

Viruses in the sediments around the trenches harbor diverse survival mechanisms

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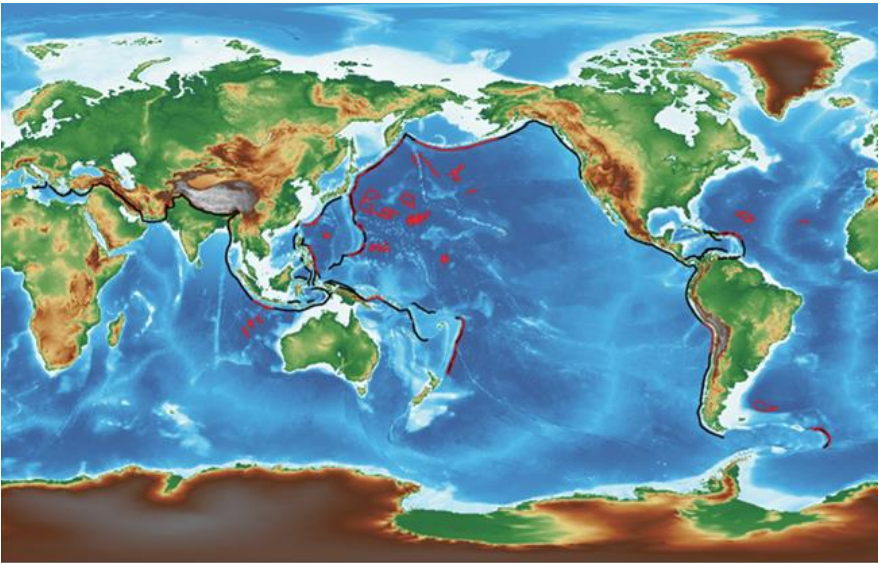
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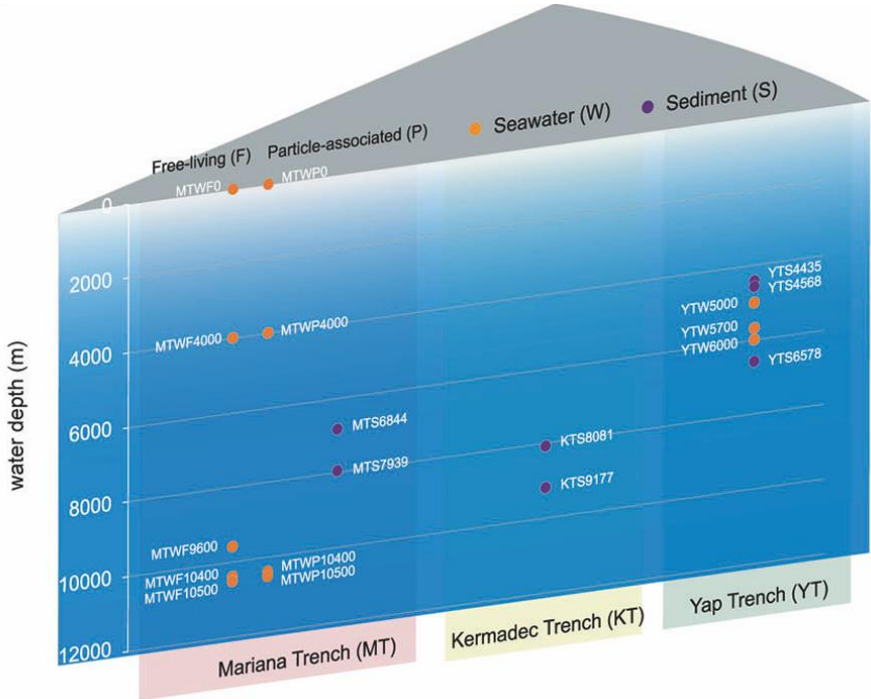
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iMetaOmics 3: e70124. <https://doi.org/10.1002/imo2.70124>



Introduction



Global distribution map of the trench
(Li et al. 2023)



The Oceanic Trench Viral Genome Dataset
(Jian et al. 2021.)

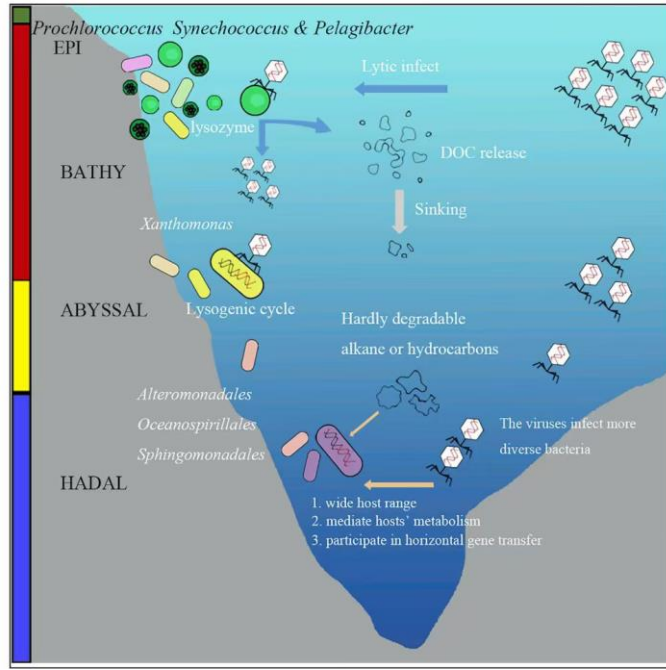


Diagram of trench virus
(Gao et al. 2021.)

The trench is characterized by **high pressure, low temperature, and the absence of light**, making it an ideal place for studying how life adapts to extreme conditions. ;

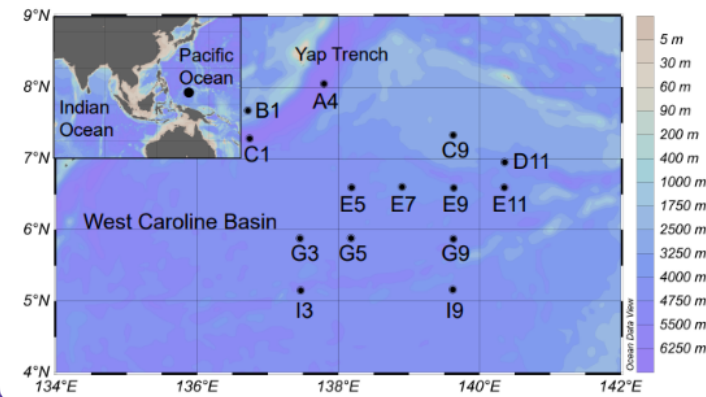
Trench viruses exhibit **different community structures** and viral communities across different trenches **may be interconnected**.

Temperate life strategies may be widespread in the trench environment.

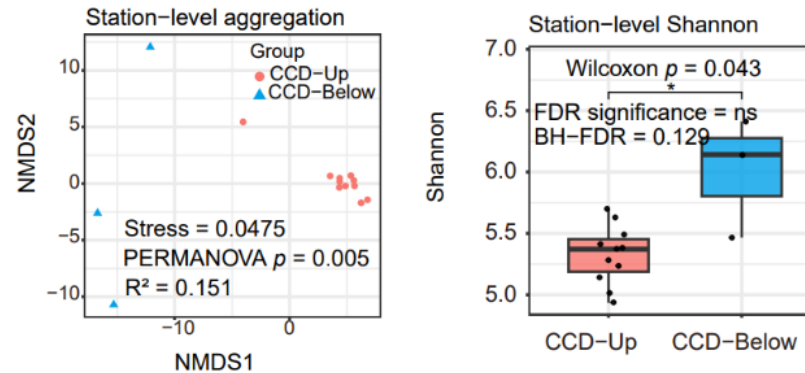
Limitation: Lack of systematic research on the survival mechanisms of viruses around the trench

Highlights

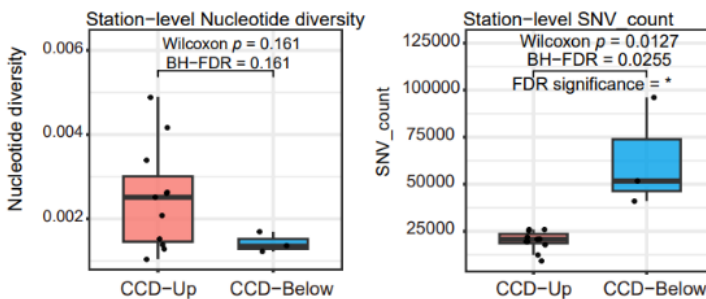
1 Sampling across the carbonate compensation depth (CCD)



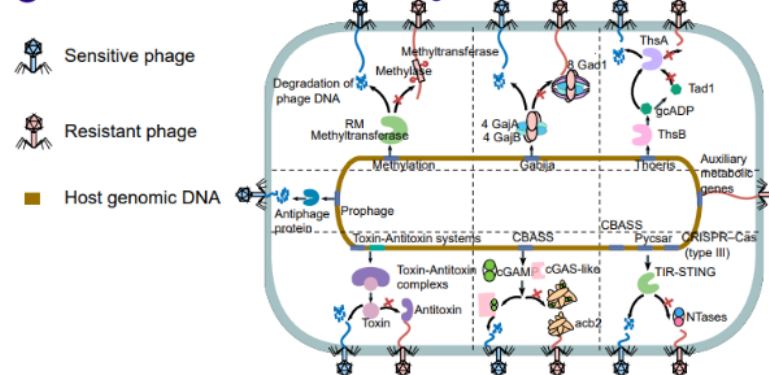
2 Highly novel, depth-structured virus



3 Microdiversity varies with depth



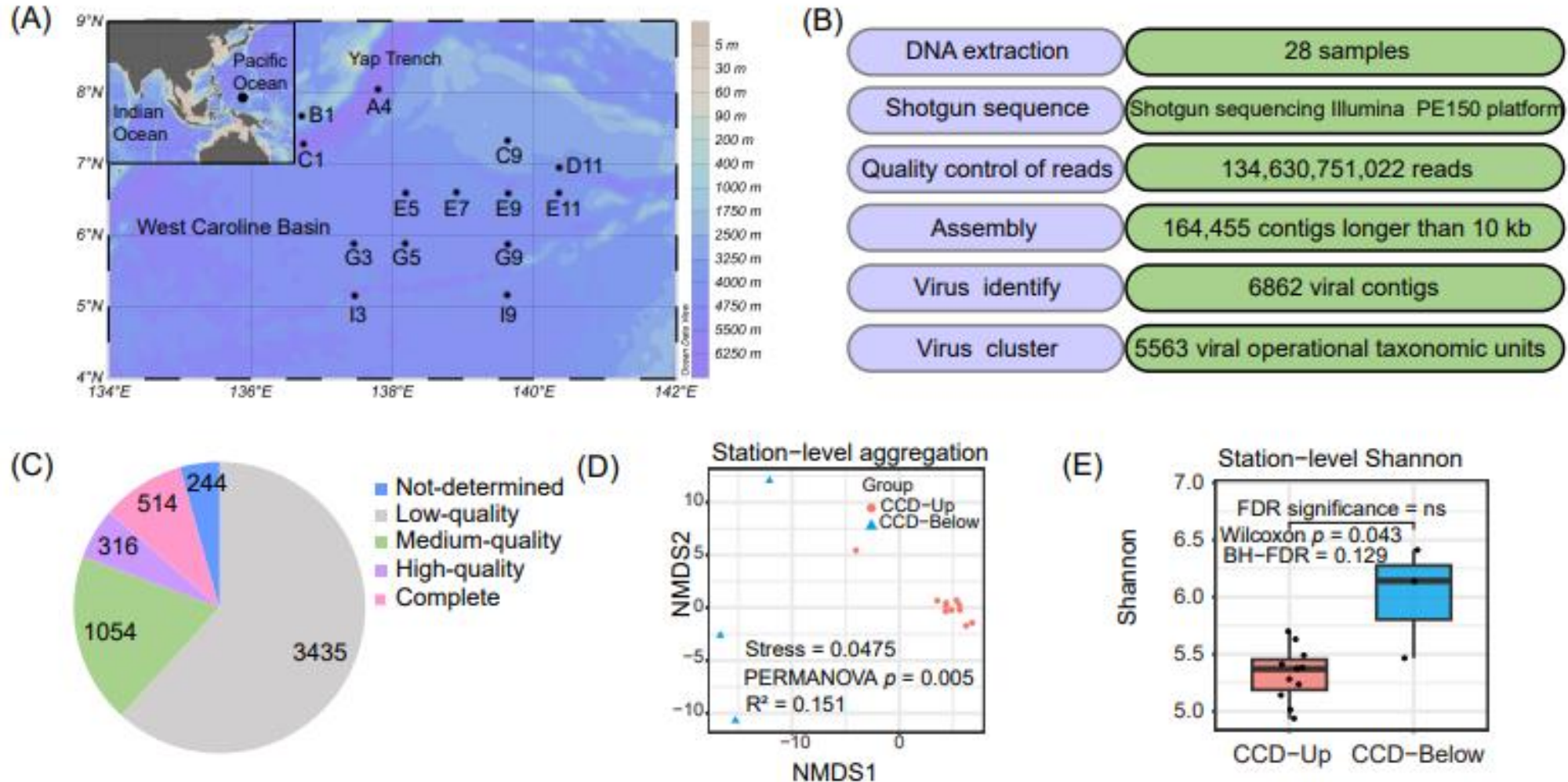
4 Virus-host interactions and ecological functions



- Metagenomic analysis reveals **highly novel viral community structures** in Yap Trench and Western Caroline Basin (YTWCB) sediments;
- Viral community composition, functional potential, and diversity **exhibit significant differentiation** along the water depth gradient;
- Abundant antiviral defense systems in host genomes and viral counter-defense proteins jointly reveal **complex host-virus antagonistic relationships** in deep-sea sediment environments.



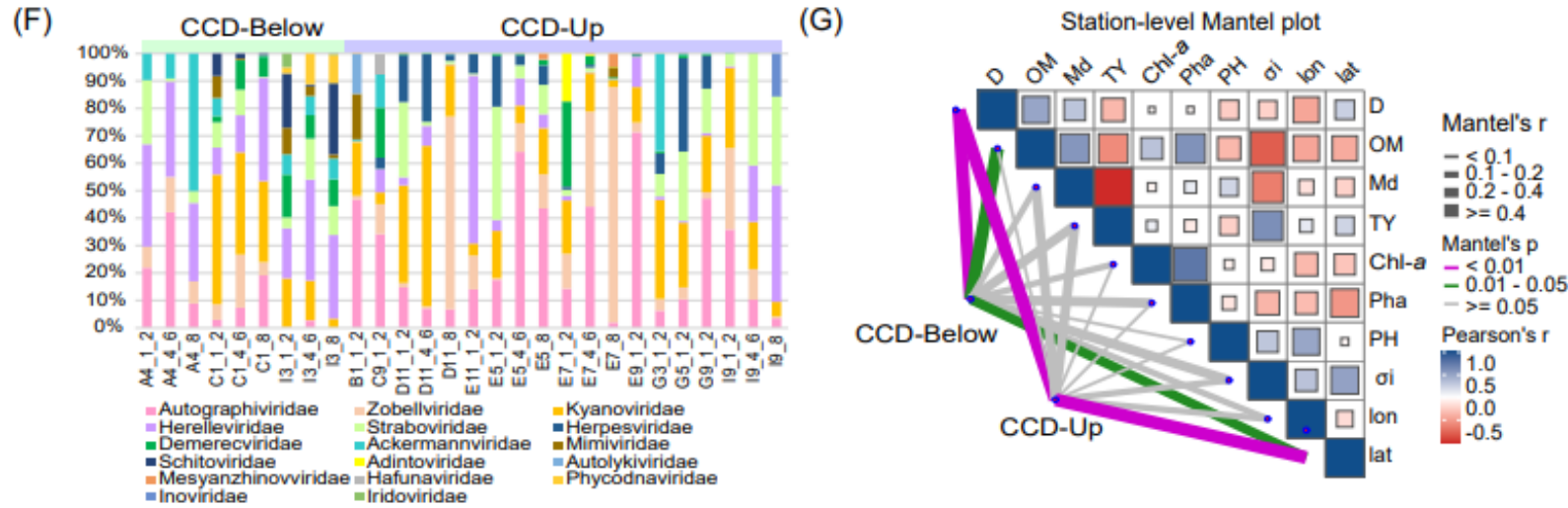
Overview of viruses in sediments from the Yap Trench and Western Caroline Basin (YTWCB)



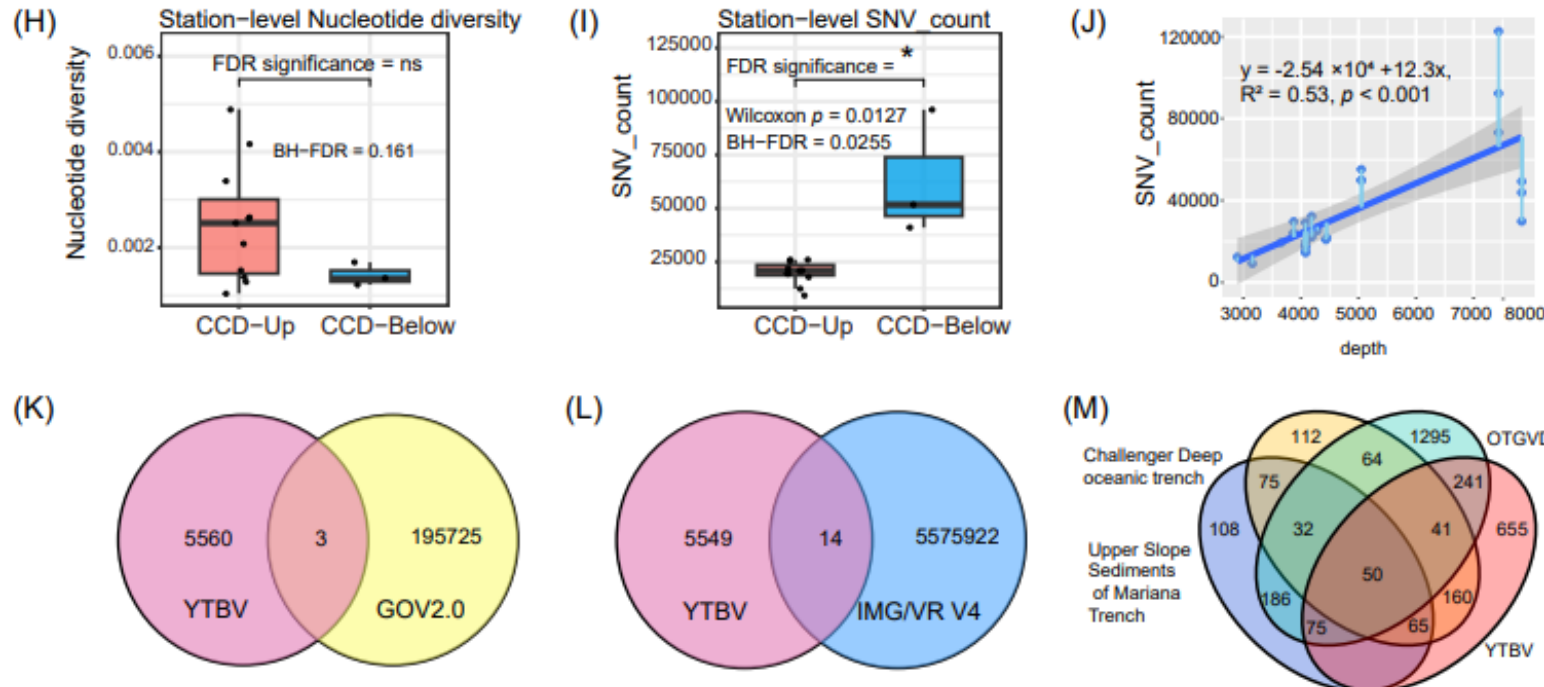
- Viral macrodiversity **differed** between the CCD-Below and CCD-Up groups;
- Viral microdiversity showed **SNV counts increasing significantly** with water depth;
- Low similarity to existing viral databases indicated **substantial novelty of sediment viruses**.



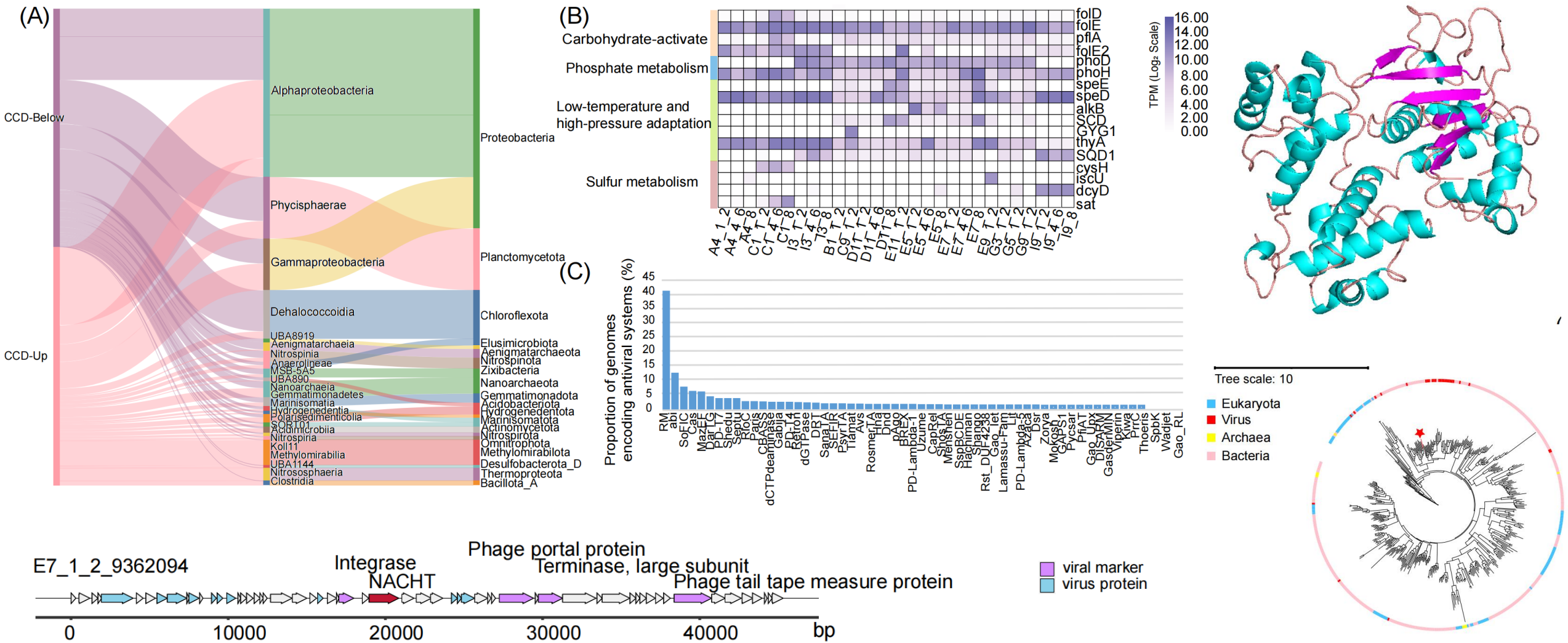
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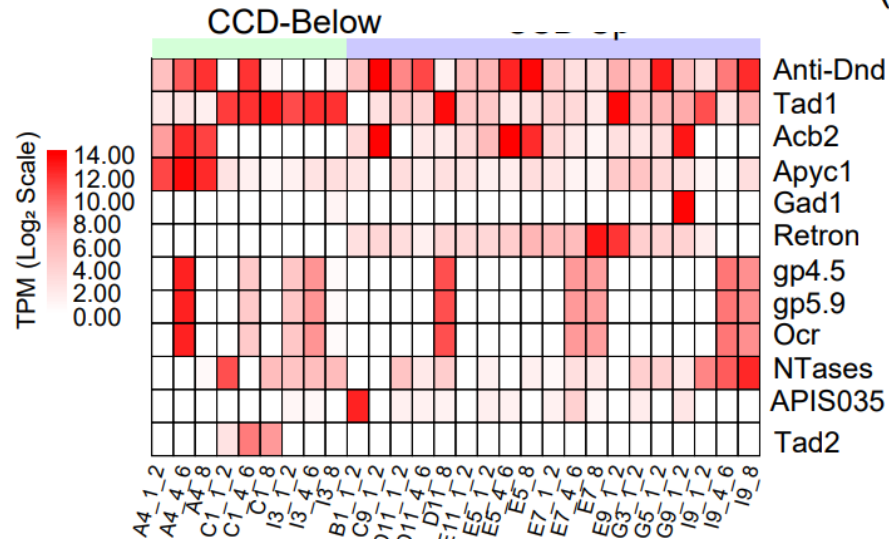
Virus-host interactions from the Yap Trench and Western Caroline Basin (YTWCB) sediments.



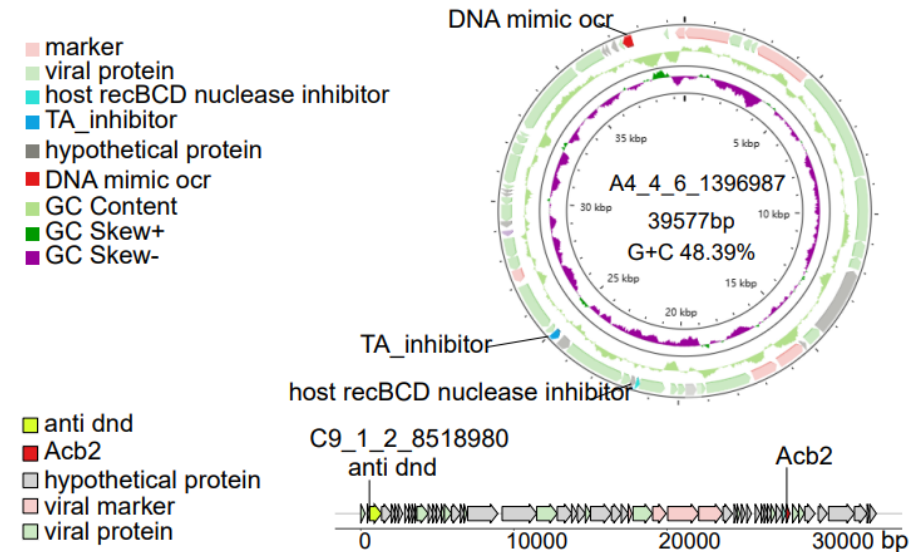
- At the functional level, viruses encoded diverse genes related to adaptation to deep-sea environments, including DNA modification, lipid metabolism, carbohydrate utilization, sulfur metabolism;

Virus-host interactions from the Yap Trench and Western Caroline Basin (YTWCB) sediments.

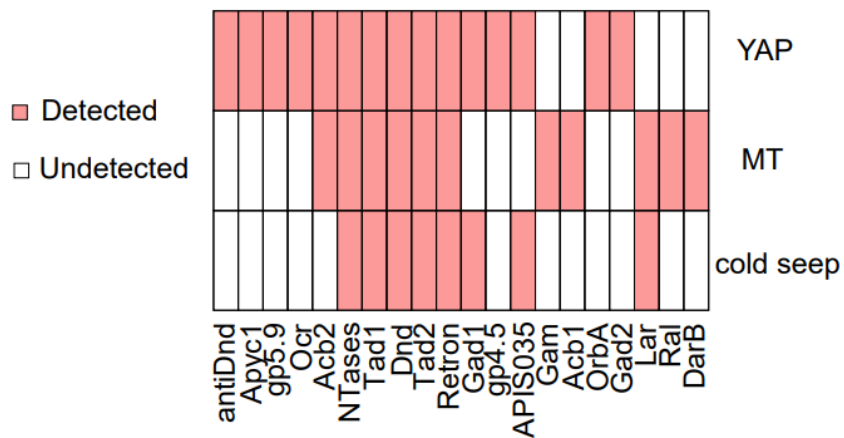
(E)



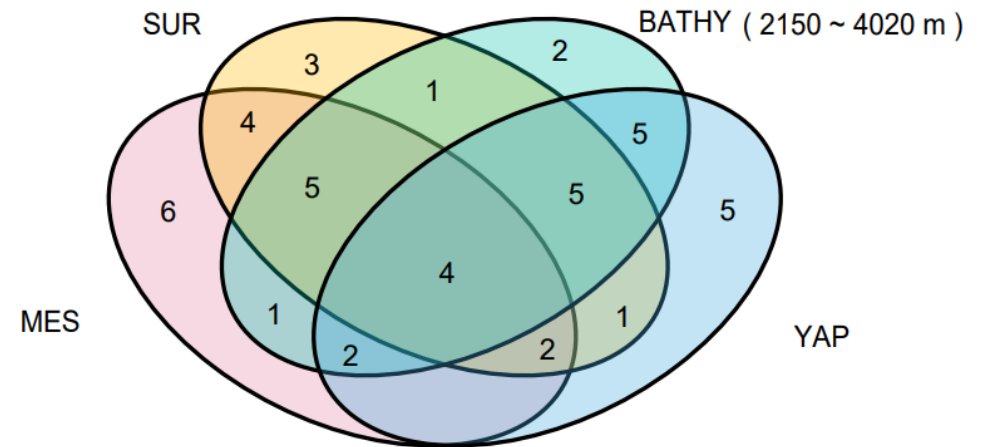
(F)



(G)



(H)



- Abundant antiviral defense systems in host genomes and viral counter-defense proteins jointly reveal **complex host-virus relationships** in deep-sea sediment environments.



Summary

- ❑ YTWCB sediments harbor highly **novel viral** communities with **low similarity to** current marine viral databases.
- ❑ Viral assemblages **differ significantly** across the carbonate compensation depth (CCD) boundary. SNV accumulation increases with depth, while nucleotide diversity (π) remains weakly differentiated, suggesting **stronger selection pressures in deeper sediments**.
- ❑ Viruses encode diverse genes involved in DNA modification, **lipid metabolism, carbohydrate utilization, sulfur metabolism, and immune evasion**, representing key genetic reservoirs that modulate host metabolism.
- ❑ Abundant antiviral defense systems in host genomes, together with viral counter-defense proteins, reveal complex host–virus interactions in deep-sea sediment environments.

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