A comparative genomics analysis of the T3SS2α pathogenicity island of *Vibrio parahaemolyticus*

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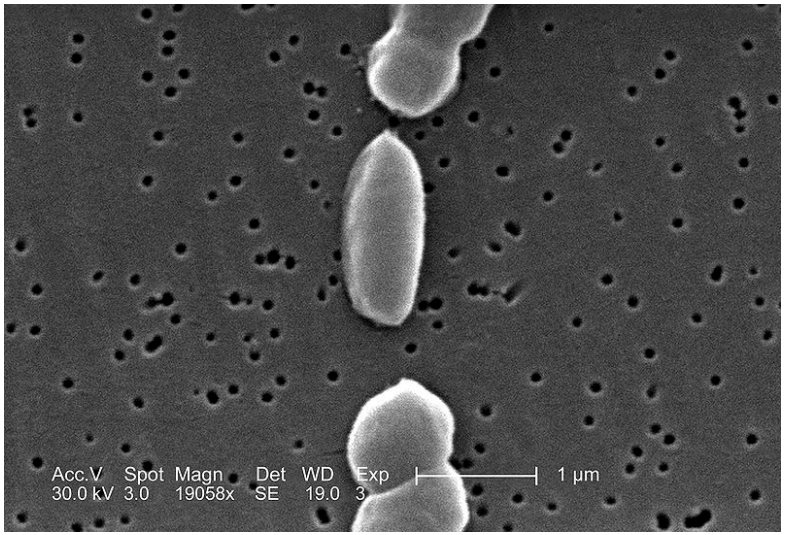
Vibrio parahaemolyticus

- ***Vibrio parahaemolyticus* (Vp)** is ubiquitous in the environment
- may acquire virulence factors that make them pathogenic
- Virulence factors have been found in pathogenicity islands
- Pathogenicity islands can be acquired or transferred in a process called horizontal gene transfer



Virulence factors of *Vibrio parahaemolyticus*

- **Virulence factors** are molecules expressed by an organism that enables them to propagate to the detriment of a host organism
- In *Vibrio parahaemolyticus*, these can be:

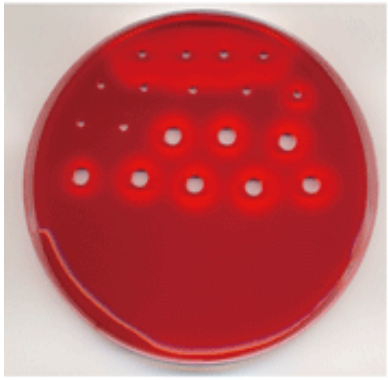
  -capsules (physical protection)

  -flagella (movement)

  -iron uptake (competition for scarce nutrient)

  -quorum sensing (communication)

  -secretion systems (transfer of genetic material/toxins)

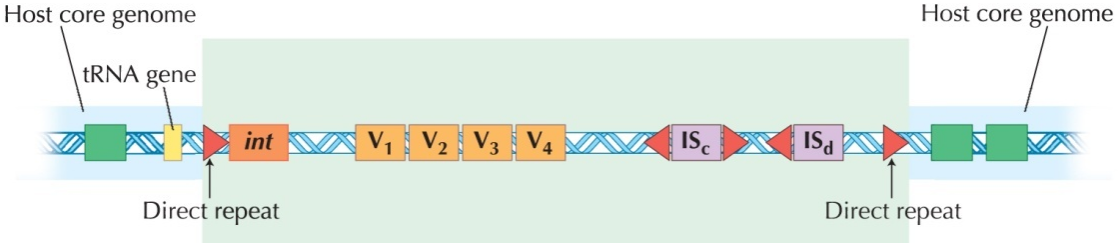


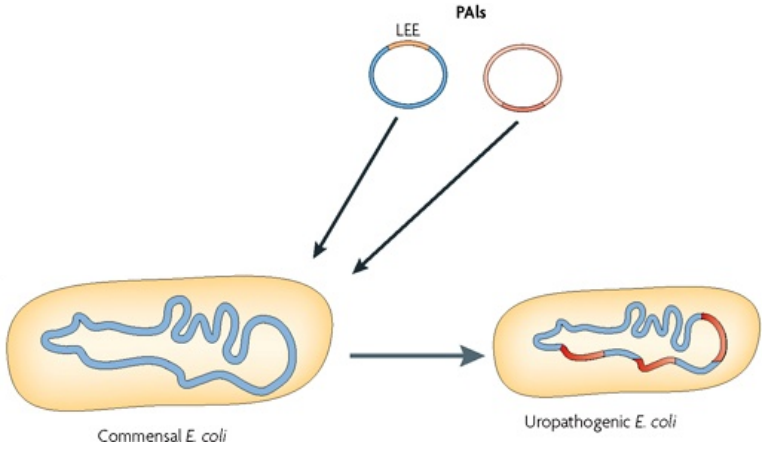
Disruption of blood cells on a blood agar plate by *Vibrio parahaemolyticus*.
-Toshio Miwatani and Takeshi Honda

- **tdh** (thermostable direct hemolysin) is a toxin that destroys host cells
- **Type 3 secretion system** (T3SS) is a secretion system that can transfer this toxin to the target cell
- Some virulence factors (T3SS, tdh toxin) are found in pathogenicity islands

Pathogenicity Islands and Horizontal Gene Transfer

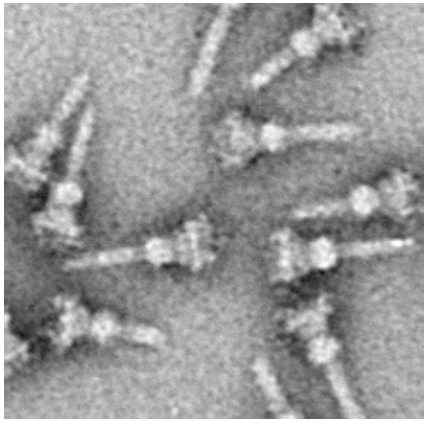
- **Pathogenecity islands (PAI)** are Discrete genetic units
- Flanked by direct repeats, insertion sequences, or tRNA
- Pathogenicity islands are unstable
- Pathogenicity islands can be acquired or transferred in a process called horizontal gene transfer





- **Horizontal gene transfer (HGT)** is the direct transfer of genes between organisms through processes such as injection of the relevant genes.
- Continuous HGT introduces variations in the PAI
- One facilitator of horizontal gene transfer is the type 3 secretion system

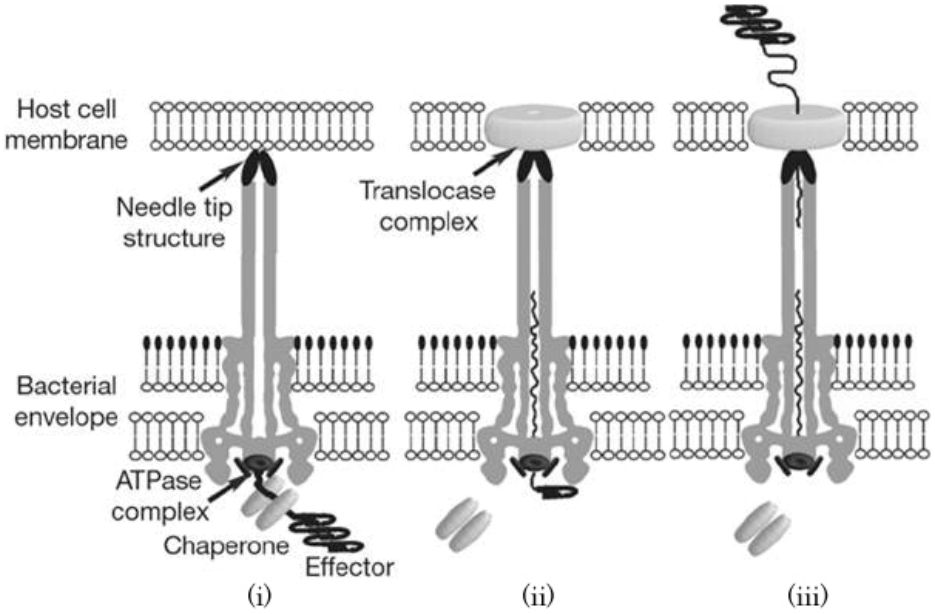
Type 3 secretion system



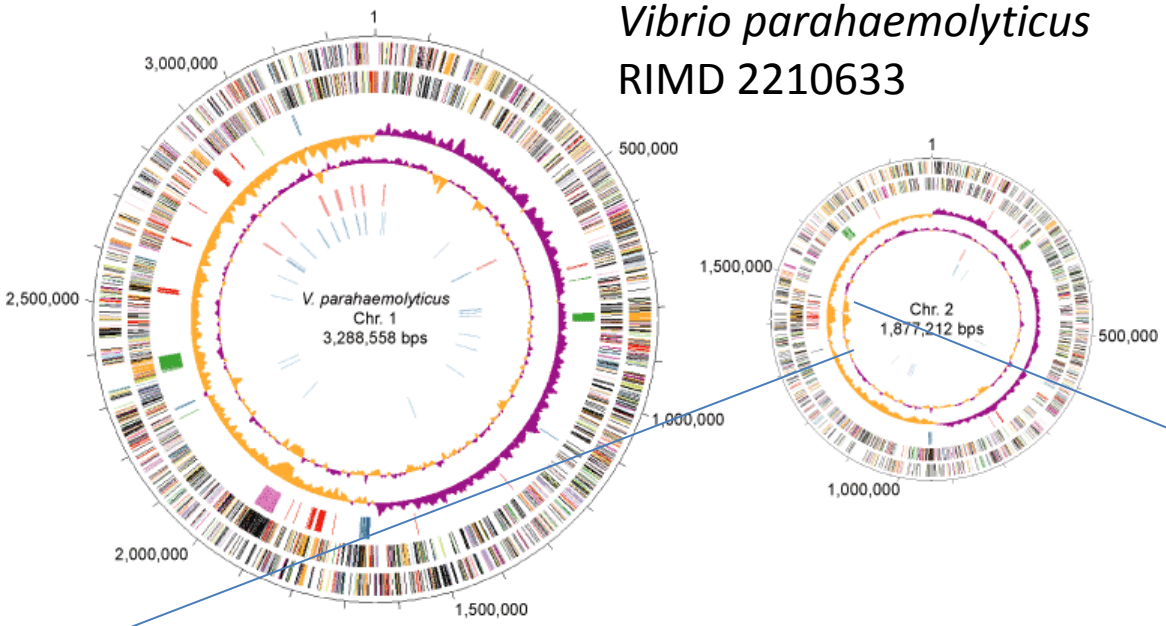
- **Type 3 secretion system (T3SS)** is a needle-like structure commonly found in pathogenic bacteria
- Some bacteria that contains has T3SS mediated virulence are *Yersinia* (plague), *Salmonella* (typhoid fever) *E. coli* (food poisoning), *Chlamydia* (STD), and *Vibrio*

- *Vibrio parahaemolyticus* has 3 known T3SS systems.
  - T3SS1
  - T3SS2α – encodes for tdh (*tdhA* & *tdhS*)
  - T3SS2β – encodes for trh

  T3SS2α and T3SS2β are variants of each other



T3SS2α pathogenicity island (VpPAI) of *Vibrio parahaemolyticus* RIMD 2210633



From the outside:

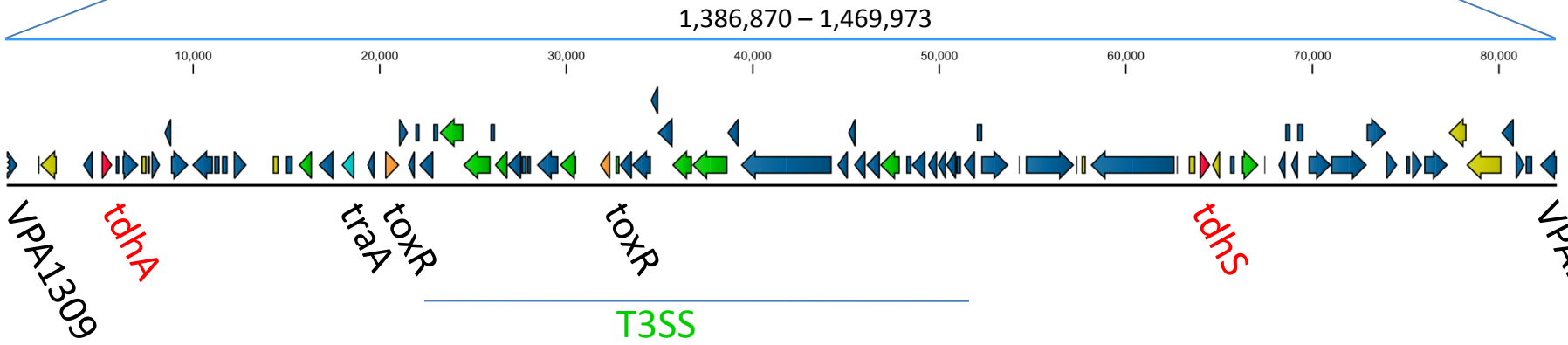
1st 2nd = CDS on the plus and minus strands

3rd = pathogenesis-related genes (red)

4th = GC skew

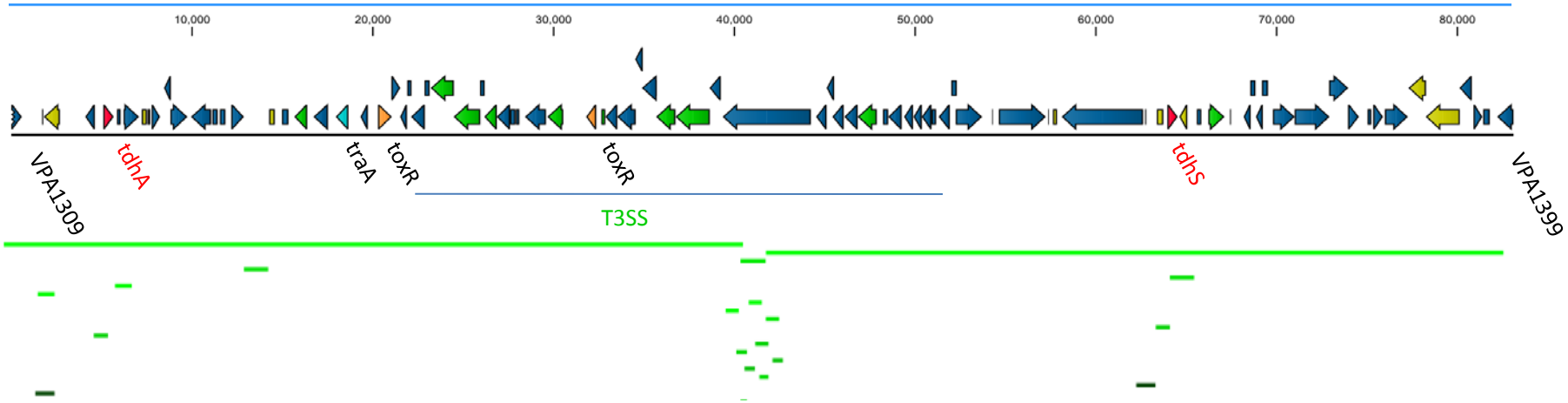
5th = percentage G+C/mean G+C

-from http://genome.bio.titech.ac.jp/

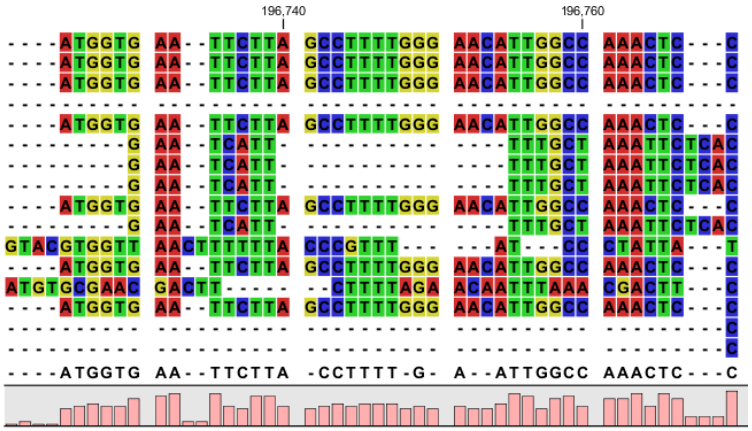


Methodology

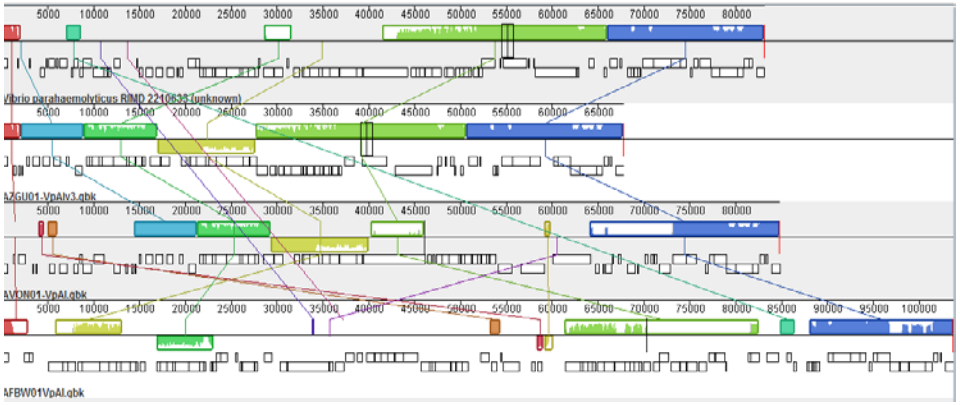
A. BLAST



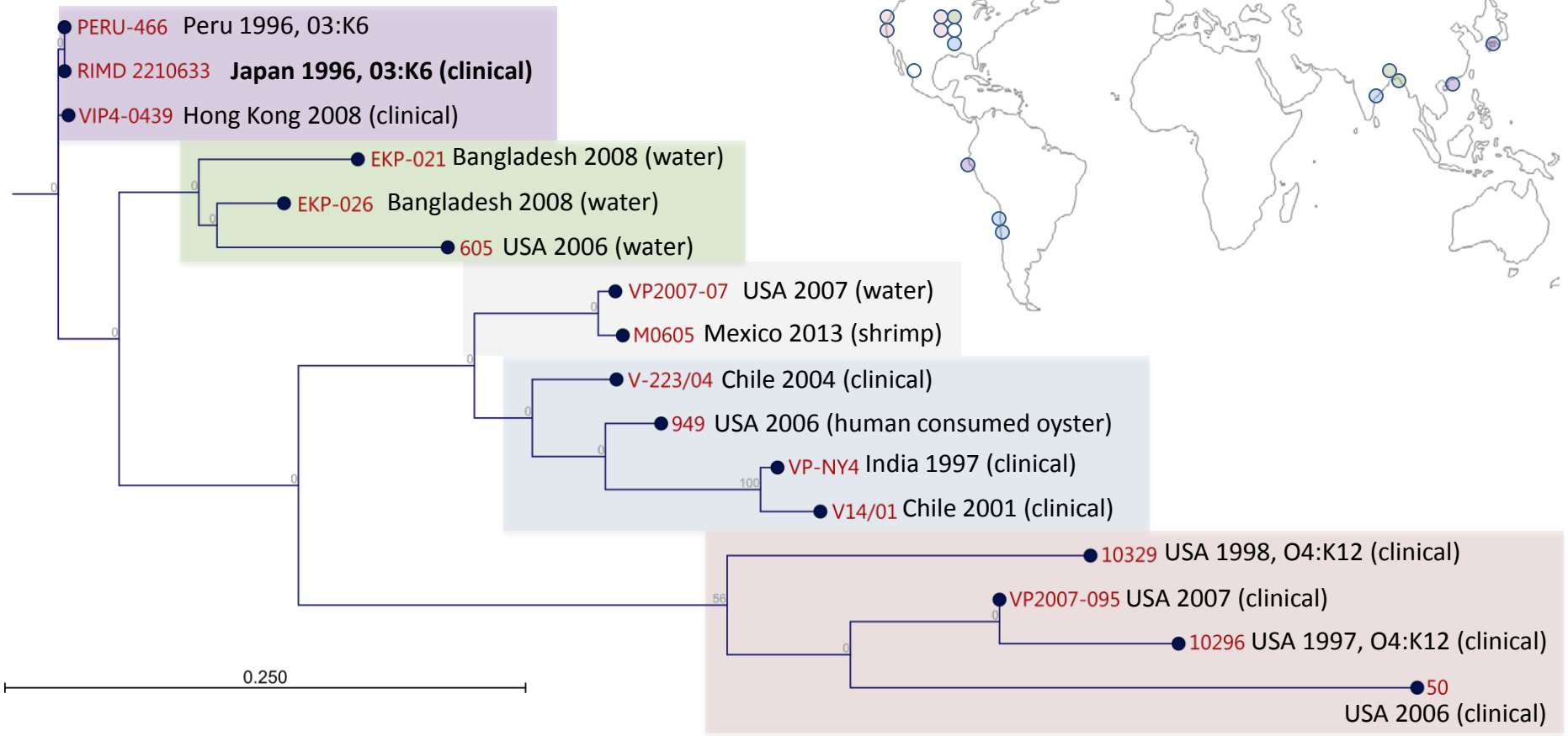
B. ALIGN

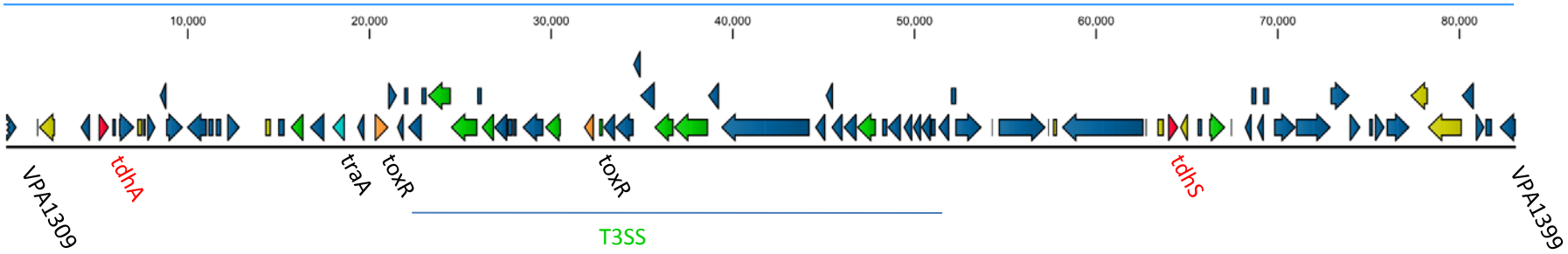


C. MAUVE

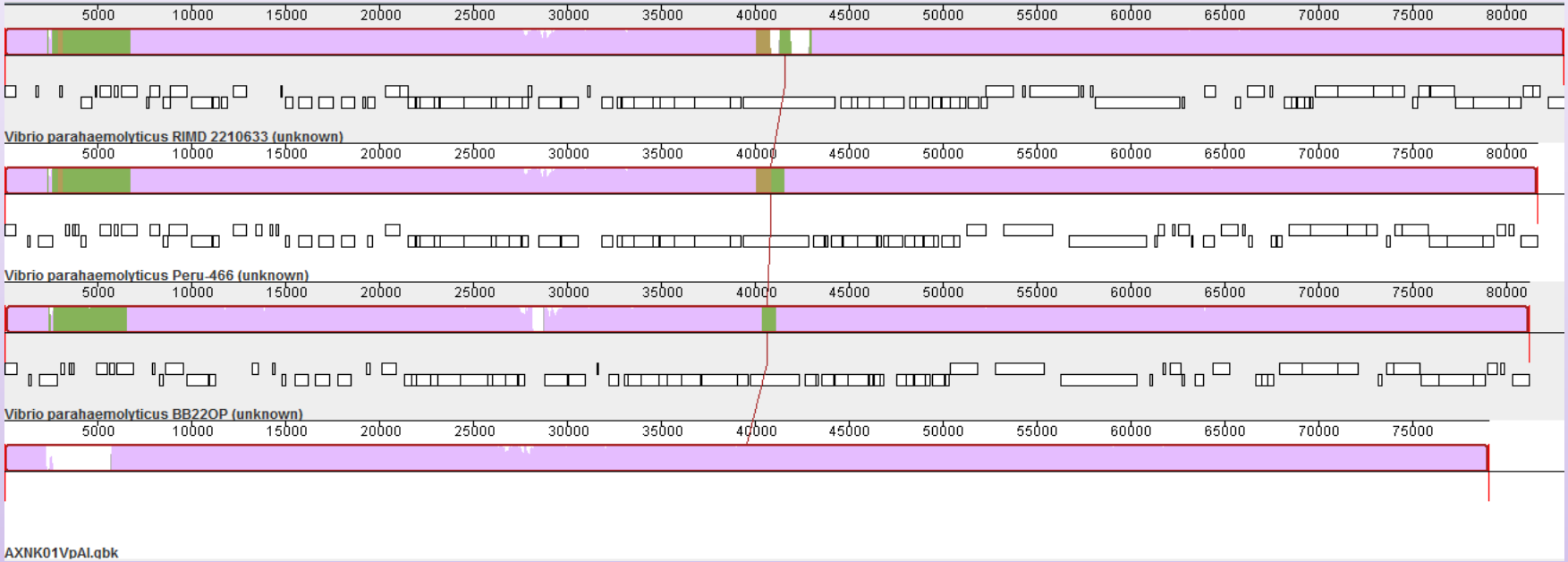


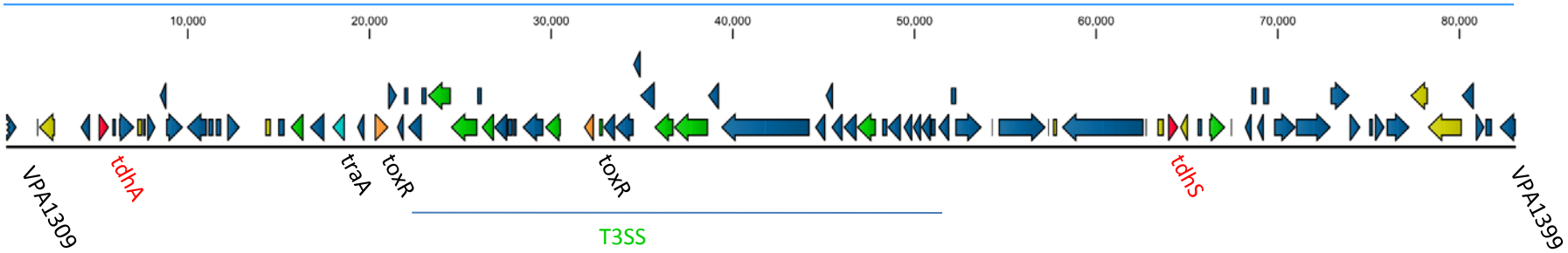
Sequences


PERU-466 Peru 1996, 03:K6
RIMD 2210633 Japan 1996, 03:K6 (clinical)
VIP4-0439 Hong Kong 2008 (clinical)
EKP-021 Bangladesh 2008 (water)
EKP-026 Bangladesh 2008 (water)
605 USA 2006 (water)
VP2007-07 USA 2007 (water)
M0605 Mexico 2013 (shrimp)
V-223/04 Chile 2004 (clinical)
949 USA 2006 (human consumed oyster)
VP-NY4 India 1997 (clinical)
V14/01 Chile 2001 (clinical)
10329 USA 1998, O4:K12 (clinical)
VP2007-095 USA 2007 (clinical)
10296 USA 1997, O4:K12 (clinical)
50
USA 2006 (clinical)
0.250

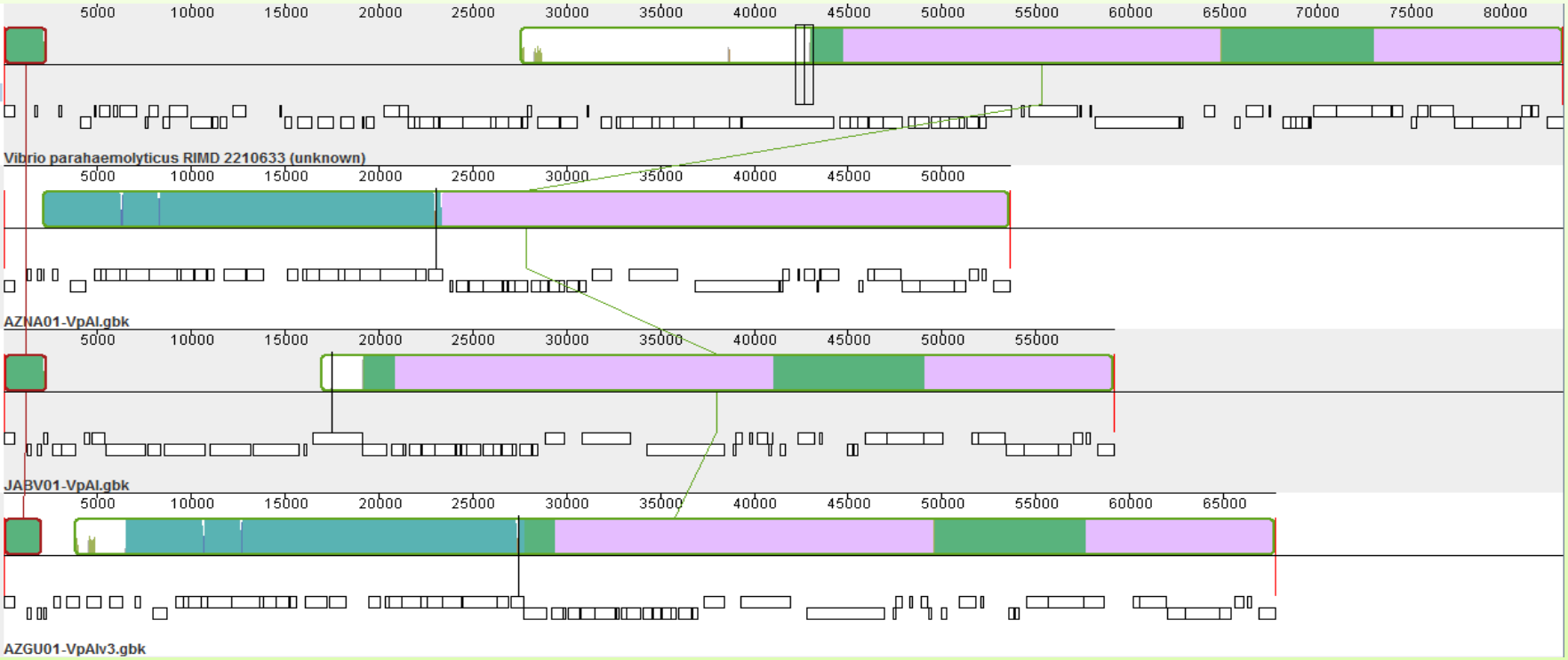


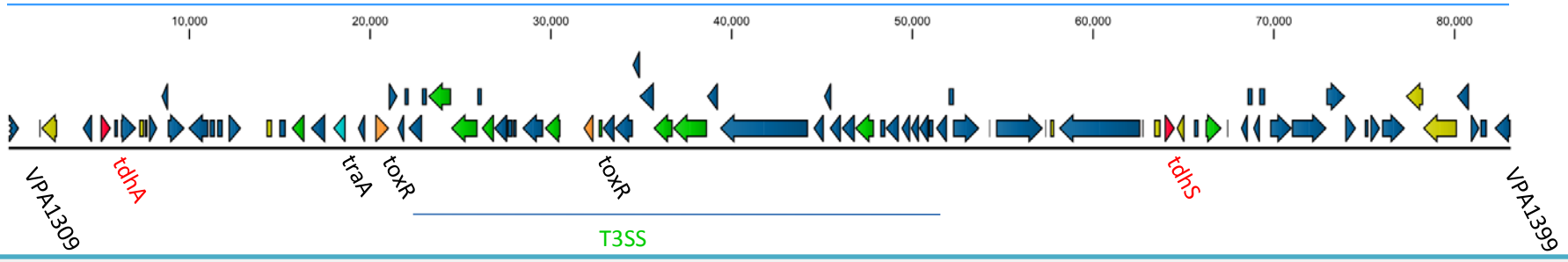
tdh+/T3SS2α+/trh-



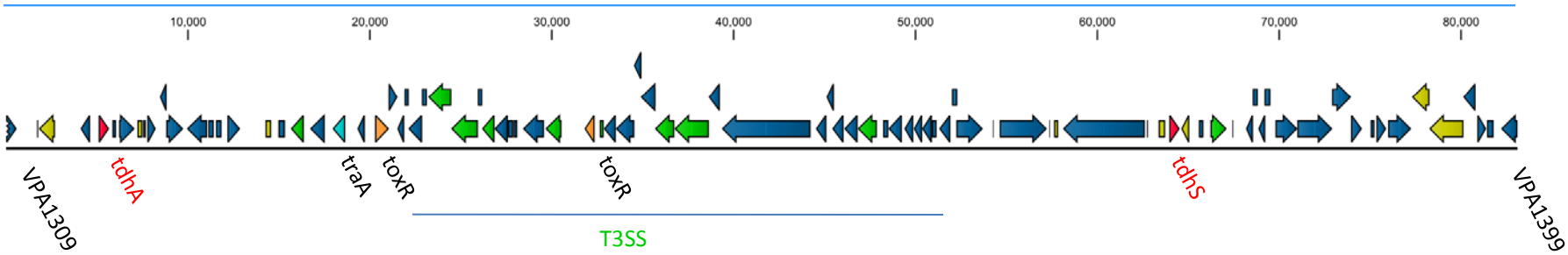


tdh+/T3SS2α+/trh-

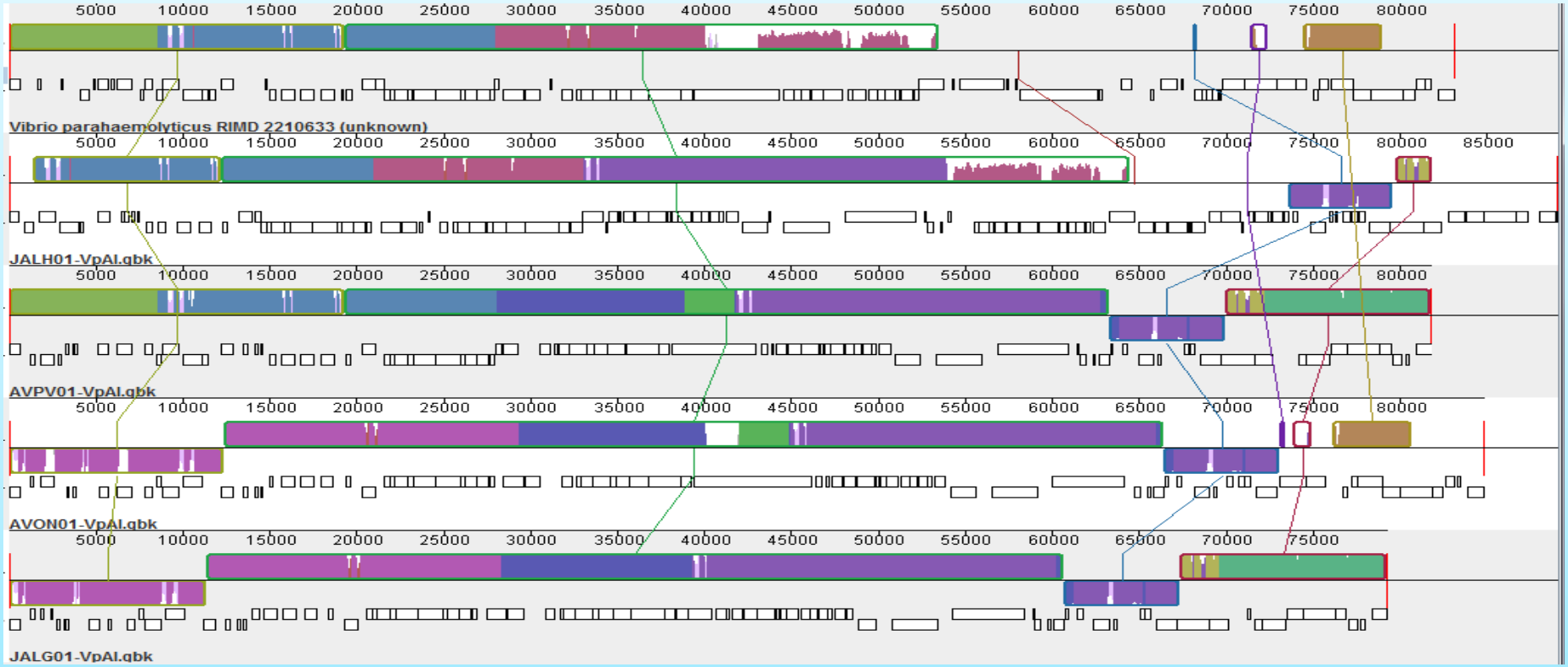


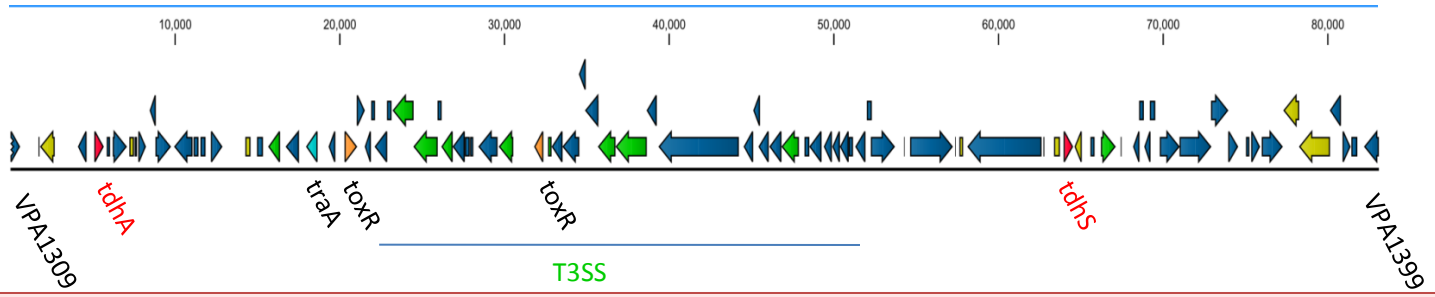


tdh-/T3SS2-/trh-

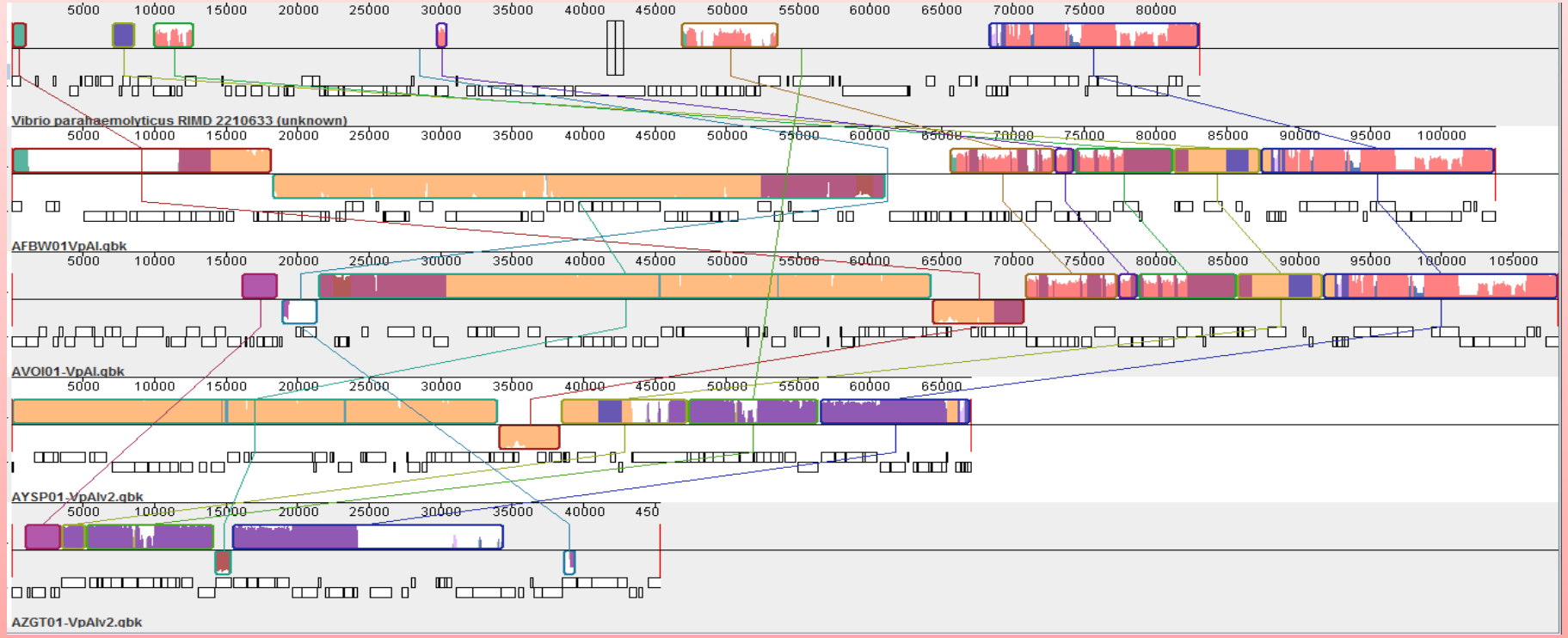


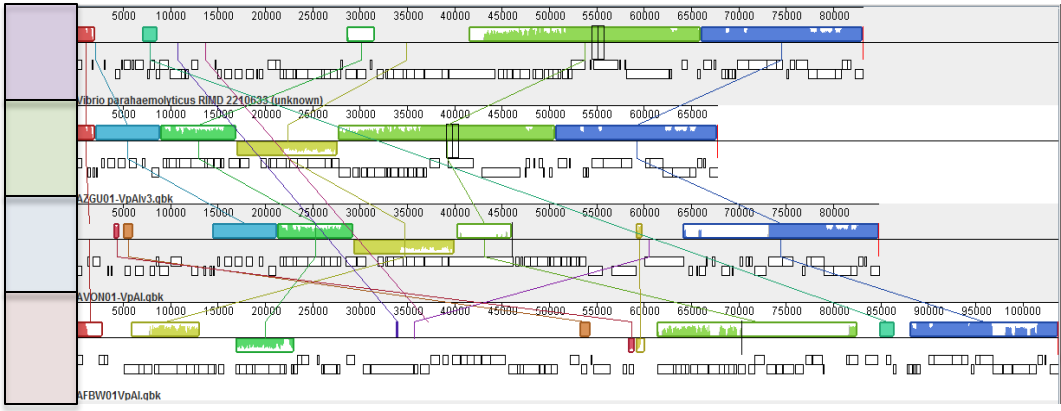
tdh+/T3SS2α+/trh-

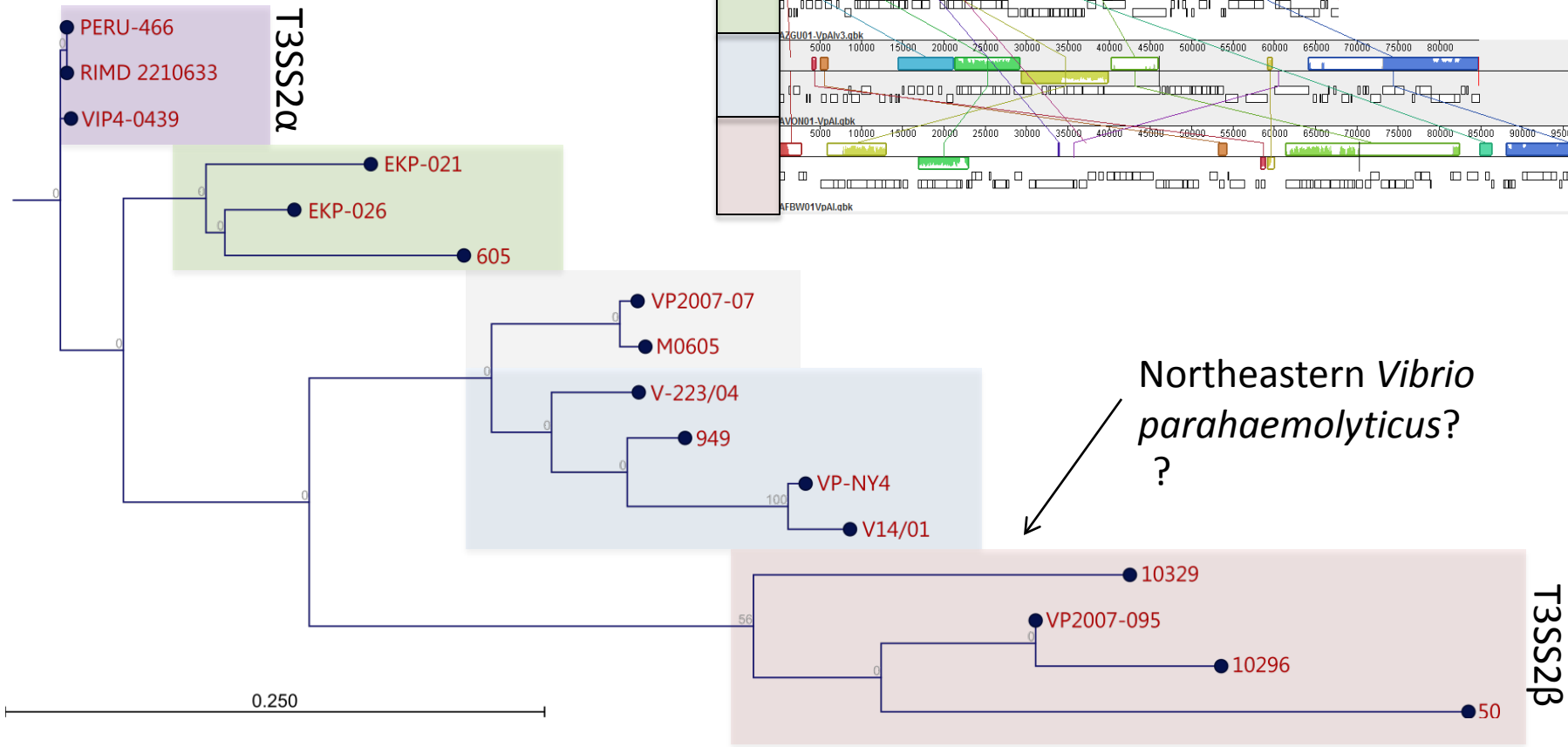




tdh+/ T3SS2β +/trh+







Northeastern *Vibrio parahaemolyticus*?
?

Summary

- The approach is a viable method to understand incompletely assembled sequences
- Several lineages of the VpPAI can be discerned
- Several lineages may be available in a single locale
- The USA *Vibrio parahaemolyticus* are mostly a tdh+ T3SS2β