

Table S1: Blast results for amplicons of the clinical samples and plasmid controls

No.	Sample Code	FECT	PCR	Sequencing primers	Sequence	Max. Score	E. value	Identity	Accession number of the maximum scored sequence
1	AsT7	plasmid control		T7-F, T7-R	GGTGATGTAATAGCAGTCGGCGGTTTCTTTTTTTT	399	2.00E-107	218/219(99%)	MK849920.1
					TGGCGGACAATTGCATGCGATTGCTATGTGTTG	399	2.00E-107	218/219(99%)	LC422643.1
					AGGGAGAAATAGGTGGCATGTTGGGCTTGTAGAA	399	2.00E-107	218/219(99%)	MF358963.1
					AGGCATGCCGTAGCGCTATTTCCCGCTATTT	399	2.00E-107	218/219(99%)	HQ721819.1
					CGTAACAACGGTGTCCATTTGGCGTCTACGCTT	383	2.00E-102	215/219(98%)	AJ000895.1
2	D27	As	As	As-F, As-R	GGTGATGTAATAGCAGTCGGCGGTTTCTTTTTTTT	390	1.00E-104	215/217(99%)	AJ000895.1
					TGGCGGACAATTGCATGCGATTGCTATGTGTTG	385	5.00E-103	216/219(99%)	MK849920.1
					AGGGAGAAATAGGTGGCATGTTGGGCTTGTAGAA	385	5.00E-103	216/219(99%)	LC422643.1
					AGGCATGGTAGCGCTATTTCCCGCTATTTGTA	385	5.00E-103	216/219(99%)	MF358963.1
					ACAACGGTGTCCATTTGGCGTCTACGCTTACC	385	5.00E-103	216/219(99%)	HQ721819.1
3	D21	As	As	As-F, As-R	GGTGATGTAATAGCAGTCGGCGGTTTCTTTTTTTT	392	3.00E-105	215/217(99%)	AJ000895.1
					TGGCGGACAATTGCATGCGATTGCTATGTGTTG	387	1.00E-103	216/219(99%)	MK849920.1
					CGGGAGAAATAGGTGGCATGTTGGGCTTGTAGAA	387	1.00E-103	216/219(99%)	LC422643.1
					AGGCATGCGTAGCGCTATTTCCCGCTATTTG	387	1.00E-103	216/219(99%)	MF358963.1
					TAACAACGGTGTCCATTTGGCGTCTACGCTTCA	387	1.00E-103	216/219(99%)	HQ721819.1
4	D25	As	As	As-F, As-R	GGTGATGTAATAGCAGTCGGCGGTTTCTTTTTTTT	392	3.00E-105	215/217(99%)	AJ000895.1
					TGGCGGACAATTGCATGCGATTGCTATGTGTTG	387	1.00E-103	216/219(99%)	MK849920.1
					AGGGAGAAATAGGTGGCATGTTGGGCTTGTAGAA	387	1.00E-103	216/219(99%)	LC422643.1
					AGGCATGCGTAGCGCTATTTCCCGCTATTTG	387	1.00E-103	216/219(99%)	MF358963.1
					TAACAACGGTGTCCATTTGGCGTCTACGCTTCA	387	1.00E-103	216/219(99%)	HQ721819.1
5	D53	NF	As+Ss+Hw	As-F, As-R	GGTGATGTAATAGCAGTCGGCGGTTTCTTTTTTTT	387	1.00E-103	214/217(99%)	AJ000895.1
					TGGCGGACAATTGCATGCGATTGCTATGTGTTG	381	6.00E-102	215/219(98%)	MK849920.1
					AGGGAGAAATAGGTGGCATGTTGGGCTTGTAGAA	381	6.00E-102	215/219(98%)	LC422643.1
					AGGCATGCGTAGCGCTATTTCCCGCTATTTG	381	6.00E-102	215/219(98%)	MF358963.1
					TAACAACGGTGTCCATTTGGCGTCTACGCTTCA	381	6.00E-102	215/219(98%)	HQ721819.1
6	D56	NF	As+Ss	As-F, As-R	GGTGATGTAATAGCAGTCGGCGGTTTCTTTTTTTT	390	1.00E-104	215/217(99%)	AJ000895.1
					TGGCGGACAATTGCATGCGATTGCTATGTGTTG	385	5.00E-103	216/219(99%)	MK849920.1
					AGGGAGAAATAGGTGGCATGTTGGGCTTGTAGAA	385	5.00E-103	216/219(99%)	LC422643.1
					AGGCATGCGTAGCGCTATTTCCCGCTATTTG	385	5.00E-103	216/219(99%)	MF358963.1
					TAACAACGGTGTCCATTTGGCGTCTACGCTTCA	385	5.00E-103	216/219(99%)	HQ721819.1
7	BK75	Hw	As+Hw	As-F, As-R	GGTGATGTAATAGCAGTCGGCGGTTTCTTTTTTTT	390	1.00E-104	215/217(99%)	AJ000895.1
					TGGCGGACAATTGCATGCGATTGCTATGTGTTG	381	6.00E-102	215/219(98%)	MK849920.1
					AGGGAGAAATAGGTGGCATGTTGGGCTTGTAGAA	381	6.00E-102	215/219(98%)	LC422643.1
					AGGCATGCGTAGCGCTATTTCCCGCTATTTG	381	6.00E-102	215/219(98%)	MF358963.1
					TAACAACGGTGTCCATTTGGCGTCTACGCTTCA	381	6.00E-102	215/219(98%)	HQ721819.1
8	Hw-T7	plasmid control		T7-F, T7-R	AGCATTGCTTGAATGCCGCCTCAATTTTGTATTG	881	0.0	477/477 (100%)	KM891738.1
					GTGGTTAGACACACACATAAATTGTGTGGTGT	881	0.0	477/477 (100%)	LC036565.1
					GGTACCTGTTCTTGTATCAGGAAACCTTAATGAT	881	0.0	477/477 (100%)	LC036563.1
					CCTTCACATGTTAACCAATAATGCGCGCTACGTG	876	0.0	476/477 (99%)	LC088287.1
					TTATGGTGGATGGGACAATATGTGTGGACGCCAA	876	0.0	476/477 (99%)	AB793527.1
9	22	NF	Hw+Ss	Hw-F,Hw-R	AGCATTGCTTGAATGCCGCCTCAATTTTGTATTG	881	0.0	477/477 (100%)	LC088287.1
					GTGGTTGGACACACACATAAATTGTGTGGTGT	881	0.0	477/477 (100%)	AB793527.1
					GGTACCTGTTCTTGTATCAGGAAACCTTAATGAT	876	0.0	476/477 (99%)	KM891738.1
					CCTTCACATGTTAACCAATAATGCGCGCTACGTG	876	0.0	476/477 (99%)	LC036565.1
					TTATGGTGGATGGGACAATATGTGTGGACGCCAA	876	0.0	476/477 (99%)	LC036563.1
10	D53	NF	As+Hw+Ss	Hw-F,Hw-R	AGCATTGCTTGAATGCCGCCTCAATTTTGTATTG	881	0.0	477/477 (100%)	LC088287.1
					GTGGTTGGACACACACATAAATTGTGTGGTGT	881	0.0	477/477 (100%)	AB793527.1
					GGTACCTGTTCTTGTATCAGGAAACCTTAATGAT	876	0.0	476/477 (99%)	KM891738.1
					CCTTCACATGTTAACCAATAATGCGCGCTACGTG	876	0.0	476/477 (99%)	LC036565.1
					TTATGGTGGATGGGACAATATGTGTGGACGCCAA	876	0.0	476/477 (99%)	LC036563.1
11	D64	NF	As+Hw+Ss	Hw-F,Hw-R	AGCATTGCTTGAATGCCGCCTCAATTTTGTATTG	881	0.0	477/477 (100%)	LC088287.1
					GTGGTTAGACACACACATAAATTGTGTGGTGT	881	0.0	477/477 (100%)	LC036565.1
					GGTACCTGTTCTTGTATCAGGAAACCTTAATGAT	881	0.0	477/477 (100%)	LC036563.1
					CCTTCACATGTTAACCAATAATGCGCGCTACGTG	876	0.0	476/477 (99%)	LC088287.1
					TTATGGTGGATGGGACAATATGTGTGGACGCCAA	876	0.0	476/477 (99%)	AB793527.1
12	D90	As+Hw	As+Hw	Hw-F,Hw-R	AGCATTGCTTGAATGCCGCCTCAATTTTGTATTG	881	0.0	477/477 (100%)	LC088287.1
					GTGGTTGGACACACACATAAATTGTGTGGTGT	881	0.0	477/477 (100%)	AB793527.1
					GGTACCTGTTCTTGTATCAGGAAACCTTAATGAT	876	0.0	476/477 (99%)	KM891738.1
					CCTTCACATGTTAACCAATAATGCGCGCTACGTG	876	0.0	476/477 (99%)	LC036565.1
					TTATGGTGGATGGGACAATATGTGTGGACGCCAA	876	0.0	476/477 (99%)	LC036563.1

					CACAAAATATTAACITTTTACATTTGATGTTTGCAG ATGATCGTGACTTCATCTTAGTCGTACATTAGAC TCCACTAGCTTCAGCCATCGATCCCTCCATTCCG	876	0.0	476/477 (99%)	LC036563.1
						876	0.0	476/477 (99%)	AF217891.1
13	D97	As+H w	As+Hw	Hw-F,Hw-R	AGCATTGCTTGAATGCCGCCTCAATTTTGTATTG GTGGTTGGACACACACATAACTTGTGTGGTGT GGTACCTGTTCTTGTGATCAGGAAACCTTAATGAT CCTTCACATGTTAACCAATAATGCGCGCTACGTG TTATGGTGGATGGACAATATGTGGACGCCAA CACAAAATATTAACITTTTACATTTGATGTTTGCAG ATGATCGTGACTTCATCTTAGTCGTACATTAGAC TCCACTAGCTTCAGCCATCGATCCCTCCATTCCG	881	0.0	477/477 (100%)	LC088287.1
						881	0.0	477/477 (100%)	AB793527.1
						876	0.0	476/477 (99%)	KM891738.1
						876	0.0	476/477 (99%)	LC036565.1
						876	0.0	476/477 (99%)	LC036563.1
						876	0.0	476/477 (99%)	AF217891.1
						876	0.0	476/477 (99%)	AF217891.1
14	Ss4-T7	plasmid control		T7-F, T7-R	GAATCCAAGTAAACGTAAGTCATTAGCTTACATT GATTACGTCCCTGCCCTTTGTACACACCCGCCGT CGGTGCCCGGAACTGAGCAATATCCAGAGGCA	176	1.E-40	100/102 (98%)	M84229.1
						172	2.E-39	99/102 (97%)	AF036605.1
						171	6.E-39	99/102 (97%)	XM_024646606.1
						171	6.E-39	99/102 (97%)	LC038066.1
						171	6.E-39	99/102 (97%)	LM524975.1
						171	6.E-39	99/102 (97%)	LM524969.1
						171	6.E-39	99/102 (97%)	AB923889.1
15	6	NF	Ss	Ss-F, Ss-R	GAATCCAAGTAAACGTAAGTCATTAGCTTACATT GATTACGTCCCTGCCCTTTGTACACACCCGCCGT CGCTGCCCGGAACTGAGCAATATCCAGAGGCA	187	5.E-44	101/101 (100%)	M84229.1
						182	3.E-42	100/101 (99%)	XM_024646606.1
						182	3.E-42	100/101 (99%)	LC038066.1
						182	3.E-42	100/101 (99%)	LM524975.1
						182	3.E-42	100/101 (99%)	LM524969.1
						182	3.E-42	100/101 (99%)	AB923889.1
						182	3.E-42	100/101 (99%)	AB923888.1
16	3	NF	Ss	Ss-F, Ss-R	GAATCCAAGTAAACGTAAGTCATTAGCTTACATT GATTACGTCCCTGCCCTTTGTACACACCCGCCGT CGCTGCCCGGAACTGAGCAATATCCAGAGGCA	187	5.E-44	101/101 (100%)	M84229.1
						182	3.E-42	100/101 (99%)	XM_024646606.1
						182	3.E-42	100/101 (99%)	LC038066.1
						182	3.E-42	100/101 (99%)	LM524975.1
						182	3.E-42	100/101 (99%)	LM524969.1
						182	3.E-42	100/101 (99%)	AB923889.1
						182	3.E-42	100/101 (99%)	AB923888.1
17	15	NF	Ss	Ss-F, Ss-R	GAATCCAAGTAAACGTAAGTCATTAGCTTACATT GATTACGTCCCTGCCCTTTGTACACACCCGCCGT CGCTGCCCGGAACTGAGCAATATCCAGAGGCA	187	5.E-44	101/101 (100%)	M84229.1
						182	3.E-42	100/101 (99%)	XM_024646606.1
						182	3.E-42	100/101 (99%)	LC038066.1
						182	3.E-42	100/101 (99%)	LM524975.1
						182	3.E-42	100/101 (99%)	LM524969.1
						182	3.E-42	100/101 (99%)	AB923889.1
						182	3.E-42	100/101 (99%)	AB923888.1
18	8	NF	Ss	Ss-F, Ss-R	GAATCCAAGTAAACGTAAGTCATTAGCTTACATT GATTACGTCCCTGCCCTTTGTACACACCCGCCGT GCTGCCCGGAACTGAGCAATATCCAGAGGCA	180	9.E-42	100/101 (99%)	M84229.1
						174	4.E-40	99/101 (98%)	XM_024646606.1
						174	4.E-40	99/101 (98%)	LC038066.1
						174	4.E-40	99/101 (98%)	LM524975.1
						174	4.E-40	99/101 (98%)	LM524969.1
						174	4.E-40	99/101 (98%)	AB923889.1
						174	4.E-40	99/101 (98%)	AB923888.1
19	27	Ss	Ss	Ss-F, Ss-R	GAATCCAAGTAAACGTAAGTCATTAGCTTACATT GATTACGTCCCTGCCCTTTGTACACACCCGCCGT CGCTGCCCGGAACTGAGCAATATCCAGAGGCA	187	5.E-44	101/101 (100%)	M84229.1
						182	3.E-42	100/101 (99%)	XM_024646606.1
						182	3.E-42	100/101 (99%)	LC038066.1
						182	3.E-42	100/101 (99%)	LM524975.1
						182	3.E-42	100/101 (99%)	LM524969.1
						182	3.E-42	100/101 (99%)	AB923889.1
						182	3.E-42	100/101 (99%)	AB923888.1
20	33	Ss	Ss	Ss-F, Ss-R	GAATCCAAGTAAACGTAAGTCATTAGCTTACATT GATTACGTCCCTGCCCTTTGTAAACCCGCCGT GCTGCCCGGAACTGAGCAATATCCAGAGGCA	180	9.E-42	100/101 (99%)	M84229.1
						174	4.E-40	99/101 (98%)	XM_024646606.1
						174	4.E-40	99/101 (98%)	LC038066.1
						174	4.E-40	99/101 (98%)	LM524975.1
						174	4.E-40	99/101 (98%)	LM524969.1
						174	4.E-40	99/101 (98%)	AB923889.1
						174	4.E-40	99/101 (98%)	AB923888.1
21	28	Ss	Ss	Ss-F, Ss-R	GAATCCAAGTAAACGTAAGTCATTAGCTTACATT GATTACGTCCCTGCCCTTTGTACACACCCGCCGT CGCTGCCCGGAACTGAGCAATATCCAGAGCA	182	2.E-42	98/98 (100%)	M84229.1
						176	1.E-40	97/98 (99%)	XM_024646606.1
						176	1.E-40	97/98 (99%)	LC038066.1
						176	1.E-40	97/98 (99%)	LM524975.1
						176	1.E-40	97/98 (99%)	LM524969.1
						176	1.E-40	97/98 (99%)	AB923889.1
						176	1.E-40	97/98 (99%)	AB923888.1
22	44	Hw	Ss	Ss-F, Ss-R	GAATCCAAGTAAACGTAAGTCATTAGCTTACATT GATTACGTCCCTGCCCTTTGTACACACCCGCCGT CGCTGCCCGGAACTGAGCAATATCCAGAGGCA	187	5.E-44	101/101 (100%)	M84229.1
						182	3.E-42	100/101 (99%)	XM_024646606.1
						182	3.E-42	100/101 (99%)	LC038066.1
						182	3.E-42	100/101 (99%)	LM524975.1
						182	3.E-42	100/101 (99%)	LM524969.1
						182	3.E-42	100/101 (99%)	AB923889.1
						182	3.E-42	100/101 (99%)	AB923888.1

23	H19	Hw	Ss	Ss-F, Ss-R	GAATTCCAAGTAAACGTAAGTCATTAGCTTACATT GATTACGTCCTGCCCTTTGTACACACCGCCCGT CGCTGCCCGGAACTGAGCAATATCCAGAGGCA	187	5.E-44	101/101 (100%)	M84229.1
						182	3.E-42	100/101 (99%)	XM_024646606.1
						182	3.E-42	100/101 (99%)	LC038066.1
						182	3.E-42	100/101 (99%)	LM524975.1
						182	3.E-42	100/101 (99%)	LM524969.1
						182	3.E-42	100/101 (99%)	AB923889.1
24	D63	NF	As+Ss	Ss-F, Ss-R	GAATTCCAAGTAAACGTAAGTCATTAGCTTACATT GATTACGTCCTGCCCTTTGTACACACCGCCCGT CGCTGCCCGGAACTGAGCAATATCCAGAGGCA	187	5.E-44	101/101 (100%)	M84229.1
						182	3.E-42	100/101 (99%)	XM_024646606.1
						182	3.E-42	100/101 (99%)	LC038066.1
						182	3.E-42	100/101 (99%)	LM524975.1
						182	3.E-42	100/101 (99%)	LM524969.1
						182	3.E-42	100/101 (99%)	AB923889.1
25	D73	NF	As+Ss	Ss-F, Ss-R	GAATTCCAAGTAAACGTAAGTCATTAGCTTACATT GATTACGTCCTGCCCTTTGTACACACCGCCCGT CGCTGCCCGGAACTGAGCAATATCCAGAGGCA	187	5.E-44	101/101 (100%)	M84229.1
						182	3.E-42	100/101 (99%)	XM_024646606.1
						182	3.E-42	100/101 (99%)	LC038066.1
						182	3.E-42	100/101 (99%)	LM524975.1
						182	3.E-42	100/101 (99%)	LM524969.1
						182	3.E-42	100/101 (99%)	AB923889.1
26	D98	As	As+Ss	Ss-F, Ss-R	GAATTCCAAGTAAACGTAAGTCATTAGCTTACATT GATTACGTCCTGCCCTTTGTACACACCGCCCGT CGCTGCCCGGAACTGAGCAATATCCAGAGGCA	187	5.E-44	101/101 (100%)	M84229.1
						182	3.E-42	100/101 (99%)	XM_024646606.1
						182	3.E-42	100/101 (99%)	LC038066.1
						182	3.E-42	100/101 (99%)	LM524975.1
						182	3.E-42	100/101 (99%)	LM524969.1
						182	3.E-42	100/101 (99%)	AB923889.1
27	22	NF	Hw+Ss	Ss-F, Ss-R	GAATTCCAAGTAAACGTAAGTCATTAGCTTACATT GATTACGTCCTGCCCTTTGTACACACCGCCCGT CGCTGCCCGGAACTGAGCAATATCCAGAGGCA	187	5.E-44	101/101 (100%)	M84229.1
						182	3.E-42	100/101 (99%)	XM_024646606.1
						182	3.E-42	100/101 (99%)	LC038066.1
						182	3.E-42	100/101 (99%)	LM524975.1
						182	3.E-42	100/101 (99%)	LM524969.1
						182	3.E-42	100/101 (99%)	AB923889.1
28	D53	NF	As+Hw+Ss	Ss-F, Ss-R	GAATTCCAAGTAAACGTAAGTCATTAGCTTACATT GATTACGCACTGCCCTTTGTACACACCGCCCGT GCTGCCCGGAACTGAGCAATATCCAGAGGCA	174	4.E-40	99/101 (98%)	M84229.1
						169	2.E-38	98/101 (97%)	XM_024646606.1
						169	2.E-38	98/101 (97%)	LC038066.1
						169	2.E-38	98/101 (97%)	LM524975.1
						169	2.E-38	98/101 (97%)	LM524969.1
						169	2.E-38	98/101 (97%)	AB923889.1

FECT: Formalin ethyl acetate concentration technique

As: Ascaris lumbricoides

Hw: Hookworm

Ss: Strongyloides stercoralis

NF: Not found