

Supplementary Table 2. Number of reads from the DNA or RNA mNGS library aligning to viral sequences.

*re-classified to a higher taxonomic rank because reads aligned equally well to multiple different organisms that shared the same species, genus or family

species ^a	genus	family	host	DNA NTC	RNA NTC
Human mastadenovirus F	Mastadenovirus	Adenoviridae	human vertebrates	0	68
GB virus C	Pegivirus	Flaviviridae	human vertebrates	0	0
Cercopithecine herpesvirus 5	Cytomegalovirus	Herpesviridae	human vertebrates	0	32
Human herpesvirus 5	Cytomegalovirus	Herpesviridae	human vertebrates	0	0
*	*	Papillomaviridae	human vertebrates	1	0
Alphapapillomavirus 2	Alphapapillomavirus	Papillomaviridae	human vertebrates	39	16
Betapapillomavirus 1	Betapapillomavirus	Papillomaviridae	human vertebrates	0	30
Betapapillomavirus 2	Betapapillomavirus	Papillomaviridae	human vertebrates	0	0
*	Lentivirus	Retroviridae	human vertebrates	0	0
Human immunodeficiency virus	Lentivirus	Retroviridae	human vertebrates	0	0
Human immunodeficiency virus 1	Lentivirus	Retroviridae	human vertebrates	0	0
Simian-Human immunodeficiency	Lentivirus	Retroviridae	human vertebrates	0	0
Gammapapillomavirus 1	Gammapapillomavirus	Papillomaviridae	vertebrates	14	0
Gammapapillomavirus 10	Gammapapillomavirus	Papillomaviridae	vertebrates	0	12

^aViruses assigned to bacterial, plant, insect, parasitic, or fungal hosts are not shown

Abbreviations: NTC, no template control; PC, positive control; CSF, cerebrospinal fluid; mNGS, metagenomic next-generation sequencing

DNA PC	RNA PC	DNA Patient CSF	RNA Patient CSF
0	0	0	0
0	1,406	0	2
0	0	0	0
3,026	0	0	0
0	0	0	0
0	0	0	0
0	0	0	0
0	0	0	72
0	172	0	0
0	1	0	0
0	3,895	0	0
0	57	0	0
0	0	0	0
0	60	0	0