



HAL
open science

Detection of an archaeal-specific viral family, previously thought to infect exclusively hyperthermophiles, in human gut metaviromes

Vuong Quoc Hoang Ngo, Cédric Midoux, Olivier Rué, Mahendra Mariadassou, Violette Da Cunha, Valentin Loux, François Enault, Ariane Bize

► To cite this version:

Vuong Quoc Hoang Ngo, Cédric Midoux, Olivier Rué, Mahendra Mariadassou, Violette Da Cunha, et al.. Detection of an archaeal-specific viral family, previously thought to infect exclusively hyperthermophiles, in human gut metaviromes. Phages in Grenoble, Oct 2019, Grenoble, France. . hal-04360160

HAL Id: hal-04360160

<https://hal.inrae.fr/hal-04360160>

Submitted on 21 Dec 2023

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Detection of an archaeal-specific viral family, previously thought to infect exclusively hyperthermophiles, in human gut metaviromes

H. Ngo¹, C. Midoux^{1,2}, O. Rué², M. Mariadassou², V. da Cunha³, V. Loux², F. Enault⁴, A. Bize¹

¹ Irstea, UR PROSE, 92761 Antony Cedex, France

² INRA, MaIAGE, Université Paris-Saclay, 78350, Jouy-en-Josas, France

³ Institut Pasteur, BMGE, 75724 Paris Cedex 15, France

⁴ UCA, LMGE, 63178 Aubière Cedex, France



H. Ngo



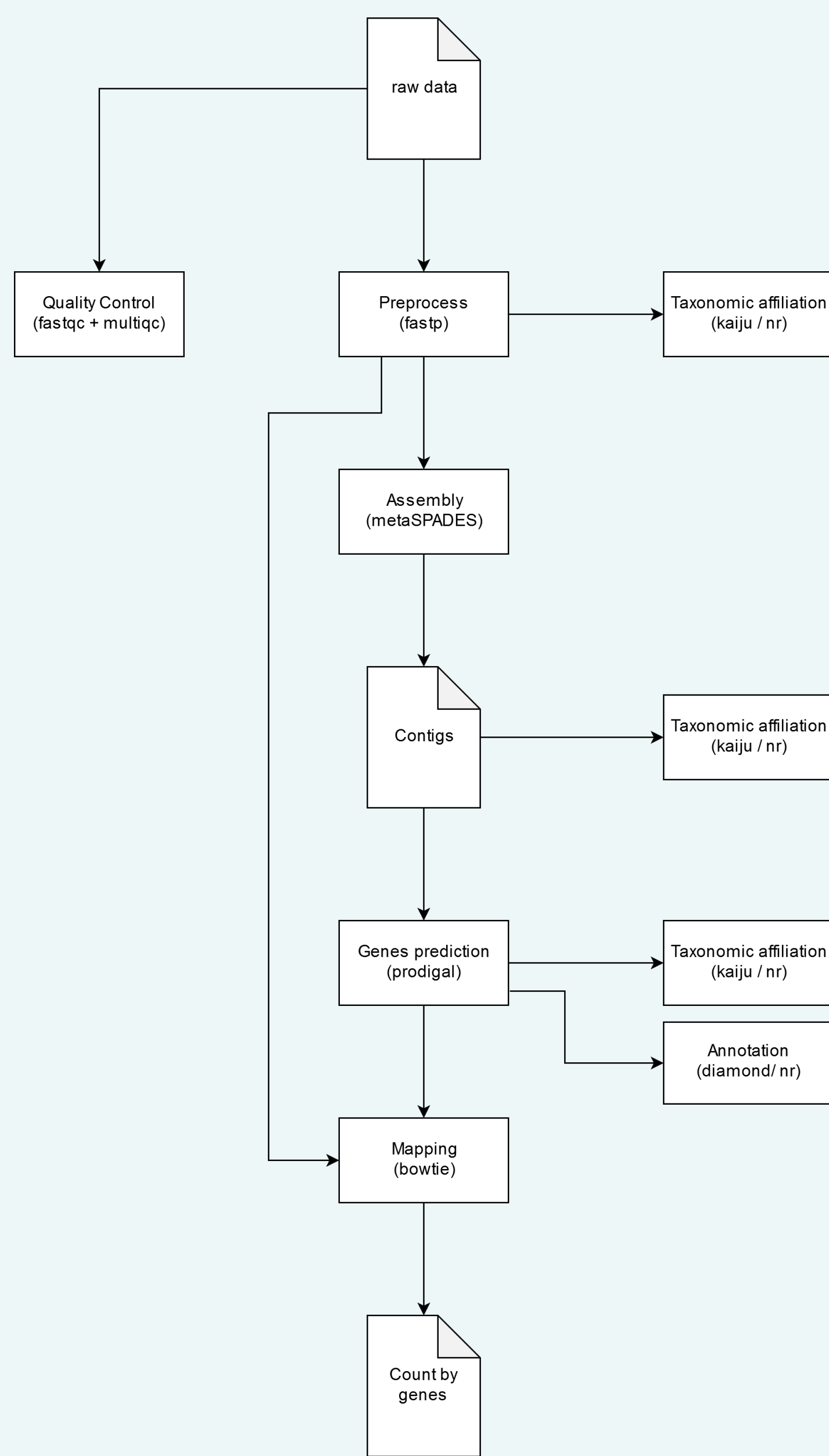
A. Bize

Context

Development of a metagenomics pipe-line for the study of archaeal viruses in anaerobic digestion ecosystems

- Test of the pipe-line on 4 previously published human gut metaviromes from healthy individuals [1]
- Analysis of contigs predicted to belong to known archaeal virus families

Metagenomics pipe-line



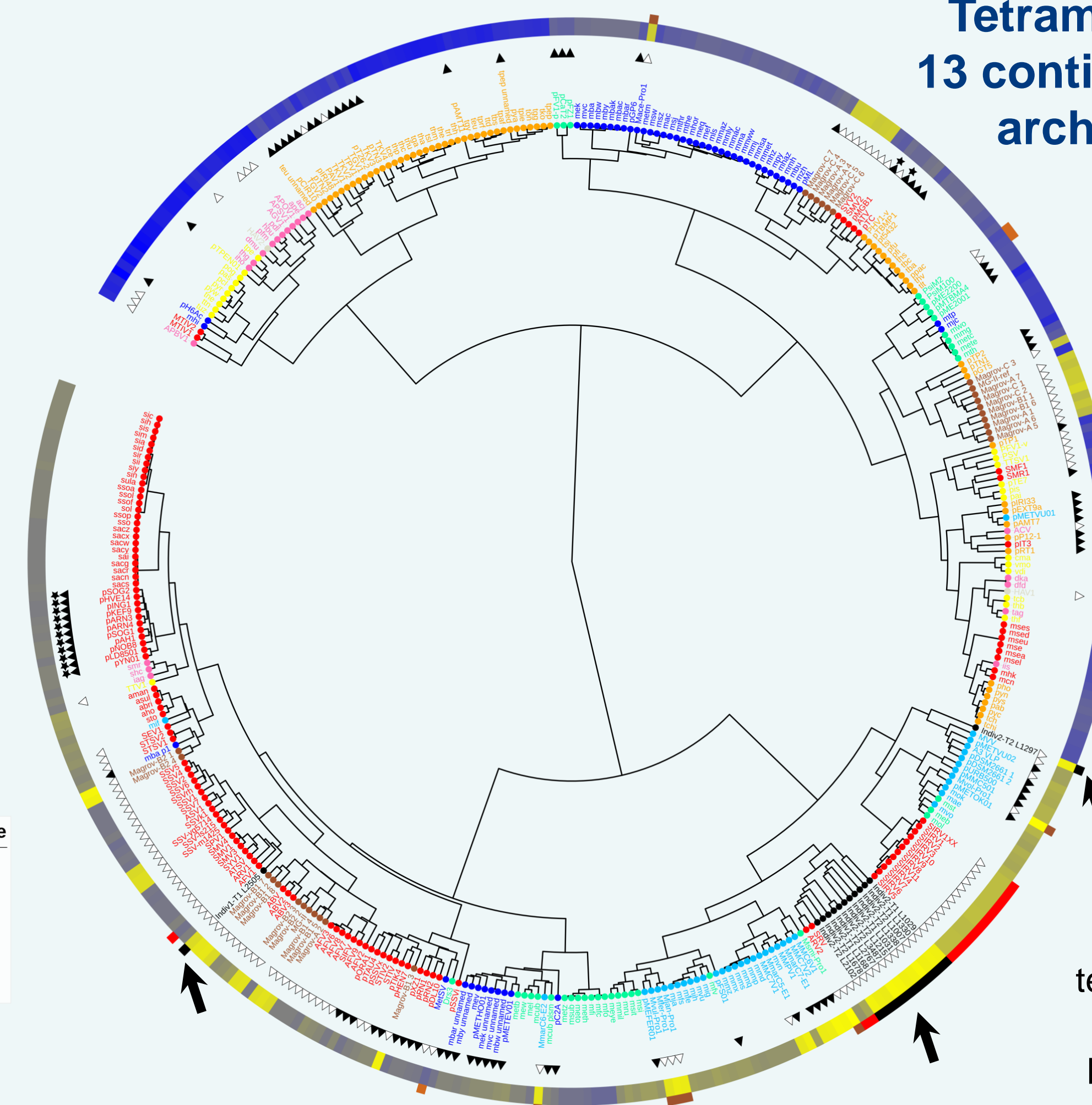
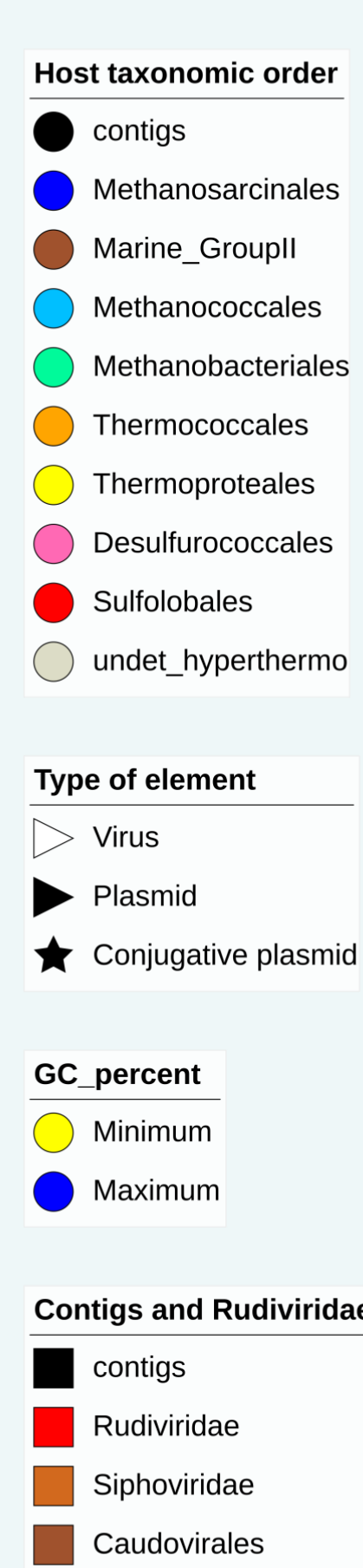
Basic statistics on the obtained metaviromes

	Indiv1-T1	Indiv1-T2	Indiv2-T1	Indiv2-T2
Reads				
# raw read pairs (M Seqs)	2.9	3.8	3.3	3.6
# filtered read pairs (M Seqs)	2.85	3.7	3.3	3.5
filtered read GC (%)	38.10%	40.30%	37.90%	38.10%
Assembly				
# contigs (>= 1000 bp)	3272	5946	1082	2002
Largest contig	177458	408314	227678	161497
Total length (>= 1000 bp)	12201808	20209687	5703620	7776961
N50	7235	6573	35485	11643
N75	2171	1830	3646	2215
L50	233	326	36	113
L75	1101	2052	193	585
GC (%)	33.75	40.73	40.36	44.02
Predicted genes				
# predicted genes (unique)	16257	26350	7675	11373
# predicted genes (>= 300 bp)	11858	19538	5405	7633
# predicted genes (>= 1500 bp)	1036	1764	554	639

13 contigs assigned to Rudiviridae, an archaea-specific viral family whose described members are rod-shaped and infect acidothermophilic crenarchaea from terrestrial acidic hot springs

Sample	Nb contigs	Length	Coverage	GC%	Taxomic affiliation (kaiju / nr)	Predicted host (WiSH [2])
Indiv1-T1	1	2505	2.1	19.76	Rudiviridae; ARV2	<i>Methanosarcina thermophila</i>
Indiv1-T2	1	2707	2.8	14.40	Rudiviridae; NA	<i>Sulfurisphaera tokodaii</i>
Indiv2-T1	4	1029	2.0	15.99	Rudiviridae; SIRV11	<i>Methanosarcina barkeri</i>
		1031	1.8	15.37	Rudiviridae; NA	<i>Acidianus hospitalis</i>
		1168	1.25	16.86	Rudiviridae; NA	<i>Methanobrevibacter millerae</i>
		1330	1.7	15.49	Rudiviridae; SIRV10	<i>Methanosphaera stadtmanae</i>
Indiv2-T2	7	1007	2.5	15.95	Rudiviridae; SIRV9	<i>Sulfurisphaera tokodaii</i>
		1215	1.75	15.71	Rudiviridae; SIRV9	<i>Sulfurisphaera tokodaii</i>
		1297	1.75	15.71	Rudiviridae; SIRV3	<i>Sulfurisphaera tokodaii</i>
		1338	1.5	14.34	Rudiviridae; NA	<i>Sulfurisphaera tokodaii</i>
		1678	2.9	16.05	Rudiviridae; SIRV3	<i>Sulfurisphaera tokodaii</i>
		2102	3.1	15.53	Rudiviridae; NA	<i>Sulfurisphaera tokodaii</i>
		3487	2.5	14.70	Rudiviridae; NA	<i>Sulfurisphaera tokodaii</i>

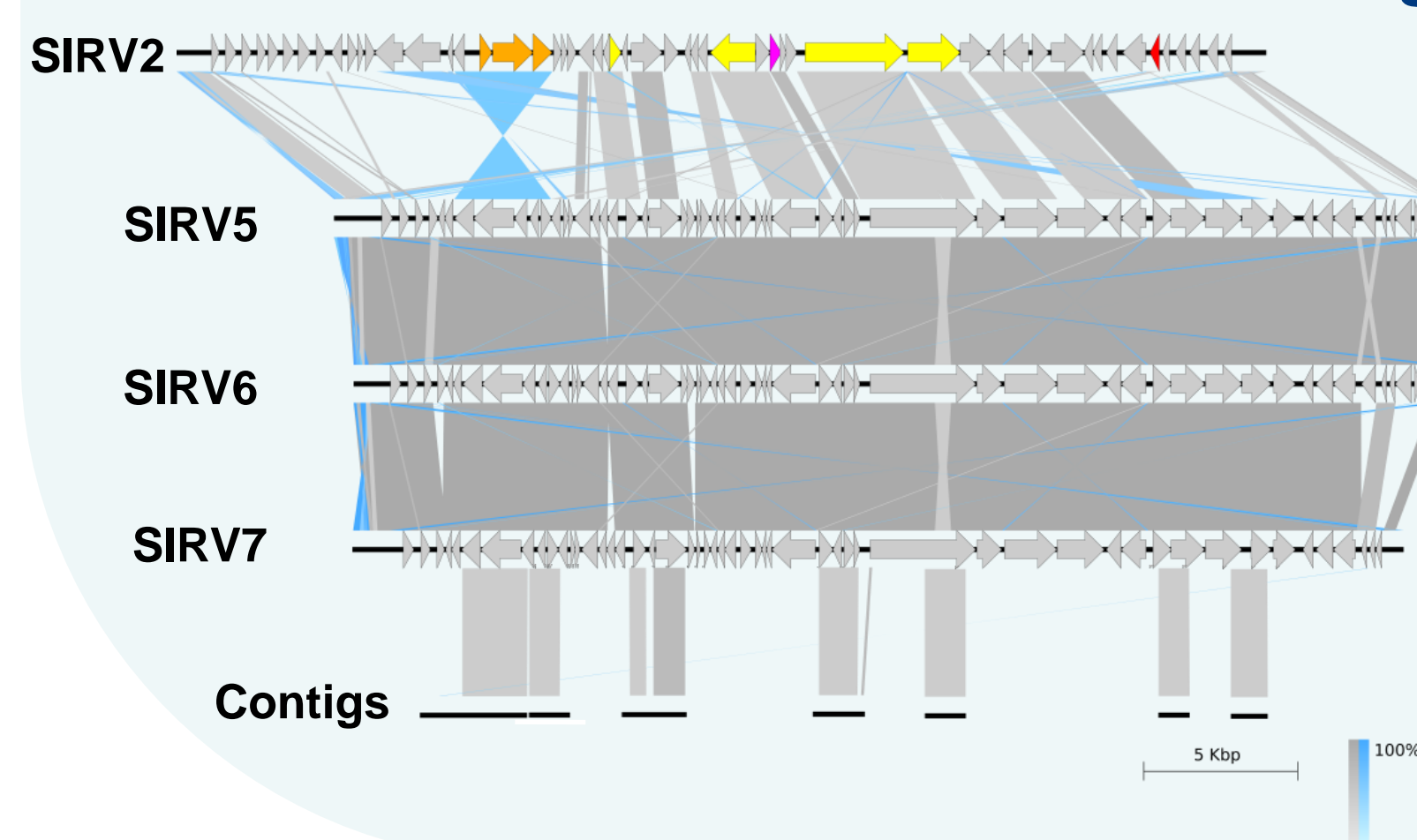
Tree scale: 0.1



Tetramer composition of the 13 contigs compared to some archaeal viruses and cells

The position of the contigs in the dendrogram based of tetramer frequencies is in most cases consistent with the predicted taxonomy and hosts

Indiv2-T2 Rudiviridae contigs: alignments with length > 900 pb



- Alignment regions are distributed all along the considered Rudiviridae genomes
- Some contigs cover conserved regions of the Rudiviridae genomes, including portions of genes coding for virion structural proteins

Conclusions and perspectives

- DNA from viruses similar to rudiviruses seems to be present in the studied metaviromes, especially in Indiv2-T2
- A contamination issue cannot be excluded. However, some authors have recently reported the detection of morphotypes and sequences, similar to viral families specific for acidothermophilic archaea, in anaerobic digestion samples [3]. We also observed unusual morphotypes in anaerobic digestion microcosms [Poster 1].
- Enrichment approaches could be interesting to study these putative unknown archaeal viruses, which are in low abundance

References

[1] Manrique P, Bolduc B, Walk ST, van der Oost J, de Vos WM, Young MJ. Healthy human gut phageome. *PNAS*. 2016 113:10400-5.

[2] Galez C, Siebert M, Enault F, Vincent J, Söding J. WiSH: who is the host? Predicting prokaryotic hosts from metagenomic phage contigs. *Bioinformatics*. 2017 33:3113-4.

[3] Calusinska M, Marynowska M, Goux X, Lentzen E, Delfosse P. Analysis of ds DNA and RNA viromes in methanogenic digesters reveals novel viral genetic diversity. *Environ. microbiol*. 2016 18:1162-75