

## SUPPLEMENTARY FILE

### **High genomic identity between clinical and environmental strains of *Herbaspirillum frisingense* suggests pre-adaptation to different hosts and intrinsic resistance to multiple drugs**

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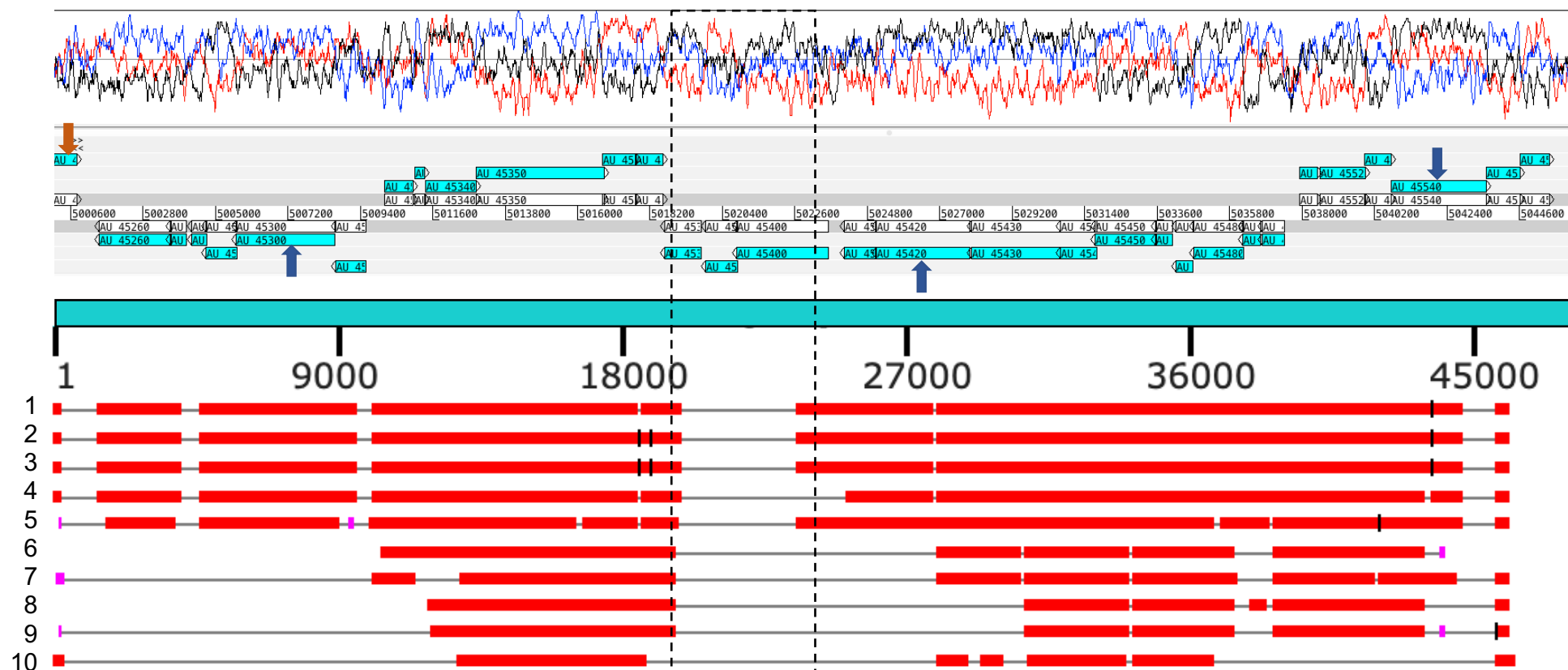
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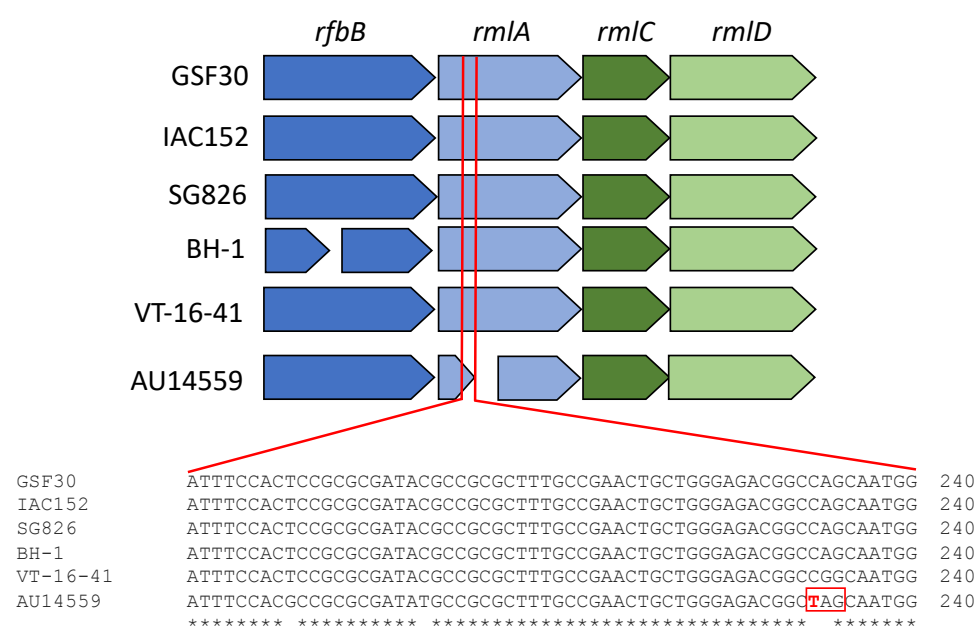
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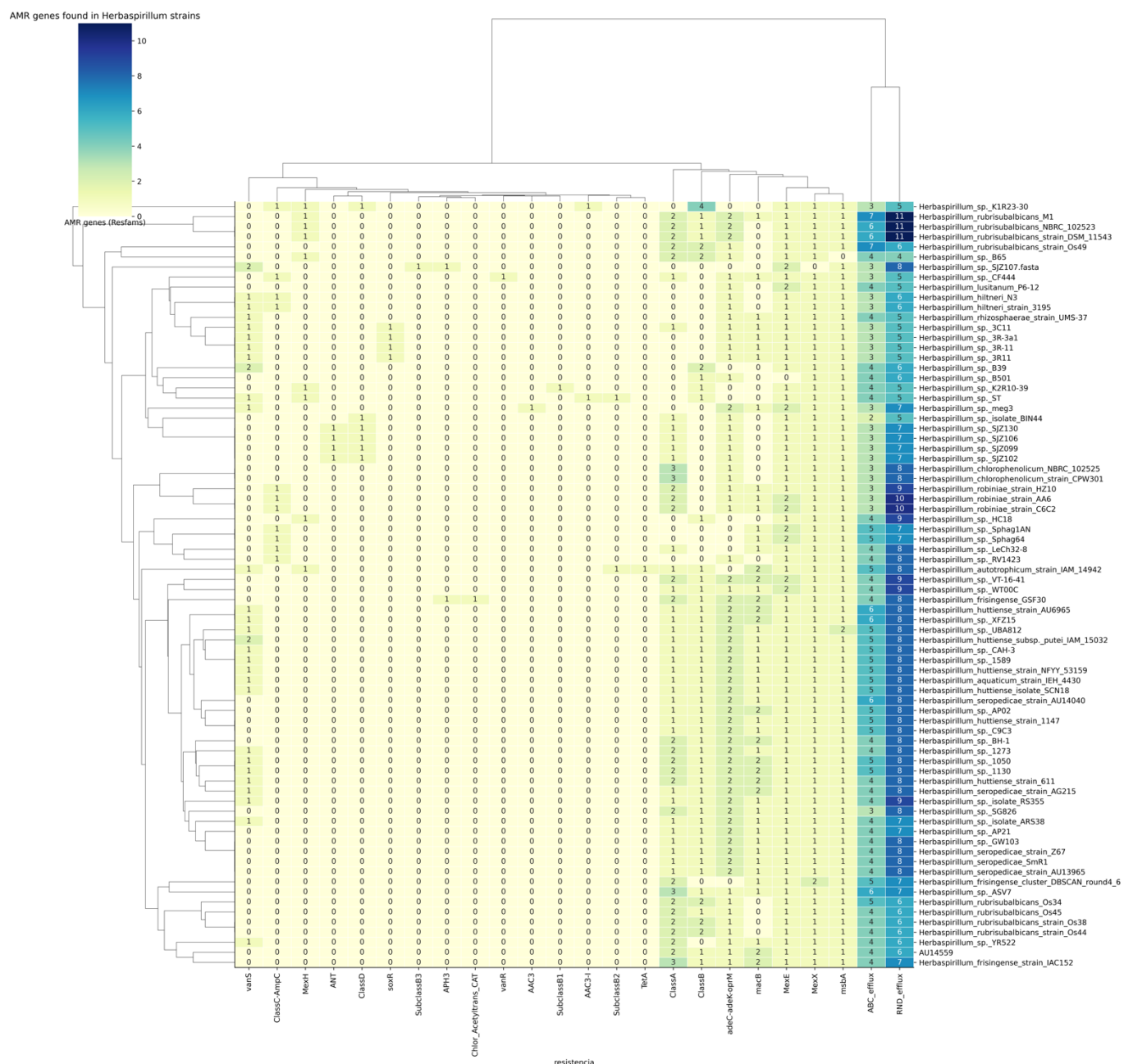
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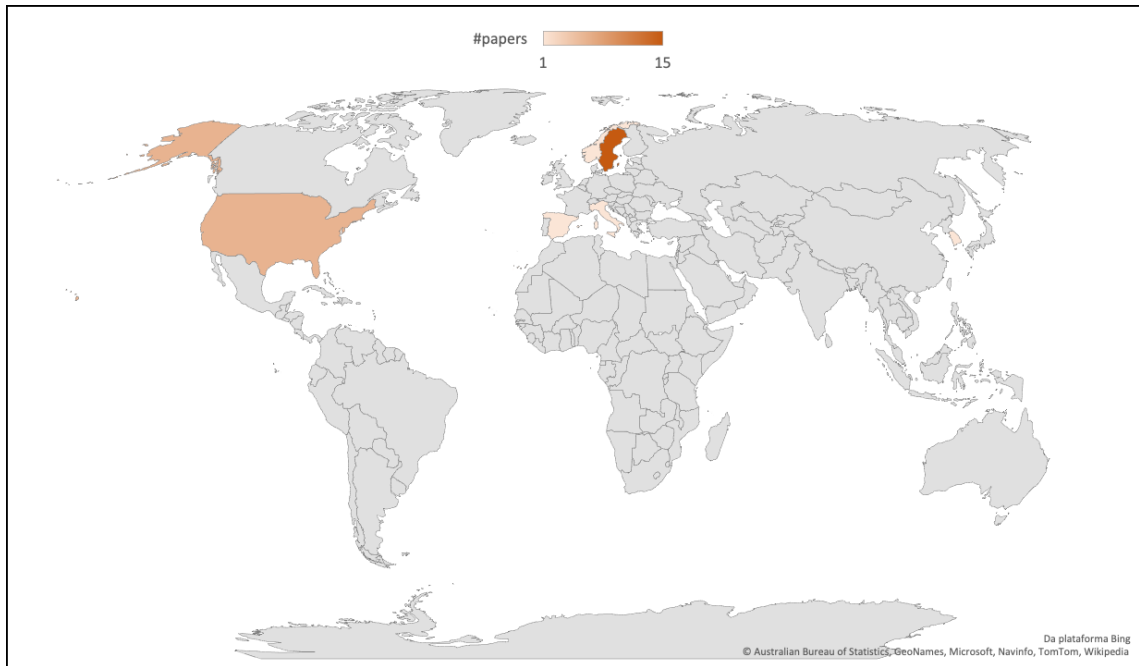
**Figure S1:** Genomic region of *H. frisingense* AU14559 containing the type VI secretion system (T6SS). The upper part of the figure represents the GC% content in Framplot format. The cyan arrows represent the genes encoded in that region. The lower part represents the blastn alignment score in the following descending order of score: 1- *H. seropedicae* AU14040; 2- *H. seropedicae* Z67; 3- *H. seropedicae* SmR1; 4- *H. seropedicae* AU13965; 5- *H. robiniae* AA6; 6- *H. rubrisubalbicans* Os34; 7- *H. huttiense* NFYY53159; 8- *H. rubrisubalbicans* M1; 9- *H. rubrisubalbicans* DSM11543; 10- *H. frisingense* IAC152. The orange arrow indicates a transposase. The dark blue arrows indicate the 3 *vgrG* genes. The dotted box indicates the region of *clpV* that underwent recombination.



**Figure S2:** Schematic representation of the *rfbBrlmACD* operon identified in the genomes of *H. frisingense* strains. The highlighted region represents the multiple sequence alignment by ClustalW identifying the mutation responsible for the insertion of a premature stop codon in the *rmlA* gene of *H. frisingense* AU14559.



**Figure S3:** Antibiotic resistance genes found in *Herbaspirillum* genomes. The predicted proteome of each strain was compared with the Resfams database using the HMM Resfams core model. The lines in the heatmap represent the strains, and the numbers in the squares indicate the number of genes in that column found in the strain.



**Figure S4:** Distribution of clinical isolates of the genus *Herbaspirillum* according to published papers.