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Human reference gut virome

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The human gut microbiome is one of the most studied metagenomes, followed by the human oral microbiome. Dysbiosis of the gut microbiome can contribute to the onset of intestinal and systemic diseases, including inflammatory bowel disease, ulcerative colitis and other cancers, cardiovascular disease, and diabetes. However, most of the gut microbiome studies have been focused on the bacteriome with least attention on the gut virome. Since being called viral dark matters, gut viral genomes have been known as direct or indirect modulators of numerous human diseases for decades. Nevertheless, a lack of reference gut viral genome database restricts human gut virome research, leaving most of the gut viral dark matter unexplored. Here, we established the human reference gut virome database, HRGV, which is the most comprehensive, complete, and utilizable human gut reference viome database. We collected and analyzed 16,499 publicly available gut metagenomes encompassing 41 countries across 6 continents, and created human reference gut virome, HRGV, comprising 883,418 non-redundant high quality gut viral genomes from 17.0M putative viral sequences. We also applied viral binning processing for the first time to recover the more complete and gigantic viral genomes, which has not been viable through conventional contig-based viral genome recovering, resulting over 11.6M of fragmented viral sequences to be binned. Human reference gut virome most comprehensively explains the variations in association to host geography, demography, and multiple associate features including age, diseases, sex, etc. To sum up, human reference gut virome will provide new resources and insights for future metagenomic virome research, enlarging the understanding of the human gut virosphere.