

Supporting information for

Treatment of antibiotic-manufacturing wastewater enriches for *Aeromonas veronii*, a zoonotic antibiotic-resistant emerging pathogen

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Figure S1. The bioinformatics analysis workflow.

Figure S2. Changes of selected physicochemical properties of the wastewater samples through all treatment units. (a) Suspended solids; (b) Colority; (c) pH; (d) Total organic carbon; (e) Chemical oxygen demand; (f) Biochemical oxygen demand for five days; (g) Total nitrogen; (h) Ammonia nitrogen; and (i) Total Phosphorus.

Figure S3. Microbial profiles of all the samples. (a) α -diversity indices of ARGs. (b) Abundance of microbes at the kingdom level; (c) abundance of bacteria at the phylum level; (d) α -diversity indices of bacterial communities.

Figure S4. RDA analysis of the relationships between environment variables with (a) bacteria and (c) ARGs, respectively. Red arrows represent the phylum level of bacteria and blue arrows represent environment factors. Total explained variance ratio were calculated and visualized in (b) and (d), respectively.

Figure S5. Hosts of ARGs at the phylum levels obtained from contigs statistical analysis.

Figure S6. Co-shared (a) *dfrA16*-ARG-carrying and (b) *tetG*-ARG-carrying contigs and their putative hosts in different samples.

Figure S7. (a) The Partial least squares-path modeling analysis showing the effects of antibiotics, physicochemical variables, MGEs, and bacteria on ARG compositions. The solid and dashed lines indicate the positive and negative effects, respectively. The numbers adjacent to each arrow are partial correlation coefficients at the significance level of *** ≤ 0.001 , ** ≤ 0.01 , or * ≤ 0.05 . The R^2 values represent the proportion of variance explained for each factor. (b) The standardized total effect of antibiotics, physicochemical variables, MGEs, and bacteria on the ARG compositions.

Figure S8. Comparisons of (a) *bacA* and (b) *OXA-12* genes in two assembled *A. veronii* MAGs and *A. veronii* reference genome.

Figure S9. (a) NCBI Multiple Sequence Alignment of the 16S rRNA gene of the *A. veronii* obtained from the effluent and the most similar sequences. (b) Unrooted phylogenetic tree constructed by partial *ropB* gene of effluent obtained and some other isolated *A. veronii* strains.

Figure S10. (a) Branch length ignored phylogenetic tree to show inner nodes clearly. Nodes used in figure b is shown with circle. (b) Welch Two Sample t-test result of phylogenetic distance for genomes in sub-clade 1 and sub-clade 2 (right) and result of the parent node at the next level (left).

Figure S11. The circos map of *A. veronii* genomes' chromosome. Rings from inside to outside are: genome alignment results of (1) 2nd COT1 bin.80 vs reference genome (FDAARGOS 632), (2) CT2 bin.95 vs reference genome and (3) genome from diarrhea patient (GCF 016729485.1) vs reference genome; GC content of reference genome; GC skew of reference genome; genome annotation (+); genome annotation (-); positions related to ARG or HGT.

Figure S12. Multiple sequence alignment result for protein of *OXA-12* and *bacA*.

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Additional file 1. Detailed ARG profiles in all samples.

Additional file 2. Some ARGs with identical host.

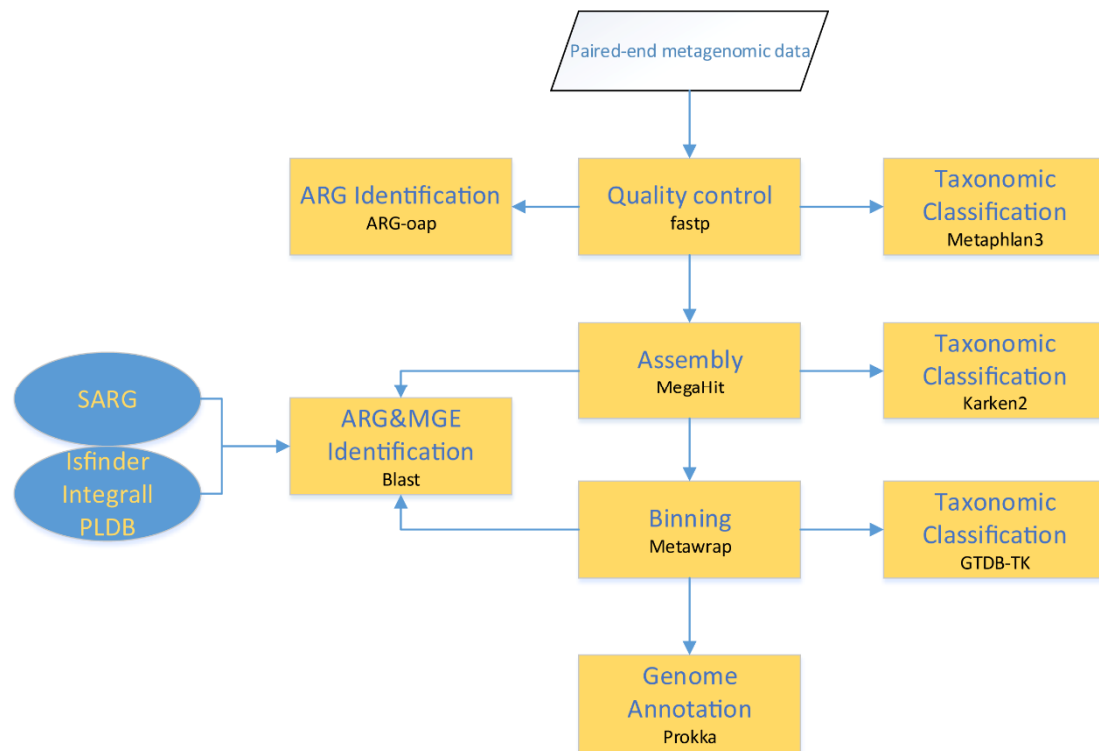


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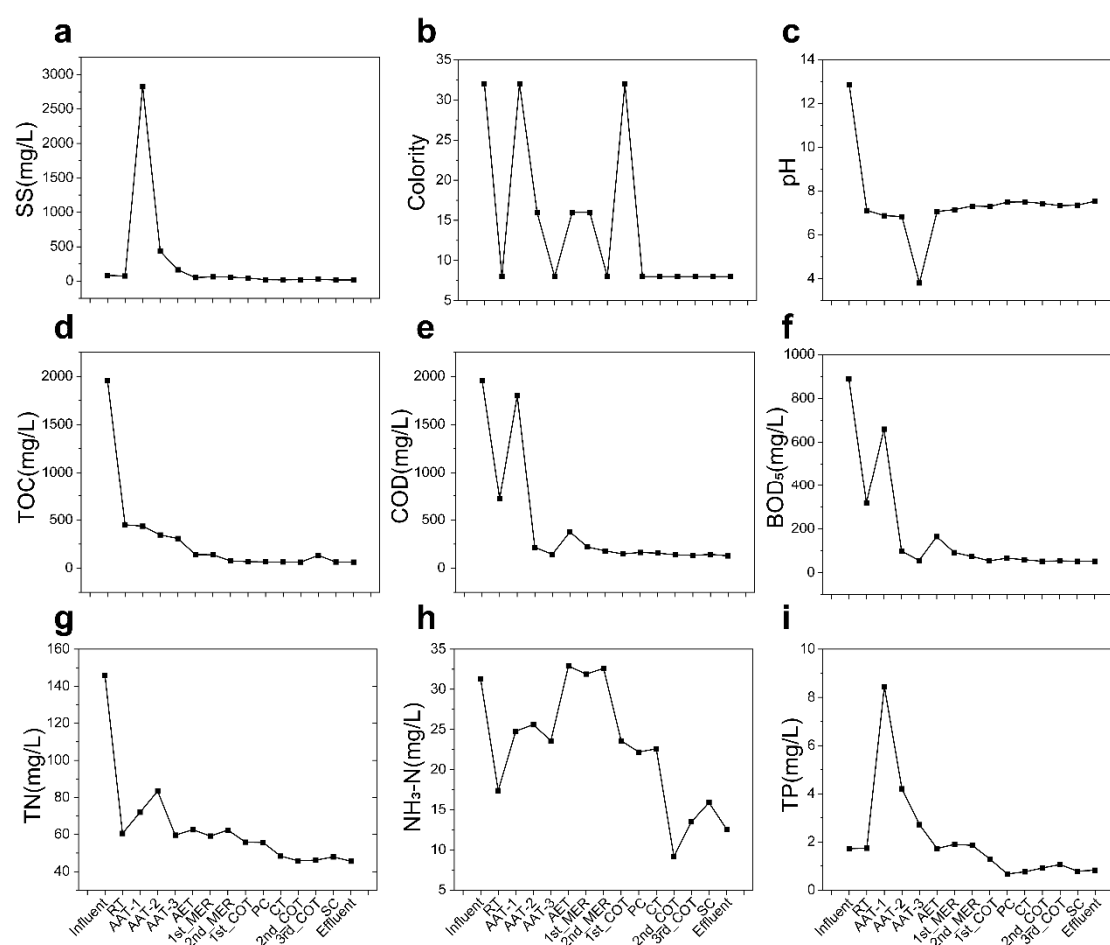


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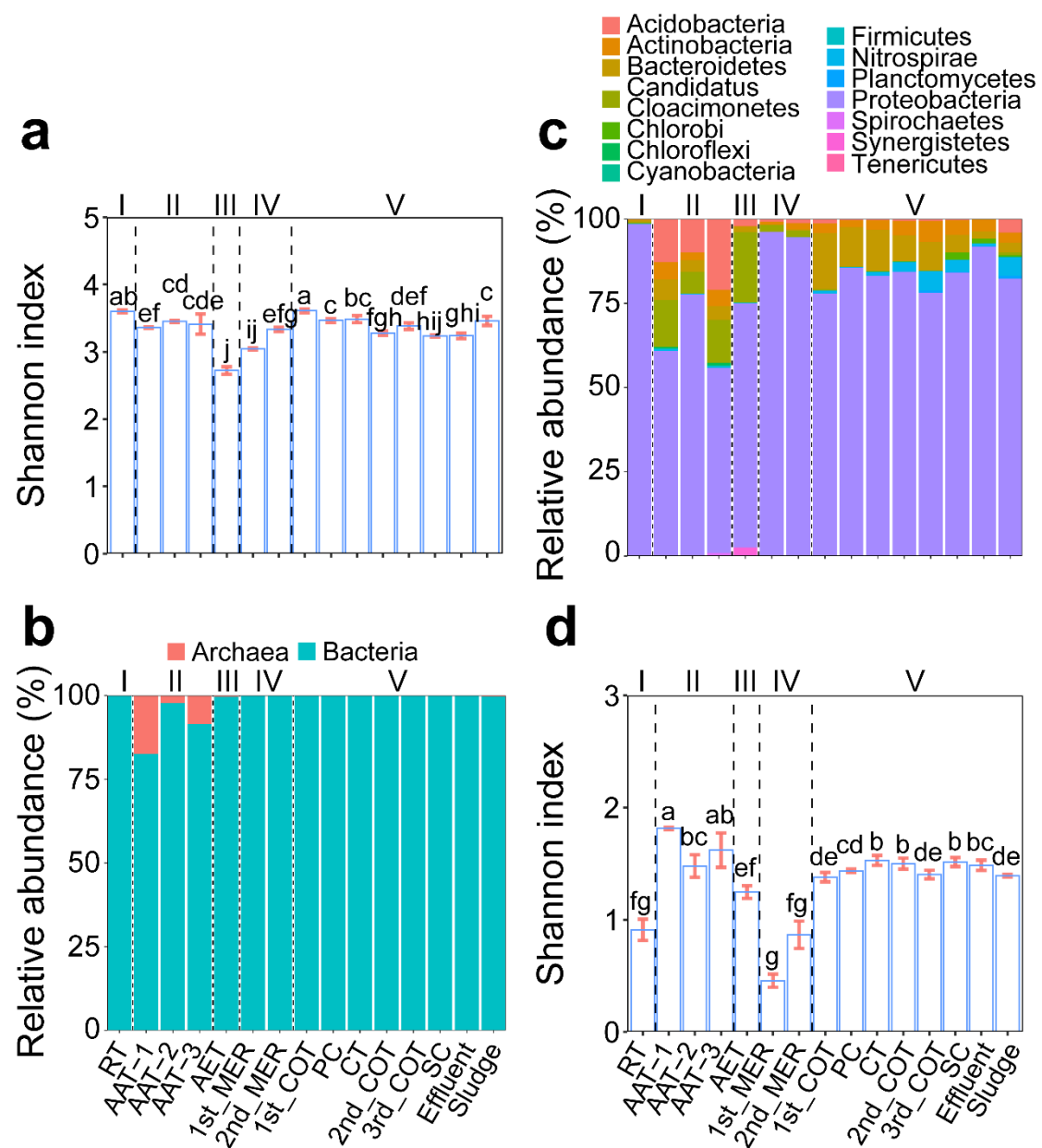


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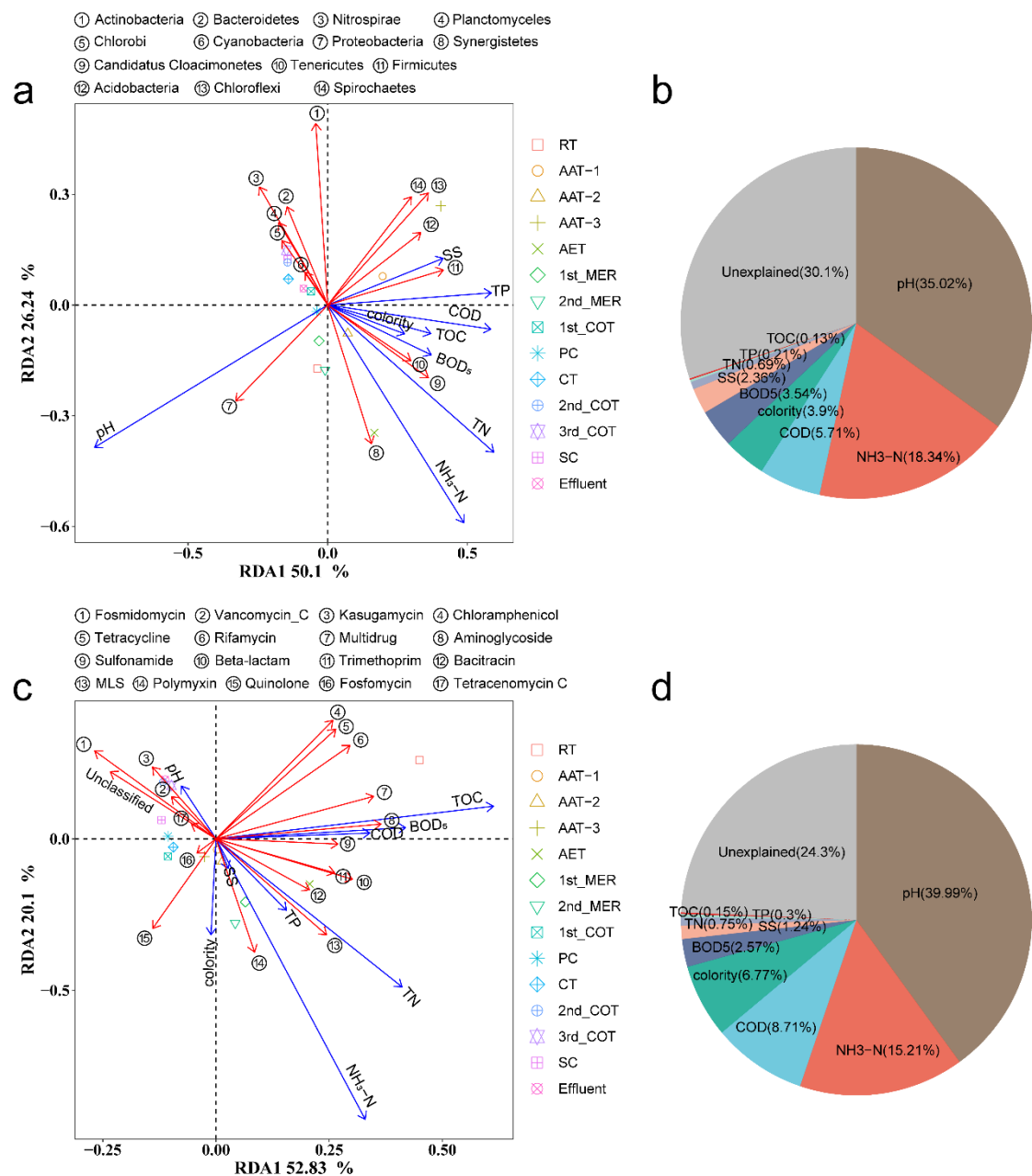


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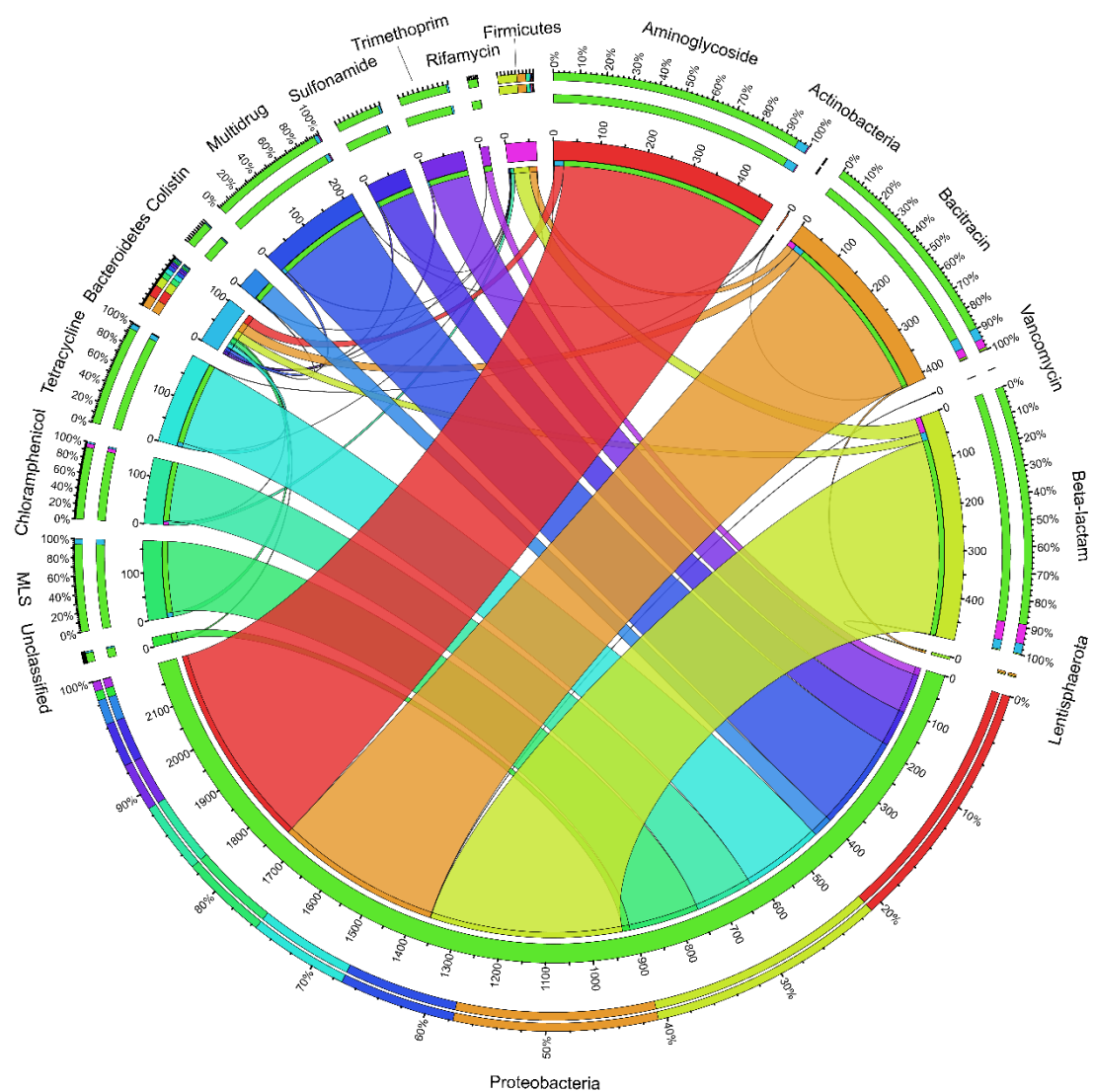


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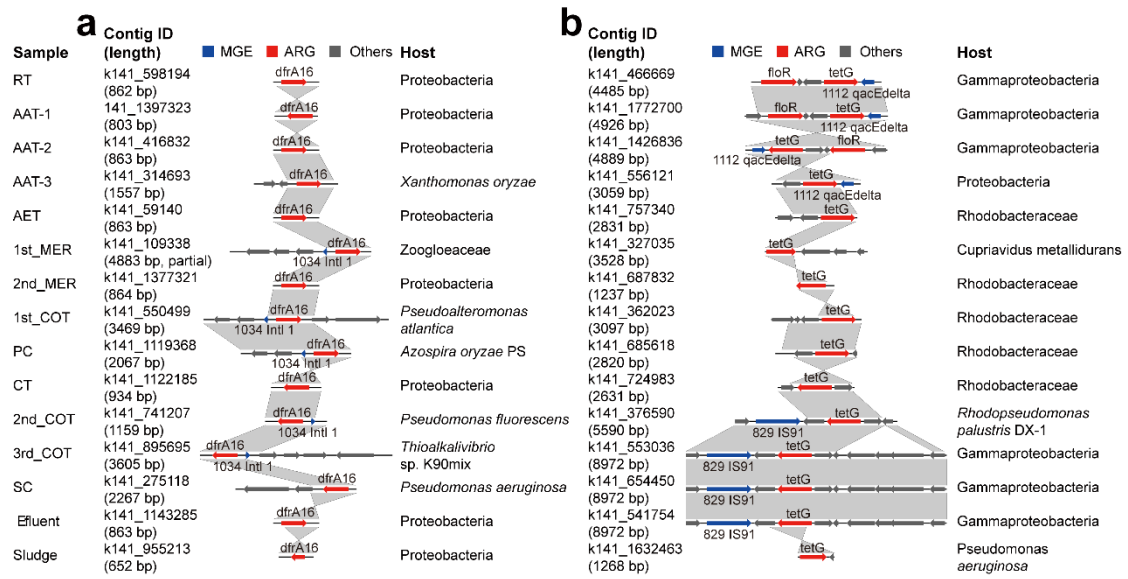


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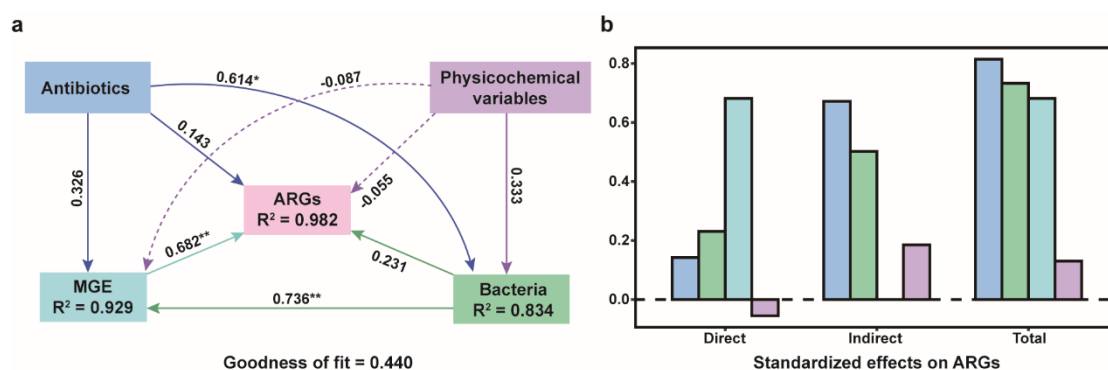


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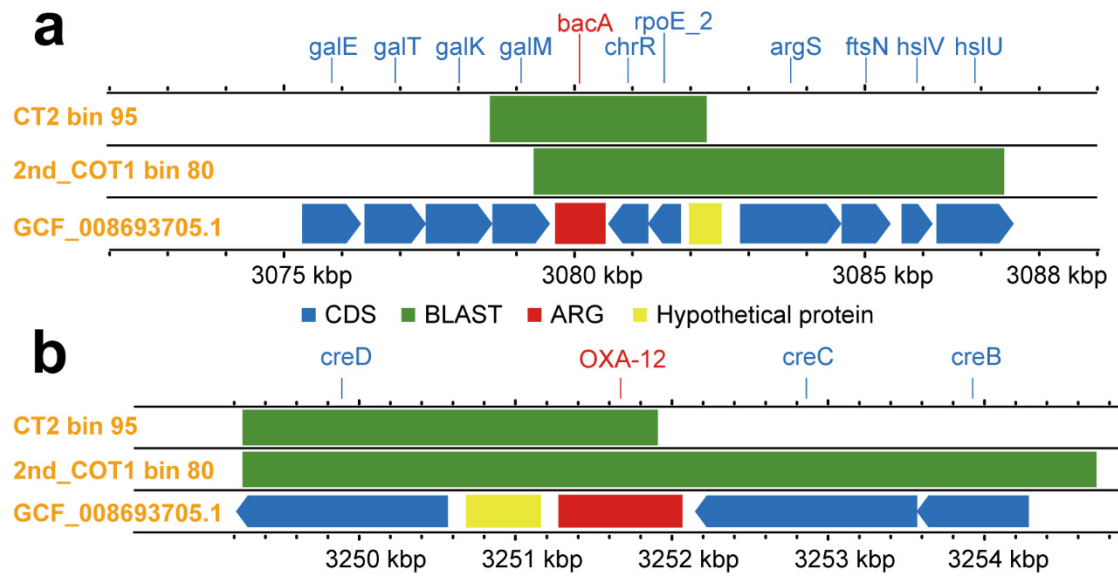


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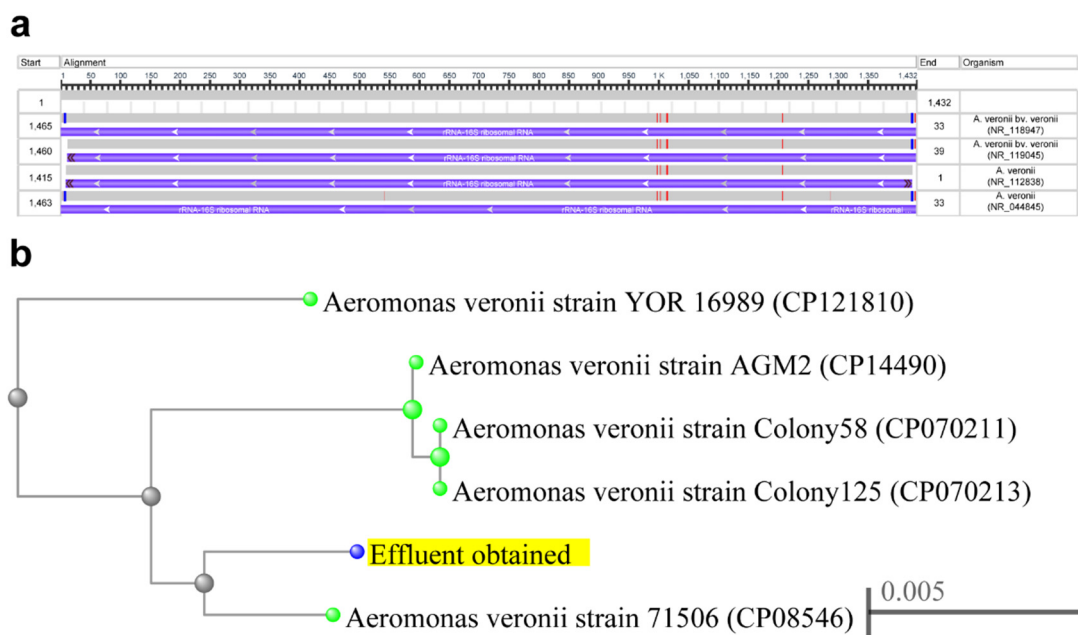


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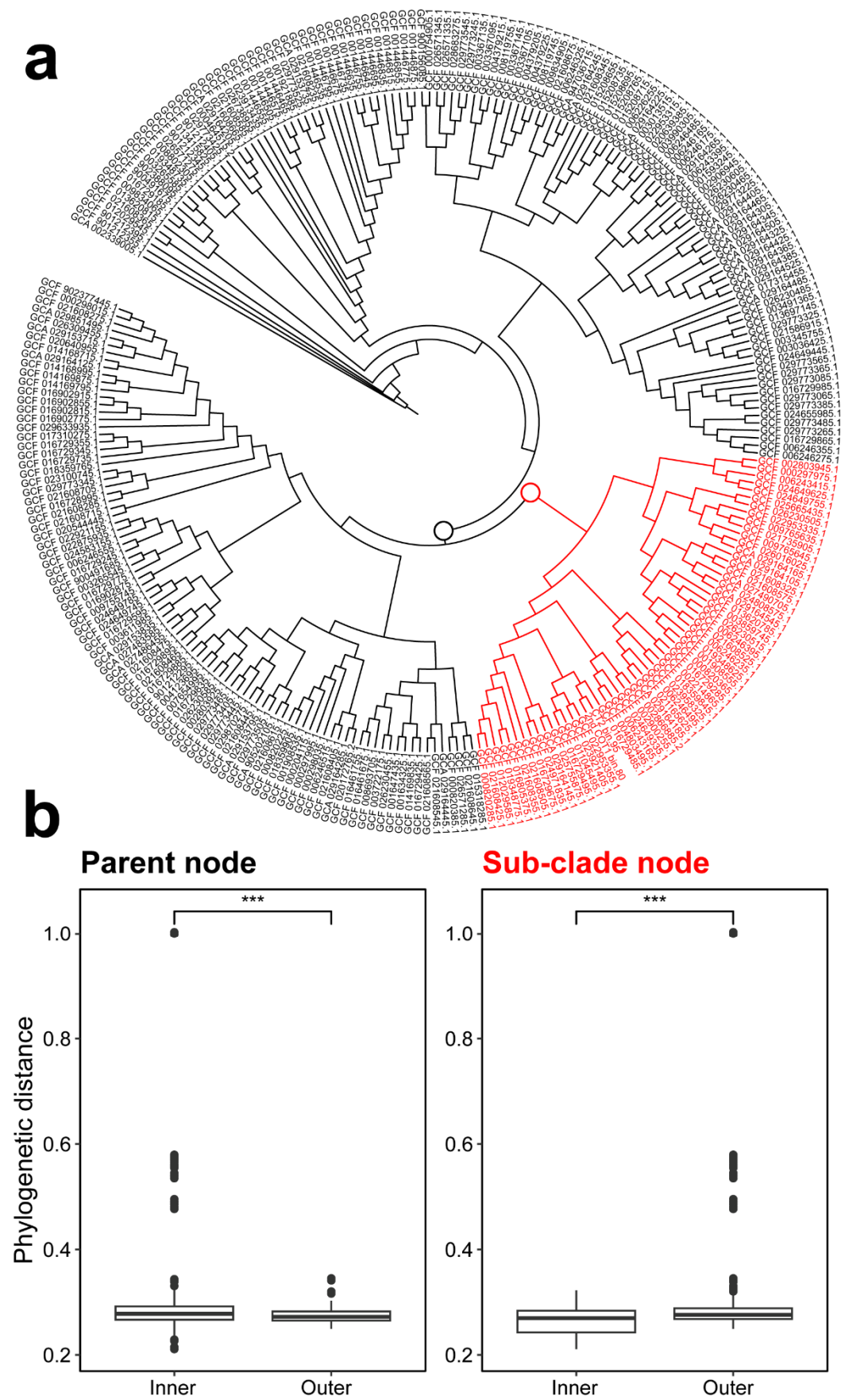


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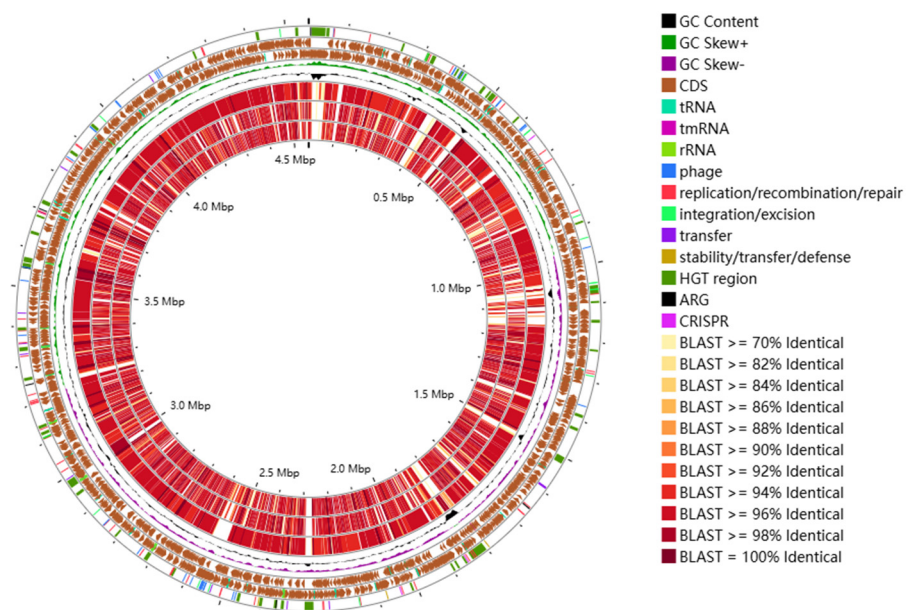


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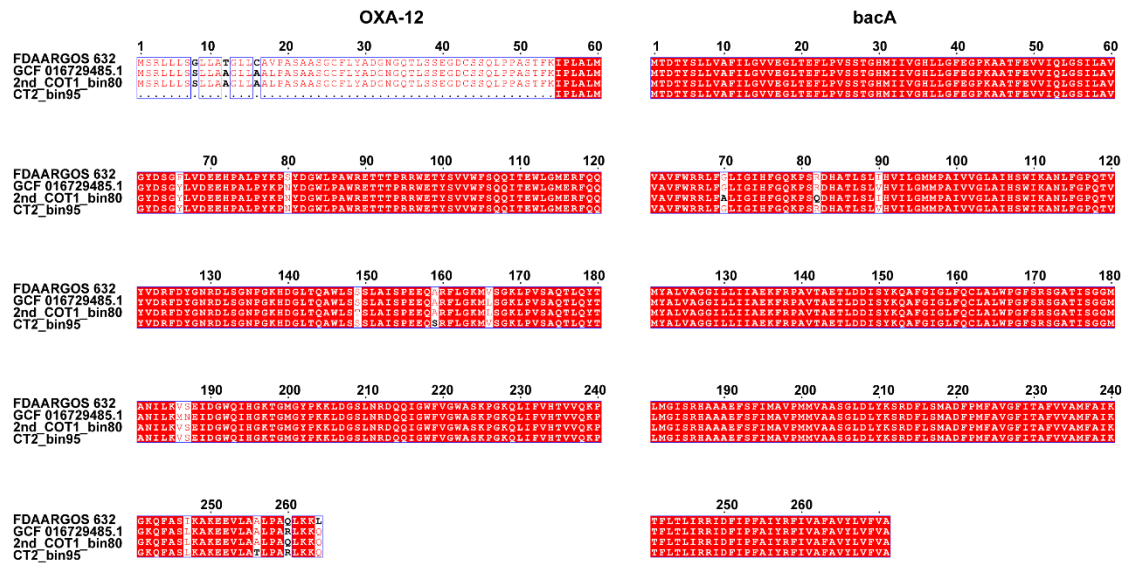


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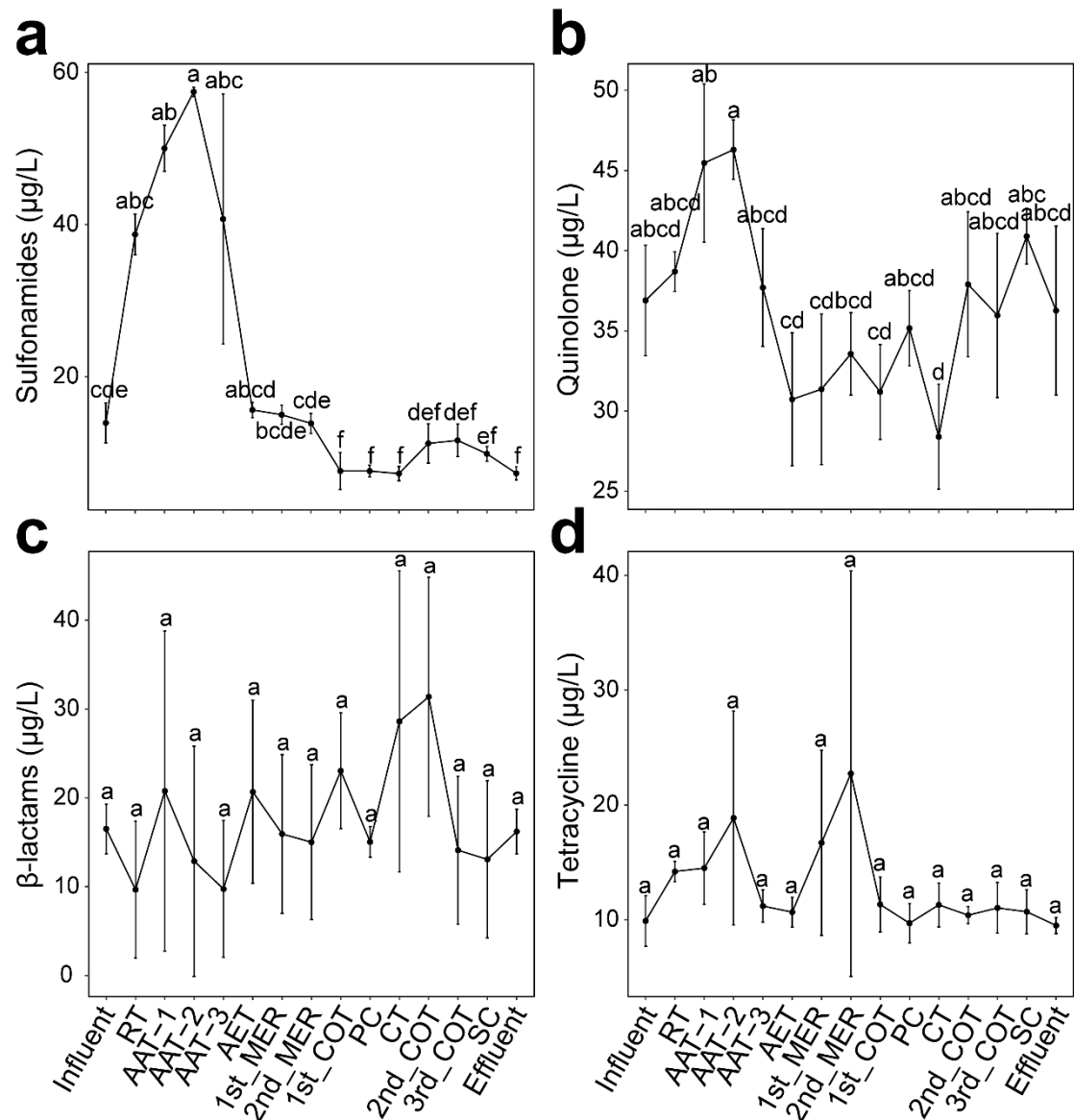
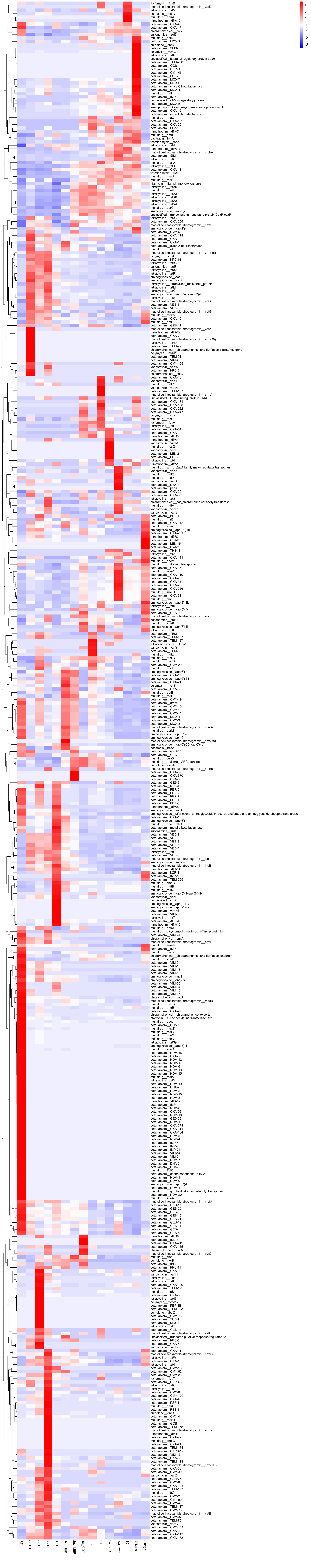
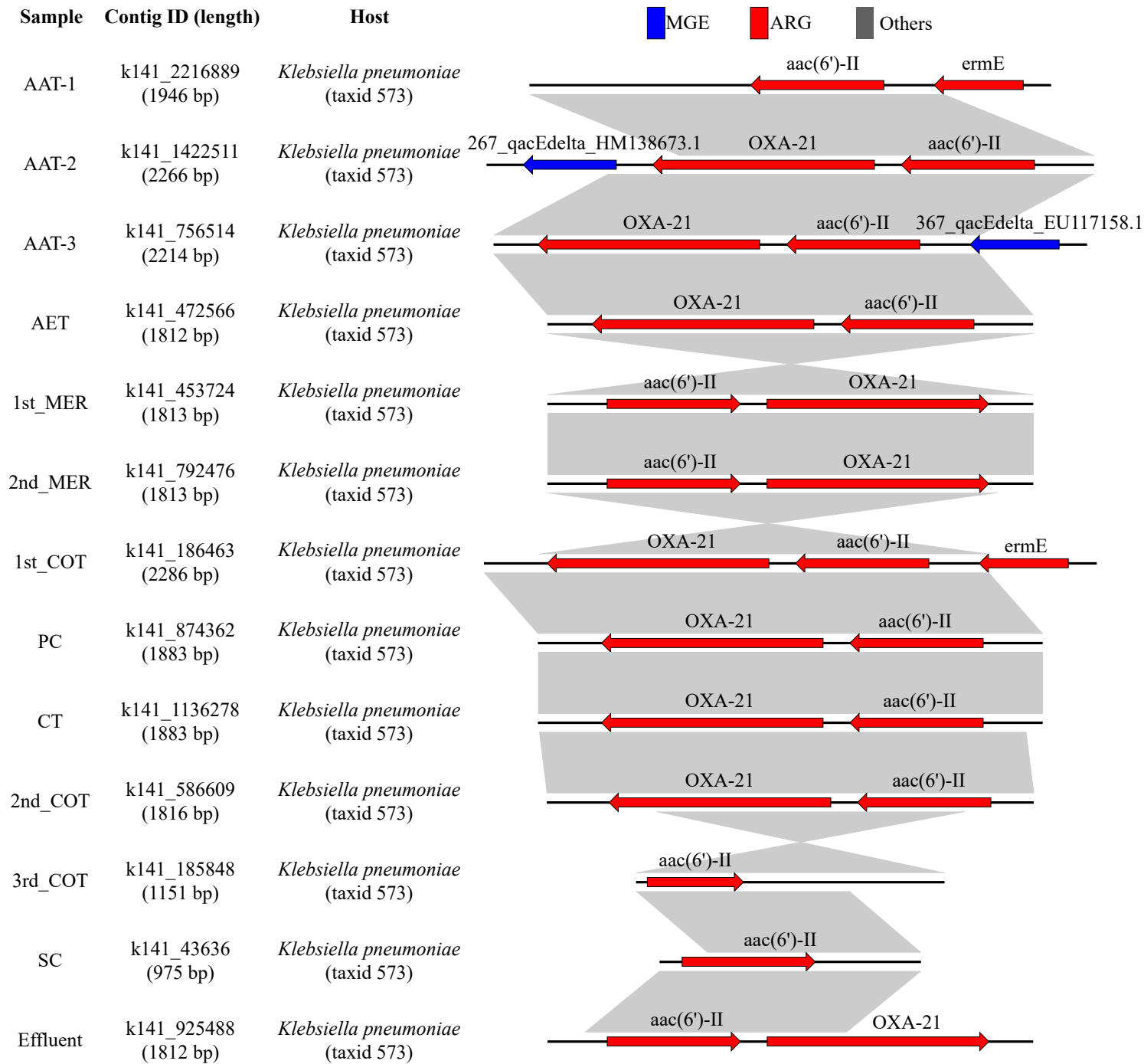
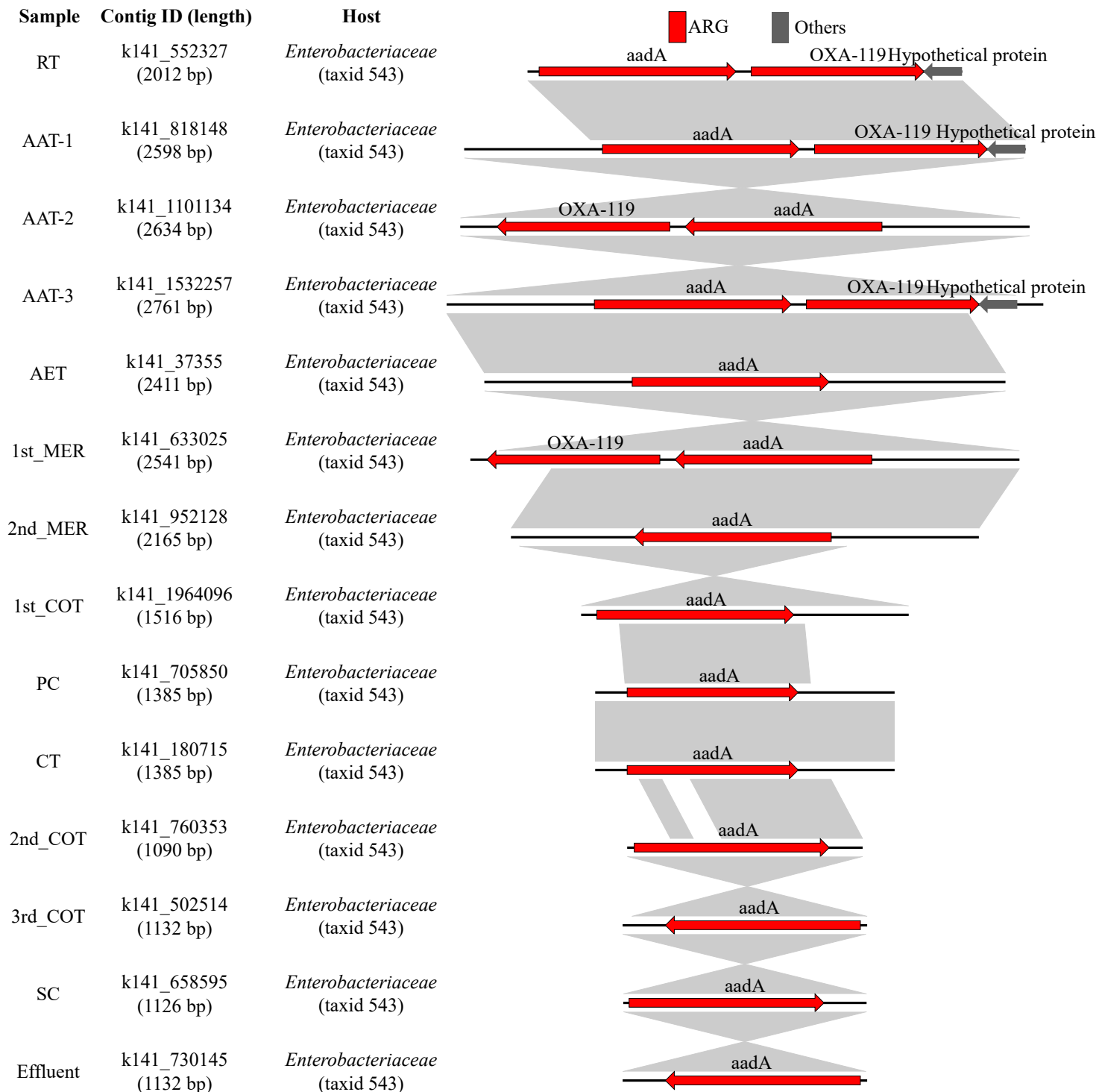


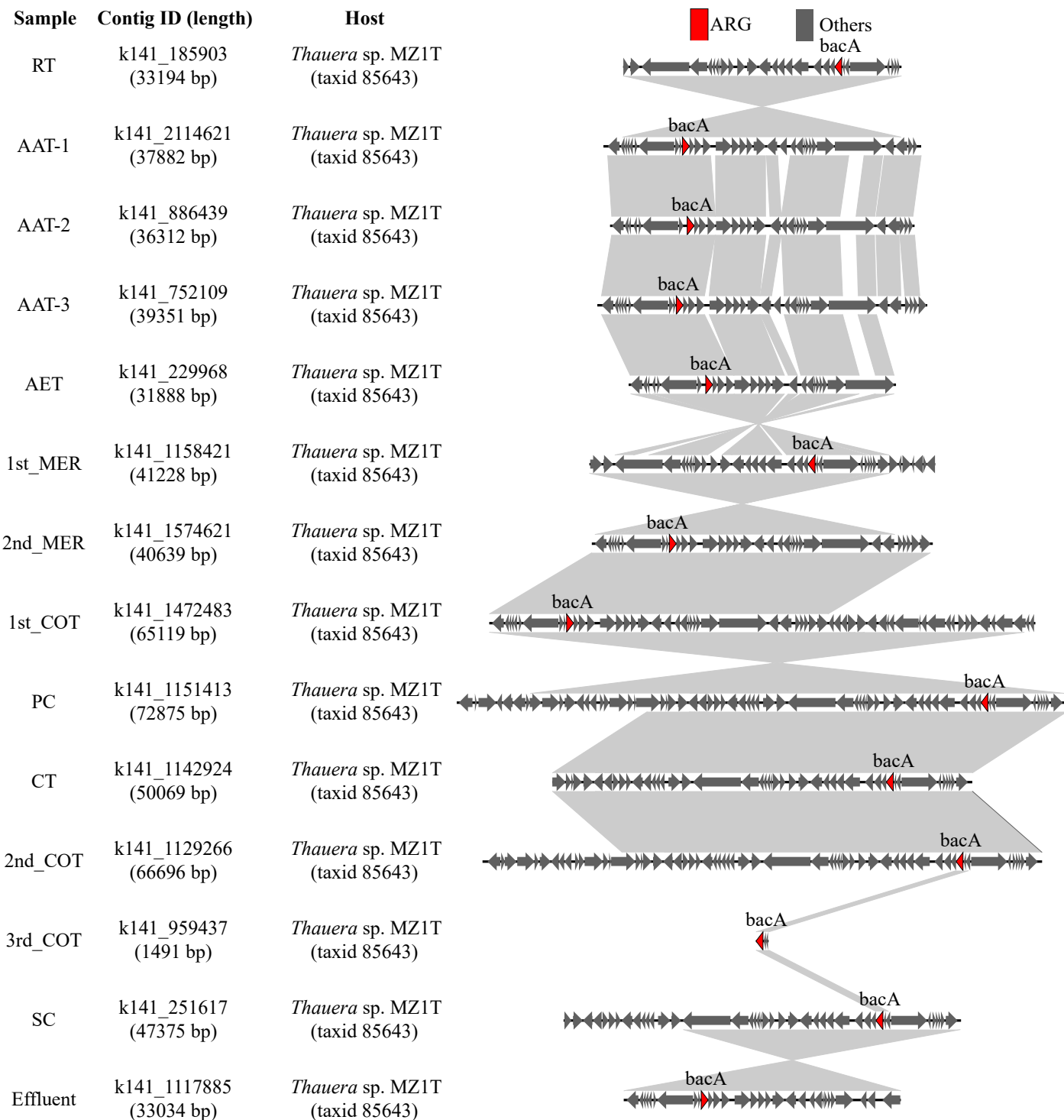
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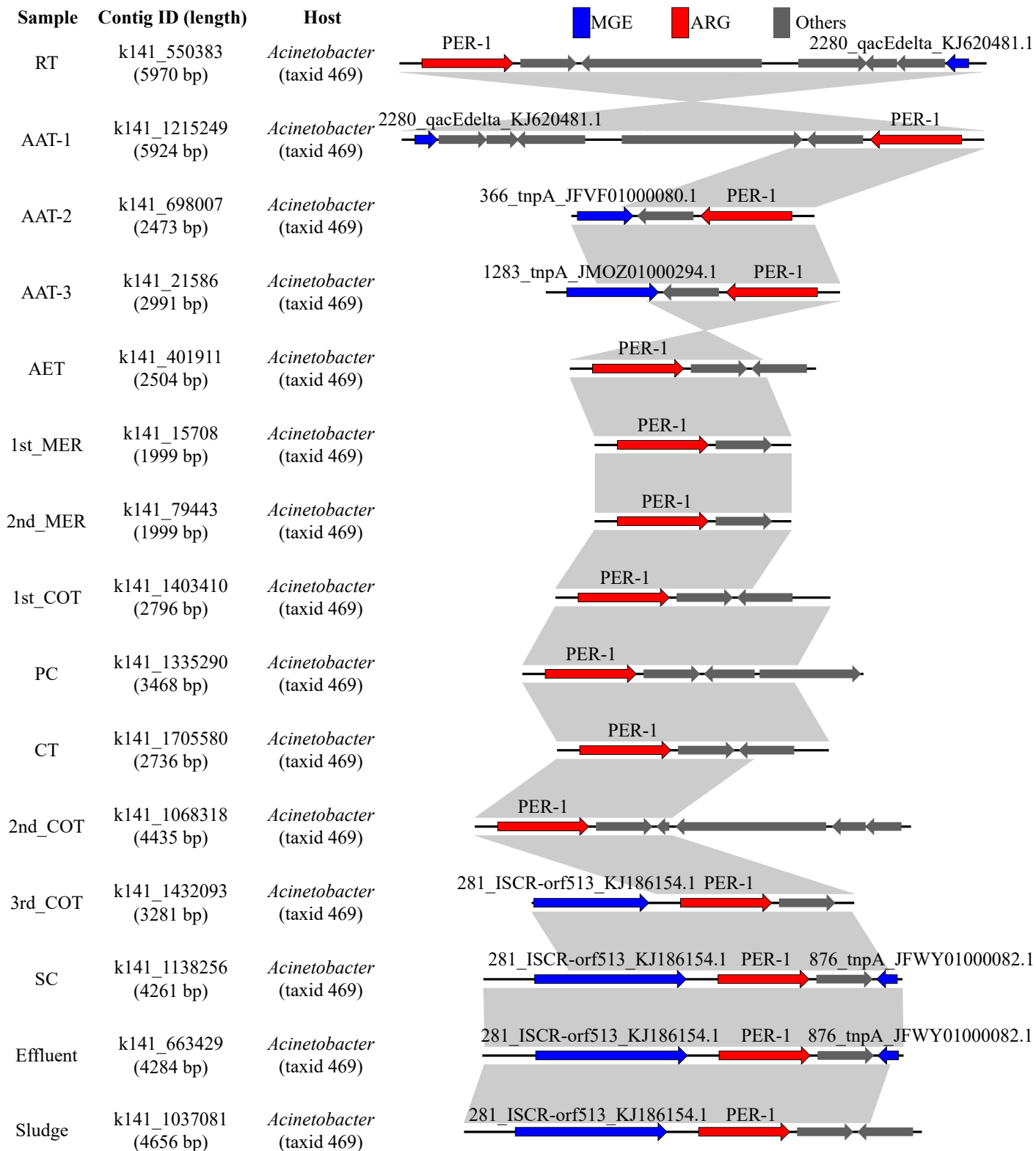


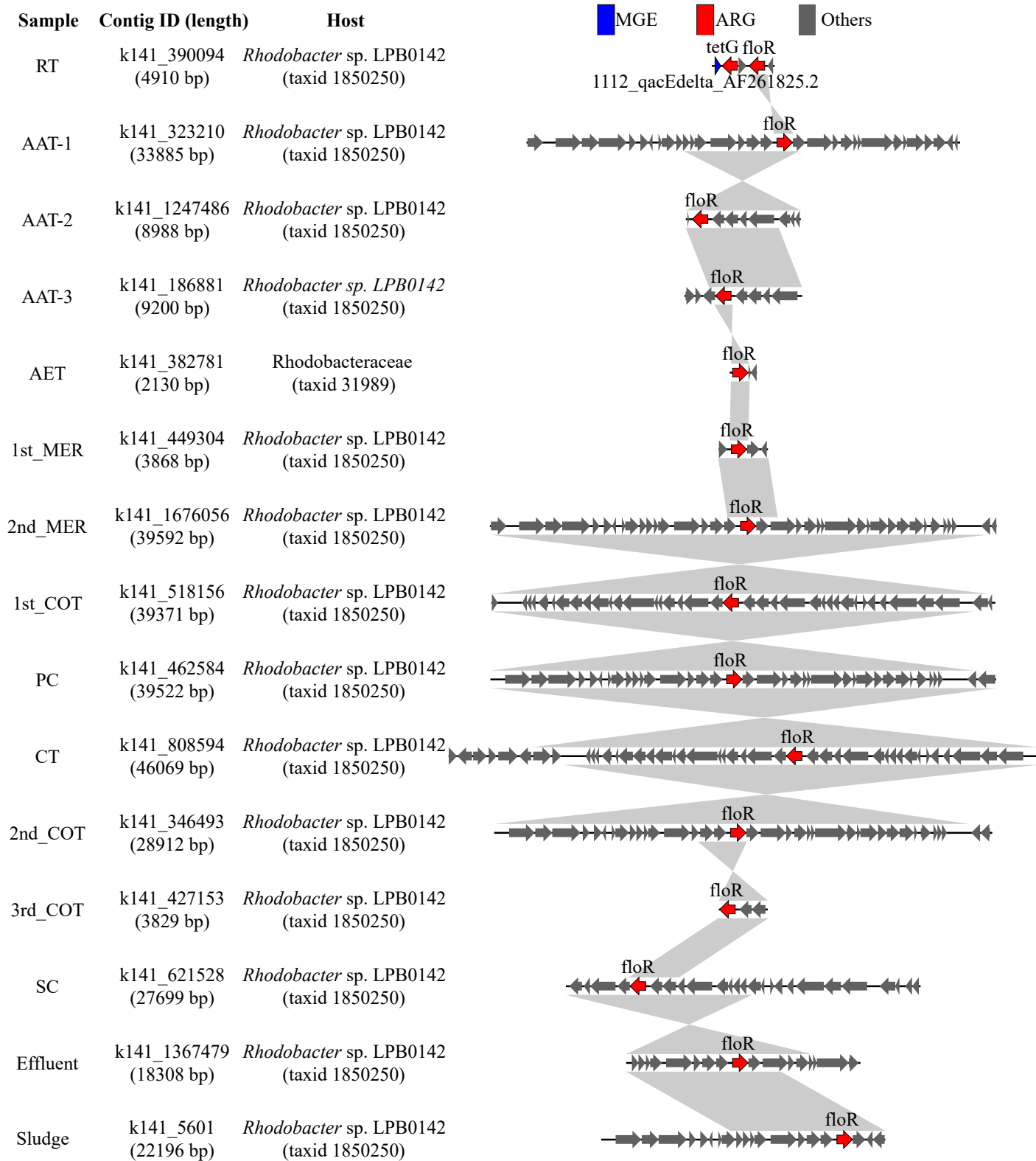
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a

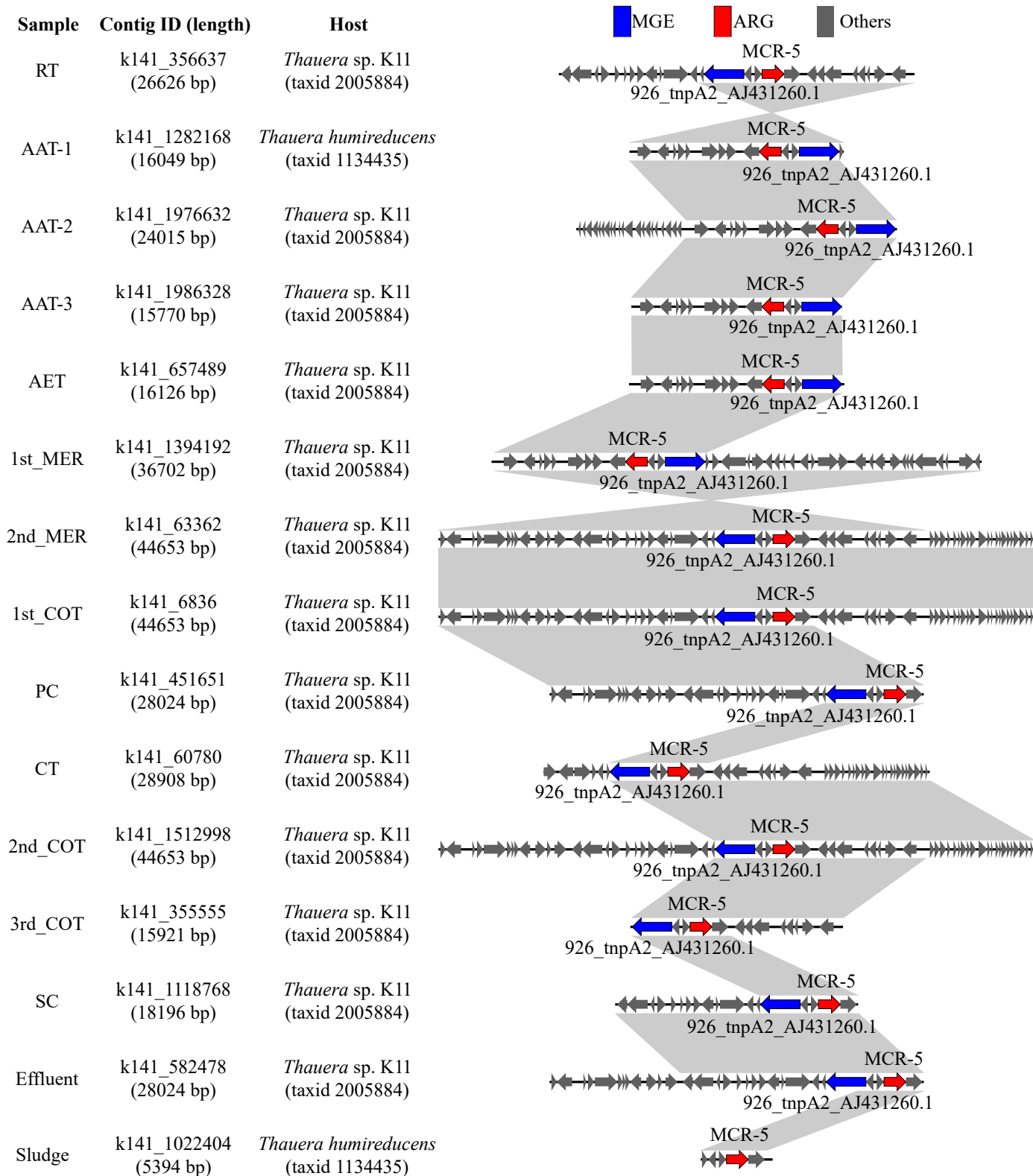
b

C

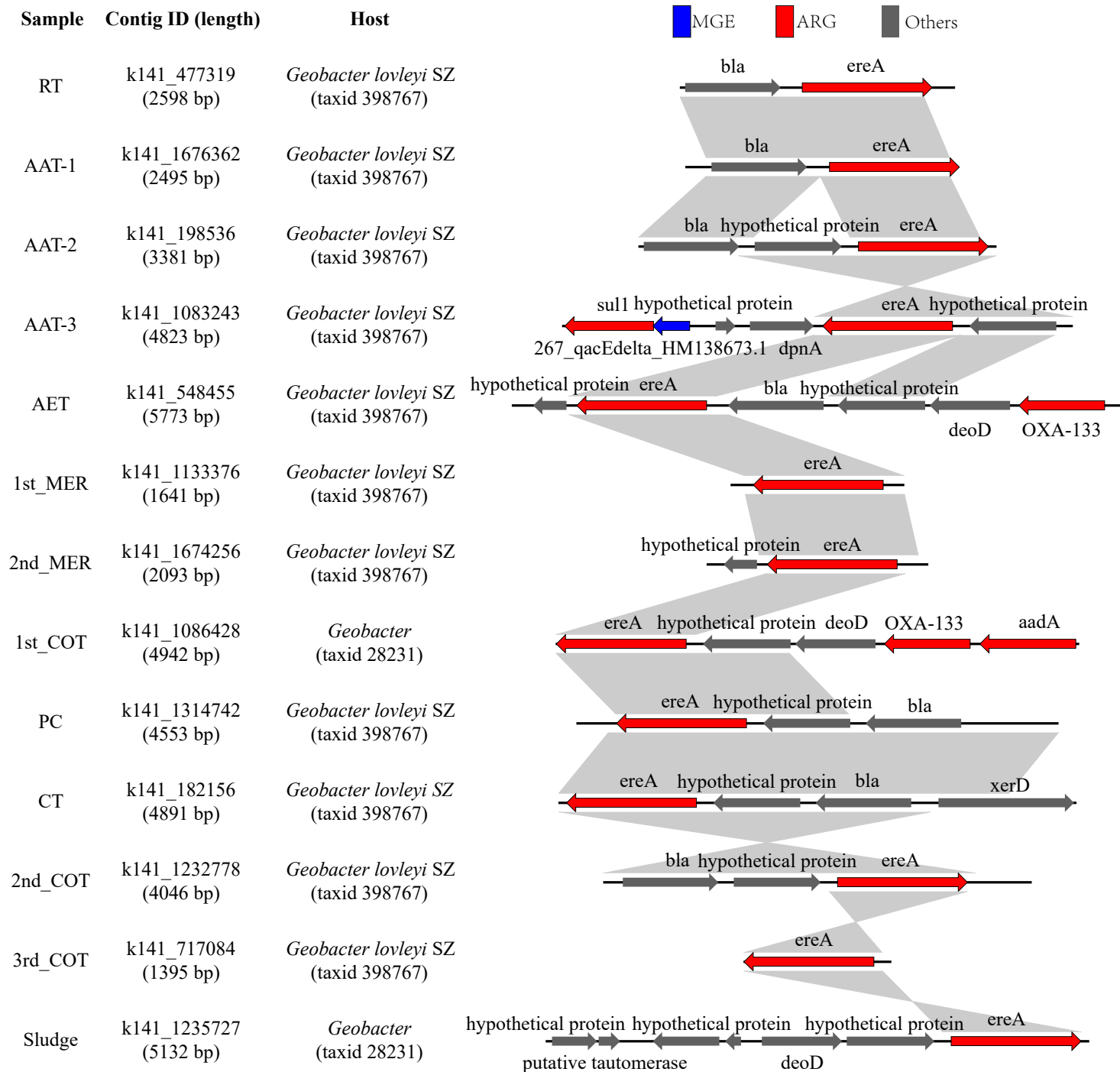
d

e

f



g



Additional file 2. (a-g) Some ARGs with identical host.