

Table S1. Sequencing data quality for the analyzed samples expressed by: input — number of reads in raw fastq files; filtered — number of reads after preliminary quality filtering; denoised (F/R) — number of reads after quality filtering; merged — number of merged forward-reverse reads; nonchim — number of merged reads after removal of chimera sequences; % passed — relative number of passed reads after all the above steps.

Host	Input	Filtered	Denoised F	Denoised R	Merged	Nonchim	% passed
<i>Monodelphis domestica</i>	35704	27750	27657	27656	27594	27445	99.46%
<i>Thylamys macrurus</i>	73610	67151	66772	66936	65233	61250	93.89%
<i>Oecomys mamorae</i>	146617	123626	123201	123124	121734	120501	98.99%
<i>Thrichomys fosteri</i>	39032	28847	28758	28726	28585	28559	99.91%
<i>Clyomys laticeps</i>	70233	59959	59868	59873	59779	59468	99.48%
<i>Holochilus chacaris</i>	52097	47846	47779	47818	47662	47662	100.00%