

Table S2. Transcripts in the *Ascaris suum* genome (PRJNA62057) encoding proteins with high identity to isotype 1 β -tubulin from *Haemonchus contortus*

Transcript ID ^a	Nomenclature Roose et al. [43]	Nomenclature Martin et al. [16]	Annotated C. <i>elegans</i> ortholog ^b	Length (bp/aa ^c)	Query coverage ^d (%)	Identity ^d (%)	Similarity ^e (%)	Location genome ^f	Location cDNA ^f
AgB01_g251_t03	bt-F	tbb-3	<i>mec-7</i>	1329/443	95	91.6	96.3	AgB01: 3782705 – 3795903 (-)	
AgB01_g252_t02	bt-E	tbb-4	<i>tbb-4</i>	1335/444	97	90.8	96.6	AgB01: 3803075- 3814443 (-)	
AgB02_g235_t03	<i>bt-A</i>	<i>tbb-5</i>	n.a.	1353/450	98	93.2	97.7	AgB02: 3973132- 3980469 (+)	
AgE31_g003_t01	bt-C	tbb-6	n.a.	1941/646	100	86.4	94.6	AgE31:35111 - 46174 (+)	
AgE31_g003_t01me	bt-C	tbb-6	n.a.	1641/546	97	87.8	95.9	AgE31: 35111 - 35167 (+) 35988 - 36096 (+) 36896 - 37122 (+) 37774 - 37902 (+) 38297 - 38459 (+) 38927 - 39117 (+) 39342 – 39437 (+)	

[illegible]

AgR043_g091_t01	bt-D	tbb-7	n.a.	1356/452	99	80.9	91.3	AgR043: 1472802 - 1487383
n.a.	bt-G	tbb-9	n.a.	1425/47485.5	99	82	91	CM024173.1: 10203269 - 1 - 57 10203325 (+) 10204246 - 58 - 166 10204354 (+) 10204989 - 167 - 394 10205216 (+) 10206197 - 395 - 422 10206324 (+) 10206637 - 423 - 585 10206799 (+) 10207440 - 586 - 776 10207630 (+) 10209713 - 777 - 872 10209808 (+) 10209991 - 873 - 1059 10210177 (+) 10211570 - 1060 - 1425 10211835 (+)

^aFor each locus, only the best matching transcript was included.

^bAnnotated *Caenorabditis elegans* ortholog in WormBase ParaSite

^cCoding sequence including stop codon in base pairs/amino acids

^dUsing *Haemonchus contortus* isotype 1 β -tubulin as query in a TBLASTN search.

^eBased on the BLOSUM62 similarity matrix.

^fDetails for individual exons are only provided if a different gene model than in the genome annotation was used.

^gVersion after manually editing the cDNA sequence.

n.a., not available