Supplementary Table S2. Guide RNA enrichment in affinity purified editing complexes. Read count is provided after filtering raw datasets against nuclear genome of *T. brucei* TREU927 (release 5.0, www.tritrypdb.org). Term: RNA sample was treated with Terminator exonuclease.

Complex	**Sample**	**Read count**	**Candidate gRNA read count**	**Candidate gRNA percentage**	**Relative enrichment**
GRBC	Mock	3914121	157749	3.99	significant
	Term	5002206	214833	4.25	significant
RGG2	Mock	4270129	176531	4.10	significant
	Term	6065063	256843	4.20	significant
PAMC1	Mock	4650970	190143	4.06	significant
	Term	8152879	360282	4.39	significant
RET2	Mock	956535	28618	2.91	none
	Term	2882095	48434	1.67	none
Mito RNA	Mock	17024977	287178	1.69	N/A
	Term	13788483	373389	2.71	N/A