

CHAPTER 7

APPENDIXES

7.1 Appendix A

Primer name	Primer sequence
SL1	CCGTCACGGTTTTACTCTTG
Smp_102510_R	GCAAATGCTGTCCATAAAGC
Smp_024110_R	CAGCCAAAGACTCCCAAT
Smp_027360_R	TTTTACTATTAGGACTTTGTGGTGATG
Smp_016410_R	GACTACACGGCGGTACAGGA
Smp_141320_R	TGAATGATGAGGTGTTGGACA
Smp_136960_R	TTCACTTTCCCGCAGTTTT
Smp_124050_R	CATTGCATTTCCATATTGTTCA
Smp_176420_R	AAAACCTTCTGTCTTAATTGTGGTG
Smp_176590_R	AATGCGGGTACGTCTGATATG
Smp_030020_R	CAGCACCAAGTGGAAGTAA
Smp_048880_R	ATTCTTCTGCAGCCTCGTTG
Smp_045200_R	AACTACTTGCCATACACGACCA
Smp_045200_F	ATGGCAACCGAGACGAAAT
enolase_poly_F	TGTTCCGATTCAACAATGCT
enolase_poly_R	TCCACCTCAACTGTGGGATT
Smp_006980-70_F	ATGAGGGGTGCACTTACGAC
Smp_006980-70_R	ATTTCAAACCTCGGGACATGC
Smp_084900-890_F	5' GGCTGATGTTGAAGCACAAA
Smp_084900-890_R	5' AGGAGTGAAACGCTGCAAAT
Smp_084890_R	GATCGACTGGATGACGACCT
Smp_079750-60_F	GCAGATTTGACGGAAAATTCA
Smp_079750-60_R	CGTTAATACGAGCTCCACGA
Smp_079760_R	TCATTTGCAGCATCCACATT
Smp_023160-70_F	ACTCCCACAATGTTGCCATA
Smp_023160-70_R	CCGAAATCCCAGACTGACTC
Smp_023170_R	AGGCTCGCACATCCTTAAAA
VAL6_F	CCGGATCAGCAAATAATGACA
VAL6_R	TGATCCCAGTAACATTTGCATC

7.2 Appendix B

GeneDB_ID	Product description
Smp_152660.1	glial cells missing related
Smp_199740.1	Conserved oligomeric Golgi complex component 4, putative;with=UniProt:Q5R7R6
Smp_182910.1	hypothetical protein
Smp_191250.1	hypothetical protein
Smp_159840.1	dynein heavy chain, putative
Smp_156080.1	dynein heavy chain, putative
Smp_194890.1	subfamily S1A non-peptidase homologue (S01 family);with=UniProt:P12546
Smp_006510.1	cercarial elastase (S01 family);with=UniProt:P12546
Smp_112090.1	cercarial elastase (S01 family);with=UniProt:P12546
Smp_167120.1	leishmanolysin-2 (M08 family);with=UniProt:Q8BMN4
Smp_185230.1	arginine/serine-rich splicing factor, putative
Smp_190370.1	rab2, putative
Smp_107700.1	hypothetical protein
Smp_179410.1	hypothetical protein
Smp_185190.1	cercarial elastase (S01 family);with=UniProt:P12546
Smp_119130.1	cercarial elastase (S01 family);with=UniProt:P12546
Smp_190590.1	hypothetical protein
Smp_136830.1	subfamily A1A unassigned peptidase (A01 family);with=UniProt:Q05744
Smp_135320.1	Hypothetical protein, putative
Smp_173950.1	hypothetical protein
Smp_147890.1	Rootletin (Ciliary rootlet coiled-coil protein), putative
Smp_151860.1	inositol 1,4,5-trisphosphate receptor, putative
Smp_133640.1	hypothetical protein
Smp_177900.1	hypothetical protein
Smp_151260.1	Adenine phosphoribosyltransferase, putative

7.3 Appendix C

Gene Ontology enrichment (Biological processes) among transcripts up regulated in the cercariae vs. schistosomula comparison. The comparisons are indicated in each table

Table C.1 – cercariae vs. 3-hours old schistosomula

GO term ID	GO term description	Annot.	Sig.	p-value
GO:0006355	regulation of transcription DNA-dependent	881	113	0
GO:0007275	multicellular organismal development	301	59	0
GO:0007186	G-protein coupled receptor protein signalling	165	32	0
GO:0007156	homophilic cell adhesion	61	15	0
GO:0030154	cell differentiation	82	19	0
GO:0016055	Wnt receptor signaling pathway	26	8	0.001
GO:0007155	cell adhesion	235	42	0.001
GO:0051258	protein polymerization	44	8	0.001
GO:0007229	integrin-mediated signaling pathway	8	4	0.001
GO:0006813	potassium ion transport	81	13	0.004

Table C.2 – cercariae vs. 3-hours old schistosomula.

GO term ID	GO term description	A	S	p-value
GO:0007156	homophilic cell adhesion	61	13	0
GO:0007186	G-protein coupled receptor protein signalling	165	18	0
GO:0007229	integrin-mediated signaling pathway	8	4	0
GO:0001503	ossification	4	3	0
GO:0007155	cell adhesion	235	31	0
GO:0051216	cartilage development	5	3	0
GO:0007160	cell-matrix adhesion	7	3	0.001
GO:0006811	ion transport	389	27	0.003
GO:0045596	negative regulation of cell differentiatton	3	2	0.003
GO:0030514	negative regulation of BMP signaling pathway	3	2	0.003
GO:0006813	potassium ion transport	81	8	0.006
GO:0015749	monosaccharide transport	4	2	0.007

Table C.3 – cercariae vs. 3-hours old schistosomula.

GO term ID	GO term description	A	S	p-value
GO:0007156	homophilic cell adhesion	61	40	0
GO:0007186	G-protein coupled receptor protein signa...	165	61	0
GO:0007275	multicellular organismal development	301	94	0
GO:0007155	cell adhesion	235	96	0
GO:0006811	ion transport	389	86	0
GO:0006814	sodium ion transport	67	22	0
GO:0007229	integrin-mediated signaling pathway	8	6	0
GO:0030154	cell differentiation	82	24	0.001
GO:0007160	cell-matrix adhesion	7	5	0.001
GO:0006813	potassium ion transport	81	22	0.001
GO:0007399	nervous system development	27	9	0.006
GO:0001503	ossification	4	3	0.009
GO:0008643	carbohydrate transport	36	12	0.009