

Supplementary Table S3. Multiple alignment of the 5'- and 3- regulatory sequences of the bonafide actin-encoding genes of *T. vaginalis*.

Group	Name	TVAG_	
5'-regulatory regions			
I	TvACT1	160060	CTATCGTTCTGAAAACCCACATATTTTCTAGCAAGTTGCCCG AAAAAAT CAGAGTTGTGATACAGAAATAATT TCAC ⁺¹ TTTCTCTTAATG
	TvACT2	172680	CTTAGATGTCCTGGTTATAAATTTTGAAGACTCT AACCGTTG TCTAAAGAAGTGAAATGATTGGAATGTTAACT TCATT TTCTGGAATG
	TvACT3	200190	TTGACACAAAAAACCCACAATGACATGTGAATGATGCCCTTAAATTTGAGAGCGGATT GAAAAATG CTATGACT TCACA TTCTCTTAATG
	TvACT4	249200	TCGTTCTGAAAACCCACATGAAAGCAAAGGTATGCCCTATCAAATCAGCATAAAACCG TCATTTT TGATCAGT TCACA TTCTCTTAATG
	TvACT5	310030	CCACTAATCCGATA AAAGTGAC AGAAGAGTTCATCTTGCCCG AAAAAAT TCAGGGACATTATCAAAATTATAAT TCAC TTTCTCTTAATG
	TvACT6	485210	ACTAAATGGGACAAAAGACAGAAGGTTTCCCAAATTGAATGGAAGTGACGTGAGAATATTGCCCATTTCAAAG TCAC TTTCTCTTAATG
	TvACT7	149090	CTTCACTTGTTTCA AACCGTTT TTTATATGAATTAATTTGAGAACTTTACAGGTCATAAGAAACACTTTTTCTT TCAC TTTCTCTTAATG
	TvACT8	054030	GACGAAATAAACCA AAAGTGAC GATCCACTTCATATTGCCCGAAATAATTGAGAGGTTTTGGCAAAAAGAATG TCAC TTTCTCTTAATG
	TvACT9	090470	TGAGATTCTATCGTTTGAAAACCCACAAGTCCACTTCACGTTTGCCCTATTTCTGAGGGAAGTGAATGACT TCACA TTTCTCTTAATG
	TvACT10	337240	CCATATTTGAATTCCTCTCAAAATATAAAATCCCTTTCAAAAAGAGATTGAAAGAAGGGCAAATT AAAGTGAC TCATT TTCTCTTAATG
3'-regulatory regions			
I	TvACT1	160060	TAA ACAATTTCCGGTATAATATATTTAAATCAAATCAATTTT TTTTATTTT CTATCCTAATTTATAACTAATTCATAATACTTTATGGCAATAAAGTTAATA
	TvACT2	172680	TAA ACAATTTCCGGTATAATATATTT CAAAATTAATTAAC TTTTTCTTTAGTGAACCTGTTTGGAAATCACTTCATTAATATTGTGTTTTAATGGTTTATA
	TvACT3	200190	TAA AAAGTTTTTTTTTCGTTGTCTCCAATT TAATCAAAAAATATTTTTT CATTATTTACTTGATATAGCTATCTTTAAGCTGAACATTCAATATAATACATAT
	TvACT4	249200	TAA ATTTTCCGGTTTATTTGATAATT TTCTCTCTTTTTAATAATTTCTCATCTT ATTATATGATAACTATTGCATGATCTTTTGTACTACTACAAATG
	TvACT5	310030	TAA CAACTTCGGTATATATTTTATAATT TATCAACTTTTTTCCTTTTTT TATGAAAATTTATCTCAGATTGTTTCCAAAGTGAAGATAATTTAAGGATAA
	TvACT6	485210	TAA ATTTTCCGGTCTTTATATTACTACAAATTT ACTTACTTTTTTACTTTTT TACCAAGCATTCTAGAAATAATTCATTTACTTTATTGGAAATCTATAAGTT
	TvACT7	149090	TAA ACAATTTCCGAATA TAAT ATTTATTGAATTCGAAAAAAAT TTCTTTTAATTT CAAAAAGATTTATGTTTATTAGCAAATGAAG TTTAATTTCTTATATC
	TvACT8	054030	TAA AAAGTTTTTTTTTCGTTGTCTCCAATTATTCAAATC TTTTTTTT TATTACTGTTTCAATTCATTAGAAAGTGAAGT TTTTTAAAGCACTATCTGGCC
	TvACT9	090470	TAA ACTATATTTTATTAGCTTCCAGTTAA CAAAATTTATCAGTTTTTT AAATATTTTCAATATTTGAAATTAATCATTCTCAACTGGCCAATTACTA
	TvACT10	337240	TAA ACAATTTGAAATGTTTCAGATTCCAAATTTCTAAT TTTTTTAACTTTTTT ACTCTTTTACAACATCTTTATCAATCTACGCCTTATATAATTCCT

The 5'- and 3'-regulatory regions of all actin-like encoding sequence 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 10 sequences containing the necessary elements to be expressed, such as a start codon (ATG, red letter), stop codon (TAA, red letter), 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 M1**, highlighted in yellow; **motif M2**, highlighted in purple, **motif M3**, highlighted in green; **M4**, highlighted in blue; **PS**, underlined capital letters; **CS**, highlighted in gray; **DSE**, bold capital letters. See Suppl. Table S5 for more information.