

**Table S.4. Number of viral contigs by rodent species/habitats and viral families.**

Total number of contigs are given for each species habitat and across species habitats. Genome types are mentioned along the viral family names as follow \*\* = dsDNA, \* = ssDNA, ++ = dsRNA, + = ssRNA (+), - = ssRNA (-), °° = DNA-retrotranscribing, ° = RNA-retrotranscribing. Left row represent host-type (Vertebrate, Invertebrate, Plants...).

Host	Rodent species Environments / Viral family	<i>Proechimys guyannensis</i>		<i>Proechimys cuvieri</i>		<i>Oecomys auyantepui</i>	<i>Oecomys bicolor</i>	<i>Hylaeamys yunganus</i>	<i>Hylaeamys megacephalus</i>		<i>Zygodontomys brevicauda</i>			Total
		Pristine forest	Disturbed forest	Pristine forest	Disturbed forest	Disturbed forest	Disturbed forest	Disturbed forest	Pristine forest	Disturbed forest	Savannah	Disturbed forest	Peri-urban	
Amoeba	<i>Mimiviridae</i> **	18	0	0	0	0	0	0	0	0	0	0	0	18
	<i>Chuviridae</i> -	0	0	0	3	0	0	0	0	2	0	0	0	
	<i>Iflaviridae</i> +	0	0	0	0	0	0	0	0	1	0	0	0	
	<i>Nudiviridae</i> **	4	0	0	0	0	0	0	0	0	0	0	0	
	<i>Picornaviridae</i> +	0	0	0	0	0	0	0	0	1	0	0	0	
	<i>Polycipiviridae</i> +	0	0	0	0	0	7	0	0	12	9	10	0	
Invertebrates	Total	4	0	0	3	0	7	0	0	16	9	10	0	49
Plants	<i>Alphaflexiviridae</i> +	1	0	0	0	0	0	0	0	0	0	0	0	
	<i>Caulimoviridae</i> °°	0	0	0	1	0	0	0	0	0	0	0	0	
	<i>Luteoviridae</i> +	0	0	0	0	0	1	0	1	0	0	0	0	



[illegible]