

Table S1. Transcripts in the *Parascaris univalens* genome (PRJNA386823) 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 <i>C. elegans</i> ortholog ^b	Length (bp/aa ^c)	Query coverage ^d (%)	Identity ^d (%)	Similarity ^e (%)	Location genome ^e	Location cDNA ^e
PgB04_g135_t01	bt-F	tbb-3	<i>mec-7</i>	1329/442	95	91.3	96.0	PgB04:1,953,671- 1,964,238 (-)	
PgB04_g136_t01 ^{f,g}	bt-E	tbb-4	<i>tbb-4</i>	916/305	68	92.1	97.7		
PgB04_g136_t01me ^h	bt-E	tbb-4	<i>tbb-4</i>	1278/426	95	91.5	96.9	PgB04: 1982336 - 1982392 (-)	1 - 57
								1981706 - 1981814 (-)	58 - 166
								1981151 - 1981261 (-)	167 - 277
								1980417 - 1980532 (-)	278 - 393
								1979909 - 1980037 (-)	394 - 522
								1979599 - 1979714 (-)	523 - 638
								1978892 - 1978987 (-)	639 - 735
								1978310 - 1978409 (-)	736 - 872
								1977262 - 1977448 (-)	973 - 1159
								1972810 - 1972928 (-)	1160 - 1278
PgB10_g062_t01	bt-D	tbb-7	n.a.	1356/451	99	79.8	91.3	PgB10:929520 - 937009 (+)	
PgE153_g002_t01	bt-C	tbb-6	n.a.	1353/450	100	85.7	94.0	PgE153:8,032 - 15,428 (+)	
PgR003_g161_t04	bt-B	tbb-8b	<i>tbb-6</i>	1368/455	97	90.8	96.6	PgR003:3157208 - 3178515 (+)	
PgR007_g022_t01	bt-A	tbb-5	n.a.	1353/450	98	93.2	97.7	PgR007:407010 - 413041 (+)	

PgR045_g070_t01	bt-G	tbb-9	<i>tbb-6</i>	1488/495	99	78.7	87.0	PgR045:1372050 - 1381671 (+)	
PgR045_g070_t01me ^f	bt-G	tbb-9	<i>tbb-6</i>	1428/475	99	82.1	90.8	PgR045: 1372050 - 1372106	1 - 57
								(+)	
								1373392 - 1373500	58 - 166
								(+)	
								1374127 - 1374353	167 - 393
								(+)	
								1375326 - 1375454	394 - 522
								(+)	
								1375747 - 1375909	523 - 685
								(+)	
								1377235 - 1377425	686 - 876
								(+)	
								1379551 - 1379646	877 - 972
								(+)	
								1379832 - 1380018	973 - 1159
								(+)	
								1381403 - 1381671	1160 - 1428
								(+)	

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

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

^cUsing *Haemonchus contortus* isotype 1 β -tubulin as query in a TBLASTN search against the cDNA.

^dBased on the BLOSUM62 similarity matrix.

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

^fVersion after manually editing the cDNA sequence.

^g5'- and 3'-ends are missing.

^h3'-end is missing.