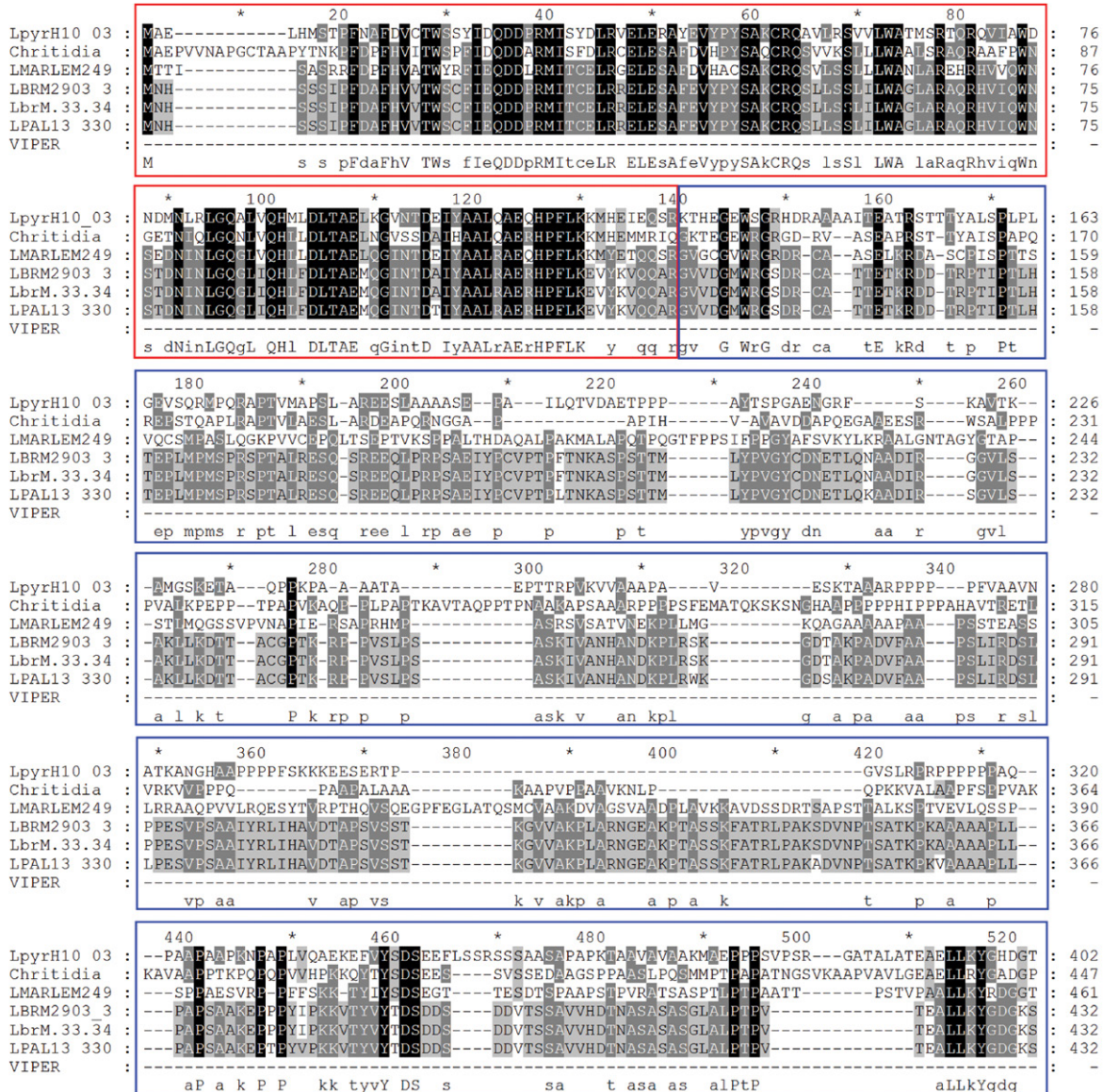


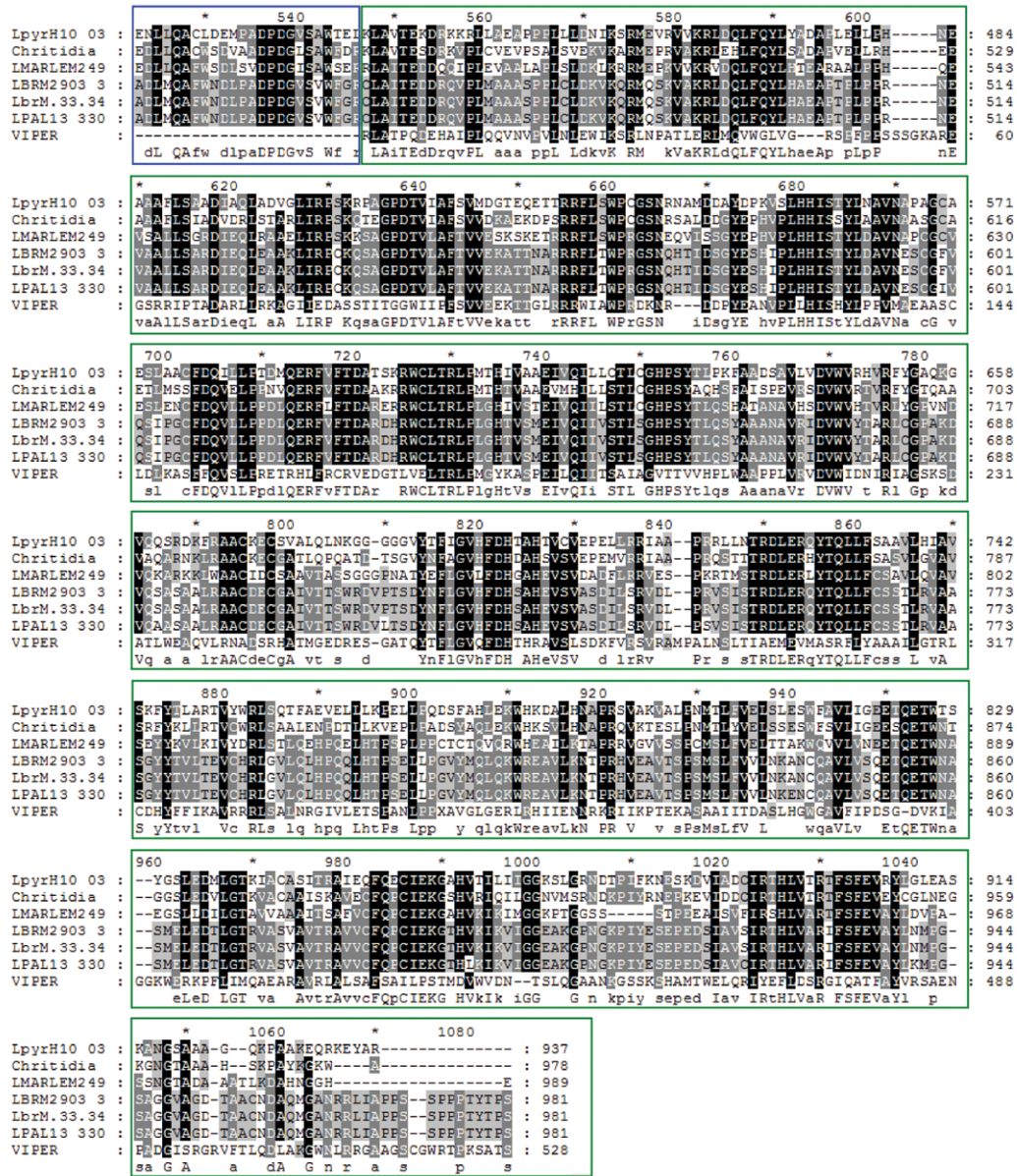
TABLE

TryTripDB gene identification (ID) of the orthologous genes located up and downstream the domesticated gene. The upstream gene is annotated for some species as “Zn-finger in Ran binding protein and others” and the downstream gene is annotated as “hypothetical protein, conserved”. Species that contain the domesticated gene are shown in bold. The IDs of orthologous genes from species where the domesticated gene was not found were also provided

Organism	Upstream gene	Downstream gene
<i>Crithidia fasciculata</i> strain Cf-C1	CfaC1_21: 1262421- 1263227*	CFAC1_210044900
<i>Endotrypanum monterogei</i> strain LV88	EmoLV88_33: 1359639- 1360553*	EMOLV88_330037700
<i>Leishmania panamensis</i> L13	LPAL13_330041700	LPAL13_330041900
<i>Leishmania aethiopica</i> L147	LAEL147_000701800	LAEL147_000701900
<i>Leishmania arabica</i> strain LEM1108	LarLEM1108_33: 1307955- 1308869*	LARLEM1108_330039800
<i>Leishmania braziliensis</i> MHOM/BR/75/M2903	LBRM2903_330043500	LBRM2903_330043700
<i>Leishmania braziliensis</i> MHOM/BR/75/M2904	LbrM.33: 1456663-1457580*	LbrM.33.3500
<i>Leishmania donovani</i> BPK282A1	Ld33_v01s1: 1435155-1436069	LdBPK_333370.1
<i>Leishmania enriettii</i> strain LEM3045	LENLEM3045_330042100	LENLEM3045_330042200
<i>Leishmania gerbilli</i> strain LEM452	LGELEM452_330042900	LGELEM452_330043000
<i>Leishmania infantum</i> JPCM5	LinJ.33: 1429595-1430509*	LinJ.33.3370
<i>Leishmania major</i> strain LV39c5	LMJLV39_330045400	LMJLV39_330045500
<i>Leishmania major</i> strain SD 75.1	LMJSD75_330044200	LMJSD75_330044300
<i>Leishmania mexicana</i> MHOM/GT/2001/U1103	LmxM.32: 1390571-1391485*	LmxM.32.3220
<i>Leishmania</i> sp. MAR LEM2494	LMARLEM2494_330040600	LMARLEM2494_330040800
<i>Leishmania tarentolae</i> Parrot-TarI	LtaP33.3470	LtaP33.3480
<i>Leishmania tropica</i> L590	LTRL590_330041700	LTRL590_330041800
<i>Leishmania turanica</i> strain LEM423	LTULEM423_330043000	LTULEM423_330043100
<i>Leptomonas pyrrocoris</i> H10	LpyrH10_03_5680	LpyrH10_03_5700
<i>Leptomonas seymouri</i> ATCC 30220	Lsey_0124_0160	Lsey_0124_0180
<i>Trypanosoma brucei</i> Lister strain 427	Tb427.02.6070	Tb427.02.6080
<i>Trypanosoma brucei</i> TREU927	Tb927.2.6070	Tb927.2.6080
<i>Trypanosoma brucei</i> gambiense DAL972	Tbg.972.2.4240	Tbg.972.2.4250
<i>Trypanosoma congolense</i> IL3000	TcIL3000_2_1690	TcIL3000_2_1700
<i>Trypanosoma cruzi</i> CL Brener Esmeraldo-like	TcCLB.507105.20	TcCLB.507105.30
<i>Trypanosoma cruzi</i> CL Brener Non-Esmeraldo-like	TcCLB.506815.40	TcCLB.506815.50
<i>Trypanosoma cruzi</i> Dm28c	TCDM_07380	TCDM_07379
<i>Trypanosoma cruzi</i> Sylvio X10/1	TCSYLVIO_004016	TCSYLVIO_004017
<i>Trypanosoma cruzi</i> marinkellei strain B7	Tc_MARK_2783	Tc_MARK_2784
<i>Trypanosoma evansi</i> strain STIB 805	TevSTIB805.2.3440	TevSTIB805.2.3450
<i>Trypanosoma grayi</i> ANR4	Tgr.572.1040	Tgr.572.1050
<i>Trypanosoma rangeli</i> SC58 ¹	TRSC58_00071	Not found
<i>Trypanosoma vivax</i> Y486	TvY486_0202070	TvY486_0202080

*: non annotated orthologues. The chromosomal position of the open reading frame is indicated; ¹: the downstream gene was not found for this species and the upstream gene is located in a small contig.





Alignment view of amino acid sequences of the domesticated gene from different species and the C-terminal portion of the third VIPER protein. The distinct regions I, II, and III of the protein are represented by red, blue, and green boxes, respectively. The order of genes from top to bottom is LpyrH10_03_5690, *Critidia* non-annotated gene, LMARLEM249_330040700, LBRM2903_330043600, LbrM.33.3490, LPAL13_330041800, and VIPER.