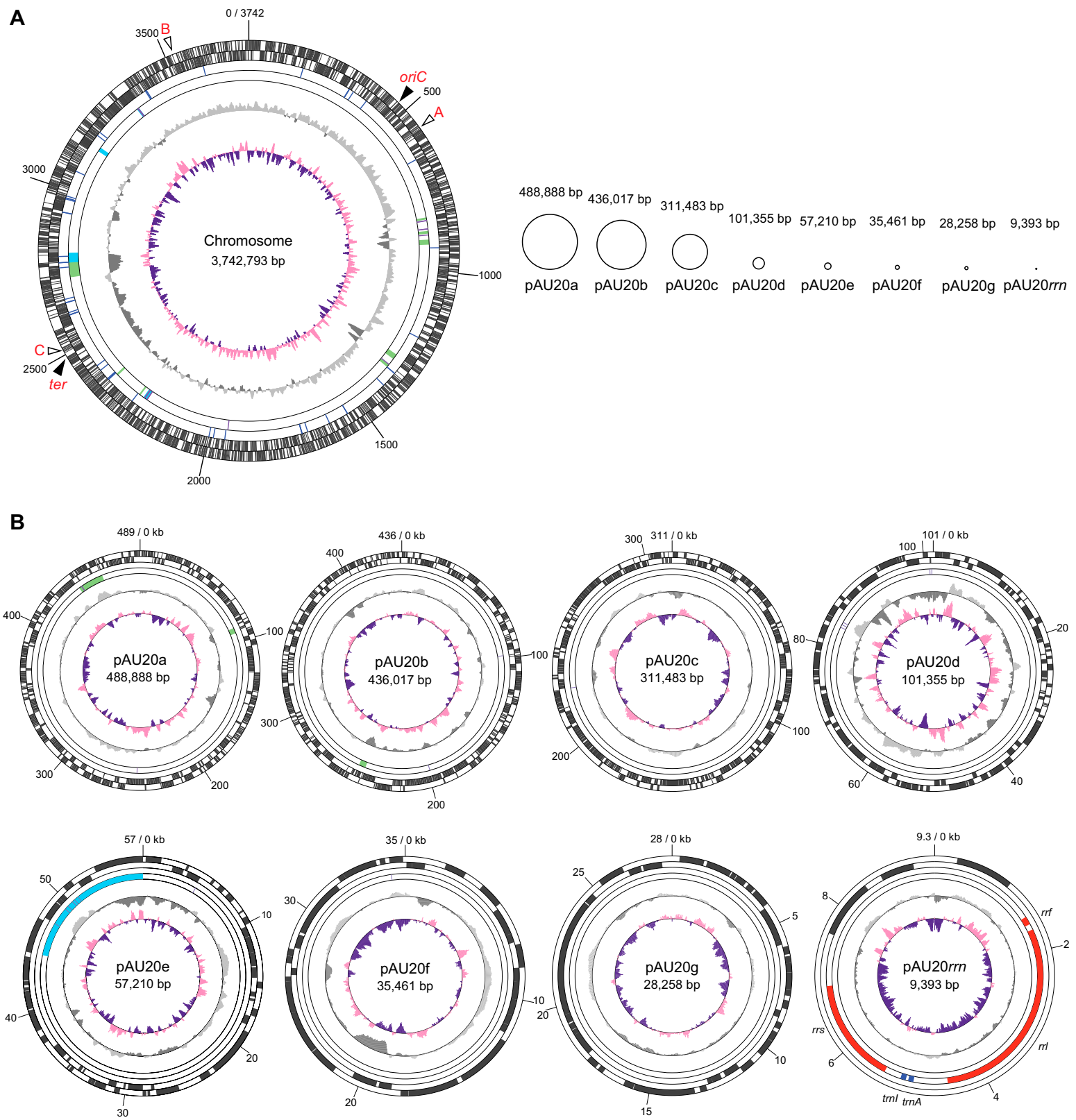


# Supporting Information

Anda et al. 10.1073/pnas.1514326112



**Fig. S1.** Schematic representation of the *Aureimonas* sp. AU20 genome. (A) Nine replicons are shown on the same relative scale. For the chromosome, circles, from the outermost inward, show (i) predicted protein-coding genes in the clockwise orientation; (ii) predicted protein-coding genes in the counterclockwise orientation; (iii) genes for tRNA (blue) or rRNA (red); (iv) putative genomic islands (yellow green), prophages (light blue), or insertion sequences (purple); (v) G+C content deviation (light gray for values higher than the average and dark gray for values lower than the average); and (vi) GC-skew values (pink for plus values and violet for minus values). (B) Extrachromosomal replicons are shown on different scales. Circles show the same information as the circles for the chromosome in A. Genomic islands, prophage regions, and insertion sequences were predicted by using IslandViewer (38), PHAST (39), and ISSaga (40), respectively. The G+C contents and GC-skew values were calculated by using ArcWithColor ([www.ige.tohoku.ac.jp/joho/gmProject/gmdownload.html](http://www.ige.tohoku.ac.jp/joho/gmProject/gmdownload.html)) with a window of 10 kb (for the chromosome), 5 kb (for pAU20a, pAU20b, and pAU20c), 1 kb (for pAU20d), 0.5 kb (for pAU20e, pAU20f, and pAU20g), or 0.1 kb (for pAU20rrn). Positions marked in red with A, B, and C on the chromosome indicate the loci showing synteny with the *rnaA*, *rnaB*, and *rnaC* regions, respectively, on the chromosomes of other strains (Fig. S5). The origin (*oriC*) and terminus (*ter*) of replication are also noted.

**A**

```

tRNA-Ala (M673_01770)  GGGGCCATAGCTCAGCTGGGAGAGCGCTTGAATGGCATTCAAGAGGTCGTCGGTTCGATCCCATTGGCTCCACCA
tRNA-Ala (pAU20rrn)   GGGGCTTTAGCTCAGCTGGGAGAGCACTGCTTTGCAAGCAGGGGGTCGTCGGTTCGATCCCAGCAAGCTCCACCA
tRNA-Thr (M673_13785) GCCGGCTTAGCTCAGCTGGTAGAGCACTGATTTGTAATCAGGGGGTCGCGGTTTCGAGCCCTGCAGCCGCACCA
    
```

**B**

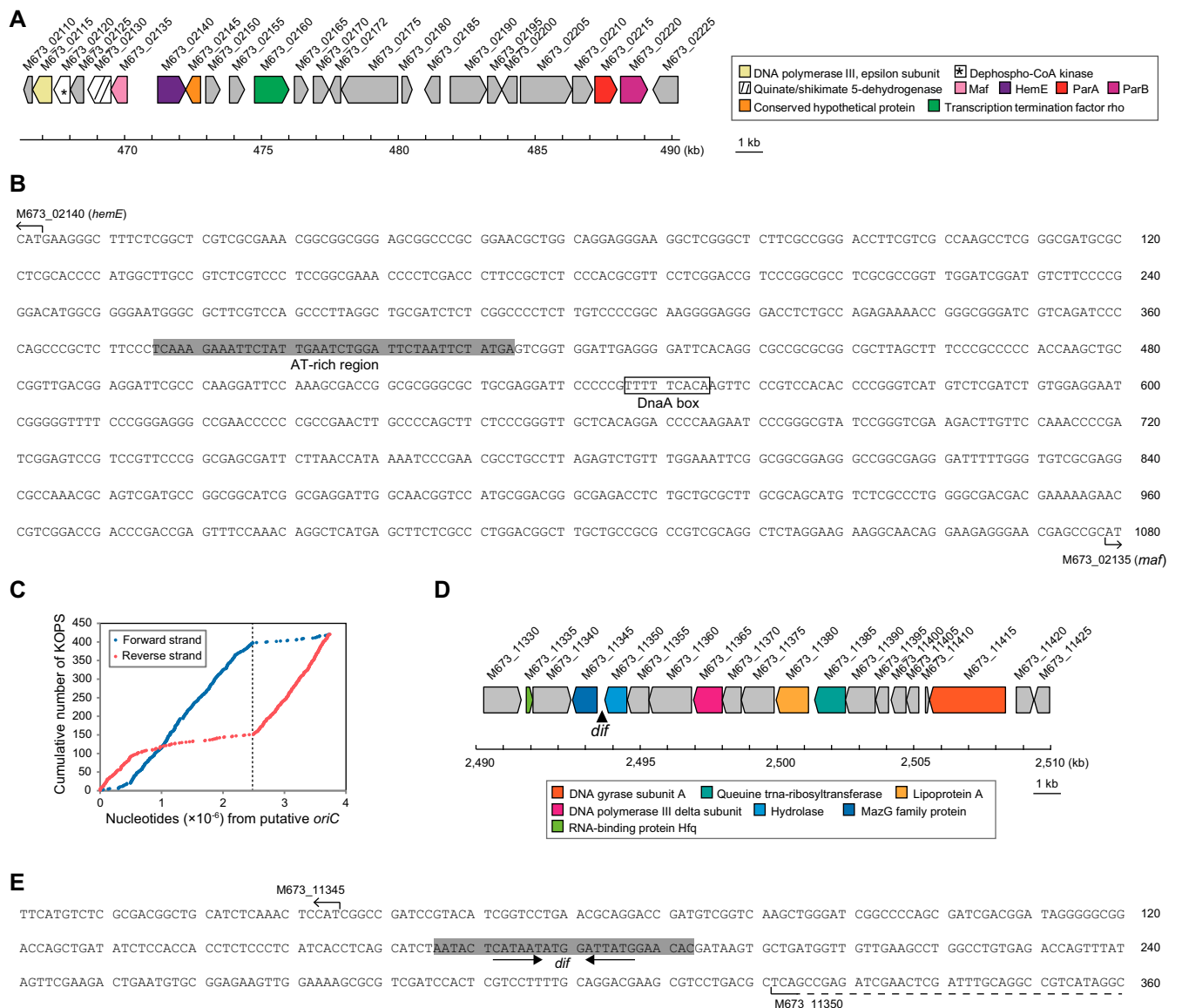
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                UP element          -35          -10
pAU20rrn  GGGTTCCACCCCTTTTTCATCACAAGAGGTGTGACCTTCCCTGAAGAATCCCTTATAAGCCGCTCA-CGACAACGGCGCTGAGGCGGGTGTGGCGG -464
pAUTrrn   GATTCGGTTCAATTTTCCTGACAGAGGTGTGACCTCCCCGAGAATCCCTTATAAGCCGCTCA-TCATCGACGACGGCTTG--GCCTGTGC-GGGCG -460
AU4_rrnC  GCAAAATATTGAAATTTCTCAAAAACCGCTTACCCGCCGCTGTGGCTTTCATAAACCCTG-TCATCGACGACGGTGGTGGCGCCGGGGCGGTTGG -456
AU22_rrnC GTTTTCCTTCAAATTTTCCTGACCAACCCCGGCTGCGCCCTTATAAGCCGCTCA-TCATCGACGACGGCGGTGGCGCCGGGGCGGACGGG -464
          * * * * *
pAU20rrn  ACGGACCGGCTGGAA---GGCTCGTTTGTTCGCGTT-GAGCTGACGTTTGGTTCCTCG-GAAATTTTCAGGGGTAAGCTGGTGGCTTGTTTTTG -370
pAUTrrn   ACAAGCCGGCTGGAA---GGCTCGTTTGTTCGCGGTAGAGCTGACGTTTGGTTCCTTG-GTTACCAAGGGGGTTGAGCTGGTGGCTTGTTTTTG -365
AU4_rrnC  ACGAGCCGCTTTGGTGC-TGGTCTGGTTTCCGGGAAGTTGAGCT-GCGGTTGGTTCGCGGGGATTTCTCCGGGGTTGGCTTGGC-GGCTCGGTTTTG -359
AU22_rrnC ACGGGCACTGCGGTGCATCGAGCGGATGCCGGGAAGTTGAGCTAGCGGTAGCGGCTGGGTGGTAAAGCTGGGGATAG-CTGACTGGCTCGGTTTTG -365
          * * * * *
pAU20rrn  CGCCTTCGGGTGCAGAAGTTTCAAGATGTCGTTGGATGCTTTGCGAGGTTGGCCTCAGGTTGACCGACGGTGGCTTGTTC----- -286
pAUTrrn   CGCCTCCGGGTGCAACCCGTTTCGAAGTGTCTGTTGGATGCTTTGCAAGGATGGCCTGAGGGCGATCCGACGGTGGTTCGT-CC----- -282
AU4_rrnC  CGCCTTCTGCTTGGTGTGCGGACGAGATCT---GAGTATTCCTGAGGGATGC-TTGAGGTTTCTGCGGGGAGCTGGAGATCCGGACGACGGGCTTTT -264
AU22_rrnC GCCTCTTGCAT--GTGTCGG-CGAGATTTTCGAGTATGCGTTGAGCTTGGAGGGTGGTGGCTGGCTGGTTCACCCGACGGCGGACTTTT -269
          * * * * *
                BoxA-like          16S processing stalk
pAU20rrn  -----GCCGTGATCTTTGAAACTGAAGAGTG-TTGGAGAAAGAGAACTGGAACGGCGCTTGGCC-GAGGACCGCTCTGGATGGTATTTCCTT -195
pAUTrrn   -----GCCGTGATCTTTGAAACTGAAGAGTG-TTGGAGAAAGAGAACTGGAACGGCGCTTGGCC-GAGGACCGCTCTGAAATGGTATTTCCTT -191
AU4_rrnC  TTGGTCTGGCGTGTCTTTTGAACCTGCATAATG-CGAAGCAAGAGAGACTGCAACCGCGCTTGGCC-TGAGGACGAGAA-GGGCTGGCTTATCCTT -166
AU22_rrnC GTTT--GCCGGTGTGTTGAGAATTGAAGAGAGAACTGGAAGAGAGAGACTGGAACGGCGCTTGGCC-GAGGACG-GCTTGGAGCGATATC-CCTT -175
          * * * * *
pAU20rrn  TCCATCTGAGTGACGTCGAGAGAACTCGACGAA-ACACGTTTCGCAAGAGA-TGAGAGTGTACGCGCTCCGGTTTGGCTGGAGTGTTTGGCGAT -97
pAUTrrn   TCCATTTGAGTGACGTCGAGAGAACTCGACGAA-ACACGTTTCGTT-GAGA-TGAGAGTGTACGCGCTCCGACTCGGTTGGAGTGTTC-GACGAT -95
AU4_rrnC  TGCTGGTCTG-GACGTCGAGGAAACGAGCCGACCG--ACACGTTTCGTTGAGAGAAATGAAGT-----GGGTAG -100
AU22_rrnC TCCTTTGGTGTATGTCGAGAGCTAAGACCGACGAGTACAGCTTTCGTT-AAGA-TGAGAG-----CAGGCACGGT -105
          * * * * *
                16S rRNA
pAU20rrn  CATGTTGGCTGGTGGCTTTCGGCTGGCGGTTGTTTGGTCTGTTCT-----CTCGTCGAT-GCTTTGAGACAGTGACTAGTCGGGAACAGCTCTTA-ATCAA
pAUTrrn   CATGT-GCGCTGGTTGGCTTTCGGCTGGCGGTTGTTTGGTCTGTTCT-----CTCGTCGAT-GCTTTGAGACAGTGACTAGTCGGGAAGAACTCTT--ATCAA
AU4_rrnC  GTTTTGGGCTGGTTGGGATGATCCTGGCTGG--GTTTGGGTTTAT--CTGCACTTCGCTTTTGGCTTTGAGACAGTGT-TGGTCAGGCAAG-CTCTTATATCAA
AU22_rrnC GTTTGCTGGCTGGTTGAGCAGAGCTTGGCGGTTGGTTTTCGCTGCTGACATAACTCTCGTTGAT-GCTTTGAGACAGTGACTAGTCGGGAACAACTCTT--ATCAA
          * * * * *
    
```

**C**

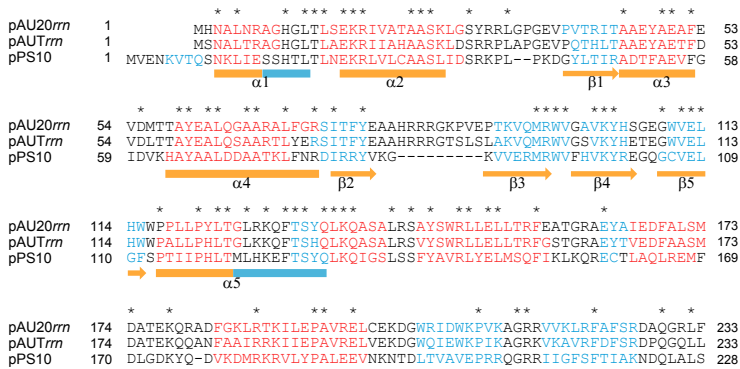
5S rRNA	$\Delta G$ (kcal)
pAU20rrn TCTGCCAATCGCATCTTCTCTCTTCTTCCCTTCAAAAAACCCCGTTCTCTCCGAGGCGGGGGTTTTGCTTGTCTG	-17.1
pAUTrrn TCTGCCAATCACATCCTTCTCTTCCCTTCTTCAAAAAACCCCGTTCTCTCGTAGGCGGGGGTTTTGTCATGCTCT	-18.0
AU4_rrn TCTGCCCATCGCATCCCTCTCTTCCATCCACCAAAAAACCCCGCCAGGTTGAAACCTGCGGGCGGCTTTGGTCTG	-27.4
AU12_rrn TCTGCCAATCGCATCAACTCTTCTCCGACCCCTCAACGCCCGGCTCAAAAGCCGGGGCGTTTTGGCGTTTCAGT	-21.6
AU22_rrn TCTGCCAATCGCATCCTTCTCTCTTCTCTTCCCTTCAACGCCCGCCAGGTTGCGCTTGGCGGGCGTTTTGCTCTC	-19.5

**Fig. S2.** Sequence comparison between the *rrn*-plasmids and the chromosomes in the genus *Aureimonas*. (A) Sequence alignment of the tRNA<sup>Ala</sup> gene on pAU20rrn and the tRNA<sup>Ala</sup> and tRNA<sup>Thr</sup> genes on the AU20 chromosome (locus tags indicated in parentheses). (B) Regions upstream of the 16S rRNA genes. The sequences were from *rrn*-plasmids (pAU20rrn from AU20 and pAUTrrn from *A. ureilytica*) and chromosomes (*rrnC* from AU4 and AU22). For the numbering of nucleotides, the 5'-terminus of the 16S rRNA gene (shown in white letters on a black background with an arrow at the bottom right) is set to +1. Asterisks below the alignment mark nucleotides identical in the four sequences. The positions of the -35 and -10 consensus hexamers of the putative core promoters are marked; these hexamers are similar to the hexamers of the *rrn* operons in *Sinorhizobium meliloti*, a species belonging to the order Rhizobiales (41, 42). The position of A+T-rich segments preceding the -35 hexamers, which possibly act as the UP elements (13, 43), is also marked (A and T are shown in white letters). Segments similar to BoxA of the *E. coli rrn* operons (43) are labeled "BoxA-like," although an associated stem-loop is present only in the AU22 sequence (indicated by arrows below the alignment upstream of the BoxA-like sequence). A position for the upstream arm of the putative 16S processing stalk (44) is marked (nucleotides complementary to those nucleotides in the other arm downstream of the 16S rRNA gene are shown in white letters). (C) Putative rho-independent terminators located downstream of the 5S rRNA genes. The sequences were from pAU20rrn; pAUTrrn; and the genomes of AU4, AU12, and AU22 (note that the corresponding sequences were identical in all of the *rrn* operons within each strain). The 3'-terminus of the 5S rRNA gene is shown in white letters with a horizontal line. Nucleotides involved in the stem structure (underlined) and the associated change in free energy ( $\Delta G$ ) (shown on the right) were predicted by GENETYX (GENETYX Corporation).

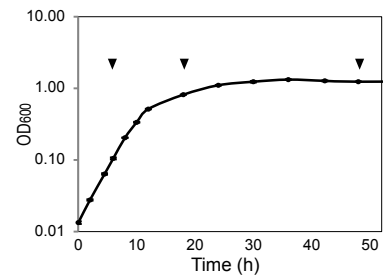


**Fig. S3.** Prediction of the *oriC* and *ter* regions on the AU20 chromosome. (A) Map of the predicted *oriC* region. This region was located at a position showing a GC-skew shift (45) that was in the vicinity of *hemE* and *maf* homologs, which are among the genes typically localized near *oriC* (46). Locus tags for the ORFs are shown above the map. Annotations are shown with the color code on the right. (B) Nucleotide sequence of the intergenic region between *hemE* and *maf* homologs. The start positions and the orientations of these ORFs (indicated by arrows), an AT-rich region (shaded), and a putative DnaA box similar to the *E. coli* consensus sequence 5'-TTATCCACA-3' (boxed) are marked. (C) Cumulative numbers of FtsK orienting polar sequence (KOPS) motifs (with the sequence 5'-GGGNAGGG-3') plotted against the distance from the predicted *oriC* site on both strands of the chromosome. The inflection points on the lines suggest that the *ter* region was located on the chromosome at coordinates 2,491–2,495 (kb) (47). (D) Map of the predicted *ter* region. This region was located on the basis of the GC-skew and the distribution of KOPS motifs over the chromosome. Locus tags for the ORFs are shown above the map. Annotations are shown with the color code below. (E) Nucleotide sequence of the intergenic region between M673\_11345 and M673\_11350. The start position of M673\_11345 (indicated by an arrow); the stop position of M673\_11350 (indicated by a dashed line); and a predicted *dif* site [a site for site-specific recombination to resolve dimeric chromosomes; shaded (an inner palindrome is shown by arrows)], which is similar to the 28-nt motif identified in some members of the order *Rhizobiales* (48), are marked on the sequence.

**A**



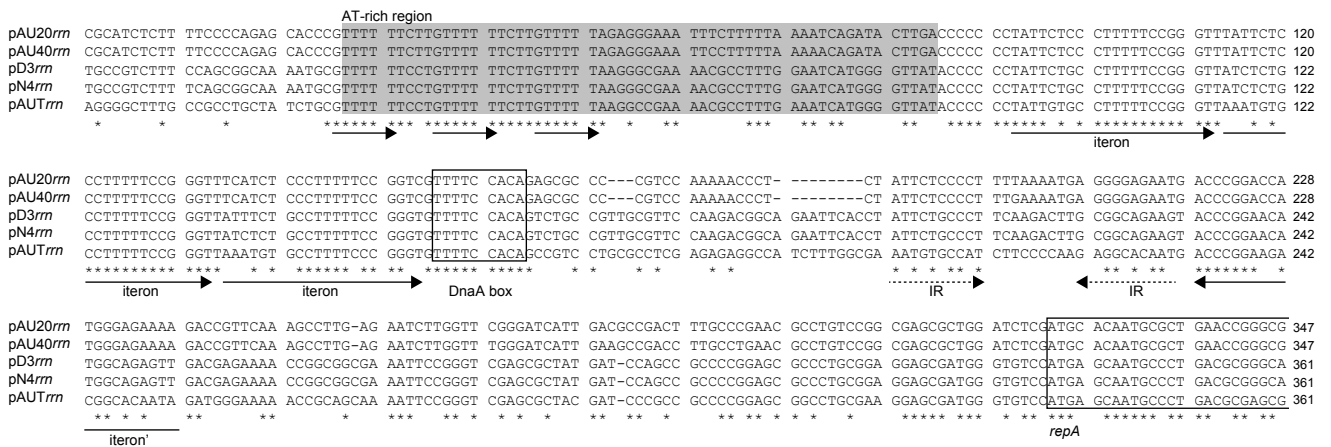
**C**



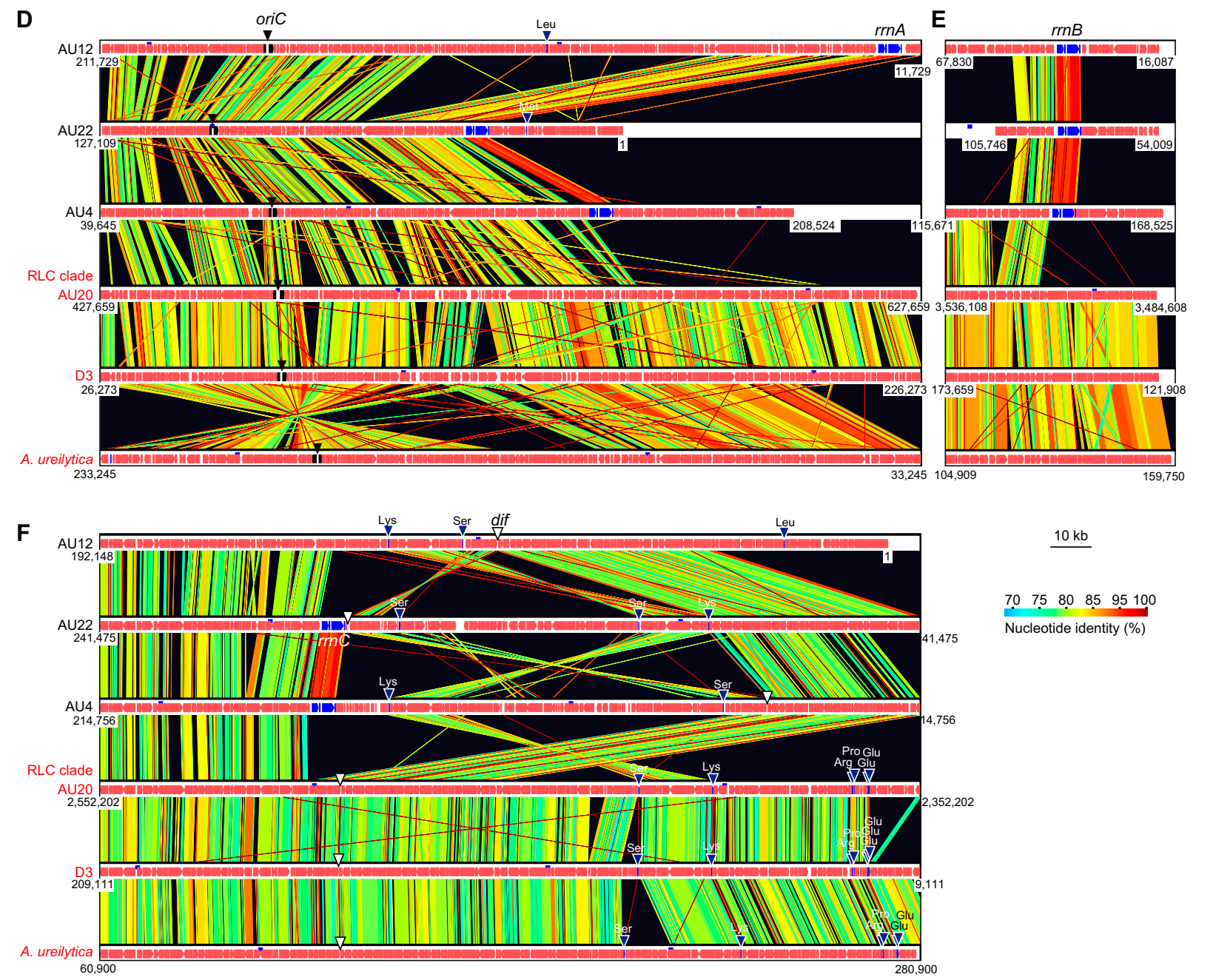
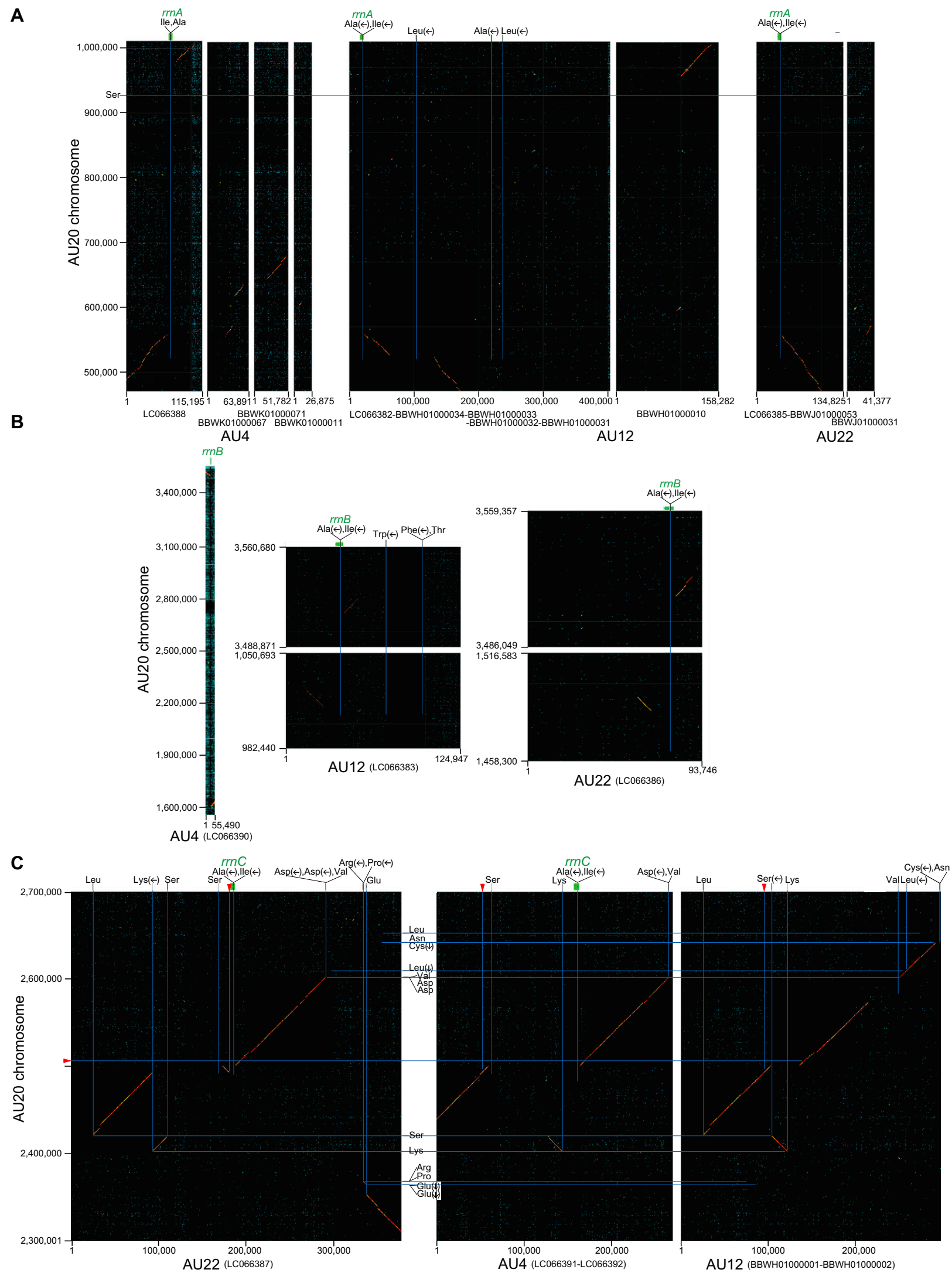
**D**

Time (h)	No. ( $\times 10^5$ ) of molecules per ng of total DNA		Ratio ( <i>rrs</i> / <i>rpsB</i> )
	<i>rrs</i>	<i>rpsB</i>	
6	25.0 $\pm$ 4.5	1.18 $\pm$ 0.25	21.2
18	28.2 $\pm$ 8.8	0.83 $\pm$ 0.26	34.0
48	25.1 $\pm$ 2.2	1.38 $\pm$ 0.10	18.2

**B**



**Fig. S4.** Features of the *rrm*-plasmid. (A) Sequence comparison among RepA proteins from pAU20rrn (234 aa), pAUTrrn (233 aa), and pPS10 (230 aa; accession no. CAA41700). Asterisks above the alignment mark residues identical in the three sequences. Residues shown in red and blue are those residues predicted by the Jpred 3 server (49) to adopt  $\alpha$ -helix and  $\beta$ -sheet secondary structures, respectively. The secondary structure elements evidenced from the crystal structure of the dimeric N-terminal domain of the pPS10 RepA (17) are shown below the sequence; the  $\alpha$ -helical segments that can be remodelled into loops or  $\beta$ -strands in the monomeric RepA are indicated in blue. (B) Multiple sequence alignment of putative *oriV* sites on the five *rrm*-plasmids. An AT-rich region (shaded), including three 5'-GTTTTT-3' repeats (indicated by arrows); a putative iteron consisting of three 20-nt tandem repeats and an additional repeat of the opposite orientation with the sequence 5'-(T/A)ATTCT(C/G)CCTTTTCCGGGT-3' (indicated by arrows labeled iteron and iteron', respectively); a putative DnaA box matching at eight of nine positions with the one located at *oriC* (Fig. S3) (boxed); an inverted repeat with each arm matching half of the repeat in the iteron (indicated by dashed arrows); and the *repA* ORF (boxed) are shown in the aligned sequences. (C) Growth curve of AU20 harvested to determine copy numbers of pAU20rrn. The optical density at 600 nm ( $OD_{600}$ ) is shown as the mean of three independent cultures ( $\pm$ SD, as indicated by the error bars, which are not visible because of small variations). Arrowheads indicate the time points at which aliquots of the culture were sampled for DNA extraction. (D) Number of molecules of *rrs* (pAU20rrn marker) and *rpsB* (chromosome marker) contained in the total AU20 DNA (mean  $\pm$  SD;  $n = 3$ ).



**Fig. 55.** Chromosomal synteny breaks of the *rrn* regions in the genus *Aureimonas*. (A and D) *rrnA*. (B and E) *rrnB*. (C and F) *rrnC*. (A–C) Dot plots comparing the AU20 chromosome (on vertical axes) with scaffolds (or contigs) from strains AU4, AU12, and AU22 (on horizontal axes) by GenomeMatcher (33) using tblastx with a parameter set “-F -W 3 -e 0.01.” Positions of tRNA genes are indicated by blue lines with three-letter symbols for their charged amino acids, and arrows in parentheses indicate orientations of the genes (otherwise, the opposite orientations). The blue line with a red arrowhead indicates a *dif* site. (D–F) Multiple alignments comparing sequences of the AU20 chromosome and scaffolds from strains AU12, AU22, AU4, D3, and *A. ureilytica* (the scaffolds are listed in Table S3) by GenomeMatcher using blastn with a parameter set “-F -W 21 -e 0.01.” Strain names are shown on the left; maps in D and E are from the same strains when compared horizontally. A line color represents the percentage (%) of nucleotide identity between connected sites. In each map, *rrn* (oriented rightward in all drawings) is indicated in blue, *maf* and *hemE* in black, tRNA genes by blue arrowheads, *oriC* by a black arrowhead, and *dif* by an open arrowhead.

**Table S1. Strains sequenced in this study**

Strain	Source (location)	Ref.
<i>Aureimonas</i> sp. AU20	Soybean stem (Miyagi, Japan)	11
<i>Aureimonas</i> sp. AU40	Soybean stem (Miyagi, Japan)	11
<i>Aureimonas</i> sp. D3 [= Pd-E-(l)-m-D-e (3)]	Rice shoot (Shiga, Japan)	19
<i>Aureimonas</i> sp. N4 [= Pd-S-(l)-l-N-4 (3)]	Rice shoot (Shiga, Japan)	19
<i>Aureimonas ureilytica</i> NBRC106430 <sup>T</sup> (= 5715S-12 <sup>T</sup> )	Air dust (Suwon, Korea)	18
<i>Aureimonas</i> sp. AU12	Soybean stem (Miyagi, Japan)	11
<i>Aureimonas</i> sp. AU4	Soybean stem (Miyagi, Japan)	11
<i>Aureimonas</i> sp. AU22	Soybean stem (Miyagi, Japan)	11
<i>Aureimonas altamirensis</i> DSM21988 <sup>T</sup> (= S21B <sup>T</sup> )	Terrestrial cave (Altamira Cave, Spain)	50
<i>Aureimonas frigidaquae</i> JCM14755 <sup>T</sup> (= CW5 <sup>T</sup> )	Water-cooling system (Gwangyang, Korea)	51
<i>Aurantimonas coralicida</i> DSM14790 <sup>T</sup> (= WP1 <sup>T</sup> )	Diseased coral (Florida Keys, United States)	52
<i>Aurantimonas manganoxydans</i> DSM21871 <sup>T</sup> (= SI85-9A1 <sup>T</sup> )	Fjord water (Sannich Inlet, Canada)	53
<i>Fulvimarina pelagi</i> DSM15513 <sup>T</sup> (= HTCC2506 <sup>T</sup> )	Sea water (Western Sargasso Sea)	54

**Table S2. Outline for draft assemblies of the genome sequences**

Strain	No. of reads	Total length, bp	No. of contigs	Estimated genome size, Mb	Coverage	Contig accession no.
<i>Aureimonas</i> sp. AU40	1,336,160	270,613,677	90	5.5	49	LC066393, BBWL01000001–01000065, 01000067–01000090
<i>Aureimonas</i> sp. D3	1,214,449	194,144,157	127	5.4	36	LC066394, BBWM01000001–01000084, 01000086–01000127
<i>Aureimonas</i> sp. N4	1,336,419	255,523,246	85	5.3	48	LC066398, BBWS01000001–01000069, 01000071–01000085
<i>A. ureilytica</i>	1,434,497	298,080,307	106	5.3	56	LC066381, BBWT01000001–01000072, 01000074–01000106
<i>Aureimonas</i> sp. AU12	1,290,323	234,581,545	89	4.8	49	LC066382–066384, BBWH01000001–01000015, 01000017–01000028, 01000030–01000034, 01000036–01000041, 01000043–01000057, 01000061–01000094
<i>Aureimonas</i> sp. AU4	1,314,008	220,880,662	121	4.7	47	LC066388–066392, BBWK01000002–01000025, 01000027–01000040, 01000042, 01000043, 01000045–01000047, 01000049–01000054, 01000056–01000060, 01000062–01000072, 01000076–01000090, 01000092–01000100, 01000102, 01000103, 01000105, 01000106, 01000108, 01000109, 01000111, 01000114, 01000117, 01000119, 01000121–01000125, 01000129–01000139, 01000141
<i>Aureimonas</i> sp. AU22	1,270,908	217,991,647	84	4.7	46	LC066385–066387, BBWJ01000001–01000043, 01000046–01000051, 01000053–01000057, 01000059–01000061, 01000063–01000065, 01000067–01000073, 01000075–01000080, 01000082–01000089
<i>A. altamirensis</i>	1,308,463	278,815,906	26	4.2	66	LC066369–066371, BBWQ01000002–01000008, 01000010–01000017, 01000020–01000022, 01000024, 01000027, 01000028, 01000030, 01000032
<i>A. frigidaquae</i>	1,321,097	275,827,698	22	4.1	68	LC066375–066377, BBWR01000004–01000009, 01000011, 01000014–01000017, 01000019–01000026
<i>A. coralicida</i>	1,363,567	282,065,433	87	4.7	60	LC066372–066374, BBWN01000001–01000015, 01000017, 01000018, 01000020–01000029, 01000031–01000041, 01000043, 01000044, 01000047–01000054, 01000056–01000074, 01000076–01000085, 01000087–01000093
<i>A. manganoxydans</i>	1,224,134	251,756,642	85	4.3	59	LC066378–066380, BBWP01000001–01000015, 01000019–01000022, 01000024–01000029, 01000031–01000048, 01000050–01000059, 01000061–01000074, 01000076, 01000077, 01000079–01000084, 01000086, 01000087, 01000089–01000091, 01000093, 01000094
<i>F. pelagi</i>	1,434,753	300,888,349	50	3.8	79	LC066395–066397, BBWO01000001–01000004, 01000006–01000011, 01000013–01000015, 01000018–01000026, 01000028–01000030, 201000032, 01000035–01000044, 01000046, 01000048, 01000050–01000052, 01000054, 01000055, 01000058–01000061

**Table S3. *rrn*-carrying contigs and scaffolds in the draft genome assemblies**

Strain	Scaffold	
	Order of contigs linked in the scaffold*	Length, bp
<i>A. ureilytica</i>	LC066381 (pAUTrrn)	9,969
<i>Aureimonas</i> sp. AU40	LC066393 (pAU40rrn)	9,396
<i>Aureimonas</i> sp. D3	LC066394 (pD3rrn)	9,912
<i>Aureimonas</i> sp. N4	LC066398 (pN4rrn)	9,902
<i>A. altamirensis</i>	LC066369 ( <i>oriC</i> , <i>rrnA</i> )	235,734
	LC066370 ( <i>rrnB</i> )	491,202
	LC066371 ( <i>rrnC</i> , <i>dif</i> )	563,239
<i>A. frigidaquae</i>	LC066375 ( <i>rrnA</i> , <i>oriC</i> )	709,689
	LC066376 ( <i>rrnB</i> )	251,770
	LC066377 ( <i>dif</i> , <i>rrnC</i> )	1,054,539
<i>Aureimonas</i> sp. AU22	LC066385 ( <i>rrnA</i> )–BBWJ01000053( <i>oriC</i> )	134,825
	LC066386 ( <i>rrnB</i> )	93,746
	LC066387 ( <i>dif</i> , <i>rrnC</i> )	377,401
<i>Aureimonas</i> sp. AU4	BBWK01000040( <i>oriC</i> )–LC066388( <i>rrnA</i> )	208,524
	LC066389( <i>rrnD</i> )–BBWK01000060 <sup>†</sup> –BBWK01000059 <sup>†</sup> – BBWK01000058 <sup>†</sup> –BBWK01000057 <sup>†</sup> –BBWK01000056 <sup>†</sup> – LC066390( <i>rrnB</i> )–BBWK01000027	352,520
	LC066391( <i>dif</i> )–LC066392( <i>rrnC</i> )	270,387
	LC066382( <i>rrnA</i> )–BBWH01000034 <sup>†</sup> –BBWH01000033( <i>oriC</i> ) <sup>†</sup> – BBWH01000032 <sup>†</sup> –BBWH01000031 <sup>†</sup>	403,858
<i>F. pelagi</i>	LC066383 ( <i>rrnB</i> )	124,947
	LC066384 (pAU12rrn)	13,404
	LC066395 ( <i>rrnA</i> )	210,368
<i>A. coralicida</i>	LC066396 ( <i>rrnB</i> )	89,502
	LC066397 ( <i>rrnC</i> )	624,009
	BBWN01000047( <i>oriC</i> ) <sup>†</sup> –LC066372( <i>rrnA</i> )	209,738
<i>A. manganoxydans</i>	LC066373 ( <i>rrnB</i> )	203,547
	LC066374 ( <i>rrnC</i> )	395,184
	BBWP01000039( <i>oriC</i> ) <sup>†</sup> –BBWP01000038 <sup>†</sup> –BBWP01000071– BBWP01000083–LC066378( <i>rrnA</i> )	154,368
	LC066379 ( <i>rrnB</i> )	195,490
	LC066380 ( <i>rrnC</i> )	426,327

\*Contigs are listed under their accession numbers. A copy of the *rrn* operon, a putative *oriC* or *dif* site that is present in the contig, is shown in parentheses after the accession number (*dif* sites are listed in Table S4). In the case of a contig corresponding to a small circular replicon, the replicon name is shown in parentheses.

<sup>†</sup>Contig is arranged in the reverse orientation.



**Table S4. Predicted dif sites in the contigs**

Strain	Sequence (5'→3')*	Contig	
		Accession no.	Location (nucleotide no.)
<i>Aureimonas</i> sp. AU20	AATACTCATAATATGGATTATGGAACAC	CP006367	2,493,549–2,493,576
<i>Aureimonas</i> sp. AU40	AATCCTCATAATATGGATTATGGAACAC	BBWL01000041	393,104–393,077
<i>Aureimonas</i> sp. D3	TGTTCTCATAATATGGATTATGGAACCA	BBWM01000035	69,577–69,604
<i>Aureimonas</i> sp. N4	TGTTCTCATAATATGGATTATGGAACCA	BBWS01000042	121,177–121,204
<i>A. ureilytica</i>	AATACTCATAATATGGATTATGGAACAT	BBWT01000015	119,318–119,291
<i>Aureimonas</i> sp. AU12	CGATGGCATAATATGGATTATGGAACAT	BBWH01000001	95,271–95,298
<i>Aureimonas</i> sp. AU4	AAGTGGCATAATATGCATTATGGAACCA	LC066391	52,184–52,211
<i>Aureimonas</i> sp. AU22	AAATTGCATAATATGGATTATGGAACAT	LC066387	180,819–180,792
<i>A. altamirensis</i>	AAATGGCATAAGATAGATTATGGAACCA	LC066371	279,206–279,179
<i>A. frigidaquae</i>	AAATGGCATAAGATAGATTATGGAACCA	LC066377	676,504–676,531
<i>A. coralicida</i>	AAGTTGCATAAGATAGATTATGGAACCG	BBWN01000036	70,610–70,583
<i>A. manganoxydans</i>	AAGTTGCATAAGATAGATTATGGAACCG	BBWP01000052	10,286–10,313
<i>F. pelagi</i>	AAGTTGCATAATATAGATTATGGAACCTG	BBWO01000001	132,315–132,342

\*Nucleotides involved in the palindrome are underlined.

**Table S5. Accession numbers of the genes and contigs used for phylogenetic analyses**

Strain*	<i>rrs</i>	<i>atpD</i>	<i>dnaK</i>	<i>gyrB</i>	<i>rpoB</i>	<i>rpoC</i>
<i>Aureimonas</i> sp. AU20	CP006375	CP006367	CP006367	CP006367	CP006367	CP006367
<i>Aureimonas</i> sp. AU40	AB600141	BBWL010000033	BBWL010000030	BBWL010000030	BBWL010000064	BBWL010000064
<i>Aureimonas</i> sp. D3	AB600180	BBWM010000034	BBWM010000047	BBWM010000047	BBWM010000083	BBWM010000083
<i>Aureimonas</i> sp. N4	AB600181	BBWS010000006	BBWS010000008	BBWS010000008	BBWS010000062	BBWS010000062
<i>A. ureilytica</i>	DQ883810	BBWT010000005	BBWT010000017	BBWT010000001	BBWT010000074	BBWT010000074
<i>Aureimonas</i> sp. AU12	AB600133	BBWH010000021	BBWH010000031	BBWH010000029	BBWH010000057	BBWH010000057
<i>Aureimonas</i> sp. AU4	AB600129	BBWK010000006	BBWK010000034	BBWK010000063	BBWK010000092	BBWK010000092
<i>Aureimonas jatrophae</i>	JQ346805	—	—	—	—	—
<i>Aureimonas</i> sp. AU22	AB600138	BBWJ010000047	BBWJ010000026	BBWJ010000051	BBWJ010000065	BBWJ010000065
<i>Aureimonas phyllosphaerae</i>	JQ346806	—	—	—	—	—
<i>Aureimonas rubiginis</i>	JQ864241	—	—	—	—	—
<i>Aureimonas ferruginea</i>	JQ864240	—	—	—	—	—
<i>A. altamirensis</i>	DQ372921	BBWQ010000011	BBWQ010000025	BBWQ010000020	BBWQ010000004	BBWQ010000004
<i>A. frigidaquae</i>	EF373540	BBWR010000005	BBWR010000003	BBWR010000011	BBWR010000022	BBWR010000022
<i>Aurantimonas litoralis</i> HTCC2156	AY178863	—	—	—	—	—
<i>A. coralicida</i>	AJ786361	BBWN010000008	BBWN010000017	BBWN010000001	BBWN010000056	BBWN010000056
<i>Aurantimonas manganoxydans</i>	AJ786360	BBWP010000013	BBWP010000006	BBWP010000004	BBWP010000026	BBWP010000026
<i>F. pelagi</i>	AY178860	BBWO010000012	BBWO010000012	BBWO010000001	BBWO010000032	BBWO010000032
<i>Marteella mediterranea</i>	AY649762	—	—	—	—	—
<i>Aminobacter aminovorans</i>	AJ011759	—	—	—	—	—

\*Type strains of the respective species were used unless strain names are specified.