

Supplemental Figures

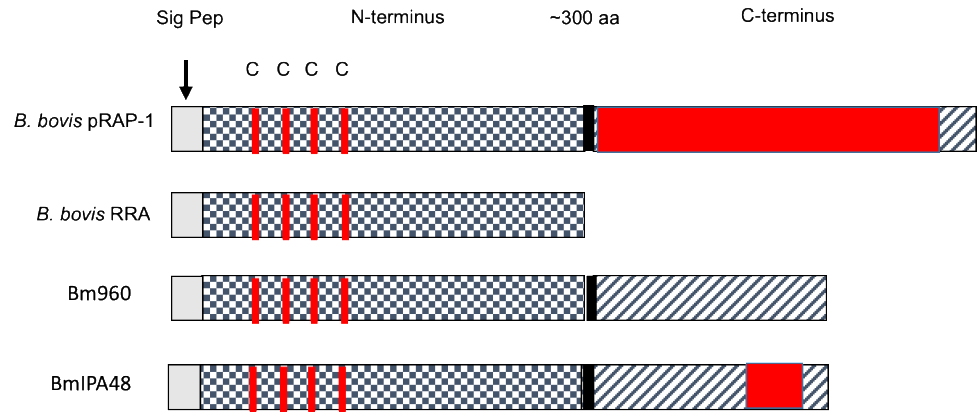


Figure S1. Schematic representation of the structural features of RAP-1 and RRA proteins. The relative location of the typical conserved Cys residues of the RAP-1 proteins is marked in red. The solid red box represents the repetitive region in the RAP-1 proteins of *B. bovis* and the RAP-1 putative *B. microti* BmIPA48 and Bm960 proteins. (The proteins are not represented in scale).

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repeats      1  MRGMFSNKWMSFVCFSILFVALKSDLEYVSAALKLLRAPPTSLFLEKLIDDGSDIPKDP
960          1  -----
consensus    1  mrgmfsnkwmsfvcfsilfvalksdleyvsalkllrappqtslflekliddgsdipkdp

repeats      61  DTDKEESQSSLFKFNINLFNKKSIWEADEKFVITIAKSRLNVILAQKLDLFLAKTCKIYT
960          1  -----MSFTATE-----LIK-----DKEQLLLETNKSCAFIN
consensus    61  dtdkeesqsslfkfnl  F  siweadekfvitL Ksrlnvi  L kF KtC

repeats      121 VDSEHSACINDIKIYAQKCTESNDLNSCYVPIQPIAKLPISR--LVGLVPHVLNFSIL
960          28 -GDLVDNCVGSIEDYIKRCSENP--YDCTLINAVPLIVYSSITTTNTDAVE--LTAALIS
consensus    121 v      Ci I Y kC E dl C vI Pi ts ttn y V hvL I

repeats      178 IFTNLRSNLDRYYIDGSKDWFSHIFMRKREFGIRNKHSYSDNRLMNKIFSRTS----
960          83 LYKEIPRRRG-FF-N--RKRIINILIRI---ITLGMYNNSDDOTLINSITHLKSGIYY
consensus    181 if l      ryyi gsk s I mRlkrf i f Dn LmN i r sgiyy

repeats      233 TTEGPDRS-----DSLISN-----YIKFGAIEYAILLNTR
960          136 KHVSPGNEQFAFSQLQLLFIGVDSLTSFIIFYRMLTSLIFSDFYSKFGISS-PIISN--
consensus    241 f P qfafsqlqlllfigvdSL S fiifyrmltstlsifdsfy KFG y Il Ntr

repeats      263 SNLVKMISSSEAHIKFVRIRLYKFYTNKKSIEGLVTRGHKPVDISN-----NPIIS
960          193 -KGRIRLYSVYFKHMKKIGRTIVSVSKSLFKDALFFTVSGVKEVYISLPNYISILSPSID
consensus    301 s km lS F HiK v k L wK e G lK V lS pnyisils i

repeats      315 DNIFKYFGKFSNNTNLSNAIA-GAFIDHYKSLFSNSTDVNCEGSSGEGPSSGEGFN----
960          252 EQQSKMFTALFASTIHNAATEVSEIVPKL--IVLDSSTQNAIDSICKNTSGEKLSLFLCL
consensus    361 dn K F T AI v l h ksl St Ng S SGE lflcl

repeats      369 -GEGS-----SGEGPSSGEGFNGE-GFDGEGSPSGEGPSGEGFNGEGFNGEGLNCEGPSGEG
960          310 RGRRTNDLKNTSPFEYTLIKATSKAEERQSRHQGKRRERDICK--NQLSGIVGFFRN
consensus    421 rG srndlk P i E S gF G ng gL G

repeats      422 PSGEGLNEWGLMNGTA
960          368 PLGKRE-----
consensus    481 P G newnglmngta

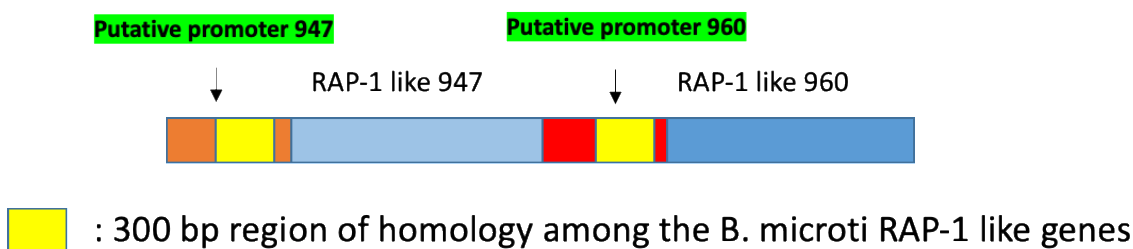
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Figure S2. Amino acid sequence alignment between the BmIPA48 and Bm960 RAP-1 like proteins. Note the alignments of the 4 conserved Cys and Tyr residues at the NT-end of the proteins.

BmIPA48

mrgmfsnkwmsfvcfsilfvalksdleyvsalkllrappqtslflekliddgsdipkdpidtdkeesqs
 slfkfnlnfnkksiweadekfvitlaksrlnvilaqkldkflaktckiytdsehsacindikiyaqkie
 sndlnscyvipiapiaklptsrlyglvphvlnfsiliftnlrsnldryyidgskdwfshifmrlkrffgirnk
 hsyfsdnrlmnkifsrtsttfgpdrsdslsnyikfgaieyailntrsnlvkmilssfahikfvrkrlykfyt
 nkwksieglvtrghlkpvdlsnnpisdnifykfgksnntnlsnaiagafldhykslfsnstdvn
 sgegpsgegfngegssgegpsgegfngegfdgegpsgegpsgegfngegfngeglngegpsge
 gpsgeglnewnglmngta

Figure S3. Amino acid sequence of the Bm947 protein. The region with repeats is marked in red font.



Query	689	tttttttAATATGAAGGAACGTATAGTAATATTAATATGCGATTGCGGTATATTAGGTT	748
Sbjct	395	TTTTTTTAAATATGAAGGAACGTATAGTAATATTAATATGCGATTGCGGTATATTAGGTT	454
Query	749	TATGTGGCTGATTAGTGCAATGTAGTAATGTCTATTG-----A----CCCAT	792
Sbjct	455	TATGTGGCTGATTAGTGCAATGTAGTAATGTCTATTGTAGTAATTGTCTATTGGCCCAT	514
Query	793	GTGCCAATGCGTGTGTTATTACACGATTATACTTAATAATCGGATGAAACCAACACAAAA	852
Sbjct	515	GTGCCAATGCGTGTGTTATTACACGATTATACTTAATAATCGGATGAAACCAACACAAAA	574
Query	853	GTTATCAATTTTGAACGTGTGCAGTATGAATTAATTTATTCTTACACAATTTTATTCCT	912
Sbjct	575	GTTATCAATTTTGAACGTGTGCAGTATGAATTAATTTATTCTTACACAATTTTATTCCT	634
Query	913	TGTTGTTATGCCGATAGTTGCAGTGCACCCATTAGCCTAATTCTTAAGTAAGGAATAC	972
Sbjct	635	TGTTGTTATGCCGATAGTTGCAGTGCACCCATTAGCCTAATTCTTAAGTAAGGAATAC	694
Query	973	ACTCACTC 980	
Sbjct	695	ACTCACTC 702	

Figure S4. Schematic representation of the 300 bp region of homology among the *B. microti* RAP-1 like genes BMR1_03g00947 (947) and BMR1_03g00960 (960).

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Pf 3752  NGDEYDGDDEYDGDDEYDGDDECDGDDEYDGDDEYDGDDEYDGDDEHNGDEYNGDEYNGDEY  3811
        NG+   G+   G+  ++G+   G+   G+  ++G+  +DG+   G+   +G+  +NG+  +NG+
Bm 353   NGE GSSGEGPSGEGFN GEGSSGEGPSGEGFN GEGFDGEGPSGEGPSGEGFN GEGFN GEGFN
                                     NG+  +G+  +G+  N  E+NG
Bm 413   NGE GPSGEGPSGEGLN--EWNG  432

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Figure S5. Amino acid alignment between BmIPA48 (Bm) and PF3D7_1324300 (Pf). The only region of homology corresponds with a G-rich repeated region.

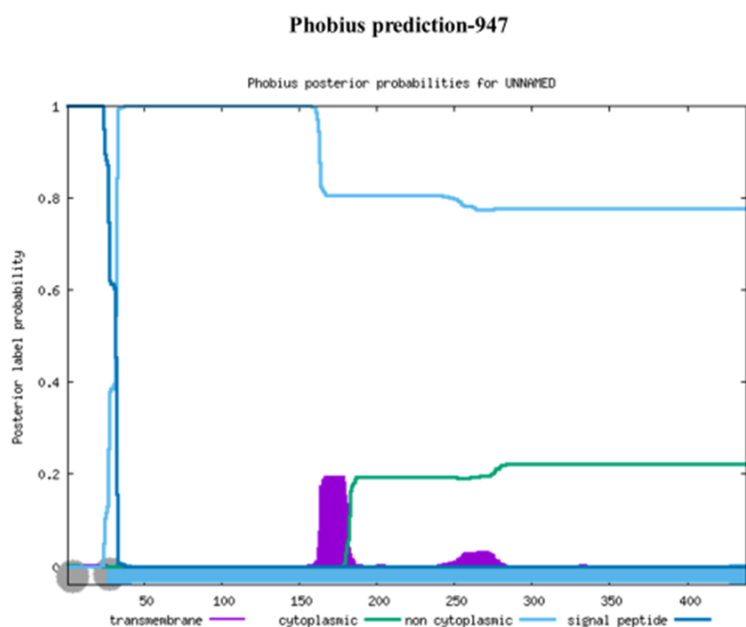


Figure S6. Secondary structure prediction of BmIPA48 using the software Phobius. Two putative transmembrane domains were confirmed by this predictive algorithm.