

Figure S1. (A) Aqueous and (B) detergent phase protein fractions from TX-114 extractions of *T. orientalis* Ikeda, Chitose and Buffeli piroplasms were electrophoresed on a 12% Tris-glycine one-dimensional SDS polyacrylamide gel. Lane 1 – PageRuler™ Prestained protein ladder (ThermoFisher Scientific); Lane 2 – *T. orientalis* protein sample. Bands from each protein sample were excised into 8-12 gel slices as indicated on the righthand side of the lane prior to processing for LC-MS/MS.

	450	460															470										480									
T.orientalis ATP-PFK	V	K	T	V	T	E	L	E	L	D	G	L	I	I	V	G	G	D	G	S	N	S	N	A	A	N	I	S	N	Y	L	A	P			
T.annulata ATP-PFK	L	K	T	V	T	E	L	E	L	D	G	L	I	I	V	G	G	D	G	S	N	S	N	A	A	N	I	S	N	Y	L	A	Q			
T.parva ATP-PFK	L	K	T	V	T	E	L	E	L	D	G	L	I	I	V	G	G	D	G	S	N	S	N	A	A	N	I	A	N	Y	L	A	Q			
T.gondii PPI-PFK	L	E	I	C	E	K	L	Q	L	N	G	L	V	V	I	G	G	D	D	S	N	T	N	A	A	I	L	A	E	Y	F	K	S			
C.parvum PPI-PFK	L	E	I	C	E	K	L	K	L	H	G	L	V	V	I	G	G	D	D	S	N	T	N	A	A	V	L	A	E	Y	F	K	R			

Figure S2. Alignment of phosphofructokinase sequences from representative apicomplexans showing the substrate-binding motif GGDG/D (boxed) which is associated with use of ATP or PPi for activity. *T. orientalis* PFK is predicted to be ATP-dependent.

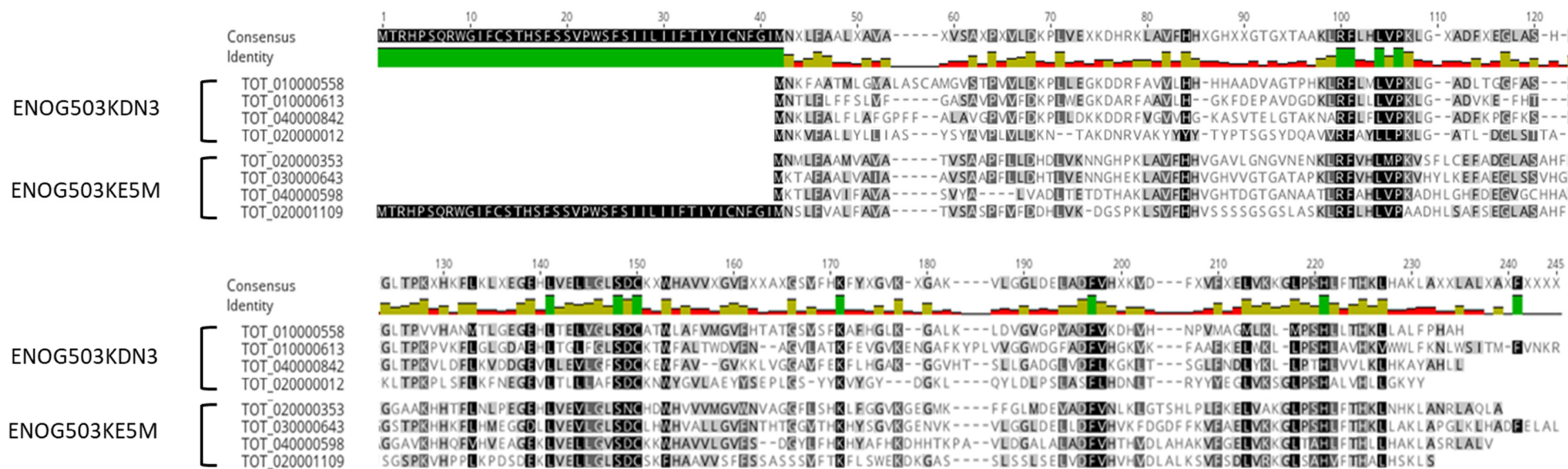


Figure S3. Alignment of uncharacterised aqueous phase proteins found to be highly abundant in the *T. orientalis* Ikeda piroplasm phase. These proteins are all orthologs and cluster into two phylogenetic groups according to EggNOG (ENOG503KDN3 and ENOG503KE5M).