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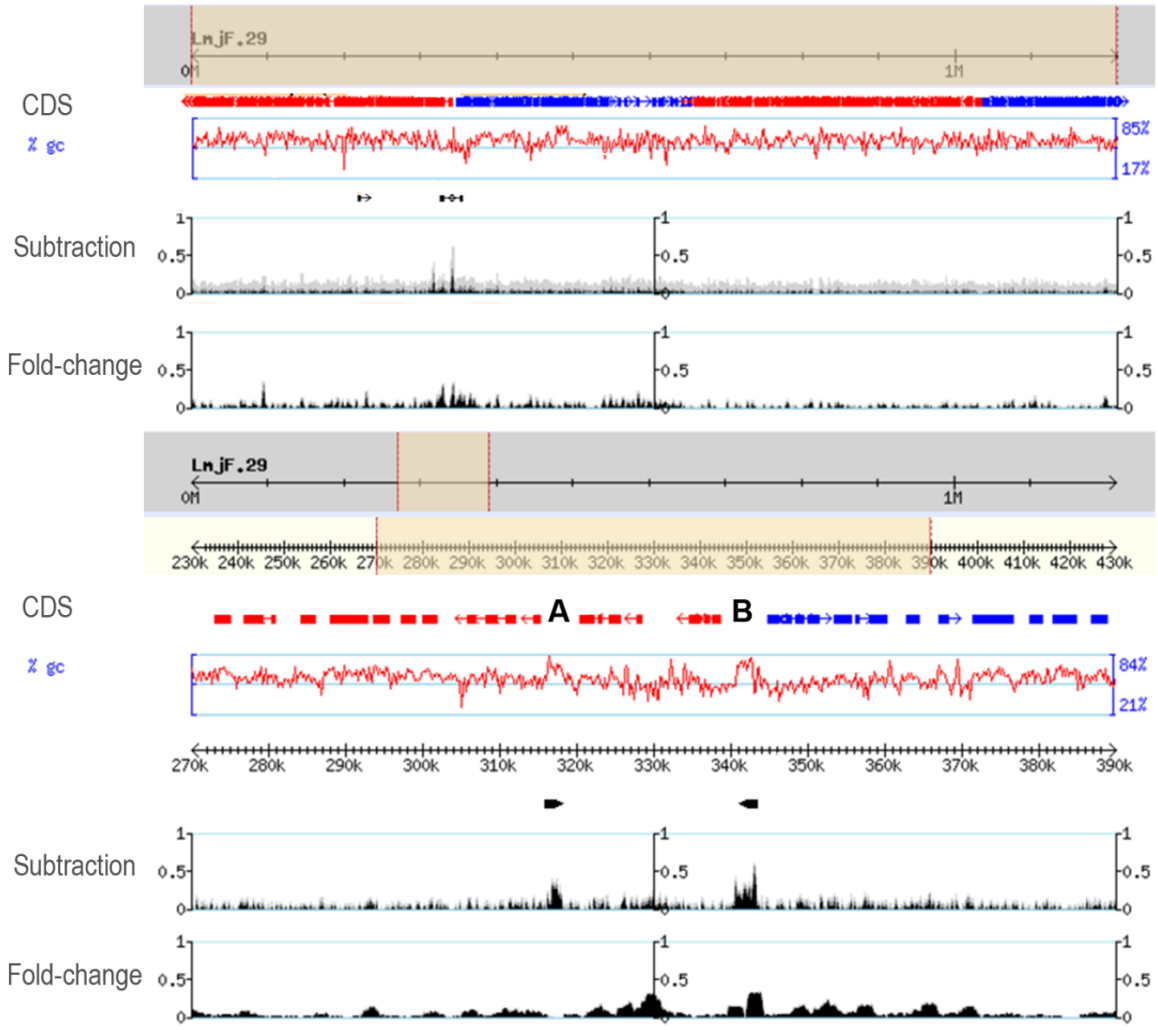
Appendix Table S1: Orthologous genes of TbKKTs in the genome of *L. major*: LmKKTs

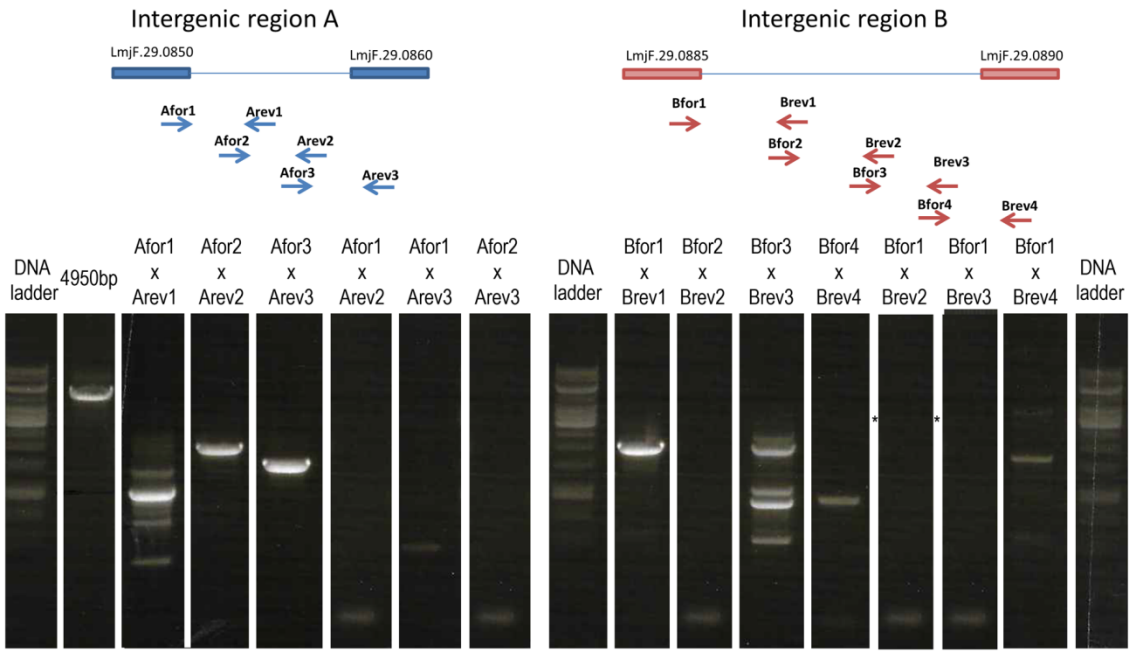
Name	*T.brucei*	*L.major*	Similarity (%)	Identity(%)
KKT1	Tb927.10.6330	LmjF.36.1900	53	36.2
KKT2	Tb927.11.10520	LmjF.36.5350	61.9	46.9
KKT3	Tb927.9.10920	LmjF.35.4050	51	38.5
KKT4	Tb927.8.3680	LmjF.10.0300	43	29.9
KKT5	Tb927.7.4850	LmjF.06.0200	57	36
KKT6	Tb927.6.1210	LmjF.12.0080	67.8	50.5
KKT7	Tb927.11.1030	LmjF.27.0430	36.6	24.4
KKT8	Tb927.4.5110	LmjF.31.2750	46.1	30
KKT9	Tb927.8.1150	LmjF.02.0610	42.8	26.2
KKT10*	Tb927.11.12410	LmjF.09.0410 LmjF.09.0400	74.3 79	65 70
KKT11	Tb927.7.2110	LmjF.22.0120	48.6	25.3
KKT12	Tb927.8.1680	LmjF.24.1400	51	29
KKT13	Tb927.7.4860	LmjF.06.0210	26	17.9
KKT14	Tb927.10.7240	LmjF.36.2800	39.6	27.5
KKT15	Tb927.6.3760	LmjF.30.2520	51.5	36.2
KKT16	Tb927.11.1000	LmjF.27.0400	45.1	24.6
KKT17	Tb927.3.2330	LmjF.25.2220	52.8	36
KKT18	Tb927.9.3800	LmjF.01.0350	43.6	28.7
KKT19*	Tb927.11.12420	LmjF.09.0410 LmjF.09.0400	71.1 74.2	62.7 66.1
KKT20	Tb927.8.4760	LmjF.10.1227	31.8	18.5

* TbKKT19 and TbKKT10 share 82.5% similarity and 79.8% identity



Appendix Figure S1: Chromosome 29: comparison of the results obtained using fold-change *versus* subtraction methods for ChIP-seq analysis.

Chromosome #29 is the only chromosome for which a clear peak was not obtained by ChIP-seq; on the contrary, it gives a very "noisy" dataset, in particular when using the fold-change-method to discriminate noise from signal. A simple subtraction after normalization to separate noise from signal; and indeed the subtraction method allowed us to distinguish a major peak and a minor peak, both being separated by 25 kb and sharing sequence similarities. Top panel: whole chromosome; lower panel: zoom-in view, A: intergenic region LmjF.29:315250..320300 and B: intergenic region LmjF.29:338691..344823.



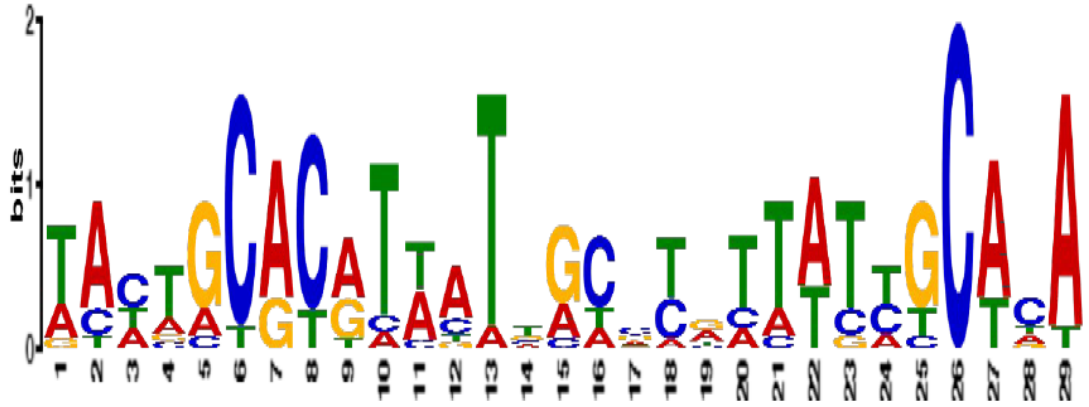
Appendix Figure S2: PCR failed to amplify intergenic regions A and B.

Chr. #29 has the same statistics regarding mapped reads as all other chromosomes, so there is no unfortunate sequencing bias that could explain this. One possible explanation is that the centromeric region of chromosome 29 may has not been properly assembled in the sequence available in TritrypDB. This same explanation had been alleged by Akiyoshi & Gull (Cell 2014) for Chr. 9, 10 and 11 of *T. brucei*. This hypothesis is further supported by the fact that both regions LmjF.29:315250..320300 and LmjF.29:338691..344823 (so-called intergenic region A and B) share sequence similarities. Indeed, a large 2244-bp region is perfectly duplicated, but inverted, in the positions LmjF.29:316100..318343 and LmjF.29:342885..340642; another smaller fragment of 114 bp was found in LmjF.29:20722..208354 (Appendix Figure S1, top panel). PCR primers were designed to map the intergenic regions A and B. The expected product sizes were 2000 bp and 5000 bp depending on the primer pairs. A 4950bp positive control was successfully amplified (Lane 2). Some of the PCR products were successfully amplified (Lane 4 (Afor2xArev2), 5 (Afor3xArev3), 10 (Bfor1xBrev1), 13 (Bfor4xBrev4) and the sequence verified by sequencing. For Bfor1xBrev2, a faint band (**) was visible at the expected size (4000bp) but could not be sequenced. All the other primer pairs failed to give a specific product at the expected size. For the list of primers see Appendix Table S2).

Appendix Table S2: List of the primers used to amplify intergenic regions A and B

	SSR A		SSR B
A-for1	ccgacatcgtgcatgatctcc	B-for1	taattgcagcttcccgcagc
A-rev1	cagcatctttcgtcggcagc	B-rev1	acggcgtccatccttcaagg
A-for2	cccgagcacgaaaaagtcacg	B-for2	tccagacgccaaagctgacg
A-rev2	cgggaagctctctcgatgagg	B-rev2	gagcgaaagcaaccacgtcc
A-for3	ccggtcgagtcatcgtttcg	B-for3	tgggatgccgcggcttg
A-rev3	ccgcacaatctcattgcagcc	B-rev3	gtgtgggcacattcctcagc
		B-for4	tcacttagggcgtcgcttgg
		B-rev4	ccccgagaacttcctgactcc

Appendix Figure S3: DNA motifs characterizing the centromeres of *T. brucei* (TbKKT3 binding sites)



!"#$%&+2)	"#$%&+2*2,67''&&26''//)	345)	)	()	)	"#$%&+2*)2,/72,&&2,/-(.)89:
!"#$%&+.)	"#$%&+.*.-,6''&&./''//)	345)	)	+)	)	"#$%&+.*).-,26.&&.-6(''))8@:)ABC)"#$%&+.*).-/(2-&&.-/6(6)8@:)
!"#$%&+,)	"#$%&+,*,'6-''&&,('(//)	345)	)	()	)	"#;<=>?+*)HJ5KL4A#)KM4)I4BKL1#4L\I)54GH4BI4)O\KM)+,)EJ)\IB1$HC4C)\IB)KM4)I4BKL1#4LI\) 54GH4BI4)
!"#$%&+6)	"#$%&+6*/-7+''&&/-6.//)	01)	)	)	)	
!"#$%&+-)	"#$%&+-*-+('''&&-+7-//)	345)	)	()	)	"#$%&+-*)-+(/.'&&-++7'2)8@:
!"#$%&+/)	"#$%&+/*72'2''&&7277//)	345)	()	()	()	"#=<?>*)"#$%&+/*)72('(.&&72+/(,)89:)ABC)"#;<=>?+*)"#$%&+/*)727++-&&727-''))89:
!"#$%&7')	"#$%&7'*++/.''&&+7+6//)	01)			)	
!"#$%&7()	"#$%&7(*66-('''&&6-(((//)	345)	)	()	)	"#$%&7(*)6-'7,-&&6-'-2-)8@:
!"#$%&7+)	"#$%&7+*((,/'''&&((6+7//)	345)	)	+)	)	"#$%&7+*)((,--'+&&))((,/+,')89:)ABC)"#$%&7+*)((6'(62&&((6',(6)89:
!"#$%&77)	"#$%&77*6,(/''&&6,.'//)	345)	)	()	)	"#$%&77*)6,2-(-&&6,.7/,)89:
!"#$%&72)	"#$%&72*+//+''&&7'+,//)	345)	)	()	)	"#$%&72*)7'++.-&&7'+6'+)89:)
!"#$%&7.)	"#$%&7.*.2,6''&&.2/-//)	01)			)	
!"#$%&7,)	"#$%&7,*(((+('''&&(((.-//)	345)	()		)	"#$%&7,*)(((+(6+))(((+2(+)89:
		K1KA$)	/)	+,)	2)	