Category	Metadata	Description	Details	Specificity to virome
General sample metadata	Sample name	Name of the sample		Identical MIMAG / MISAG/ UViG
	Sample type	Sample type, including by not limited to: tissues, blood, swabs, faeces, filters, feathers, skin, etc.		
	sample collection time	Collection date	dd/mm/yyyy	Identical MIMAG / MISAG/ UViG
	geographic location (latitude and longitude)	The geographical origin of the sample as defined by latitude and longitude. The values should be reported in decimal degrees and in WGS84 system	decimal degrees	Identical MIMAG / MISAG/ UViG
	geographic location (depth)	Follow the definitions of depth in the environmental packages		Identical MIMAG / MISAG/ UViG
	geographic location (altitude/elevation)	Follow the definitions of either altitude or elevation in the environmental packages		Identical MIMAG / MISAG/ UViG
	geographic location (country and/or sea,region)	The geographical origin of the sample as defined by the country or sea name followed by specific region name. Name of country/sea from the INSDC country list (http://insdc.org/country.html), or the GAZ ontology (v 1.512) (http://purl.bioontology.org/ontology/GAZ)	country or sea name (INSDC or GAZ);region(GAZ);specific location name	Identical MIMAG / MISAG/ UViG
	host biological information	Host information including age, sex, health/disease status, season, and phenotype		New
	Sample storage	Type and condition of sample storaged and shipping (i.e. media, or RNAlater)		New
Sample preparation	Pooling strategy	Type of protocol including number of samples per pool, how samples were selected per pool (e.g. same species, location, date), how individual sample concentrations were taken into consideration		Comparable to UViGs and improved
	Extraction methods	Name of kit and distributer and any modifications from manufacurers instructions	Kit name, distributer, country	Comparable to UViGs and improved
	Enrichment/depletion/amplification method	Outline of protocol, and if kits use, the name of kit and distributer and any modifications from manufacurers instructions	Kit name, distributer, country	Comparable to UViGs and improved
	Negative/Positive controls	How controls were constructed		New
Sequencing methodology	sequencing approach	Approaching to sequencing to contextualise results	Specify if: metagenome (not viral targeted) | viral fraction metagenome (virome) | sequence-targeted metagenome | metatranscriptome (not viral targeted) | viral fraction RNA metagenome (RNA virome) | sequence-targeted RNA metagenome | microbial single amplified genome (SAG) | viral single amplified genome (vSAG) | isolate microbial genome | other	Comparable to UViGs and improved
	sequcing methods	Sequencing machine, and flowcell, read length, paired-end or single-end and number of reads per library		Comparable to UViGs and improved
Bioinformatic approaches	quality control & trimming	Software used for reads quality controls and trimming	software name, version number, and specific parameters	Comparable to UViGs and improved
	assembly software	Tool(s) used for assembly and/or binning, version number and parameters	software name, version number, and specific parameters used	Identical MIMAG / MISAG /UViGs
	Read mapping	Tool (s) used for remapping reads back to contigs	software name, version number, and specific parameters used	
	Genome abundance and coverage	Tool(s) of reads mapping tools and the number of reads mapped back to genome	software name, version number, and specific parameters used	Comparable to UViGs and improved
	Contig statistics	Number of contigs, maximum/minimum/average contig length		New
	Viral identification software	Tool(s) used for the identification of viral genome, software or protocol name including version number, parameters, and cutoffs used	software name, version number, and specific parameters used	Identical MIMAG / MISAG /UViGs
	Relationship to most closely related viruses	Top hit name, the similarity and its accession number,the percent nucleotide or protein similarity thresholds		Comparable to UViGs and improved
Checks and balances	Index hopping	Check the balance of sequencing and reads percentage		New
	Reagent contamination	Checking with existing known contaminants, inclusion of no template control libraries to identify putative reagent contamination,	reference of contaminant list used. software name, version number, and specific parameters used	New

Category	Item	Description	Format/Parameters	Comparison
Annotation	Mis-assembly	Mapping back reads to virus contigs to check if there is assembly error	software name, version number, and specific parameters used	Comparable to UViGs and improved
	ORFs found	Presentation of all putative ORFs in each viral genome	Presenation of ORFs, software name, version number, and specific parameters used	Identical to UViGs
	Domains, motifs, mature pepties, IRES sites, etc	Presentation of key domains/motifs/etc for each genome to ensure correct orientation and order in alignment with ICTV	software name, version number, and specific parameters used	Comparable to UViGs and improved
	Identification of EVEs	identifying truncated and/or non-functional proteins, investigating the genomic context from DNA sequencing	approach described, as well as software name, version number, and specific parameters used	New
Phylogeny	Phylogenetic analysis	phylogenetic estimate model, software, nodal support, and parameter	software name, version number, and specific parameters used	New
	Code availability	Raw data (such as alignments or nwk files) availbale	Repository and doi or similar	New
Virus Description	Virus name	Follow ICTV demarcation and novel virus naming system	Description of naming approach used	Comparable to UViGs and improved
	Virus genome completeness	Genome is complete or partial	Partial or Complete	Identical to UViGs
	Virus genome length	Virus genome length	base pair of nt, aa	Identical to UViGs
	Predicted genome type	Type of genome predicted for the viral genome	[DNA	dsDNA	ssDNA	RNA	dsRNA	ssRNA	ssRNA (+)	ssRNA (-)	mixed	uncharacterized]	Identical to UViGs
	Predicted genome structure	Expected structure of the viral genome	[segmented	non-segmented	undetermined]	Identical to UViGs
Host association	Broad host classification	Clarity of whether virus is host infecting, or likely "host associated" (e.g. a virus of diet or microbome)		New
Data Sharing	Desposit reads	Deposit reads into NCBI Sequence Read Archive (or similar) with associated metadata	Repository and accession numbers	Comparable to UViGs and improved
	Desposit viral genomes	Deposit fully annotated (including ORFs) viral genome into publically accessible database (e.g. GenBank, ENA) with associated metadata	Repository and accession numbers	Comparable to UViGs and improved
	Code availability	Novel or updated pipelines/code should be depositied in publically avalilable repository (e.g. Github, FigShare).	Repository and doi or similar	New