Supplementary Table S3. Overview of sequences used for bait capture of target gene groups and baited sequences (hits) with annotations. Heat shock protein sequences can be accessed using the protein IDs (Aguoru et al. 2022) at *UniProt* (Bateman et al. 2023). Annotations were inferred from *PANNZER2* (Törönen & Holm 2022) (see Fig. 2).

Bait sequence				**Hits**		**Annotations**
Name	Family	Species	*GenBank* Accession	Protein ID (*C. casuarinus*)	*HybPiper*	Description
Cytochrome P450 (CYP)		*Schistosoma mansoni* *Opisthorchis felineus* *Echinococcous multilocularis*		—	—	—
Glutathione peroxidase (GPx)		*S. mansoni*	Q00277.2	XXXXX	Group 1: all but *K. limnotrissae*	Glutathione peroxidase
				XXXXX	Group 2: all	Glutathione peroxidase
Glutathione *S*-transferase (GST)	Microsomal (MGST)	*E. multilocularis*	CDS61239	XXXXX	All	Microsomal glutathione S-transferase 3
	Alpha-class (GSTA)	*Ciona intestinalis*	XP_002119784.1 XP_002120526.1 XP_009861494.1	—	—	—
	Zeta-class (GSTZ)	*Clonorchis sinensis*	GAA48819.1	XXXXX	All but *K. limnotrissae*	Maleylacetoacetate isomerase
	Mu-class (GSTM)	*E. multilocularis*	CDS58059.1 CDS58060.1 CDS58083.1 CAA59739.1	XXXXX	Group 1: all	Glutathione S-transferase class-mu 26 kDa isozyme
			CDS58090.2 CDS58091.1 CDS58092.1	XXXXX XXXXX XXXXX	Group 2a: *Cichlidogyrus* spp. without *C. sclerosus*	Glutathione transferase
			CDS58086.2 CDS58094.2 CDI96481.2		Group 2b: all	Glutathione transferase
	Pi-class (GSTP)	*Homo sapiens* *Danio rerio*	NP_000843.1 NP_001156323.1	—	—	—
	Sigma-class (GSTS)	*E. multilocularis*	CDS59356.1 CDS57347.1	—	—	—
		C. sinensis	GAA52095.1 GAA33791.2 AAD17488.1 GAA54850.1 GAA54851.1	—	—	—
	Omega-class (GSTO)	*C. sinensis*	GAA51230.1 GAA51230.1	XXXXX	*Cichlidogyrus* spp.	unknown
				XXXXX	*Cichlidogyrus* spp.	unknown
	Mitochondrial kappa-class (GSTK)	*C. sinensis*		—	—	—
Peroxiredoxin (Prx)	1	*S. mansoni*	AAD17299.1	XXXXX		Peroxiredoxin
	2	*S. mansoni*	XP_018645129.1	—	—	—
	3	*S. mansoni*	AAG15506.1	XXXXX		Thioredoxin-dependent peroxide reductase, mitochondrial

Superoxide dismutase (SOD)	Cu-Zn	*S. mansoni*	Q01137.1	XXXXX		Superoxide dismutase [Cu-Zn]
	Mn	*Schistosoma japonicum*	AAW26480.1	XXXXX		Superoxide dismutase
Thioredoxin glutathione reductase (TGR)		*S. mansoni*	XP_018649018.1	XXXXX		thioredoxin-disulfide reductase
Heat shock protein 10 kDa		*S. mansoni*	XP_018653498.1	XXXXX		10 kDa heat shock protein, mitochondrial
Heat shock protein 40 kDa	31 members	*S. mansoni*	see Aguoru et al. (2022)	XXXXX	Group 1	DnaJ homolog subfamily A member 1
				XXXXX	Group 2	Tumorous imaginal discs, mitochondrial
				XXXXX	Group 3	DnaJ heat shock protein family (Hsp40) member B4
				XXXXX	Group 4	J domain-containing protein
				XXXXX	Group 5	DnaJ-like protein subfamily B member 8
				XXXXX	Group 6	DnaJ heat shock protein family (Hsp40) member B14
				XXXXX	Group 7	DnaJ homolog shv/DnaJ homolog subfamily B member 11
				XXXXX	Group 8	unknown
				XXXXX	Group 9	DnaJ homolog subfamily C member 1
				XXXXX	Group 10	DnaJ homolog subfamily C member 2
				XXXXX	Group 11	DnaJ homolog subfamily C member 3/putative dsrna-activated protein kinase inhibitor p58
				XXXXX	Group 12	DnaJ heat shock protein family (Hsp40) member C7
				XXXXX	Group 13	DnaJ homolog subfamily C member 8
				XXXXX	Group 14	DnaJ homolog subfamily C member 9
				XXXXX	Group 15	Mitochondrial import inner membrane translocase subunit TIM14
				XXXXX	Group 16	unknown
				XXXXX	Group 17	DnaJ subfamily C member 17
				XXXXX	Group 18	DnaJ sub C member 27, variant 2
Heat shock protein 60 kDa	HSP60	*S. mansoni*	XP_018645622.1	XXXXX		Heat shock protein 60
Heat shock protein 70 kDa	HSPA9 protein-like	*S. mansoni*	see Aguoru et al. (2022)	XXXXX	Group 1: All except *C. halli* and *C.* sp. 'kapembwa'	Heat shock protein cognate 5
				XXXXX	Group 1bis: All except *C. halli* and *C.* sp. 'kapembwa'	Heat shock protein 70
	Hypoxia up-regulated protein 1 precursor-like	*S. mansoni*	see Aguoru et al. (2022)	XXXXX	Group HYOU1: All	Molecular chaperone grp170/sil1 *Hsp*70 superfamily protein + Hypoxia up-regulated protein 1
	Endoplasmic reticulum chaperone BiP precursor-like	*S. mansoni*	XP_018649109.1	XXXXX	Group BiP1: *Cichlidogyrus* spp. except *C. halli*	Heat shock 70 kDa protein cognate 3
				XXXXX	Group BiP2: *C. casuarinus* *C. halli* *S. longicornis*	Heat shock 70 kDa protein cognate 3
	Others (4 members)	*S. mansoni*	see (Aguoru et al. 2022)	XXXXX	Group 2:	Heat shock protein 70
				XXXXX	*C. casuarinus*	
				XXXXX	*C. halli*	
				XXXXX	*S. longicornis* *Kapentagyrus* spp.	

					Group 3: *C. casuarinus* *C. cirratus* *C. sclerosus* *C. thurstonae* *C. tilapiae* *C. zambezensis* *S. longicornis*	Heat shock protein 70
					Group 4a: All	Heat shock protein 70
					Group 4b: *Cichlidogyrus* spp.	Heat shock protein 70
Heat shock protein 90 kDa	HSP 90-alpha isoform 2-like	*S. mansoni*	see (Aguoru et al. 2022)	XXXXX	Group 1: all	Heat shock protein 83
				XXXXX	Group 2: all	Endoplasmin
	TRAP1-like	*S. mansoni*	XP_018652104.1	—	—	—
	Endoplasmin precursor-like	*S. mansoni*	see (Aguoru et al. 2022)	—	—	—
Aquaporins		*Caenorhabditis elegans*	NP_001024758.1 NP_001022480.1 NP_001021552.2 NP_508515.2 NP_505727.1 NP_505691.2 NP_505512.3 NP_502044.1 NP_499821.2 NP_496105.1 NP_495973.1 NP_495510.1	XXXXX		Aquaporin/Aquaporin-3
		S. mansoni	ACI31185.1	XXXXX		unknown
foraging (*for*)		*Drosophila melanogaster*	NP_001356955.1 NP_001356896.1	XXXXX	Group 1: all	cGMP-dependent protein kinase
			NP_001356892.1 NP_001334731.1 NP_001162858.1 NP_001014464.1 NP_995629.1 NP_995628.1 NP_995626.1 NP_599146.1 NP_477490.1 NP_477489.1 NP_477487.1	XXXXX	Group 2: all except *K. tanganicanus*	cGMP-dependent protein kinase