

Supplementary Table S1. Comparison of virome enrichment strategies.

		Total Virome Enrichment Method <sup>1</sup>			
		poly-A selection	ribo-depletion	DNase treatment	Target Enrichment
Viral Target					
	viral genome - DNA	-	+	-	+
	viral genome - RNA -strand	-	+	+	+
	viral genome - RNA +stand	+	+	+	+
	viral transcripts -polyA	+	+	+	+
	viral transcripts -non polyA	-	+	+	+
Background NAs <sup>2</sup>					
	Human gDNA	-	+	-	-
	Human rRNA	-	-	+	-
	Human mRNA	+	+	+	-
	bacterial gDNA	-	+	-	-
	bacterial rRNA	-	+	+	-
	bacterial mRNA	-	+	+	-

<sup>1</sup> Plus (+) indicates the substantial presence of the genomic material in the final NGS library.

<sup>2</sup> Major sources of background genomic material in a clinical specimen. Other sources like mitochondrial transcripts, miRNAs, long-non-coding RNAs, other microorganisms and parasites etc. are omitted.