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Supplementary Information for

The esophageal gland mediates host immune evasion by the human parasite *Schistosoma mansoni*

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Movies S1 to S2

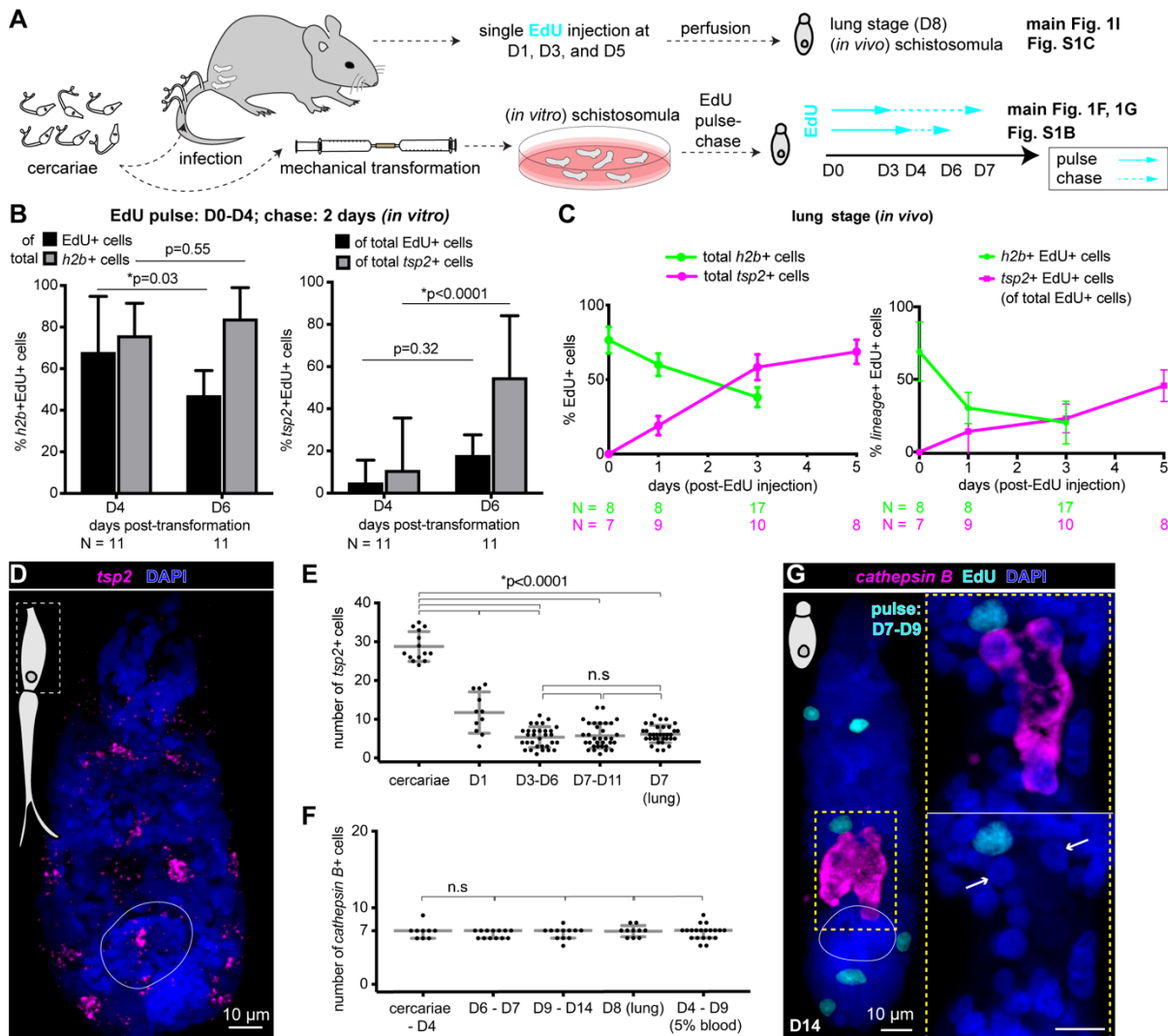


Fig. S1. Stem cell-driven differentiation of host-parasite interfaces in schistosomula. (A) Scheme of using mechanically transformed *in vitro* schistosomula and *in vivo* lung-stage schistosomula for EdU pulse-chase experiments. (B) Number of *h2b*+ EdU+ (left) and *tsp2*+ EdU+ (right) double-positive cells as percentages of total single-positive populations in *in vitro* schistosomula pulsed with EdU D0-D4 and chased until D6. Mean ± sd. Statistical analysis: Welch's t-test. (C) Number of *h2b*+ EdU+ (green) and *tsp2*+ EdU+ (magenta) cells as a percentage of total *h2b*+ or *tsp2*+ cells (left) or total EdU+ cells (right) from *in vivo* schistosomula. Mean ± sd. N: number of worms analyzed. (D) Expression of *tsp2* mRNA (marker of tegument progenitors) in cercaria, detected by FISH (maximum-intensity projection). (E) Quantification of *tsp2*+ cells from cercariae and schistosomula harvested at the indicated time points. Each dot represents a single worm. Mean ± sd. Statistical analysis: one-way ANOVA followed by Tukey's multiple comparisons test. (F) Quantification of *cathepsin B*+ cells from cercariae and schistosomula harvested at indicated time points. Each dot represents a single worm. Median with interquartile range shown. Statistical analysis: one-way ANOVA followed by Tukey's multiple comparisons test. (G) EdU pulse-chase experiment combined with FISH to detect *cathepsin B* mRNA in schistosomula that were pulsed with EdU from D7-D9 and chased until D14 (maximum-intensity projection). A magnified single confocal z-section of the boxed area is shown on the right with *cathepsin B* (top) and without *cathepsin B* (bottom). Arrows: *cathepsin B*+ cells.

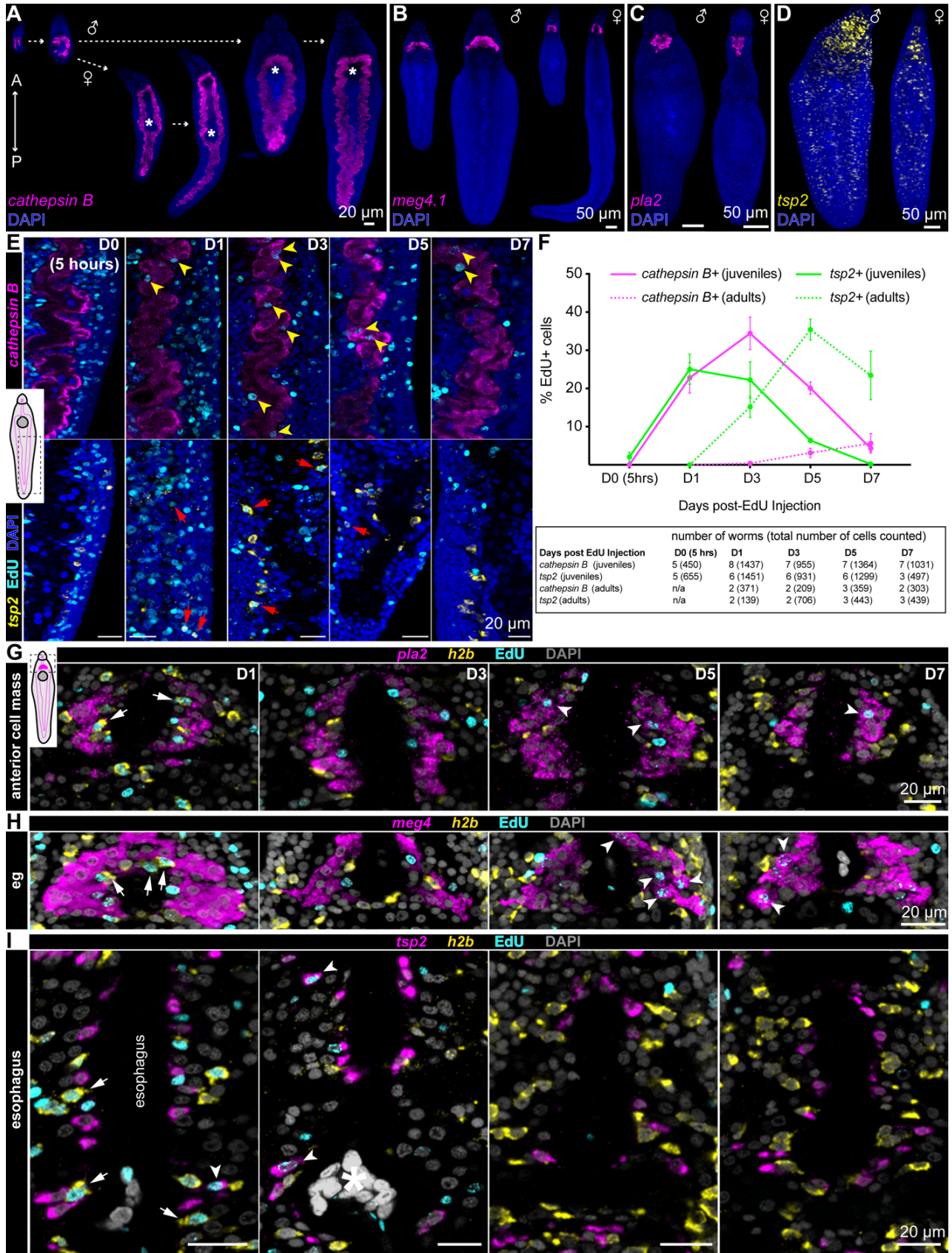


Fig. S2. Stem cell-driven development of host-parasite interfaces in juveniles. (A) Gut

development in juvenile schistosomes (3-weeks post-infection) as revealed by *cathepsin B* FISH (maximum-intensity projections). Different sizes represent different times of arrival at the hepatic portal vein, with the smallest arriving latest. Schistosomes first merge the two gut lobes in both male and female worms; branching patterns then diverge between males and females as they develop further. Asterisks: developing gonads. A: anterior; P: posterior. **(B-D)** Expression of cell type-specific markers by FISH in 3-week-old juvenile schistosomes (maximum-intensity projections): **(B)** *meg4.1* (esophageal gland); **(C)** *pla2* (esophageal anterior cell mass); and **(D)** *tsp2* (tegument progenitors). **(E-I)** EdU pulse-chase experiments in juvenile schistosomes. Parasites were harvested 3-weeks post-infection from mice that received a single EdU injection between 0-7 days prior to sacrifice. **(E)** *cathepsin B* (top) and *tsp2* (bottom) FISH in juvenile gut and tegument, respectively. Single confocal sections. Yellow arrowheads: *cathepsin B*⁺ EdU⁺ cells within the gut; red arrows: *tsp2*⁺ EdU⁺ cells near the tegument. **(F)** Quantification of *cathepsin B*⁺ EdU⁺ cells over total *cathepsin B*⁺ cells (magenta) and *tsp2*⁺ EdU⁺ cells over total *tsp2*⁺ cells (green) in juvenile parasites harvested from mice given a single EdU injection. Dotted lines indicate quantifications from adult worms for comparison to the juvenile worms. The numbers of worms and cells analyzed for each condition are listed in the box below. Mean \pm sd shown. **(G-I)** EdU incorporation and double FISH of *h2b* with **(G)** *pla2* (anterior cell mass), **(H)** *meg4.1*, or **(I)** *tsp2*, single confocal sections. Arrows: *h2b*⁺ EdU⁺ cells; arrowheads: *lineage*⁺ EdU⁺ cells; eg: esophageal gland. N=3-5 worms were analyzed for each condition.

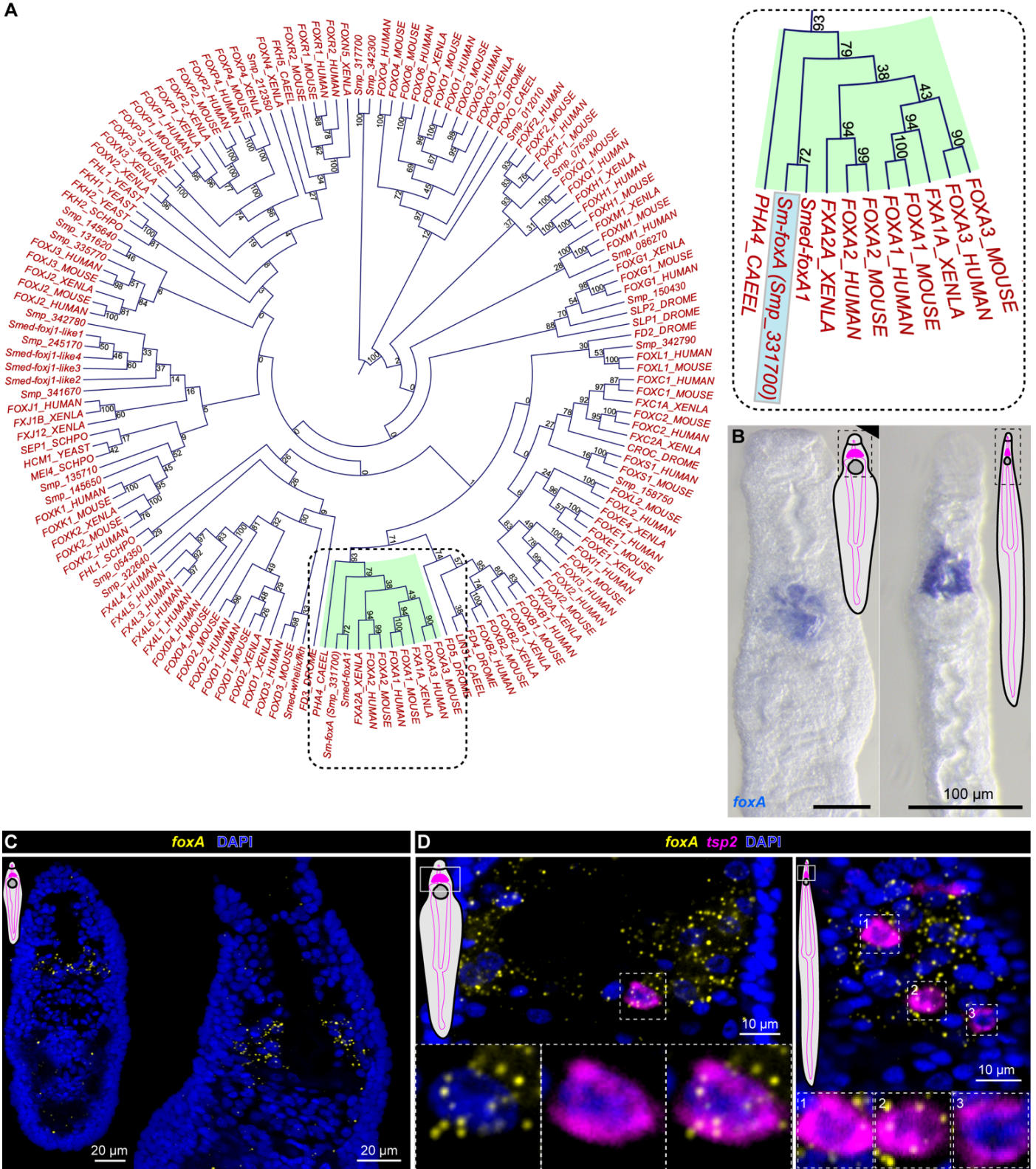


Figure S3. Phylogenetic analysis of *foxA* and its esophageal gland-enriched expression. (A) Circular cladogram including all forkhead domain-containing *S. mansoni* Fox proteins with forkhead domains of FOX proteins extracted from multiple species. Analyzed species include

human, mouse, *D. melanogaster* (DROME), *C. elegans* (CAEEL), *S. mediterranea* (Smed), *S. cerevisiae* (Yeast), *S. pombe* (SCHPO), *X. laevis* (XENLA), *X. tropicalis* (XENTR). The numbers before each branch indicate bootstrap value (%). Magnified view of the FOXA family is shown on the right. **(B)** Whole-mount *in situ* hybridization (WISH) of *foxA* in adult male (left) and female (right) worms. **(C)** *foxA* FISH in less developed (left) and more developed (right) juvenile schistosomes, single confocal sections. **(D)** Double FISH of *tsp2* and *foxA* in adult worms, showing co-localization of *foxA* with *tsp2*, a tegument progenitor marker (single confocal sections).

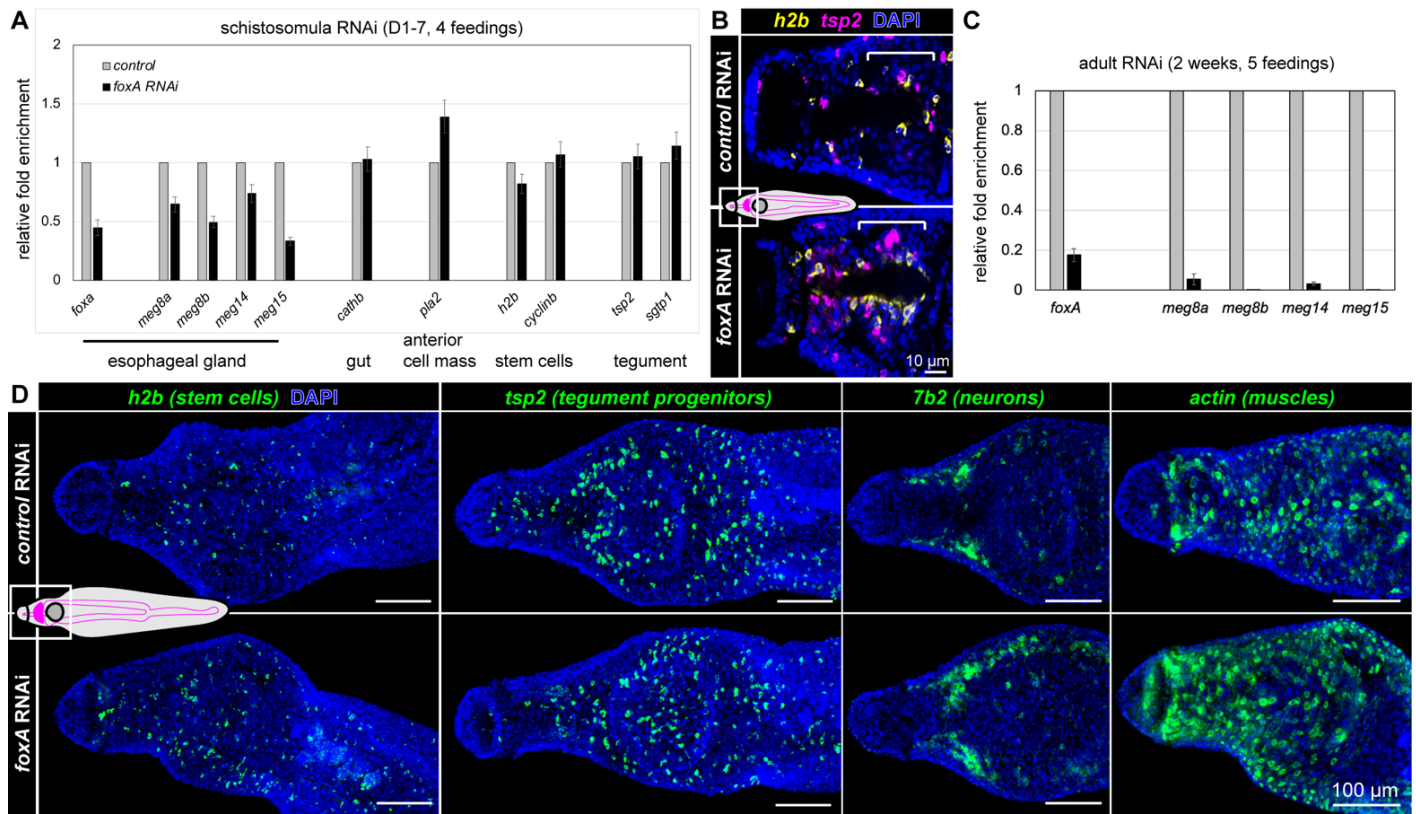


Figure S4. *foxA* RNAi results in esophageal gland loss, but other cell types are not affected. (A) qPCR analysis of schistosomula RNA collected after one week of exposure to *foxA* dsRNA. Genes known to be expressed in the esophageal gland, gut, tegument, and stem cells were tested. Mean \pm sd. (B) Double FISH of *h2b* and *tsp2* in control and *foxA* RNAi male juvenile parasites showing accumulation of stem cells (*h2b*+) and progenitor (*tsp2*+) near the missing esophageal gland (single confocal sections). Bracket: anatomical location of the esophageal gland. Number of worms analyzed: 17 control RNAi worms; 18 *foxA* RNAi worms from three independent RNAi batches. (C) *foxA* knockdown in adults leads to down-regulation of known esophageal gland markers. qPCR analysis of RNA isolated from adult head fragments collected after 2 weeks (5 feedings) of exposure to *foxA* dsRNA. Head fragments were cut posterior to the ventral sucker. Mean \pm sd. (D) FISH of different cell-type markers in adult worms showing similarities in their expression patterns between control and *foxA* knockdown animals (maximum-intensity projections). N=9 control RNAi worms; N=12 *foxA* RNAi worms.

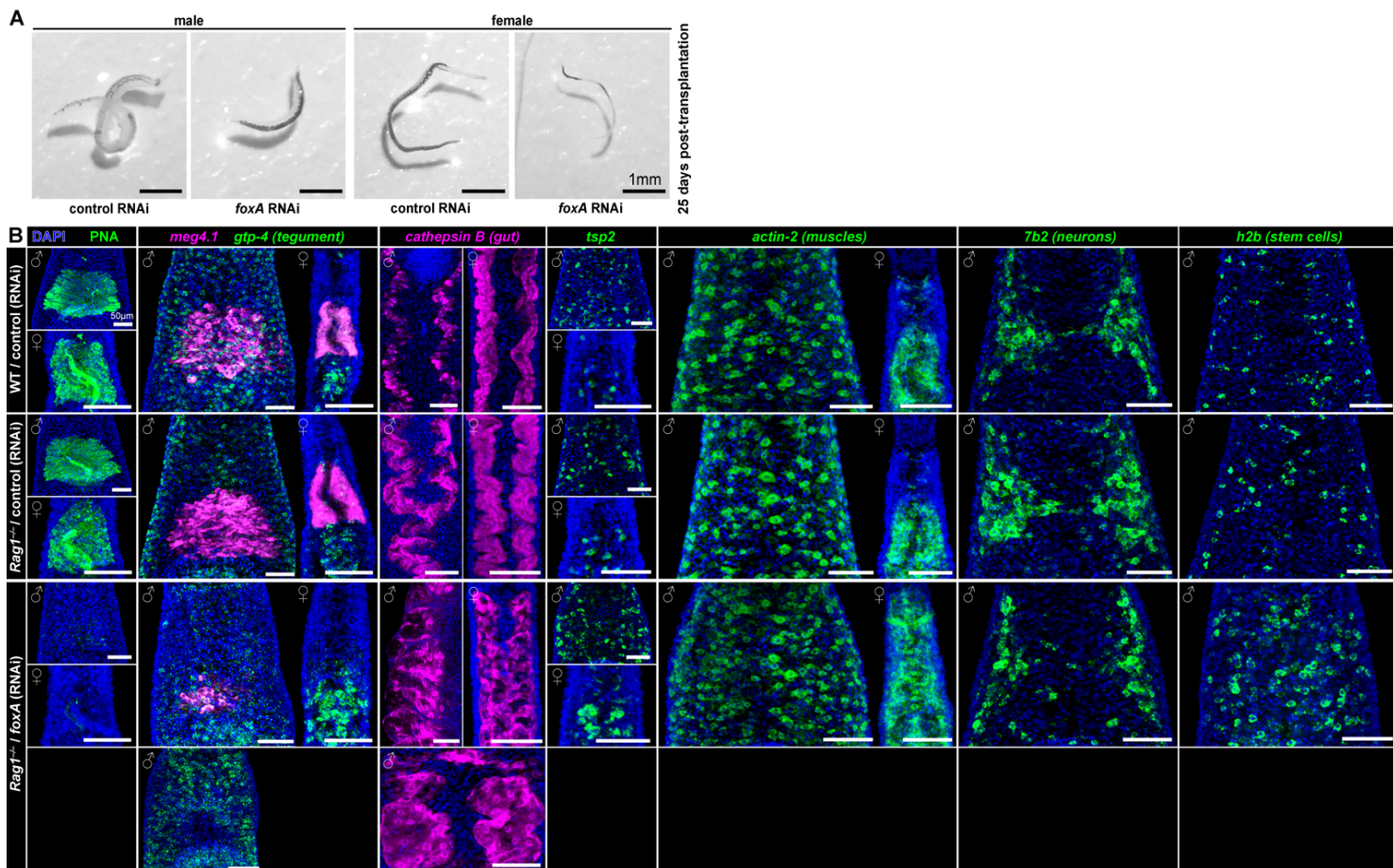


Figure S5. Characterization of stunted *foxA* RNAi parasites recovered after transplantation. (A) Representative brightfield images of recovered parasites 25 days post-transplantation. Note that *foxA* knockdown animals are shorter and thinner than control animals. (B) FISH of different cell-type markers in control and stunted *foxA* RNAi worms recovered from WT and *Rag1*^{-/-} mice >3 weeks post-transplantation. Note that *foxA* RNAi worms recovered from *Rag1*^{-/-} mice lack PNA lectin and have little or no expression of *meg4.1*, while they express *cathepsin B* at high levels along the thickened gut branch. Also, note a slight increase in the number of stem cells (*h2b*⁺) and progenitors (*tsp2*⁺) near the missing esophageal gland, similar to juvenile worms after *foxA* knockdown. Other cell-type markers are expressed at similar levels in *foxA* RNAi worms compared to control worms recovered from WT or *Rag1*^{-/-} mice (maximum-intensity projections). Scale bars: 50 μ m.

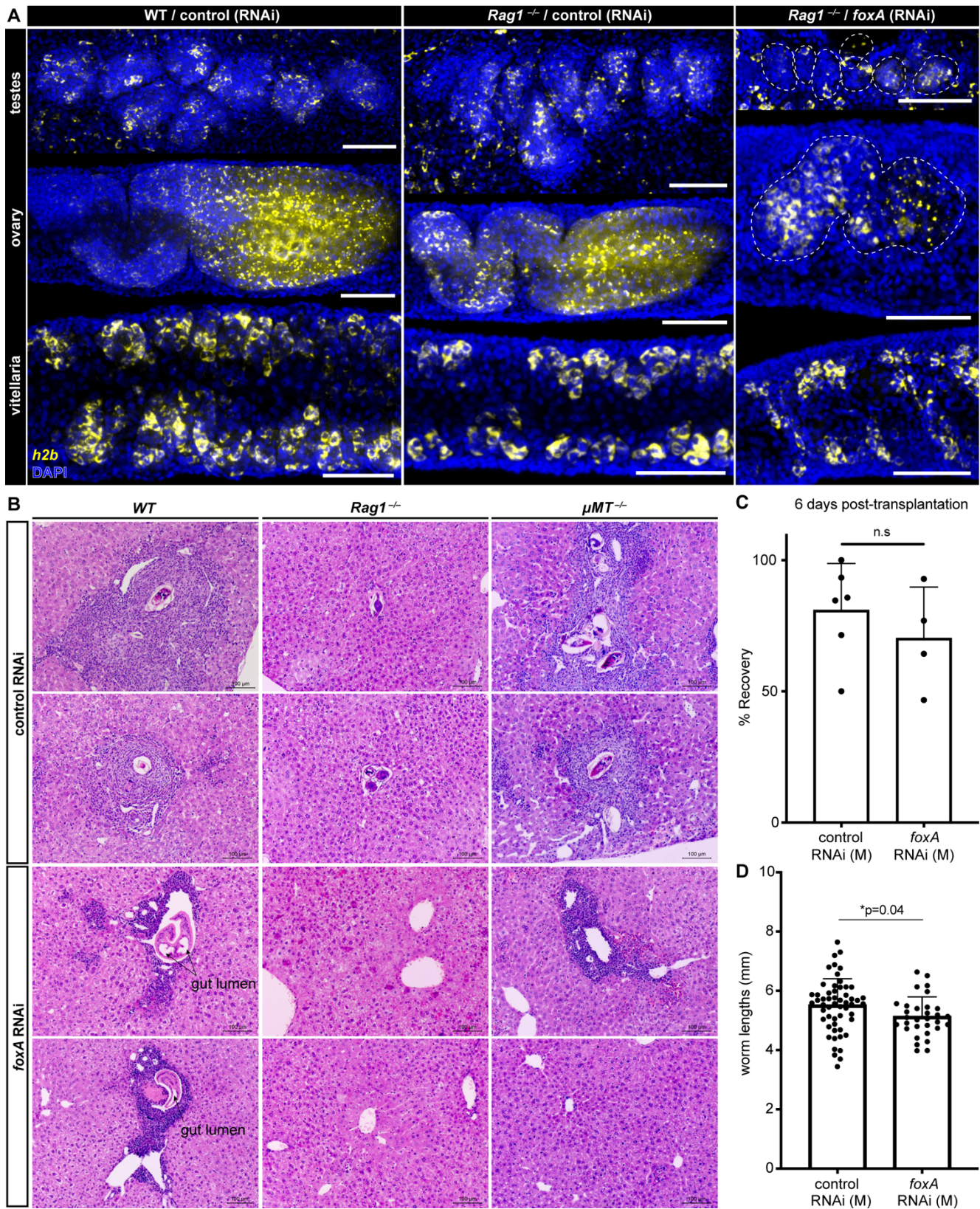


Figure S6. Reproductive system regression in *foxA* RNAi schistosomes and reduced disease pathology in host mice. (A) Characterization of the reproductive system of control and

foxA RNAi schistosomes recovered from *WT* and *Rag*^{-/-} mice >3 weeks post-transplantation. FISH to detect *h2b*, which is expressed in germ cells and vitellocytes (6), in addition to stem cells (maximum-intensity projections). Scale bars: 50 μm. **(B)** H&E staining of liver sections recovered from *WT*, *Rag1*^{-/-}, and *μMT*^{-/-} mice >3 weeks after transplantation of control or *foxA* RNAi parasites. Note that dead worms are found in *WT* mice that received *foxA* RNAi parasites but are not found in *Rag1*^{-/-} and *μMT*^{-/-} mice. Also, note that granulomas were formed around eggs laid in livers of *WT* and *μMT*^{-/-} mice but not formed around eggs laid in livers of *Rag1*^{-/-} mice. Eggs were not found in any mice that received *foxA* RNAi parasites. Scale bars: 100 μm. **(C)** Percentage of *foxA* RNAi parasites recovered 6 days after transplantation. Mean ± sd. Statistical analysis: Unpaired t-test. **(D)** Length of parasites recovered 6 days after transplantation. Each dot represents a single male worm. Mean ± sd. Statistical analysis: Unpaired t-test.

Table S1. Raw data of parasite transplantation and recovery (Figure 5A)

Experiment Number	Mouse Strain / Background	Mouse Genotype	Mouse Sex	Parasite age (post-infection) at the start of RNAi	RNAi condition	total dsRNA feedings	Days post-transplantation (recovery)	Number of male parasites injected into mouse	Number of male parasites recovered	% Recovery
Exp 1	Swiss-Webster	wild-type	female	5 weeks	pJC (control)	6 feedings	15 days	10	4	40.0
Exp 1	Swiss-Webster	wild-type	female	5 weeks	pJC (control)	6 feedings	15 days	10	9	90.0
Exp 1	Swiss-Webster	wild-type	female	5 weeks	pJC (control)	6 feedings	15 days	11	6	54.5
Exp 1	Swiss-Webster	wild-type	female	5 weeks	pJC (control)	6 feedings	15 days	12	1	8.3
Exp 1	Swiss-Webster	wild-type	female	5 weeks	foxA	6 feedings	15 days	9	0	0.0
Exp 1	Swiss-Webster	wild-type	female	5 weeks	foxA	6 feedings	15 days	12	3	25.0
Exp 1	Swiss-Webster	wild-type	female	5 weeks	foxA	6 feedings	15 days	8	1	12.5
Exp 1	Swiss-Webster	wild-type	female	5 weeks	foxA	6 feedings	15 days	9	3	33.3
Exp 1	Swiss-Webster	wild-type	female	5 weeks	foxA	6 feedings	15 days	3	1	33.3
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	pJC (control)	5 feedings	25 days	9	4	44.4
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	pJC (control)	5 feedings	25 days	11	5	45.5
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	pJC (control)	5 feedings	25 days	6	3	50.0
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	pJC (control)	5 feedings	25 days	5	4	80.0
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	pJC (control)	5 feedings	25 days	7	3	42.9
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	pJC (control)	5 feedings	25 days	9	7	77.8
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	pJC (control)	5 feedings	25 days	5	1	20.0
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	foxA	5 feedings	25 days	10	0	0.0
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	foxA	5 feedings	25 days	8	2	25.0
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	foxA	5 feedings	25 days	12	0	0.0
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	foxA	5 feedings	25 days	14	1	7.1
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	foxA	5 feedings	25 days	13	0	0.0
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	foxA	5 feedings	25 days	15	0	0.0
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	foxA	5 feedings	25 days	5	0	0.0
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	foxA	5 feedings	25 days	6	0	0.0
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	foxA	5 feedings	25 days	17	4	23.5
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	foxA	5 feedings	25 days	11	0	0.0
Exp 2	Swiss-Webster	wild-type	female	5.5 weeks	foxA	5 feedings	25 days	12	2	16.7
Exp 3	BL6	wild-type	male	5 weeks	pJC (control)	6 feedings	21 days	10	6	60.0

Exp 3	BL6	wild-type	male	5 weeks	pJC (control)	6 feedings	21 days	6	4	66.7
Exp 3	BL6	wild-type	male	5 weeks	foxA	6 feedings	21 days	9	0	0.0
Exp 3	BL6	Rag1 KO	male	5 weeks	pJC (control)	6 feedings	21 days	8	7	87.5
Exp 3	BL6	Rag1 KO	male	5 weeks	foxA	6 feedings	21 days	12	8	66.7
Exp 3	BL6	Rag1 KO	male	5 weeks	foxA	6 feedings	21 days	7	6	85.7
Exp 3	BL6	Rag1 KO	male	5 weeks	foxA	6 feedings	21 days	8	1	12.5
Exp 4	BL6	wild-type	male	5 weeks	pJC (control)	7 feedings	22 days	18	12	66.7
Exp 4	BL6	wild-type	male	5 weeks	pJC (control)	7 feedings	22 days	20	15	75.0
Exp 4	BL6	wild-type	male	5 weeks	pJC (control)	7 feedings	21 days	16	9	56.3
Exp 4	BL6	wild-type	male	5 weeks	pJC (control)	4 feedings	21 days	16	9	56.3
Exp 4	BL6	wild-type	male	5 weeks	foxA	7 feedings	22 days	16	0	0.0
Exp 4	BL6	wild-type	male	5 weeks	foxA	7 feedings	22 days	9	3	33.3
Exp 4	BL6	wild-type	male	5 weeks	foxA	7 feedings	22 days	18	2	11.1
Exp 4	BL6	wild-type	male	5 weeks	foxA	7 feedings	22 days	18	1	5.6
Exp 4	BL6	wild-type	male	5 weeks	foxA	4 feedings	21 days	16	0	0.0
Exp 4	BL6	Rag1 KO	male	5 weeks	pJC (control)	7 feedings	22 days	19	4	21.1
Exp 4	BL6	Rag1 KO	male	5 weeks	pJC (control)	7 feedings	22 days	20	9	45.0
Exp 4	BL6	Rag1 KO	male	5 weeks	pJC (control)	7 feedings	22 days	16	11	68.8
Exp 4	BL6	Rag1 KO	male	5 weeks	pJC (control)	4 feedings	21 days	16	5	31.3
Exp 4	BL6	Rag1 KO	male	5 weeks	foxA	7 feedings	22 days	10	1	10.0
Exp 4	BL6	Rag1 KO	male	5 weeks	foxA	7 feedings	22 days	17	11	64.7
Exp 4	BL6	Rag1 KO	male	5 weeks	foxA	7 feedings	22 days	17	12	70.6
Exp 4	BL6	Rag1 KO	male	5 weeks	foxA	7 feedings	22 days	19	13	68.4
Exp 4	BL6	Rag1 KO	male	5 weeks	foxA	7 feedings	22 days	17	9	52.9
Exp 4	BL6	muMT KO	male	5 weeks	pJC (control)	4 feedings	21 days	17	11	64.7
Exp 4	BL6	muMT KO	male	5 weeks	pJC (control)	7 feedings	21 days	16	2	12.5
Exp 4	BL6	muMT KO	male	5 weeks	pJC (control)	7 feedings	21 days	12	10	83.3
Exp 4	BL6	muMT KO	male	5 weeks	pJC (control)	4 feedings	21 days	16	15	93.8
Exp 4	BL6	muMT KO	male	5 weeks	foxA	7 feedings	21 days	15	9	60.0
Exp 5	BL6	wild-type	male	5 weeks	pJC (control)	8 feedings	22 days	16	9	56.3
Exp 5	BL6	wild-type	male	5 weeks	foxA	8 feedings	22 days	18	0	0.0
Exp 5	BL6	wild-type	male	5 weeks	foxA	8 feedings	22 days	16	0	0.0
Exp 5	BL6	wild-type	male	5 weeks	foxA	5 feedings	22 days	16	3	18.8
Exp 5	BL6	wild-type	male	5 weeks	foxA	5 feedings	22 days	18	0	0.0

Exp 5	BL6	Rag1 KO	male	5 weeks	pJC (control)	5 feedings	21 days	7	4	57.1
Exp 5	BL6	Rag1 KO	male	5 weeks	pJC (control)	5 feedings	21 days	18	18	100.0
Exp 5	BL6	Rag1 KO	male	5 weeks	pJC (control)	8 feedings	21 days	12	11	91.7
Exp 5	BL6	Rag1 KO	male	5 weeks	pJC (control)	8 feedings	21 days	19	17	89.5
Exp 5	BL6	Rag1 KO	male	5 weeks	foxA	5 feedings	22 days	14	9	64.3
Exp 5	BL6	Rag1 KO	male	5 weeks	foxA	5 feedings	22 days	16	12	75.0
Exp 5	BL6	Rag1 KO	male	5 weeks	foxA	8 feedings	21 days	16	3	18.8
Exp 5	BL6	muMT KO	male	5 weeks	pJC (control)	5 feedings	22 days	10	6	60.0
Exp 5	BL6	muMT KO	male	5 weeks	pJC (control)	5 feedings	22 days	20	17	85.0
Exp 5	BL6	muMT KO	male	5 weeks	pJC (control)	8 feedings	22 days	17	9	52.9
Exp 5	BL6	muMT KO	male	5 weeks	foxA	5 feedings	22 days	15	11	73.3
Exp 5	BL6	muMT KO	male	5 weeks	foxA	8 feedings	22 days	13	1	7.7
Exp 5	BL6	muMT KO	male	5 weeks	foxA	8 feedings	22 days	15	3	20.0
Exp 6	BL6	wild-type	male	5 weeks	pJC (control)	6 feedings	21 days	13	13	100
Exp 6	BL6	wild-type	male	5 weeks	foxA	6 feedings	21 days	18	1	5.55555556
Exp 6	BL6	Rag1 KO	male	5 weeks	foxA	6 feedings	21 days	15	12	80
Exp 6	BL6	muMT KO	male	5 weeks	pJC (control)	6 feedings	21 days	17	16	94.1176471
Exp 6	BL6	muMT KO	male	5 weeks	pJC (control)	6 feedings	21 days	13	13	100
Exp 6	BL6	muMT KO	male	5 weeks	foxA	6 feedings	21 days	17	14	82.3529412
Exp 6	BL6	muMT KO	male	5 weeks	foxA	6 feedings	21 days	14	12	85.7142857
Exp 6	Swiss-Webster	wild-type	female	5 weeks	pJC (control)	6 feedings	21 days	16	12	75
Exp 6	Swiss-Webster	wild-type	female	5 weeks	foxA	6 feedings	21 days	13	0	0
Exp 6	Swiss-Webster	wild-type	female	5 weeks	pJC (control)	6 feedings	21 days	18	12	66.6666667
Exp 6	Swiss-Webster	wild-type	female	5 weeks	pJC (control)	6 feedings	21 days	11	8	72.7272727
Exp 6	Swiss-Webster	wild-type	female	5 weeks	foxA	6 feedings	21 days	12	1	8.33333333
Exp 7	Swiss-Webster	wild-type	female	7 weeks	pJC (control)	8 feedings	6 days	14	12	85.7142857
Exp 7	Swiss-Webster	wild-type	female	7 weeks	pJC (control)	8 feedings	6 days	13	13	100
Exp 7	Swiss-Webster	wild-type	female	7 weeks	pJC (control)	8 feedings	6 days	13	11	84.6153846
Exp 7	Swiss-Webster	wild-type	female	7 weeks	foxA	8 feedings	6 days	14	13	92.8571429
Exp 7	Swiss-Webster	wild-type	female	7 weeks	foxA	8 feedings	6 days	13	10	76.9230769
Exp 7	Swiss-Webster	wild-type	female	7 weeks	foxA	8 feedings	6 days	15	7	46.6666667
Exp 7	UBC-GFP	wild-type	male	7 weeks	foxA	8 feedings	6 days	14	9	64.2857143
Exp 7	UBC-GFP	wild-type	male	7 weeks	pJC (control)	8 feedings	6 days	14	10	71.4285714
Exp 7	UBC-GFP	wild-type	male	7 weeks	pJC (control)	8 feedings	6 days	12	6	50

Exp 7	UBC-GFP	wild-type	male	7 weeks	pJC (control)	8 feedings	6 days	15	14	93.333333 3
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Table S2. Raw data of worm length measures (millimeters), >3 weeks post-transplantation (Figure 5B)

WT mice Control RNAi (M)	WT mice Control RNAi (F)	WT mice foxA RNAi (M)	WT mice foxA RNAi (F)	Rag1 KO Control RNAi (M)	Rag1 KO Control RNAi (F)	Rag1 KO foxA RNAi (M)	Rag1 KO foxA RNAi (F)	µMT KO Control RNAi (M)	µMT KO Control RNAi (F)	µMT KO foxA RNAi (M)	µMT KO foxA RNAi (F)
4.92	6.71	3.56	2.71	4.88	6.06	3.41	2.88	9.13	8.35	2.63	2.23
6.38	4.72	2.58		3.55	4.62	2.56	2.75	7.36	9.30	3.32	2.55
4.72	5.21	3.26		3.84	4.95	2.59	2.65	8.84	6.50	1.81	2.92
5.46	5.64	2.93		5.33	4.45	2.76	2.03	7.43	9.53	1.94	3.04
5.66	5.42	3.16		5.37	3.78	2.22	2.58	7.75	8.39	3.47	2.33
4.32	6.96	3.45		4.53	4.53	2.52	2.04	7.48	8.00	2.11	3.38
5.65	3.82	2.26		3.37	5.26	3.01	2.92	5.79	9.29	2.76	2.76
10.30	5.68	2.21		3.58	4.01	2.67	2.65	8.71	8.26	2.72	2.57
9.83	5.04	3.01		4.69	3.69	2.16	2.34	8.88	4.01	2.06	2.36
9.87	4.69	2.75		6.27	3.25	2.26	1.92	6.60	6.49	3.73	2.66
7.67	5.34	3.15		4.59	4.00	2.45	1.94	4.99	5.71	4.62	2.47
8.70	7.88			6.48	5.73	2.51	2.55	5.60	4.48	3.36	1.92
7.17	8.60			6.26	4.31	2.97	2.69	5.21	7.44	4.37	2.12
6.23	8.09			6.45	6.50	2.37	2.65	6.95	6.16	4.07	
5.81	8.39			6.04	5.44	2.67	1.83	8.44	6.93	3.04	
9.05	7.86			6.69	5.96	4.04	2.54	5.35	6.18	3.71	
8.94	8.33			3.30	6.41	2.62	4.03	7.45	4.85	3.34	
7.45	8.73			5.54	5.14	2.52	2.35	5.59	5.00	3.40	
5.55	7.82			6.15	3.54	2.82	4.09	5.23	9.12	2.28	
8.20	5.46			7.72	5.72	3.87	4.43	6.95	9.68	2.82	
7.81	9.00			4.43	5.18	3.57	2.55	6.81	7.81	3.03	
6.91	7.75			6.28	7.07	3.54	4.19	6.50	8.88	2.32	
8.88	7.29			6.19	6.24	2.87	3.14	6.32	6.72	2.91	
5.36	6.90			6.51	7.05	3.01	2.06	9.47	8.98	3.16	
7.92	7.81			4.82	5.03	2.56	3.27	7.76	8.50		
7.90	7.33			6.79	5.02	4.04	3.43	7.92	7.32		
6.94	7.19			2.97	7.90	3.07	2.51	8.52	9.46		
7.46	6.88			4.97	7.37	3.31	3.29	9.98	8.82		
7.66	7.19			4.43	7.90	2.82	4.18	8.43	8.80		
5.79	8.52			7.75	9.29	2.66	2.60	8.43	8.83		
7.48	8.27			8.98	4.82	2.97	3.79	8.80	6.07		

5.81	8.30			7.39	9.74	3.21	2.85	7.78	7.80		
6.06	7.05			7.42	6.20	2.47	2.93	8.24	6.44		
7.88	7.49			7.00	6.79	3.73	2.91	8.20	9.49		
4.19	6.80			7.78	7.29	3.74	2.86	4.51	9.65		
5.94	7.52			6.96	7.34	2.61	4.01	8.40	8.92		
4.93	7.44			6.45	7.92	4.34	3.07	8.37	10.97		
8.20	5.50			6.88	7.87	3.69	2.89	6.40	8.80		
6.84	5.14			8.01	6.99	5.26	2.83	6.77	10.48		
7.23	5.92			8.20	8.95	2.40	3.02	4.26	10.27		
7.82	6.55			8.79	9.38	4.54	2.50	6.36	10.70		
6.50	6.39			4.47	7.70	4.02	2.00	6.96	10.49		
5.64	4.92			8.19	8.48	3.64	2.84	9.49	9.96		
7.08				7.13	7.60	3.68	2.79	8.20	9.43		
6.49				8.26	9.04	3.68	3.29	9.22	10.77		
5.94				8.99	8.20	3.11	3.69	9.37	8.77		
7.56				8.72	6.74	3.30	2.30	8.80	5.54		
7.30				8.14	5.78	2.88	2.37	7.81	5.86		
6.81				9.34	9.34	3.55	2.57	4.81	4.69		
7.69				8.34	8.42	2.91	2.53	9.25	5.59		
5.59				8.49	6.93	1.98	2.54	8.97	6.31		
7.05				7.01	5.94	2.04	2.93	7.81	5.45		
2.35				8.43	6.47	3.19	2.87	8.12	6.05		
4.11				7.24	5.40	3.87	3.00	9.09	6.64		
5.98				8.38	8.37	3.21	2.28	9.28			
6.61				8.01	7.03	3.06	2.09	9.61			
6.00				6.65	5.48	3.50	2.58	7.97			
5.96				6.61	7.18	2.37	2.18	8.15			
5.77				5.89	7.31	4.03	1.94	8.97			
6.36				7.04	7.04	2.42	3.10	6.94			
6.68				6.80		2.94	2.93	5.95			
5.87				5.05		3.77	2.14	5.55			
5.96				6.98		3.77	2.84	3.96			
				6.60		3.96	2.19	3.79			
				6.11		3.28		6.38			
				7.70		3.39		6.41			
				8.37		3.17		4.76			
				6.56		2.32		3.52			
				7.55		3.19					
				7.54		3.32					

				5.37		3.74						
				6.77		2.18						
				7.36		3.36						
				7.45		3.72						
				6.65		3.35						
				7.38		2.66						
				6.91		3.51						
				6.79		3.99						
				5.38		3.20						
				6.53		3.33						
				7.17		3.00						
						2.96						
						3.45						
						2.94						
						2.74						

Table S3. Oligonucleotide sequence used for this study

Gene Name	Gene ID	Purpose	Forward Sequence	Reverse Sequence
<i>h2b</i>	Smp_108390	ISH	GCCTCCTAAAGTTGTGTCTGG	GACCCACTGTACTTCGCTCACTG
<i>tsp2</i>	Smp_181530	ISH	ATGGCTCTTGTTGTGGGTA	CCGCGCTTTATAGCCAATAG
<i>cathepsin B</i>	Smp_103610	ISH	TCGATTCCAGGAAGAAATGG	TCATCAGACCACGCACTAT
<i>meg4.1</i>	Smp_163630	ISH	TTGGTATATTATGTATTGTGGGTTTGA	ATTGATTTGTGCGTAATAGTATTTTGG
<i>foxA</i>	Smp_331700	ISH	TGGACCATCCATTTTCATTG	GAGGGTGTGTGGAGGAGAA
<i>pla2</i>	Smp_031190	ISH	TGGTGAGAATTTAGCGCTCTTT	ACTTTAGCTGTGGGCCATTTT
<i>7b2</i>	Smp_073270	ISH	GTGCGGTCAAATATTGGCTA	TGTCCCGAGACAAAATCAGTT
<i>actin</i>	Smp_307020/307010	ISH	CAGTGTCCCTCCATCGTT	GTGAACAATACCCGGACCAG
<i>gtp-4</i>	Smp_105410	ISH	ATCTCTTCGTGGTGAATCG	CTGTTCCGAGCTGTTGTTGGA
<i>foxA</i>	Smp_331700	qPCR	TCATCCCCAACAGAAAACAA	TTCTCACCTGTAGTCAATGTGGT
<i>foxA</i>	Smp_331700	qPCR	CAGGAATATGTTTGAAAATGG	TTGTTGTCGTTGTTGCCTGT
<i>meg4.1</i>	Smp_163630	qPCR	CAATTCACCGAAGAGGACAGA	AAAAATCGGCTATGGACTTAGG
<i>meg8a</i>	Smp_171190	qPCR	CCAGGAAATCCCACGAAGT	ATCGCCAACCTCTTTTCAGGA
<i>meg8b</i>	Smp_172180	qPCR	AGAACCATCATTTTGGAGACG	GTGTTCCGGTTTGGACTTTT
<i>meg14</i>	Smp_124000	qPCR	CCAAACCTTCACCTGCTAAA	TCCAAGTACGATAGGGACAGC
<i>meg15</i>	Smp_010550	qPCR	CAAGGTCAAAGAGATCCACCA	TTGCGGTTGTATGCTGAGAC
<i>pla2</i>	Smp_031190	qPCR	TGTGGCAGTCTTTTCTCTC	GGTGTCCGATCATGTTGTA

Movie S1 (separate file). Recovered *foxA* RNAi parasites >3 weeks post-transplantation are stunted.

Movie S2 (separate file). Feeding of GFP+ immune cells *in vitro* in control and *foxA* knockdown schistosomes.