

Supplementary Table 3. Sequencing and alignment results

	<i>L. donovani</i> library	<i>L. braziliensis</i> library
Total pairs of reads	1435277	1062571
Combined reads (mate 1 and mate 2 match)	1196156	912820
Uncombined reads (mates don't match)	239121	149751
Total reads used for collapsing (combined reads plus (uncombined reads x2))	1674398	1212322
Collapsed reads (cReads)	688524	538034
Unique and single copy	574049	421086
Alignment against respective reference genome LdoB, LbrM [cReads]	981412 (58.61%) [243745]	277363 (22.87%) [89414]
Alignment against LmjF reference genome [cReads]	966213 (57.7%) [234032]	641046 (52.88%) [200014]
Unaligned reads (LdoB for <i>L. donovani</i> library, LmjF for <i>L. braziliensis</i> library) [cReads]	692986 (41.4%) [444779]	571276 (47.1%) [338020]
Unaligned reads showing hits on NT-NCBI (no e-value cutoff result)	471103 (28.1%) [235745]	440511 (36.3%) [214674]
Amongst unaligned reads showing hits on NT-NCBI: reads mapping to other leishmania genomes	4.93%	4.17%
Total percentage of reads mapping to leishmania genomes	63.54%	57.01%
Reads that did not align to anything at all	13.3%	10.8%