

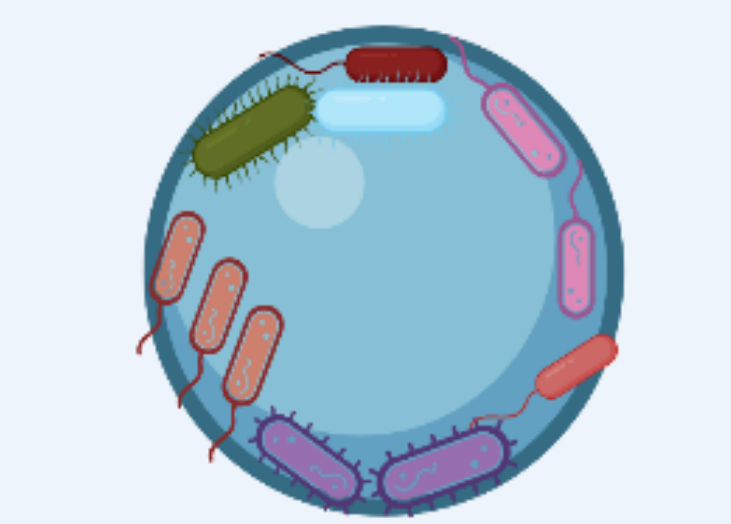
# Are Mobile Genetic Elements More Abundant in Freshwater Particle-Associated Bacteria Communities?

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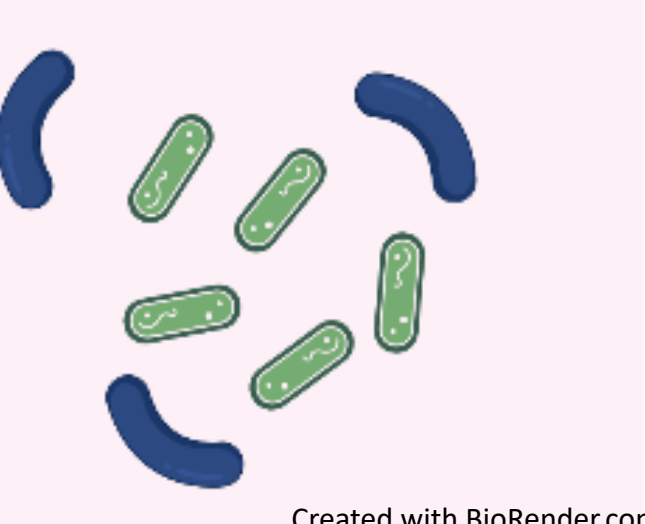
## Introduction

- Freshwater microbial communities are comprised of particle-associated and free-living bacteria.
- Particles are major sites of bacterial growth and interaction due to higher nutrient concentrations.
- Horizontal gene transfer (HGT) allows bacteria to transfer DNA and acquire novel traits.
  - Ex: Type IV secretion systems (T4SS)
- Mobile genetic elements (MGEs) are a major source of horizontal gene transfer.

### Particle-Associated



### Free-Living



- Attached to organic particles
- Copiotrophic
- Motility and chemotaxis genes
- Suspended in the water column
- Oligotrophic
- Streamlined genome

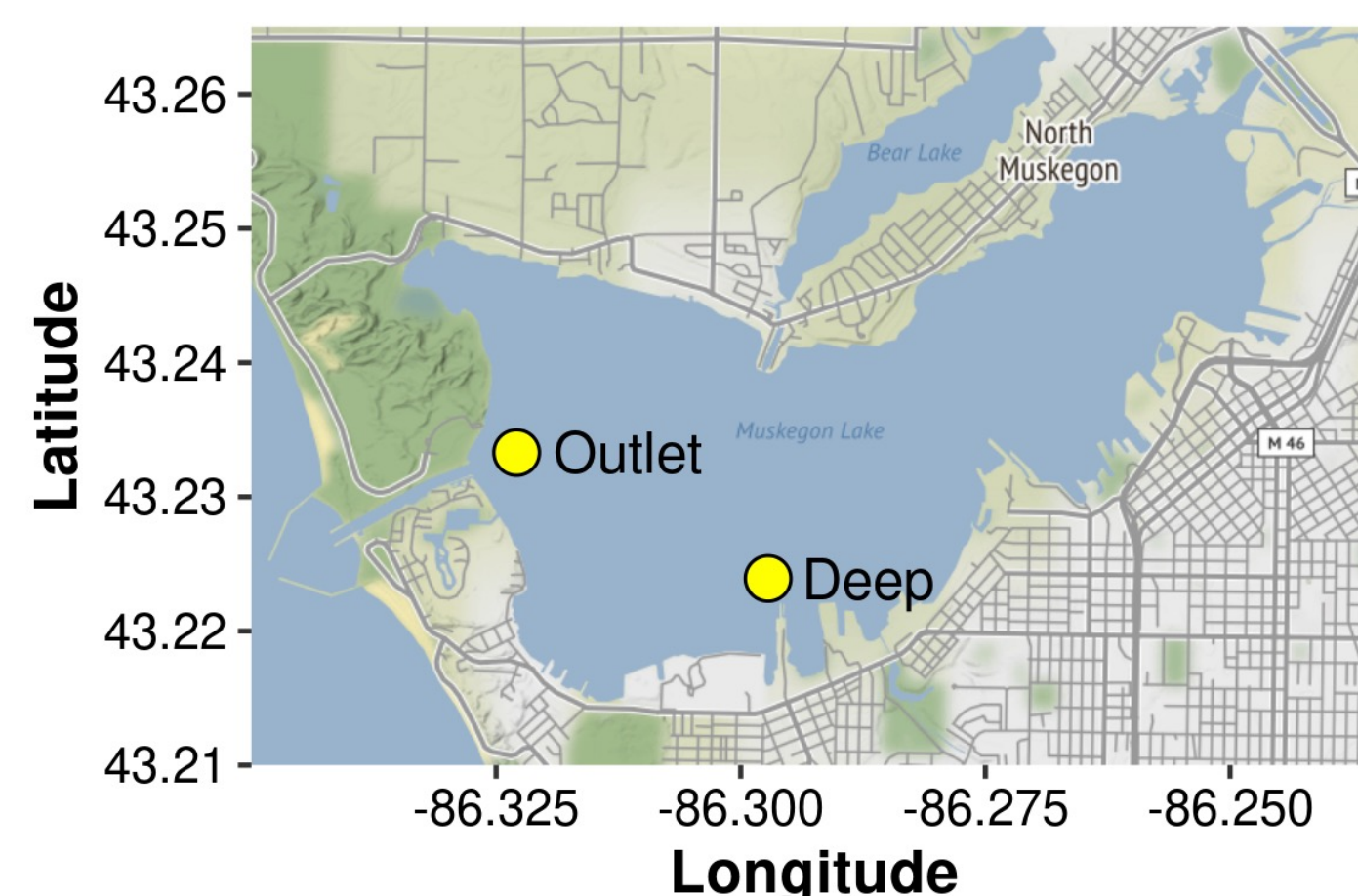
## Question

- How prevalent are mobile genetic elements in particle-associated bacteria compared to free-living bacteria?
- What genes and traits are being transferred?

## Hypothesis

- Mobile genetic elements are more prevalent in particle-associated bacteria than in free-living bacteria

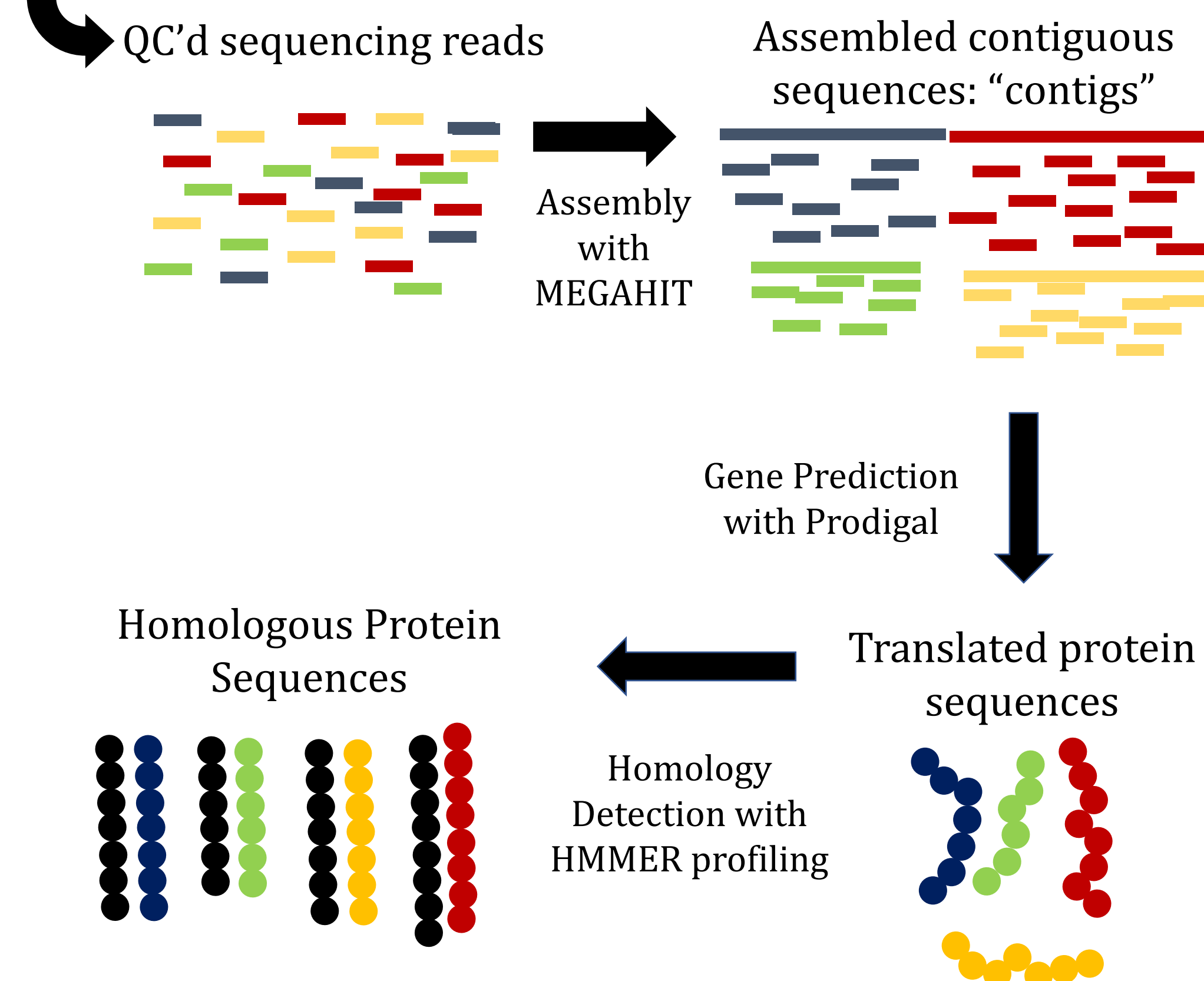
## Methods



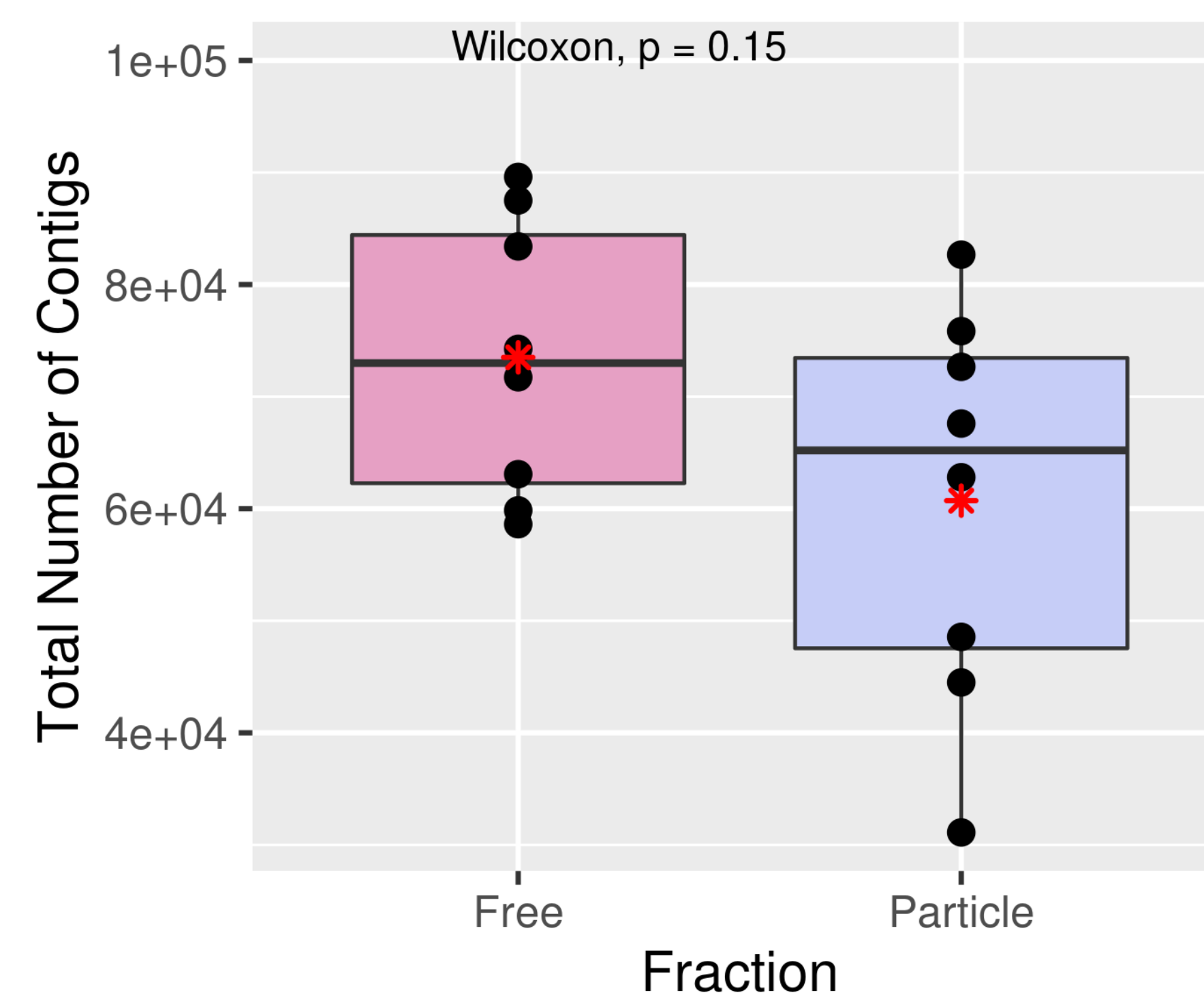
Above: Sampling stations in Muskegon Lake

## Methods (cont.)

- 16 DNA samples collected from Muskegon Lake, MI.
- 8 particle-associated, 8 free-living
- Assembly-based approach
- Raw sequencing reads obtained from Illumina shotgun metagenomic sequencing
- Raw reads were quality-controlled, adapter-trimmed, deduplicated.
- HMMER profile created from Pfam family PF02534, containing genes encoding TraG and TraD in the F-pilus complex, a T4SS.

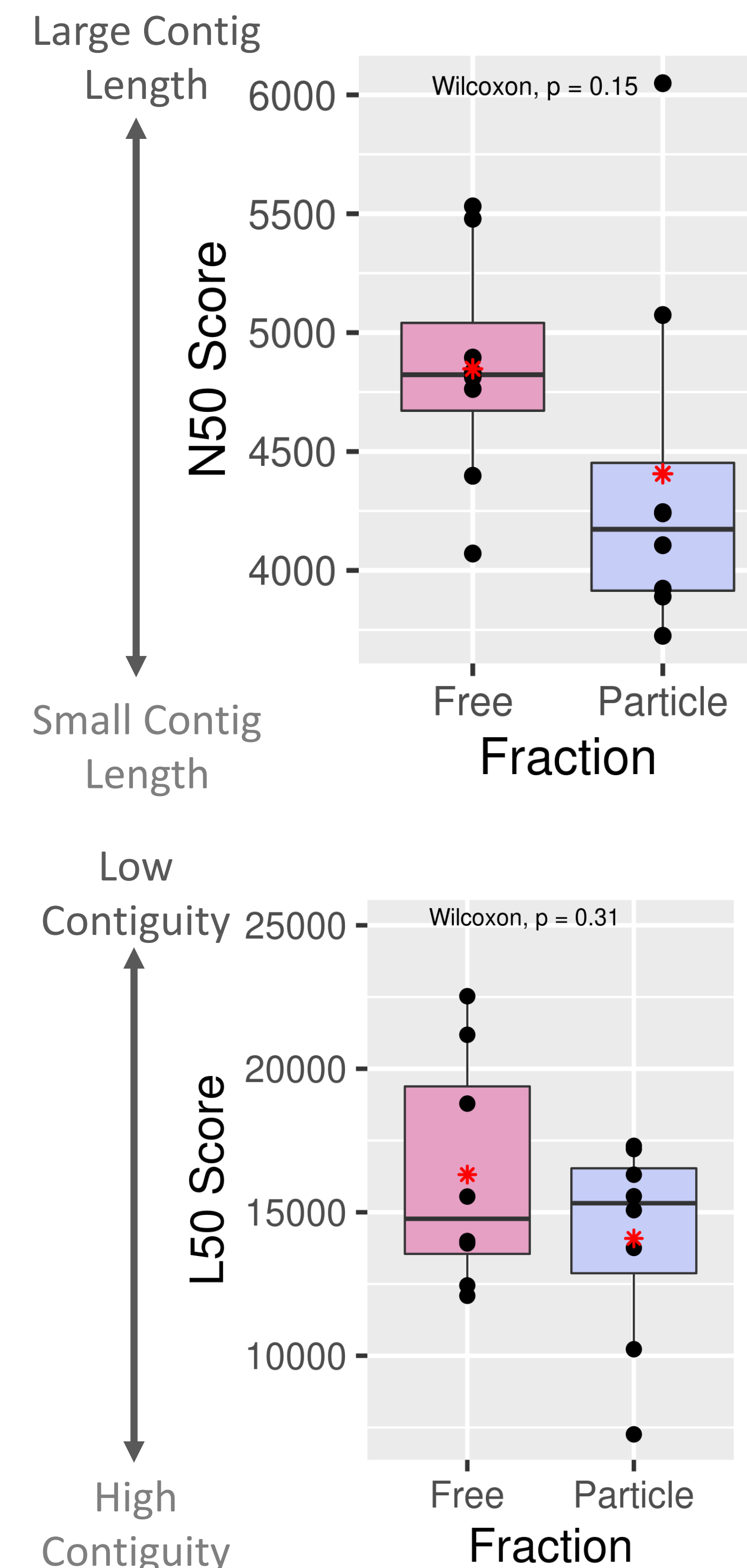


## No Significant Difference in Number of Contigs



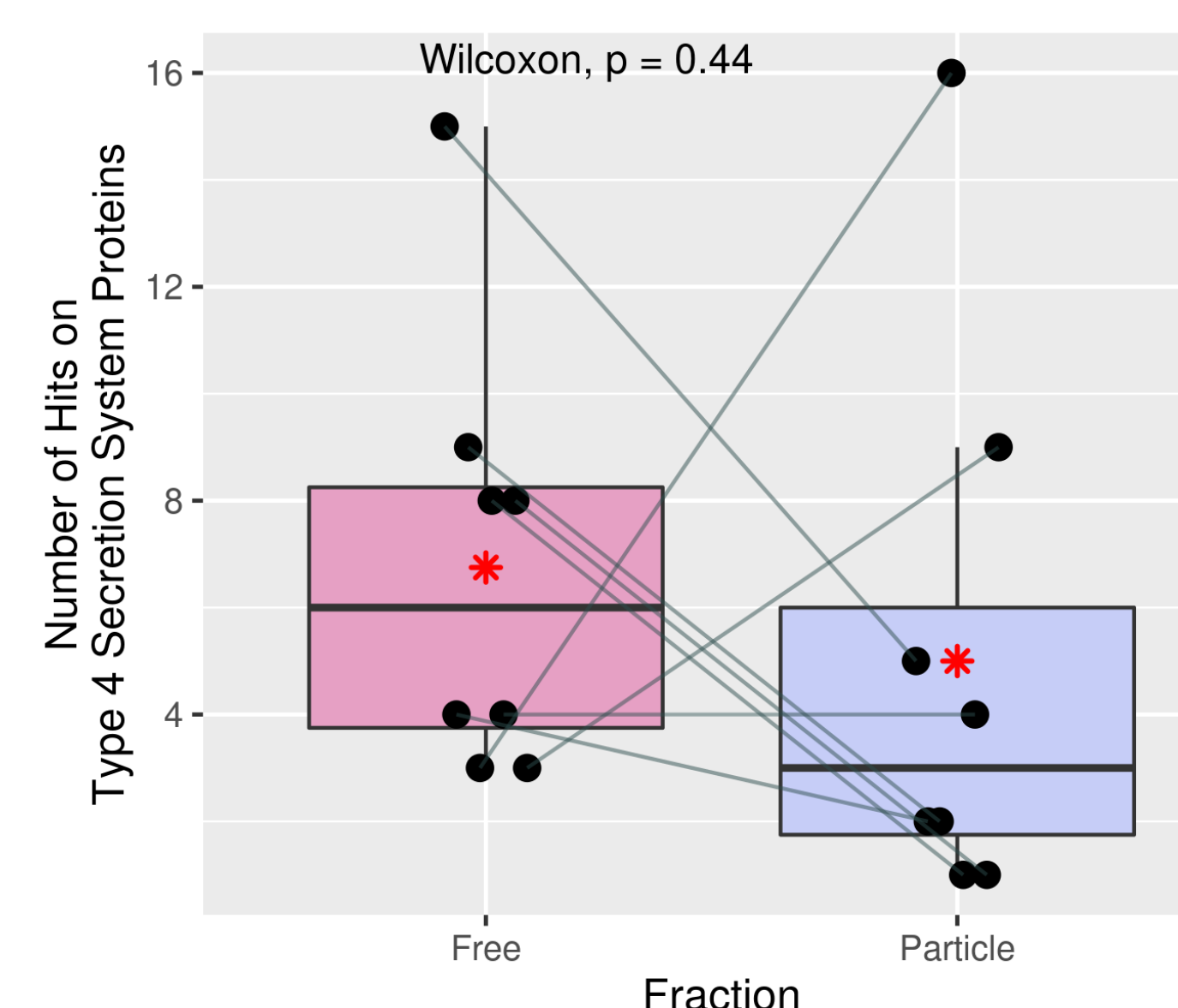
Above: Total number of contigs by habitat. Red stars indicate mean value.

## No Significant Difference in Assembly Quality



Above: N50 scores (top) and L50 scores (bottom) of sequences by habitat. Red stars indicate mean value.

## No Significant Difference in Number of Homologous Sequences



Above: Number of significant homologous sequences against the T4SS HMM profile by habitat. Red stars indicate mean value.

## Conclusion

- No significant difference in assembly quality or T4SS homologous sequences between particle-associated and free-living bacteria
  - Assembly quality affects the number of significant homologous sequences.
- Both particle-associated and free-living bacteria contained genes encoding TraG and TraD in the F-pilus complex.

## Future Work

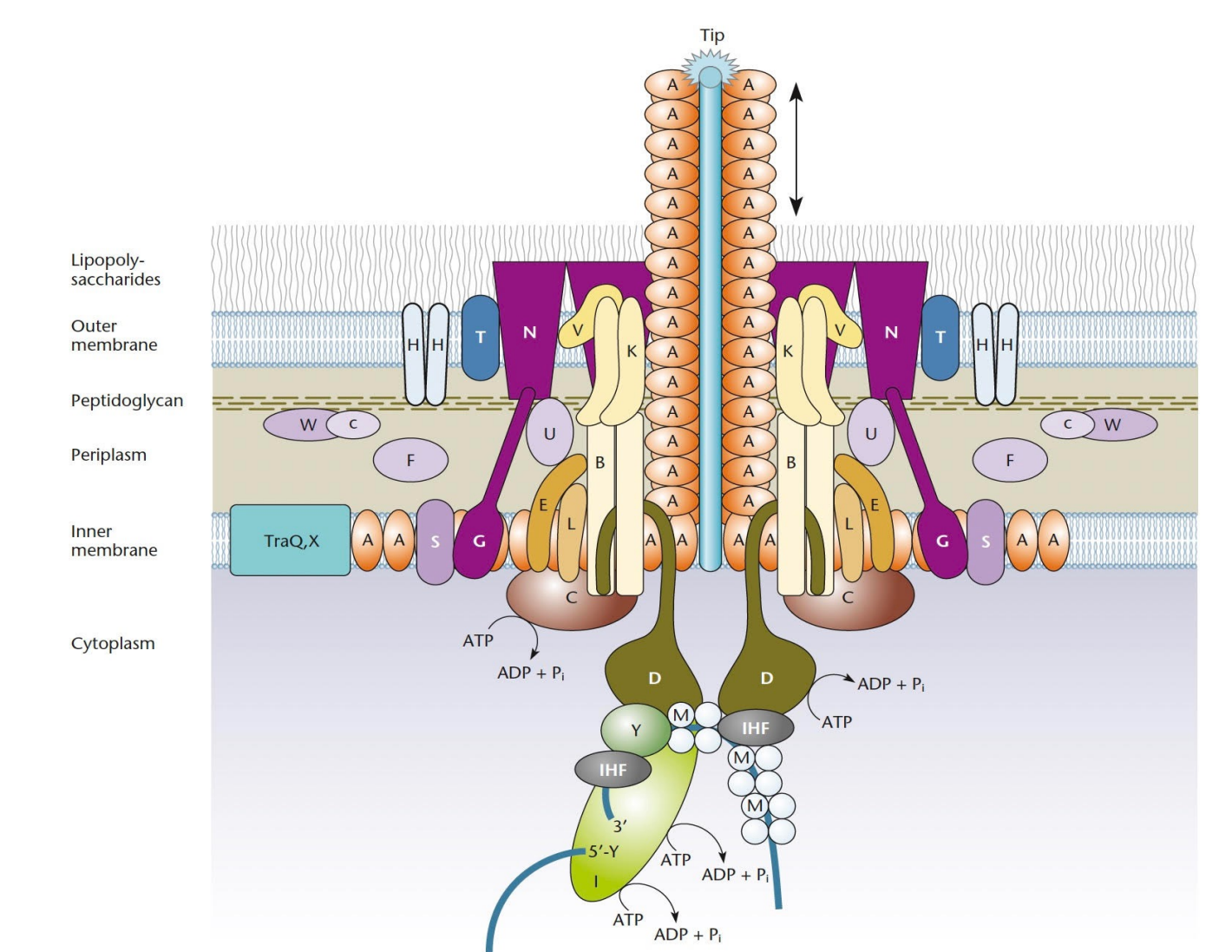
- Detection of mobile genetic elements associated with transduction, transposition, and recombination.
- Does a particular type of bacteria exhibit certain types of MGEs more than other types?

## References

Kenkin, Tina M., and Joseph E. Peters. *Snyder & Champness Molecular Genetics of Bacteria*, Fifth Edition. ASM Press, 2020.  
 Seymour, Justin R., et al. "Zooming in on the Phycosphere: The Ecological Interface for Phytoplankton-Bacteria Relationships." *Nature Microbiology*, vol. 2, Springer Nature Limited, May 2017, <https://doi.org/10.1038/nmicrobiol.2017.65>.  
 Brito, L.L. Examining horizontal gene transfer in microbial communities. *Nat Rev Microbiol* 19, 442–453 (2021). <https://doi.org/10.1038/s41579-021-00534-7>.  
 Stocker, Roman. "Marine Microbes See a Sea of Gradients." *Science*, vol. 338, no. 6107, American Association for the Advancement of Science, Nov. 2012, pp. 628–633, <https://doi.org/10.1126/science.1208929>.  
 Dinghua Li, Chi-Man Liu, Ruibang Luo, Kunihiko Sadakane, Tak-Wah Lam, MEGAHIT: an ultra-fast single-node solution for large and complex metagenomics assembly via succinct de Bruijn graph, *Bioinformatics*, Volume 31, Issue 10, 15 May 2015, Pages 1674–1676, <https://doi.org/10.1093/bioinformatics/btv033>.  
 Alla Mikhlenko, Vladislav Savilev, Alexey Gurevich, MetaQUAST: evaluation of metagenome assemblies, *Bioinformatics*, Volume 32, Issue 7, 1 April 2016, Pages 1088–1090, <https://doi.org/10.1093/bioinformatics/btv697>.  
 Hyatt, D., Chen, G.L., LoCasio, P.F. et al. Prodigal: prokaryotic gene recognition and translation initiation site identification. *BMC Bioinformatics* 11, 119 (2010). <https://doi.org/10.1186/1471-2105-11-119>.  
 HMMER 3.3.2 (Nov 2020); <http://hmmer.org/>

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Above: Structure of the F-pilus, a type IV secretion system that contributes to DNA conjugative transfer. Figure from *Molecular Genetics of Bacteria* (5th ed., p. 219).