Supplementary Table S4. Multiple alignment of the 5'- and 3'-regulatory sequences of the bonafide tubulin-encoding genes of *T. vaginalis*.

Group	Name	TVAG_	

5´-regulatory regions

+1

Group	Name	TVAG_	Sequence
	TvTUBα1	359090	AAAATAGAGGATGTCTGTTTGATTTTCCAAATACGTTATTAATAAAAATCCGTTTCTTTTTTCTAAAAAGTGTCACTCTTCATCAATG
	TvTUBα2	196270	AAAATAGAGGATGTCTGTTTGATTTTCCAAATACGTTATTAATAAAAATCCGTTTCTTTTTTCTAAAAAGTGTCACTCTTCATCAATG
	TvTUBα3	206890	ATAGCCATACAAACAAAATATCAAAAGACAAGTGAAAATCCGTTATGTTTTCTTGAGAAAGCAGATTTTGACACTCTTCATCAATG
A	TvTUBα4	312330	ATTTTTCATTGAAAATTAAAATACGTTAATTTTTGAATGCCGTTTTGTACGTTATCAAGAGACGGTTTTGCTTCACTTCATCAATG
	TvTUBα5	360870	CATTTATCCTTGACAATACTGTCTAAGCAAAATATCTAAAAATAGGAAAAAATTCGTTAGTAGTTTTTTAATTCACTCTTCATCAATG
	TvTUBα6	448380	TTGCAGCAAGATTAAAAACGGATGTGTCCGTTTTTTAATAAAAAACTCTCAGAAAATATTGTAGGGTTTGTTCAAATCACTCTTCATCAATG
I	TvTUBα7	467840	TGAATTAGTAAACTGAAAACGGATTTGCCCGTTTTTTAAATAAAAACACTCAGAAAATATTGAAATGATTCTCAAATCACTCTTCATCAATG
	TvTUBβ1	034440	TAATACGCATATTCTTTTTTATATATTTAAATTGTGATGGAGTGGTGGTTTTTTCACGTTATTCATTTTCTATCACTTCATTCTCAATG
B	TvTUBβ2	456920	AATTACGGGACAGATAAATTATAAACTGATCTTGTGAATTATTTGAGTGAAACCGCTCAATACGTTAATATCATTATTCACATG
	TvTUBβ3	008680	CACATAAATCCAGAAATAGTAAACGTGCACTTATCAAAACTATTGAGTAAAACCGCTAAATACGTTTTTAATCACTACTTTTCATG
	TvTUBβ4	062880	ATAAAAAGGCTCAAAAAATATAAACGCCCGGGCTGAATAAATTGAAATAAACCGAATAATTCGTTTTTAATCATAATTACACATG

3´-regulatory regions

Group	Name	TVAG_	Sequence
	TvTUBα1	359090	....TAAATTCGCTAATTCCTAAAACATTATTATTAATGTTCGTAATTCGATATATTTTTTTTCTCATGTTCTTTGATTTATAGTCATAATCTTA
	TvTUBα2	196270	TAAATTCGCTAATTCCTAAAACATTATTATTAATGCTCATAATTAGATATATTTTTTTTCTCATTTTCTTAAAATTATTCAGATCCAATTT
	TvTUBα3	206890	TAAATTCGCTAATTCCTAAAACATTATTATTAATGTTCGTAATTAGATATATTTTTTCTCATGTTCTTTGATTTCTAGTCATAATCTTAA
A	TvTUBα4	312330	TAAATTCGCTAATTCCTAAAACATTATTATTAATAATATATATATTTTGATCTTTGGTTTCGATTCATAATCTTAAAATTATTCAGATC
	TvTUBα5	360870	.TAAATTCGCTAATTCCTAAAAAGGTATTTTTATATCTTATGACAAACAGATTCTTTTTTTTATCTCATAATTCAAAAAGAATTTTGATA
I	TvTUBα6	448380	TAAGAACAATAAAAACATCTAACGTTTTCTCCTTTTAAAAAATTTTTAATTTTTCATCAATAAATACTCAATTATACCTTATCATATTGACTAATCCTCCATC
	TvTUBα7	467840	TAAGAAAAAAAAATTTTTTTTTAAAAATAATTCTTTTATTATAATTCTCTATTCAATCTTACTCCAGTCAACTCTTGCTAATGCAGCAGCGTTTCTTACTTCA
	TvTUBβ1	034440	TAAACAATTTTTATGTTGGTTCCTGATAACTTTTTGTAATTTTTTTAATAAAAATTATTTCAAAATTGTTTTTAATTTTCATTCT
B	TvTUBβ2	456920	TAAGTAATCTAAACGAAGTTTCACAACATACTTTTATTTTAATTTTTTATAAGTTACTTTTTTATCATCCTTTACGAGTACATCCTTGAACGGTAATTTTTTTTATTATTCCGAAATTA
	TvTUBβ3	008680	TAAGCGATTTTATATTCTGACTATAAAACATGATTTGAGTTTTGTCTTTAATCATTTCAAATTTTTACATTTTTTTCATTGTACAAATAGATTTGATAAAAAGTTTCAATTATTTTAGA
	TvTUBβ4	062880	TAAGCAGTTATTTGATTTGAACGCTAAAGAATTATTTTTTGGTGTAATAATTTTCTCATCCATTTTTAAAAACTTCATCTATAAAAATTTGAAATTAGATATTTTGTC

The 5´- and 3´-regulatory regions of all tubulin-like encoding sequences were analyzed to find putative Inr, Inr-like, motif 1 (M1), motif 2 (M2), motif 3 (M3), motif 4 (M4), motif 5 (M5), polyadenylation signal (PS), cleavage site (CS), and downstream element (DSE), respectively. The manual search of these putative elements was based on reported sequences by different groups (49-53) that resulted in 11 sequences containing the necessary elements to be expressed, such as a start codon (ATG), stop codon (TAA/TAG), putative Inr/Inr-like/motifs at the 5´upstream regulatory region and putative PS, CS, and DSE elements at the 3´downstream regulatory region. **Inr**, black and underlined capital letters; **motif M2**, highlighted in purple, **motif M3**, highlighted in green; **motif M4**, highlighted in blue; **PS**, underlined capital letters; **CS**, highlighted in gray; **DSE**, black capital letters. See Suppl. Table S6 for more information.