

## Architecture of the Trypanosome RNA Editing Accessory Complex, MRB1

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### Supplementary Data:

**Table S1. Primers used in this study**

#### Yeast two hybrid primers

Name	5' Primer	3' Primer
kPAP1	GCGCATATGAGAAAGTTTTCAGCTTTT CGGTC	GCGCTGCAGCTCGAGCTACTGATGAT TGTCGCATTTTATCC
kPAP1	GGAGGCCAGT <b>GAATTC</b> ATGAGAAAG TTTTCAGCTTTTTCGGTC	CGAGCTCGAT <b>GGATCC</b> CTACTGATGA TTGTTCGCATTTTATCC
7510	AAAAGAGATC <b>GAATTC</b> ATGCGGCACA CAATACC	TGCAGGTCGACAT <b>CGAT</b> GTTATTGTC ATCAAGTATATCC
0024	AAAAGAGATC <b>GAATTC</b> ATGCGGCGTT GGCACC	TGCAGGTCGACAT <b>CGATA</b> ACCTTGTC CTCGTCGTC
PPR5	AAAAGAGATC <b>GAATTC</b> ATGCTCCGCC GTAGTGA	TGCAGGTCGACAT <b>CGAT</b> ATATGCAGT TCCACAAACCT
3180	AAAAGAGATC <b>GAATTC</b> ATGCTTCGCT GCACTGTT	TGCAGGTCGACAT <b>CGAT</b> ATAGGGGCC ACTCGTC
PPR1	TGTATCGCCG <b>GAATTC</b> ATGTTCCAAC GCCGTTAGTGCTG	TGCAGGTCGACAT <b>CGAT</b> CTAAACATC CGCACCGGCAGC
MRB0130	AAAAGAGATC <b>GAATTC</b> ATGCGGCGG TGTTCCCTT	TGCAGGTCGACAT <b>CGAT</b> CAAACCTTAC CTTCCCTACAG
3900	AAAAGAGATC <b>GAATTC</b> ATGAATCGTA CGGGTGGG	TGCAGGTCGACAT <b>CGAT</b> CACCTTCTT GATACCCAGT
5120	AAAAGAGATC <b>GAATTC</b> ATGACATCTA GCGTAACC	TGCAGGTCGACAT <b>CGAT</b> TTTTTTTCTTC CCCTTGTTCTTTCT
GAP1	TGTATCGCCG <b>GAATTC</b> ATGCTGCGC GCGCGCCTG	TGCAGGTCGACAT <b>CGAT</b> CTAGTATGC CGAAACGGCAGTC
GAP2	AAAAGAGATC <b>GAATTC</b> ATGCTTCGCT TATTGCGG	TGCAGGTCGACAT <b>CGAT</b> CAACTTCGC CTCACAGCC
Helicase	AAAAGAGATC <b>GAATTC</b> ATGCGGGCC ATACGACTAA	TGCAGGTCGACAT <b>CGAT</b> TTACGAGTC TCCACCAGCC
MRB11870	AAAAGAGATC <b>GAATTC</b> ATGCTGCGCC ACACATCACG	TGCAGGTCGACAT <b>CGAT</b> TTATTTCTGC AGTTGATGCGTC
MERS1	AAAAGAGATC <b>GAATTC</b> ATGCGCAAGC AATTATTTTTT	TGCAGGTCGACAT <b>CGAT</b> TCACGATGC ATCTTCCCCG
MRB1820	AAAAGAGATC <b>GAATTC</b> ATGCGAACCC AAGGATCCTTCG	TGCAGGTCGACAT <b>CGAT</b> CTAGCGGGG TATTGCCCC
MRB2140	CATGGAGGCC <b>GAATTC</b> ATGTTCCGCT GGTCGTGGTG	GCAGGTCGAC <b>GGATCCT</b> CAGGTTAAG GACGCAGAAACA
MRB3010	AAAAGAGATC <b>GAATTC</b> ATGCGGAGC GCGTTGCG	TGCAGGTCGACAT <b>CGAT</b> TGCTTGCGG TGTAGACC

<b>MRB5390</b>	AAAAGAGATC <b>GAATTC</b> ATGAATGGGA GGCTGTACT	TGCAGGTCGACAT <b>CGAT</b> GCGTCTCAA TAGAAGCTG
<b>MRB4160</b>	AAAAGAGATC <b>GAATTC</b> ATGTACCCTT TCATAGAACCTCG	TGCAGGTCGACAT <b>CGAT</b> CTAATAAAG CACCTTCGCTAACAT
<b>MRB8620</b>	CGC <b>GAATTC</b> ATGAGTAACCCTTTTGA GAAAGTTGC	CGC <b>GGATCC</b> CTACTTACCACCATCTT GCGACAAC
<b>MRB8170</b>	TGTATCGCCG <b>GAATTC</b> ATGCGACGG CTAAGCCTTCTT	TGCAGGTCGACAT <b>CGAT</b> CTAACAAAA TACCTTCGCTAACAT
<b>TbRGG2</b>	AAAAGAGATC <b>GAATTC</b> ATGAAGCGCA CACCTGTT	TGCAGGTCGACAT <b>CGAT</b> CACCTTCTG ACTGGCATC
<b>TbRGG1</b>	AAAAGAGATC <b>GAATTC</b> ATGGTGTGTA GCACCATC	TGCAGGTCGACAT <b>CGAT</b> CTTTCCAC CAAACCTAGG
<b>MRB1860</b>	GCG <b>CATATG</b> CTGCTGCCACTCTCG AGCG	GCG <b>GATCTATCGATT</b> CACACCAGCT GTAAAGGCGGATTATTCAC
<b>MRB6070</b>	TGTATCGCCG <b>GAATTC</b> GATGTAAACC TAAAGTTGTGTGG	TGCAGGTCGACAT <b>CGAT</b> CTAAGAATC TGATTCTTTAGAGGCTC
<b>MRB6070</b>	CGC <b>GAATTC</b> ATGTTCAAGCGGGCTTCA GCGTGC	CGC <b>GGATCC</b> TAAGAATCTGATTCTTT AGAGGCTC
<b>MRB800</b>	TGTATCGCCG <b>GAATTC</b> ATGCGACGTC GGGTAGTTTTATG	TGCAGGTCGACAT <b>CGAT</b> CTAAAGCGA TGCTTCGTCAGGT
<b>MRB10130</b>	GCG <b>CATATG</b> CTCAACGTTCTCTCGAG CACAGC	CGC <b>GTGACT</b> CACATAACTCCGGGAG CAGCTCC
<b>MRB8180</b>	GGAGGCCAGT <b>GAATTC</b> ATGTACCGT CTTTATCGTCCGACTGTAG	CGAGCTCGAT <b>GGATCC</b> CTAAACTGCT GTGGCCAG
<b>MRB1680</b>	AAAAGAGATC <b>GAATTC</b> ATGTGTACAC ACGCGCTCATATC	TGCAGGTCGACAT <b>CGAT</b> TTACGACGT CACCTCACTTACCT
<b>MRB1590</b>	CATGGAGGCC <b>GAATTC</b> ATGTACCATC GTGGCTACGGC	GCAGGTCGAC <b>GGATCC</b> TCATCTTTTC GCAGTAACGGTCC
<b>MRB0880</b>	CGC <b>GAATTC</b> ATGAGGAGTAGCCGGG GTATTTTG	CGC <b>GGATCC</b> TACTGTGTACCGTGTT CACCCGC

**PTP construct primers**

<b>MRB6070</b>	GAGGGCCCGTTCCAGTAGGGGTGGA	GAGCGGCCGCGAATCTGATTCTTTAG
<b>MRB5390</b>	GAGGGCCCTGAACGACCAACTGTAC	GAGCGGCCCGCGTCTCAATAGAAGC
<b>MRB10130</b>	GGAAGCTTCATCCGATCACCTCATGA	GAGCGGCCGCTAACTCCGGGAGCA
<b>MRB11870</b>	GAGGGCCCATAGCAGTTGGCCACG	GAGCGGCCGCTTCTGCAGTTGATGC

**RG2 3'UTR RNAi construct primers**

<b>TbRGG2</b>	GAGGATCCAACCCTATTTACGGGAAT	GACTCGAGCCCAAAGACAATACGGT
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**TbRGG2 addback construct primers**

<b>TbRGG2</b>	GGAAGCTTATGAAGCGCACACCTGTT	GTCTAGACACCTTCTGACTGGCATC
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**Supplementary Table S2. Likely contaminants associated with MRB1 components identified by LC-MS/MS.**

<u>MRB10130 likely contaminants</u>	<u>Unique peptides</u>	<u>Amino acid coverage</u>	<u>Description</u>
Tb09.211.4511, Tb09.211.4512, Tb09.211.4513	2	27.20%	Kinetoplastid membrane protein 11 (KMP-11)
Tb927.1.2340, Tb927.1.2360, Tb927.1.2380, Tb927.1.2400	8	23.70%	Tubulin alpha chain
Tb927.3.4360, Tb11.02.4000	2	22.20%	40S ribosomal protein S15a, putative
Tb927.1.2330, Tb927.1.2350, Tb927.1.2370, Tb927.1.2390	5	20.10%	Tubulin beta chain (Beta tubulin)
Tb10.70.5650, Tb10.70.5670	7	19.20%	translation elongation factor eEF-1 alpha chain
Tb10.26.0370, Tb09.160.4450	2	12.60%	RPS3  40S ribosomal protein S3, putative
Tb09.160.4200	1	10.60%	28G16.390 60S acidic ribosomal protein, putative
Tb927.4.1800, Tb927.4.1790	2	8.90%	ribosomal protein L3, mitochondrial, putative
Tb11.0880, Tb11.50.0005, Tb927.4.1100	1	8.80%	60S ribosomal protein L21E, putative
Tb10.70.4740	2	8.60%	enolase
Tb09.211.3270, Tb09.211.3280	1	8.00%	60S ribosomal subunit protein L31, putative
Tb10.70.3510, Tb11.01.5720	1	7.80%	60S ribosomal protein L18a, putative
Tb10.6k15.0410, Tb11.02.1840	1	7.80%	60S ribosomal protein L18
Tb10.05.0220, Tb11.01.1470	1	7.00%	60S ribosomal protein L10a
Tb09.211.0110, Tb09.211.0340	1	6.60%	60S ribosomal protein L10, putative
Tb10.26.1080	3	6.20%	heat shock protein 83
Tb10.61.1810, Tb10.61.1820, Tb10.61.1830	1	5.90%	mitochondrial carrier protein, putative
Tb10.70.5110	1	5.00%	mMDH mitochondrial malate dehydrogenase

Tb11.01.3170, Tb11.01.3180	2	4.40%	Guanine nucleotide-binding protein subunit b-like protein
Tb09.244.2730, Tb09.244.2740	1	3.20%	60S ribosomal protein L5, putative
Tb927.3.5050	1	3.20%	60S ribosomal protein L4
Tb927.2.1080, Tb927.2.240, Tb11.02.2380	1	1.30%	retrotransposon hot spot (RHS) protein, putative

<b><u>MRB5390 likely contaminants</u></b>	<b><u>Unique peptides</u></b>	<b><u>Amino acid coverage</u></b>	<b><u>Description</u></b>
Tb927.1.2330, Tb927.1.2350, Tb927.1.2370, Tb927.1.2390	10	28.10%	Tubulin beta chain (Beta tubulin)
Tb10.70.5650, Tb10.70.5670	10	27.80%	translation elongation factor eEF-1 alpha chain
Tb927.1.2340, Tb927.1.2360, Tb927.1.2380, Tb927.1.2400	8	22.80%	Tubulin alpha chain
Tb10.389.0690	3	8.20%	mitochondrial carrier protein, putative
Tb927.6.4280, Tb927.6.4300	3	8.20%	GAPDH glyceraldehyde 3-phosphate dehydrogenase
Tb10.389.1500	1	7.00%	short-chain dehydrogenase, putative
Tb10.70.5110	1	5.00%	mMDH mitochondrial malate dehydrogenase

<b><u>MRB6070 likely contaminants</u></b>	<b><u>Unique peptides</u></b>	<b><u>Amino acid coverage</u></b>	<b><u>Description</u></b>
Tb09.211.4540	4	17.00%	DRBD2
Tb09.211.2150	4	9.20%	poly(A)-binding protein 1
Tb927.1.2340, Tb927.1.2360, Tb927.1.2380, Tb927.1.2400	2	5.50%	Tubulin alpha chain
Tb11.24.0006	1	2.80%	expression site-associated gene, putative
Tb10.70.5680, Tb10.70.5650, Tb10.70.5670	1	2.30%	TEF1 elongation factor 1-alpha
Tb10.70.0280, Tb10.70.0430	1	2.10%	HSP60 chaperonin Hsp60, mitochondrial precursor
Tb927.1.880	1	0.10%	putative uncharacterized protein

<b><u>MRB11870 likely containants</u></b>	<b><u>Unique peptides</u></b>	<b><u>Amino Acid coverage</u></b>	<b><u>Description</u></b>
Tb927.1.2340, Tb927.1.2360, Tb927.1.2380, Tb927.1.2400	2	5.30%	Tubulin alpha chain
Tb927.1.2330, Tb927.1.2350, Tb927.1.2370,	1	2.70%	Tubulin beta chain (Beta tubulin)
Tb10.70.5680, Tb10.70.5650, Tb10.70.5670	1	2.30%	TEF1 elongation factor 1-alpha
Tb09.211.0940	1	2.90%	hypothetical protein, conserved