Legends for supplemental figures

Fig. S1. Sequence alignment of Kazal domain-containing proteins from *Panstrongylus chinai* (Pc77 and Pc266) together with Kazal-type serine protease inhibitor-like protein from *Triatoma infestans* (accession number: ABR27896). Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment. Asterisks at the top of the amino acids denote conserved cysteine residues, and the Kazal domain is boxed.

Fig. S2. Sequence alignment of hemolysin-like proteins from *Panstrongylus chinai* (Pc60 and Pc61) together with hemolysin-like secreted salivary protein 1 from *Triatoma infestans* (accession number: ABR27902). Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment.

Fig. S3. (A) Sequence alignment of inositol polyphosphate 5-phosphatase (IP5P)-like proteins from *Panstrongylus chinai* (Pc24, Pc29, Pc31 and Pc32) together with IP5P-like protein from *Triatoma infestans*. Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment. Asterisks at the top of the amino acids denote conserved cysteine residues. (B) Phylogenetic tree analysis of IP5P-like protein from *P. chinai* (Pc24, Pc29, Pc31 and Pc32) together with IP5P-like protein from *T. infestans* (accession number: ABR27973). The numbers in parentheses indicate the number of transcripts of each contig. The scale bar represents 0.1 % divergence.

Bootstrap values are shown above branches.

Fig. S4. (A) Sequence alignment of antigen 5-related proteins from *Panstrongylus chinai* (Pc80 and Pc294) together with antigen 5-related proteins from various arthropods, *Triatoma infestans* (accession number: ABR27897), *T. dimidiata* (BAI50822), *Rhodnius prolixus* (AAQ20832), *Phlebotomus argentipes* (ABA12137), *P. duboscqi* (ABI20191), *Lutzomyia longipalpis* (AAD32191), *Drosophila melanogaster* (NP_650264), *Anopheles sinensis* (KFB42901), *Aedes aegypti* (EAT35709), *Apis mellifera* (XP_001122516), *Vespula vidua* (Q05110) and *Solenopsis invicta* (P35778). Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment. Asterisks at the top of the amino acids denote conserved cysteine residues. (B) Phylogenetic tree analysis of antigen 5-related proteins from *P. chinai* (Pc80 and Pc294) together with antigen 5-related proteins from various arthropods. The number in a parenthesis indicates the number of transcript of each contig. The scale bar represents 0.1 % divergence. Bootstrap values are shown above or below branches.

Fig. S5. Sequence alignment of a trypsin-like protein from *Panstrongylus chinai* (Pc97) together with a trypsin-like protein from *Triatoma infestans* (accession number: ABR27829) and a serine protease from *Creontiades dilutus* (AAL15154). Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment. Asterisks at the top of the amino acids denote conserved cysteine residues.

Fig. S6. Sequence alignment of a heme-binding protein-like from *Panstrongylus chinai* (Pc237) together with a heme-binding protein-like *Triatoma dimidiata* (accession number: BAI53116). Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment.