

Table S1.**Reads mapped to host and parasite genomes.**

Samples	Reads aligned to human genome (%)	Reads aligned to <i>L. braziliensis</i> genome (%)	Reads aligned to both genomes (%)	Unaligned reads (%)
LCL-01	79.42	0.07	0.002	20.50
LCL-02	78.03	0.25	0.004	21.72
LCL-03	80.23	0.18	0.003	19.59
LCL-04	82.63	0.07	0.002	17.29
LCL-05	77.23	0.17	0.003	22.59
Average	79.51	0.15	0.003	20.34
Median	79.42	0.17	0.003	20.50
ML-01	64.87	0.79	0.008	34.34
ML-02	59.13	0.91	0.010	39.96
ML-03	82.38	0.06	0.002	17.56
ML-04	80.14	0.06	0.001	19.80
ML-05	80.79	0.09	0.002	19.13
Average	73.46	0.38	0.005	26.16
Median	80.14	0.09	0.002	19.80

Alignment analysis was performed on each one of the samples. LCL = Localized cutaneous leishmaniasis group. ML = Mucosal leishmaniasis group.