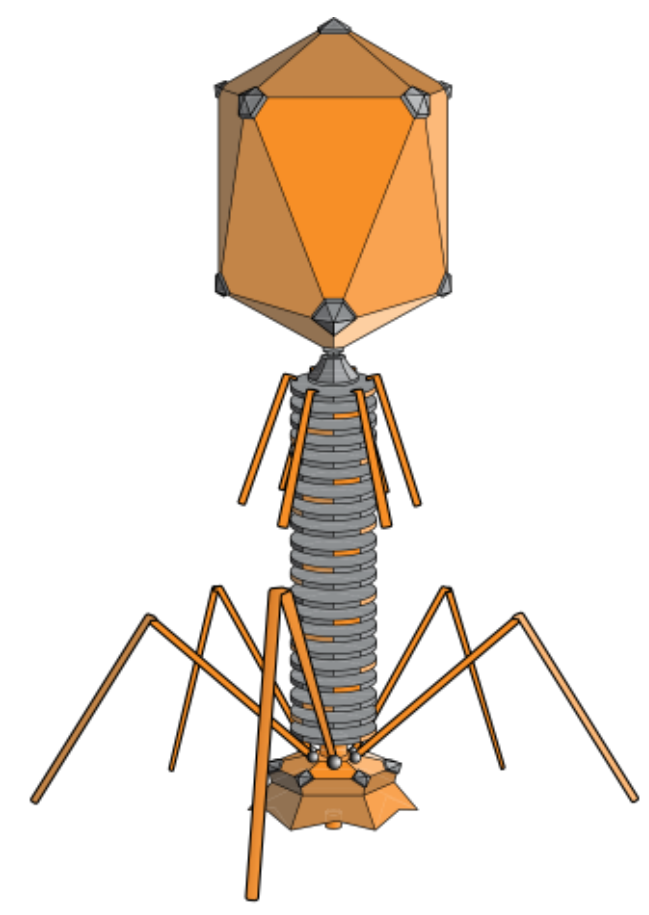
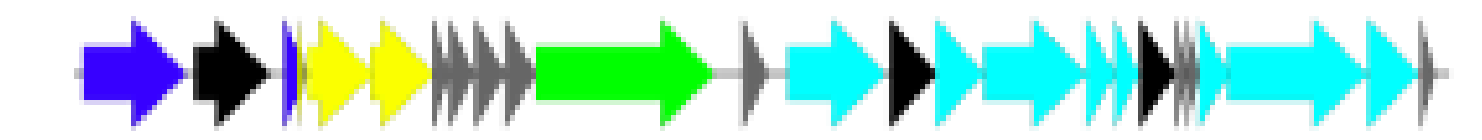




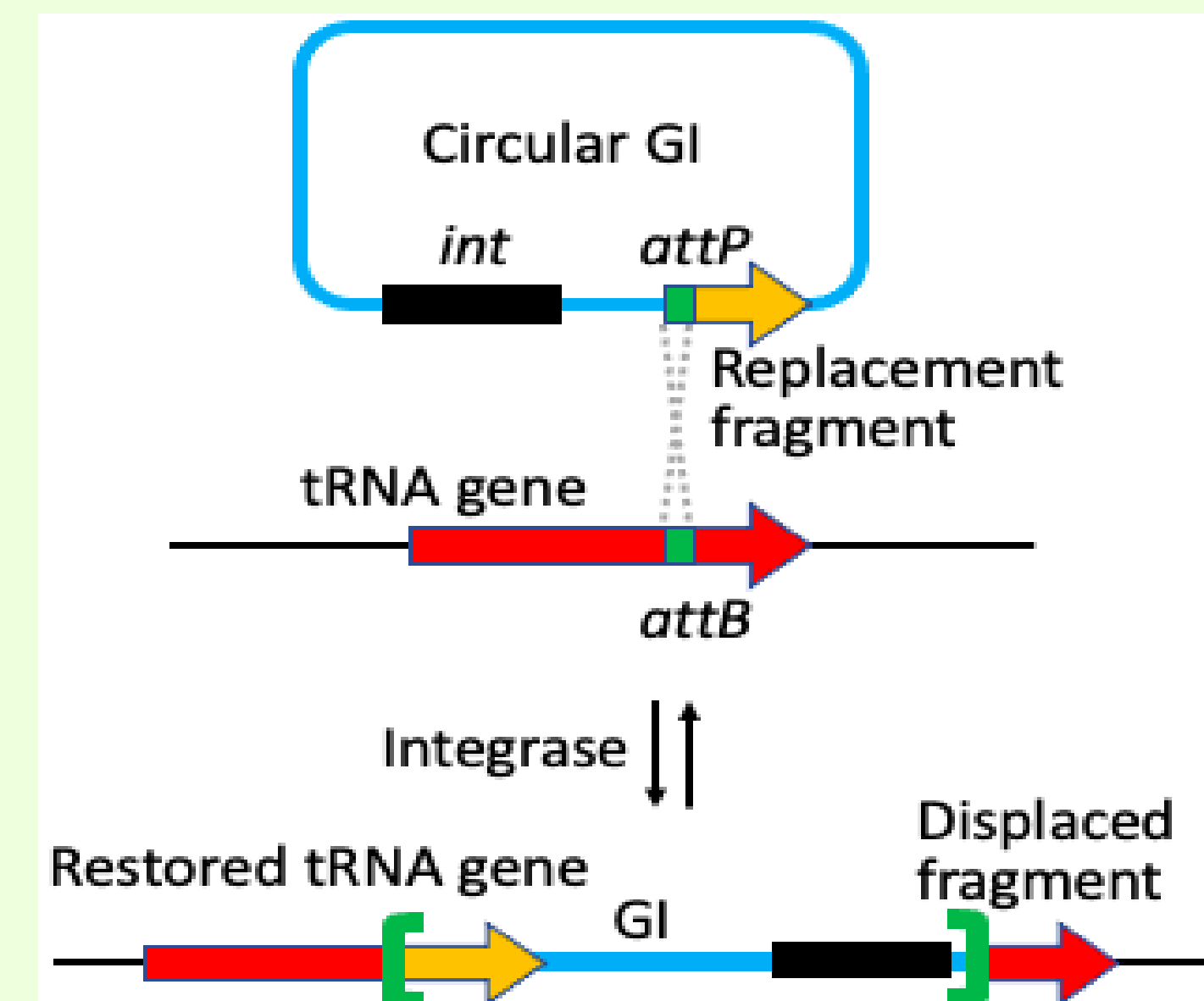
Precise Prophage Mapping

Catherine Mageeney and [Kelly Williams \(kpwilli@sandia.gov\)](mailto:kpwilli@sandia.gov)
Sandia National Laboratories, Livermore CA, USA

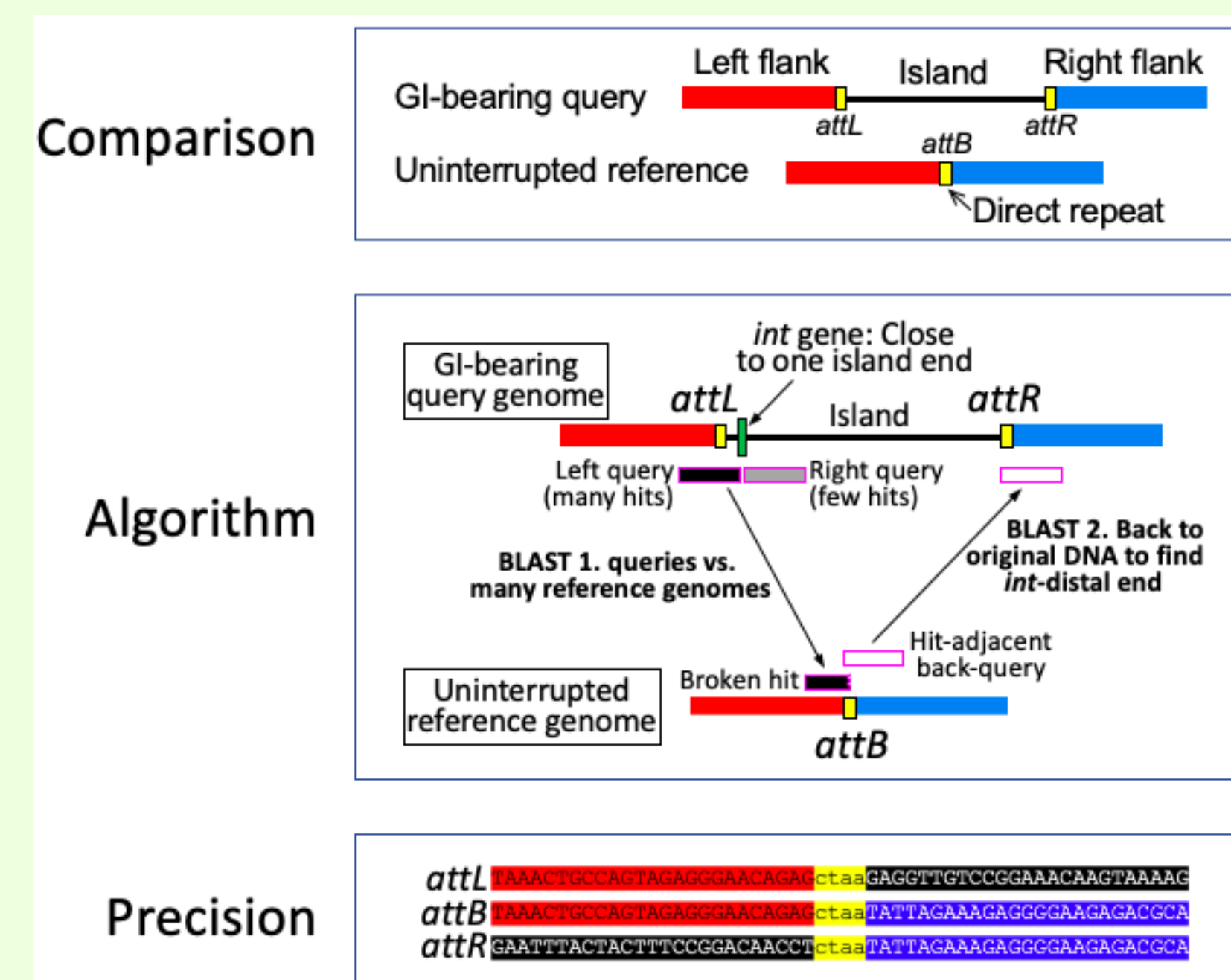


Mobilome Mapping

• Island



• TIGER

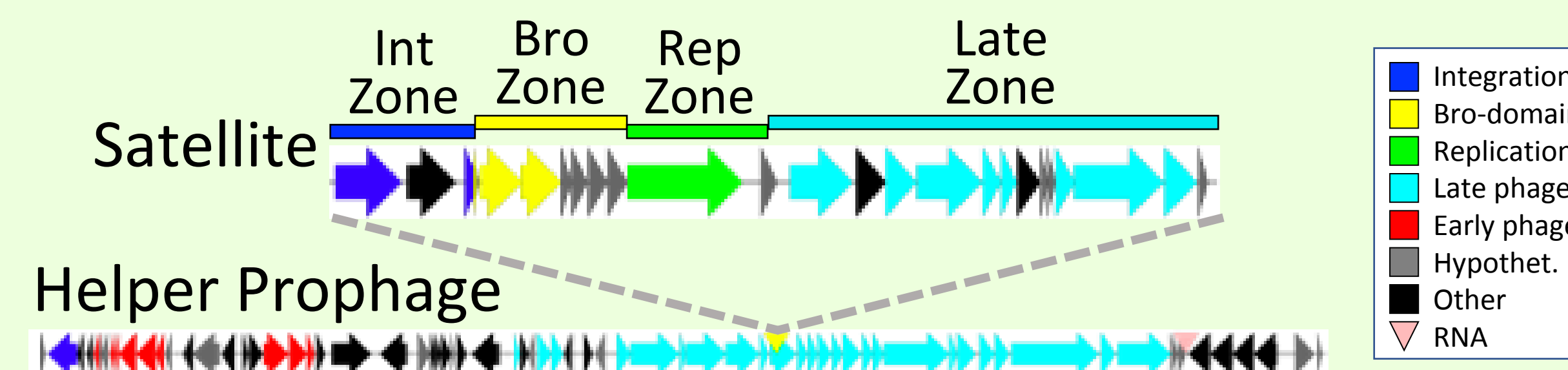


• On 350K genomes:

- 970K genomic islands
- 383K prophages

Refs (PMID): Hudson et al 2014 (25378302)
Mageeney et al 2020 (32182341)
Mageeney et al 2022 (Front Bioinfo)

Discovery: Helper-Embedded Satellites (HESs)



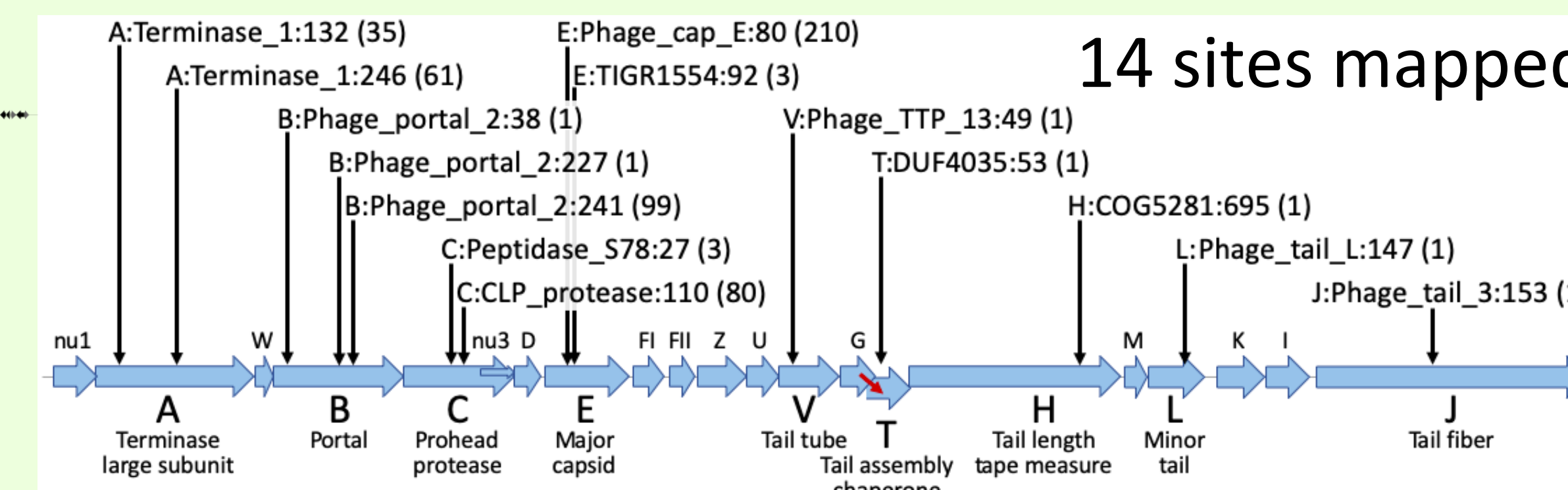
• Ordered zones in HESs/PICIs

1. Integration zone: Int + AlpA
2. Bro zone: domain-swapping regulators
3. Replication zone: Replicase + Ori
4. Late zone: gene capture from helpers

• Cis-regulation by helper

- Passive replication, late transcription
- Other satellite/helpers interact *in trans* only

• Integrate only into helper late genes



- HES always co-oriented with helper late gene

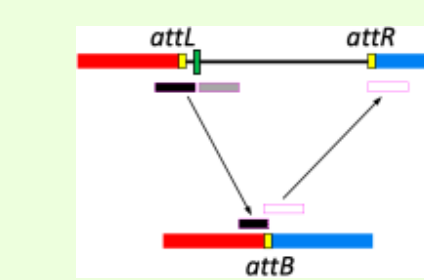
• Integrase phylogeny!!

- HESs form single clade in integrase tree
- Each late gene site-usage forms a subclade

Tommasini et al, 2022 (bioRxiv)

Application: The Phage Factory

• For any target bacterium:



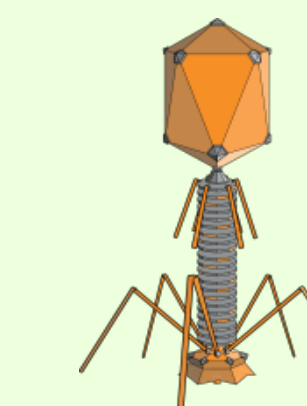
Prophage database

Identify prophage-rich
close relatives of target

Validate phages

Engineer phages

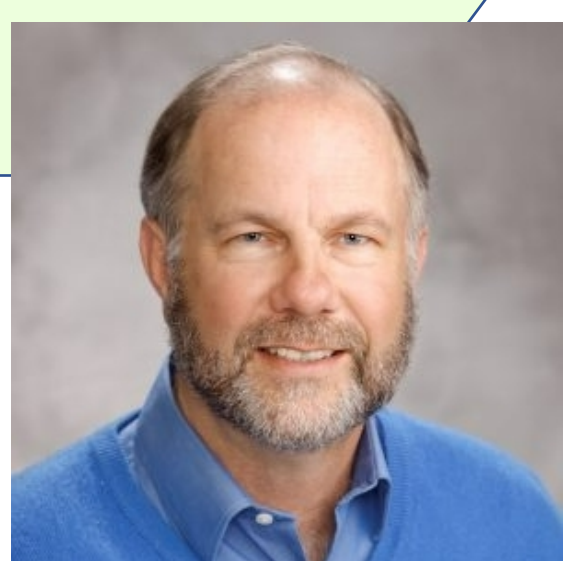
Reboot



• Proven in phage therapy

- Cocktail of five diverse phages active on *Pseudomonas aeruginosa*
- Protected waxworms from death by *Pseudomonas* infection

Mageeney et al, 2020 (32788409)



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