

***Orientia tsutsugamushi*: analysis of the mobilome of a highly fragmented and repetitive genome reveals ongoing lateral gene transfer in an obligate intracellular bacterium.**

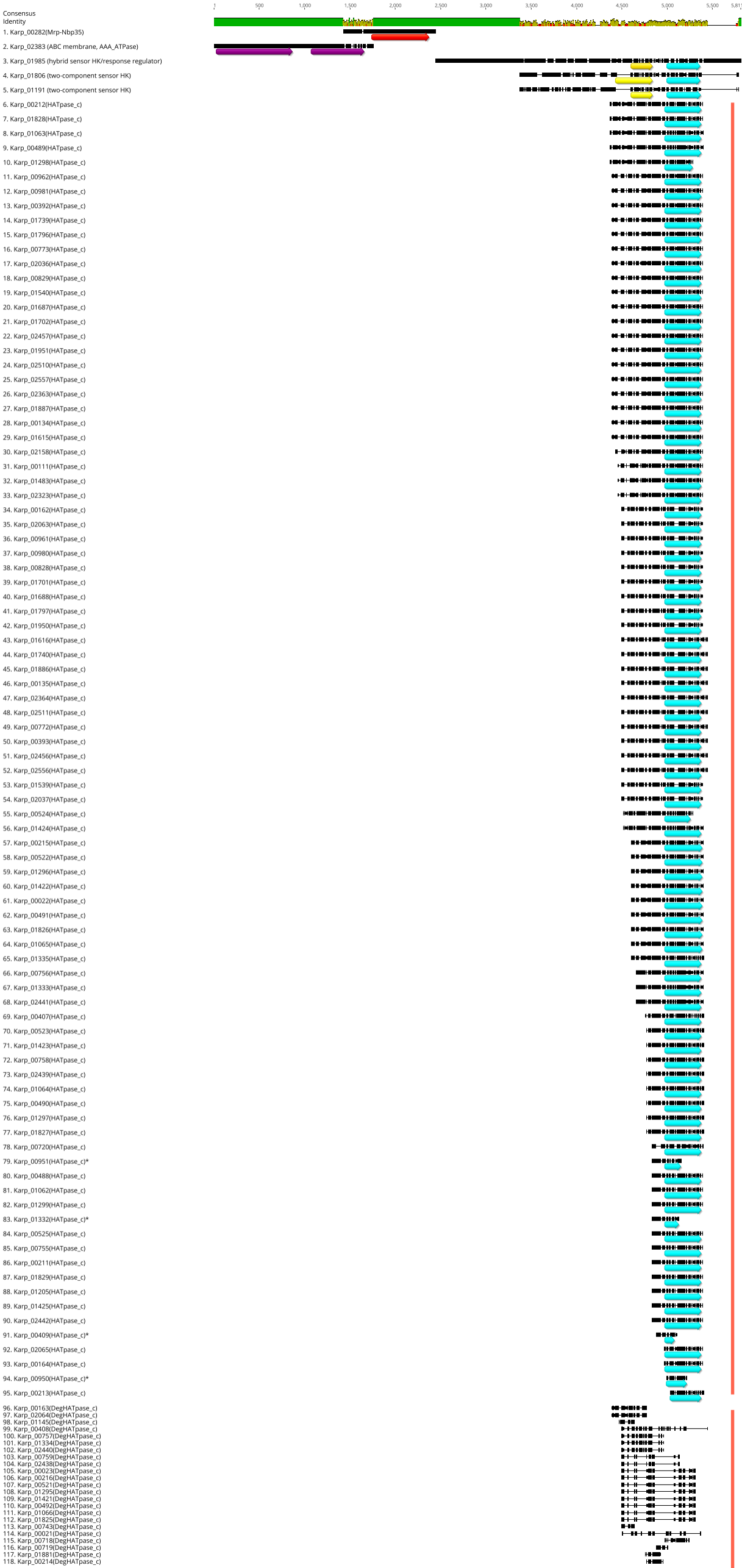
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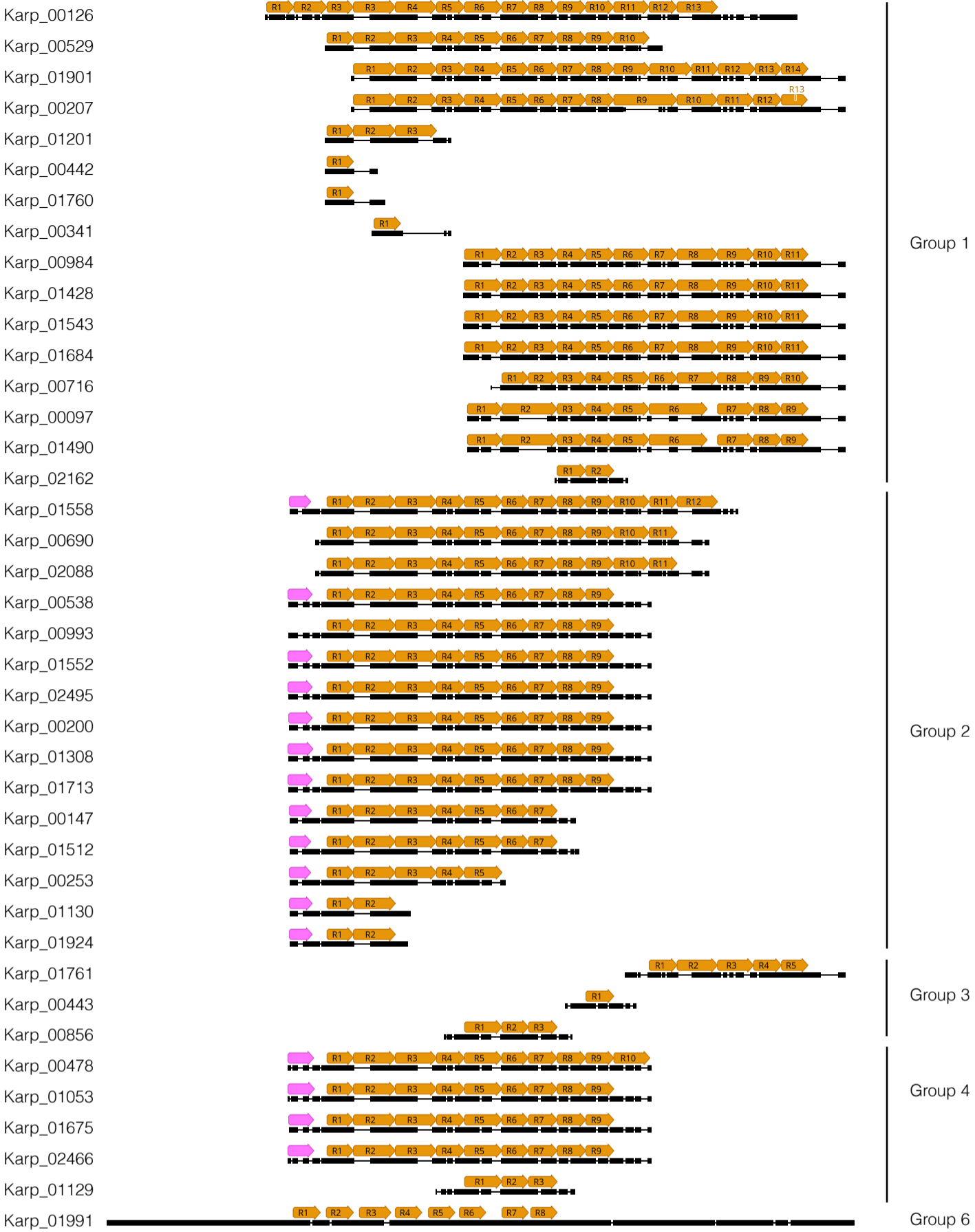


Mrp/NBP35 family ATP-binding protein
ABC_membrane and AAA - ATPases
Hybrid sensor histidine kinase/response regulator
Two-component sensor histidine kinase
Two-component sensor histidine kinase

HATPase c domain containing
protein

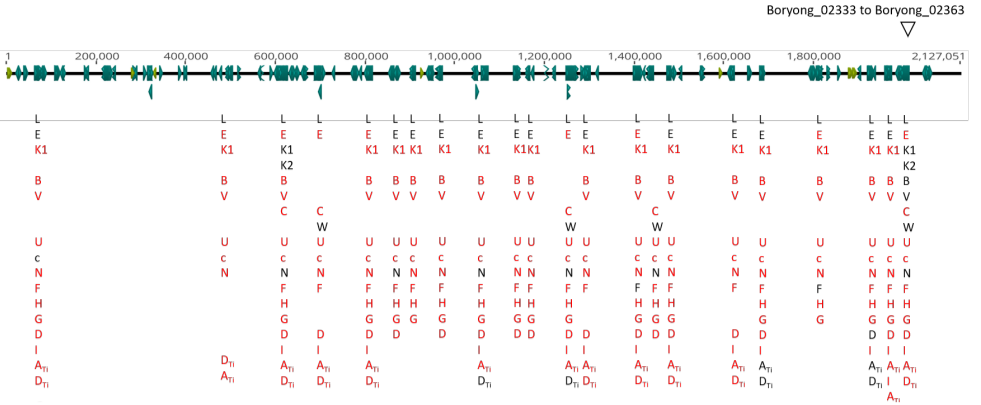
degraded HATPase c domain
containing protein

Supp. Fig. 1. Alignment of MRP and HATPase-domain genes in Ot Karp.

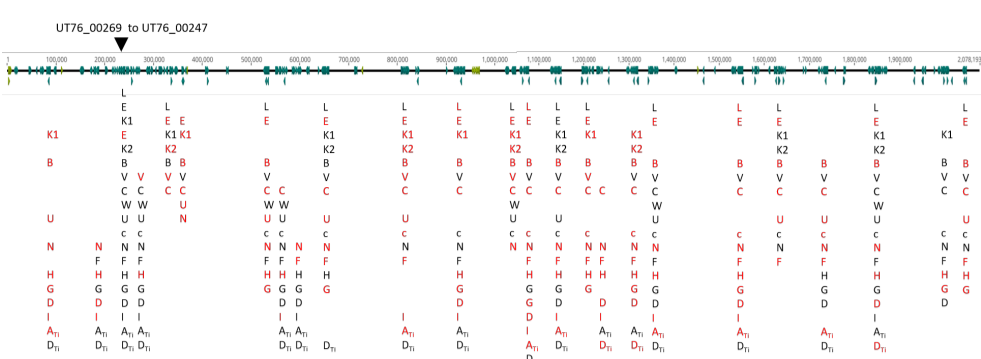


Supp. Fig. 2. Analysis of tetratricopeptide repeat containing proteins in Ot (TPRs). A. Alignment of TPR genes in Ot strain Karp showing classification into groups.

Boryong



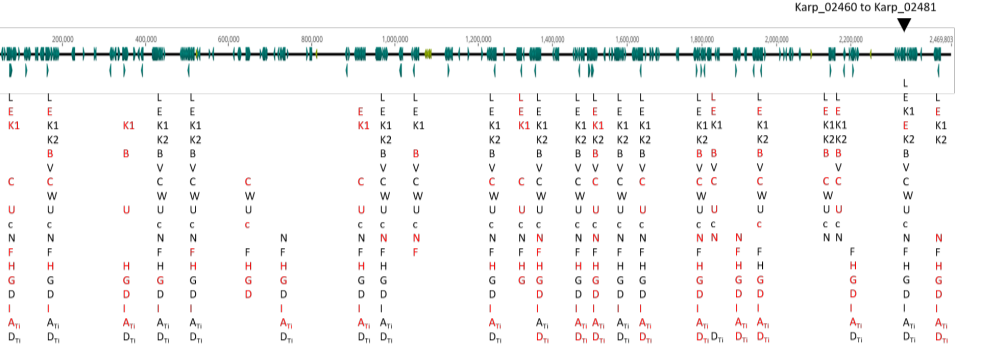
UT76



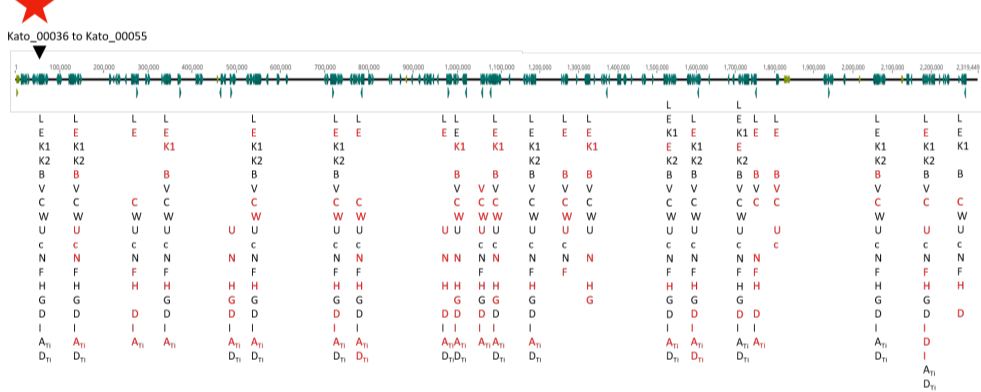
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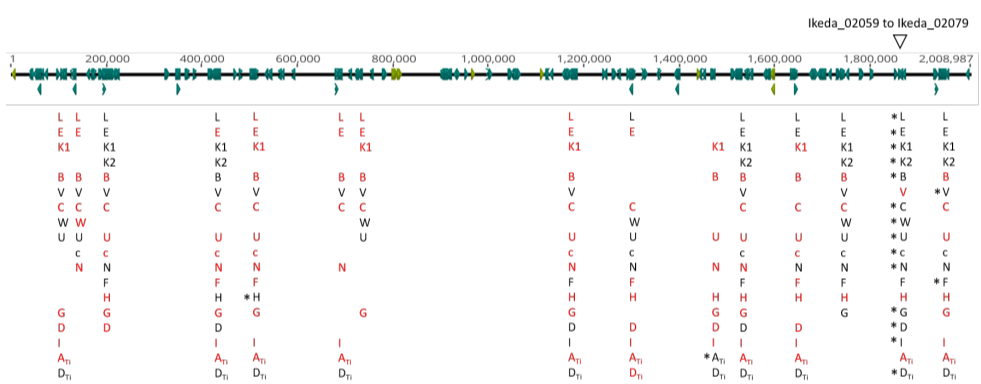
Karp



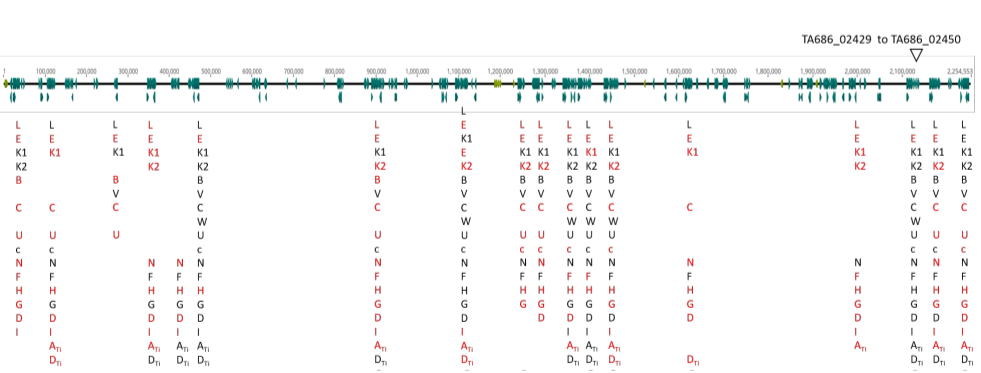
Kato



Ikeda



TA686



Gilliam



Supp. Fig. 3. Analysis of Tra genes in Ot. An overview of *tra* gene clusters in all Ot strains. Truncated genes are shown in red, and full length tones in black. Complete gene sets are shown in black arrows above, with almost complete sets in white arrows. Full gene sets located within complete RAGEs are shown by red stars.