

Supplementary to "Fecal Virome of Southeastern Maned Sloth (*Bradypus crinitus*) (Pilosa: Bradypodidae)"

Table 1 - Overview data of filtered reads (n=945,386 corresponding to 45.77% of the total sequenced) and assembled contigs (n=5,787) taxonomically classified by Diamond and Kraken2.

		Diamond	Kraken2
No hits	Reads (%)	846,692 (89.7%)	576,822 (61%)
	Contigs (%)	3,392 (58.6%)	4,577 (79%)
	(min - max)	(125 - 1,840 nt)	(125 - 4,162 nt)
Mapped reads		98,694 (10.4%)	368,564 (38.9%)
Mapped contigs		2,395	1,210
(min - max)		(186 - 6,752 nt)	(129 - 6,752 nt)
Bacteria	Reads (%)	54,910 (55.6%)	113,958 (30.9%)
	Contigs (%)	508 (21.2%)	511 (42.2%)
	(min - max)	(375 - 3,780 nt)	(131 - 4,802 nt)
Eukaryota	Reads (%)	42,975 (43.5%)	253,144 (68.7%)
	Contigs (%)	1,883 (78.6%)	683 (56.5%)
	(min - max)	(186 - 6,752 nt)	(129 - 6,752 nt)
Viral	Reads (%)	294 (0.3%)	318 (0.09%)
	Contigs (%)	2 (0.08%)	1 (0.08%)
	(min - max)	(381 - 1,441 nt)	(409 nt)
Others/ Unassigned	Reads (%)	515 (0.52%)	1,144 (0.31%)
	Contigs (%)	2 (0.08%)	15 (1.24%)
	(min - max)	(437 - 445 nt)	(186 - 735 nt)