polyA mRNA selection on oligoT beads

↓

1st strand cDNA synthesis by random hexamers

↓

2nd strand cDNA synthesis by 5' biotinylated spliced leader

↓

ligation of bar-coded paired-end 3' adapter

↓

purification on streptavidin beads

↓

PCR using mRNA-SEQ library amplification protocol

↓

size selection (120-160bp) on agarose gel

quality control by TOPO cloning and conventional sanger sequencing

sequencing on Genome Analyzer II using spliced leader primer
Figure S1

Illumina sequencing images

Basecalling of Illumina sequencing images by GAPipeline-1.3.2

Sample attribution / trimming of bar codes and 3’ adapter sequences

Read mapping to T. brucei 927 reference genome by maq

Attribution of reads to downstream genes; gene count normalisation

Loading of GFF format output into Gbrowse

Chromosome overview

Mapped reads

Chromosome zoom-in 1

Mapped reads

Chromosome zoom-in 2

annotated genes

assigned reads; read counts

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