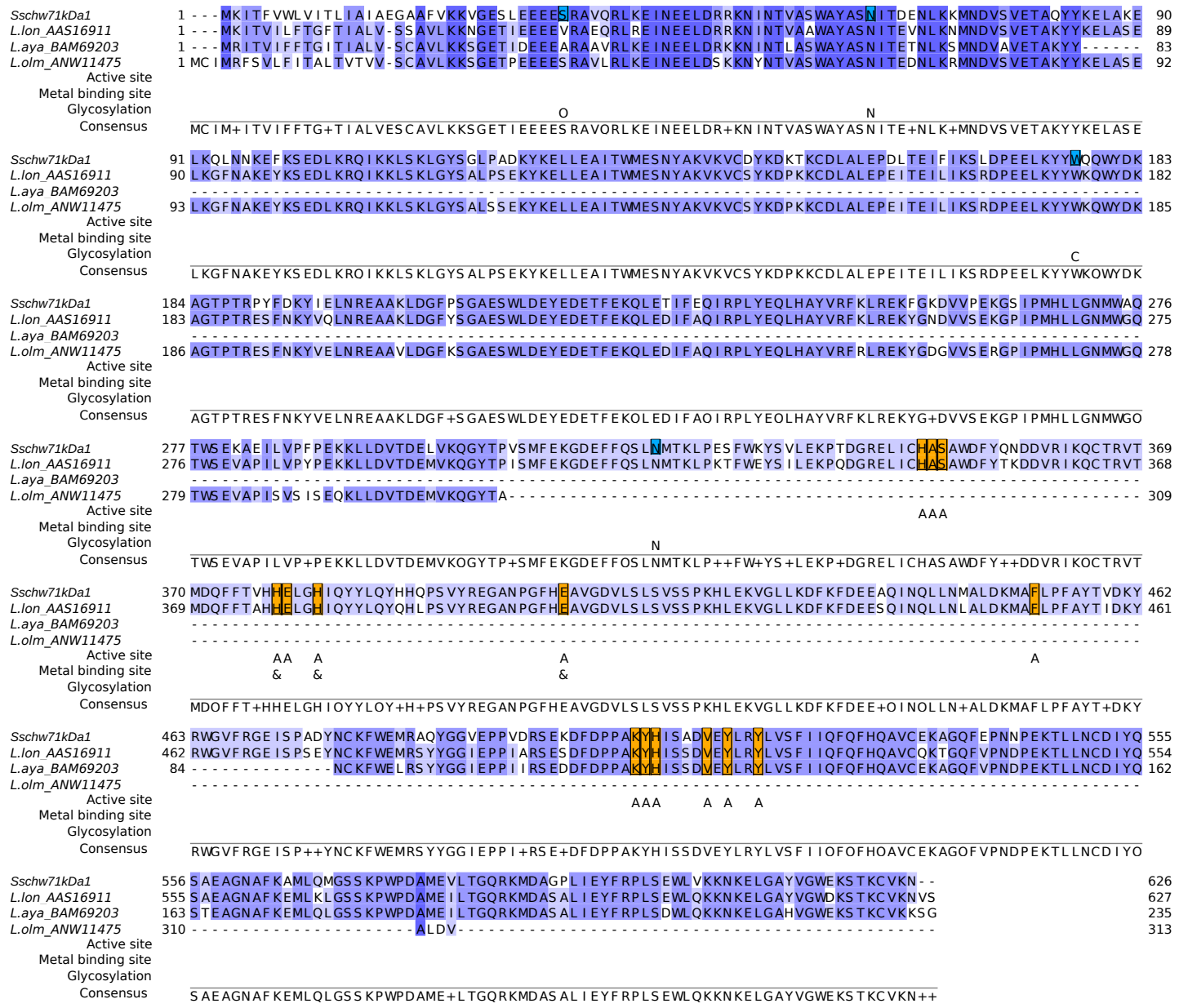
Multiple sequence alignment of *S. schwetzi* phospholipase A2 with other sand flies' phospholipases A2. Name of sequence include sand fly species shortcut (P.per – *P. perniciosus*, P.ori – *P. orientalis*, P.ari – *P. ariasi*, P.ara – *P. arabicus*) and GenBank accession number. Sequence conservation is depicted by shading of purple color. Active sites of enzyme are highlighted in orange, putative glycosylation sites in SschwPLA2_1 sequence are highlighted in blue. Lines below the alignment indicates active site of enzyme by "A", metal binding site by "&", glycosylation by "N" for N-glycosylation and "O" for O-glycosylation and consensus sequence. Alignment was made by MAFFT with L-INS-i method and visualized in Jalview.

S15 Fig. Multiple sequence alignment of sand flies' pyrophosphatases



Multiple sequence alignment of *S. schwetzi* pyrophosphatase with other sand flies pyrophosphatases. Name of sequence include sand fly species shortcut (P.per – *P. perniciosus*, P.ori – *P. orientalis*, P.ara – *P. arabicus*, P.dub – *P. duboscqi*, P.arg – *P. argentipes*) and GenBank accession number. Sequence conservation is depicted by shading of purple color. Active sites of enzyme are highlighted in orange, putative glycosylation sites in SschwPP1 sequence are highlighted in blue. Lines below the alignment indicates active site of enzyme by "A", metal binding site by "&", glycosylation by "N" for N-glycosylation and "O" for O-glycosylation and consensus sequence. Alignment was made by MAFFT with L-INS-i method and visualized in Jalview.

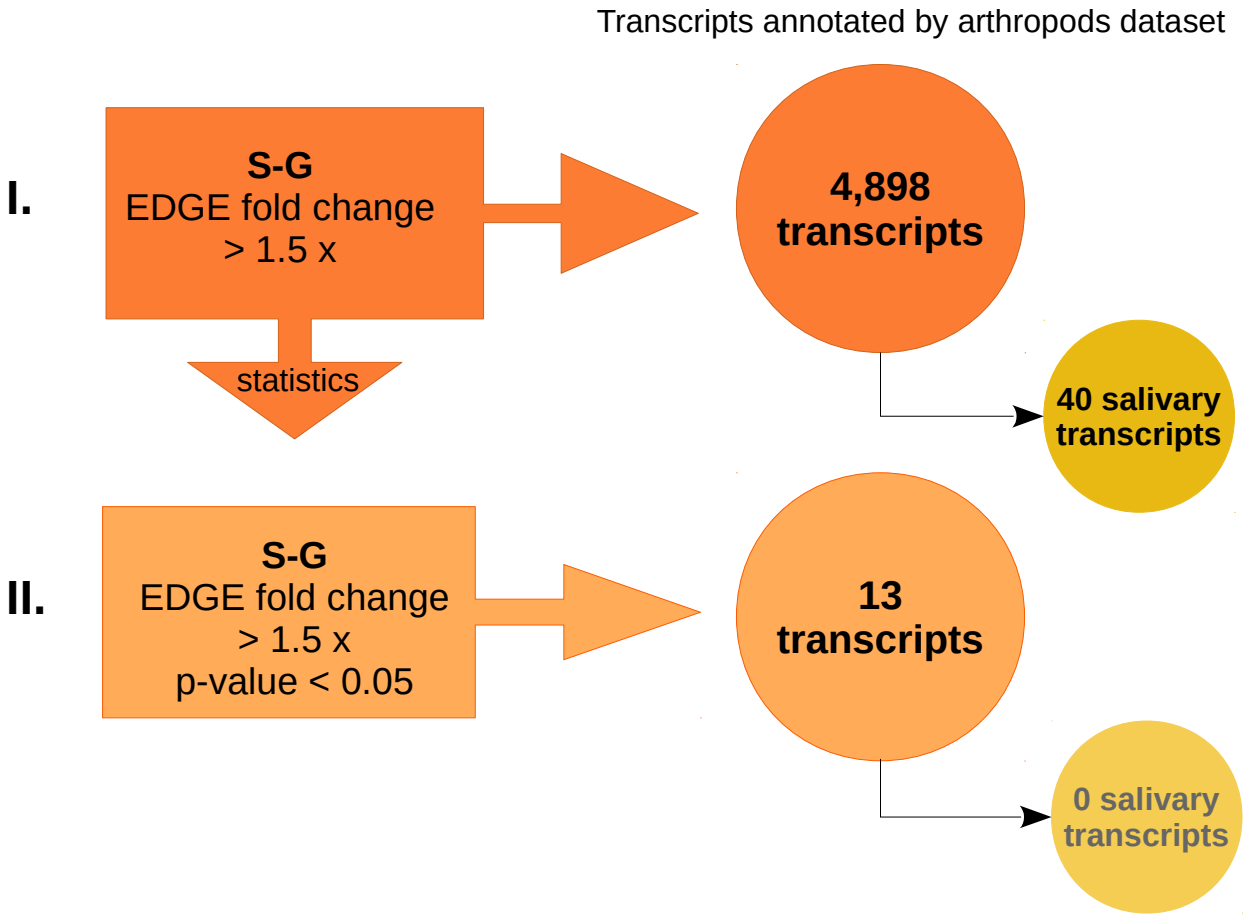
S16 Fig. Multiple sequence alignment of sand flies' 71 kDa-like proteins



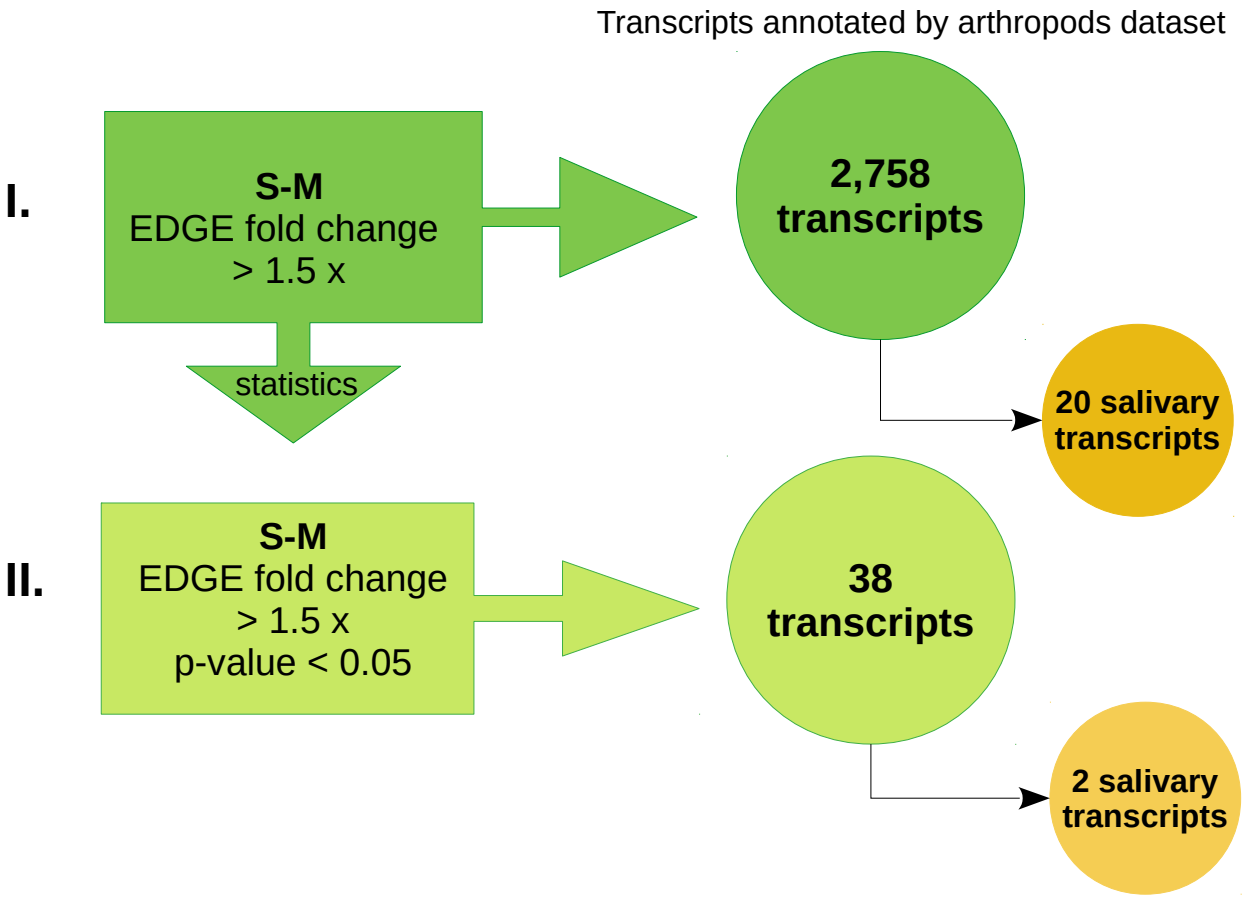
Multiple sequence alignment of S. schwetzi 71 kDa-like protein with other sand flies 71 kDa-like proteins. Name of sequence include sand fly species shortcut (L.lon – *L. longipalpis*, L.aya – *L. ayacuchensis*, L.olm – *L. olmeca*) and GenBank accession number or UniProtKB accession number. Sequence conservation is depicted by shading of purple color. Active sites of enzyme are highlighted in orange, putative glycosylation sites in Sschw71kDa1 sequence are highlighted in blue. Lines below the alignment indicates active site of enzyme by "A", metal binding site by "&", glycosylation by "N" for N-glycosylation, "O" for O-glycosylation, "C" for C-glycosylation and consensus sequence. Alignment was made by MAFFT with L-INS-i method and visualized in Jalview.

S17 Fig. RNA-seq transcriptome analysis of *S. schwetzi* salivary glands

A) Sand fly females fed on geckos (S-G lineage) transcripts up-regulation



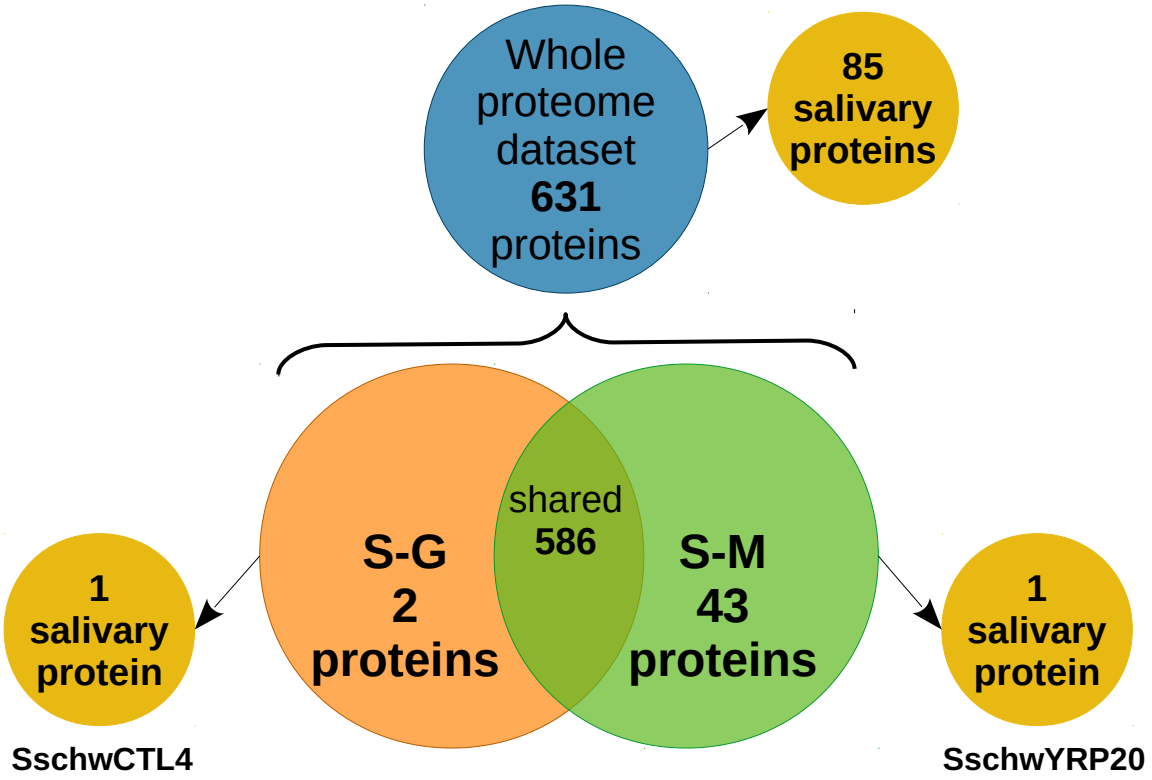
B) Sand fly females fed on mice (S-M lineage) transcripts up-regulation



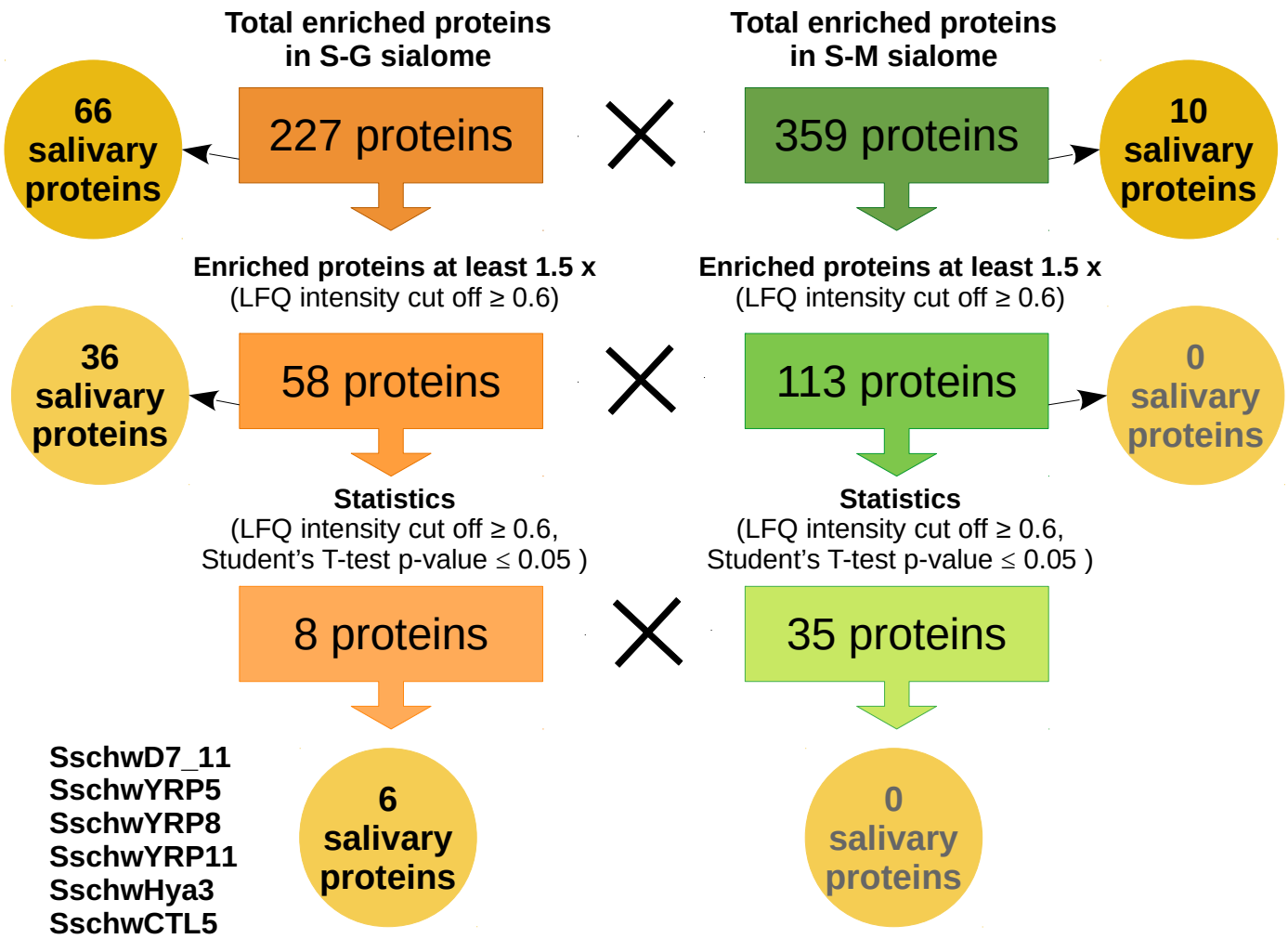
SschwSP15_5
SschwLuf3

S18 Fig. Proteome analysis of *S. schwetzi* salivary glands

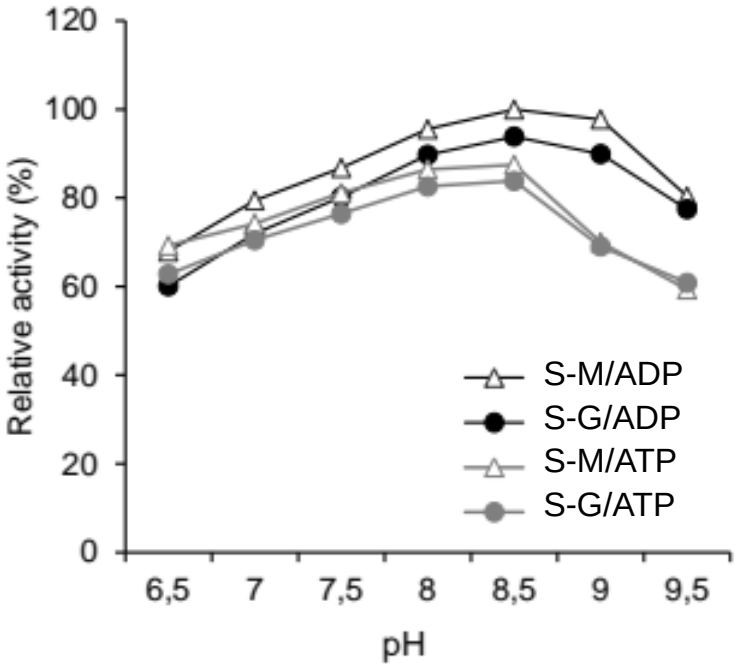
A) Distribution of the proteins from whole proteome dataset



B) Distribution of the enriched proteins either in S-G or S-M sialome



S19 Fig. Comparison of ATPase and ADPase activities and their pH optima in two *S. schwetzi* lineages



Comparison of ATPase and ADPase activities and their pH optima in two *S. schwetzi* lineages maintained on different blood-meal sources, geckos (S-G) and mice (S-M). Results represent the mean of five independent measurements.