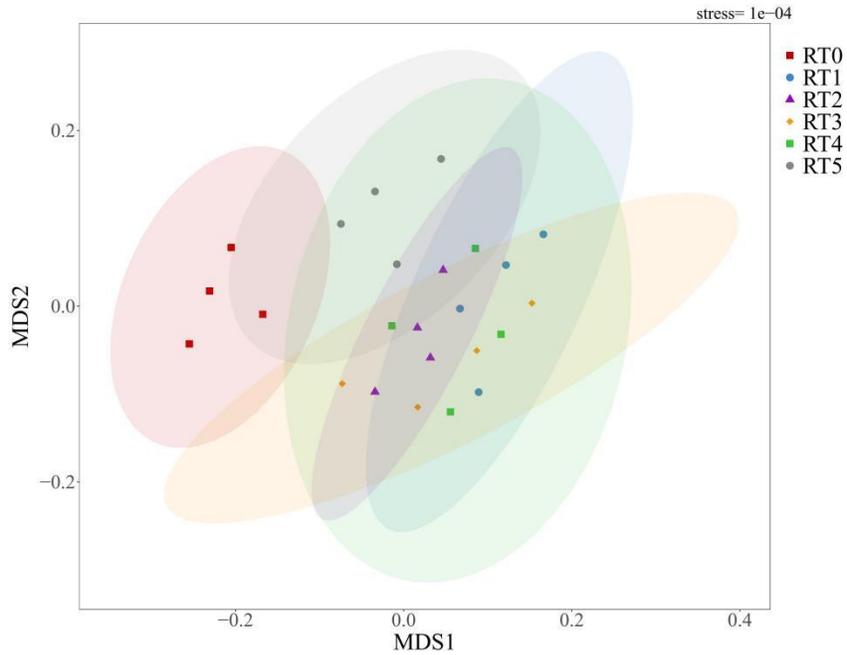
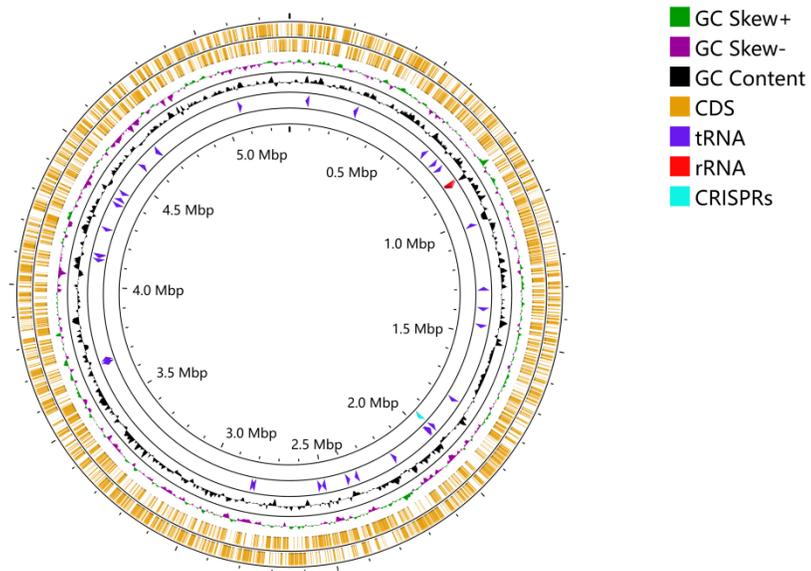


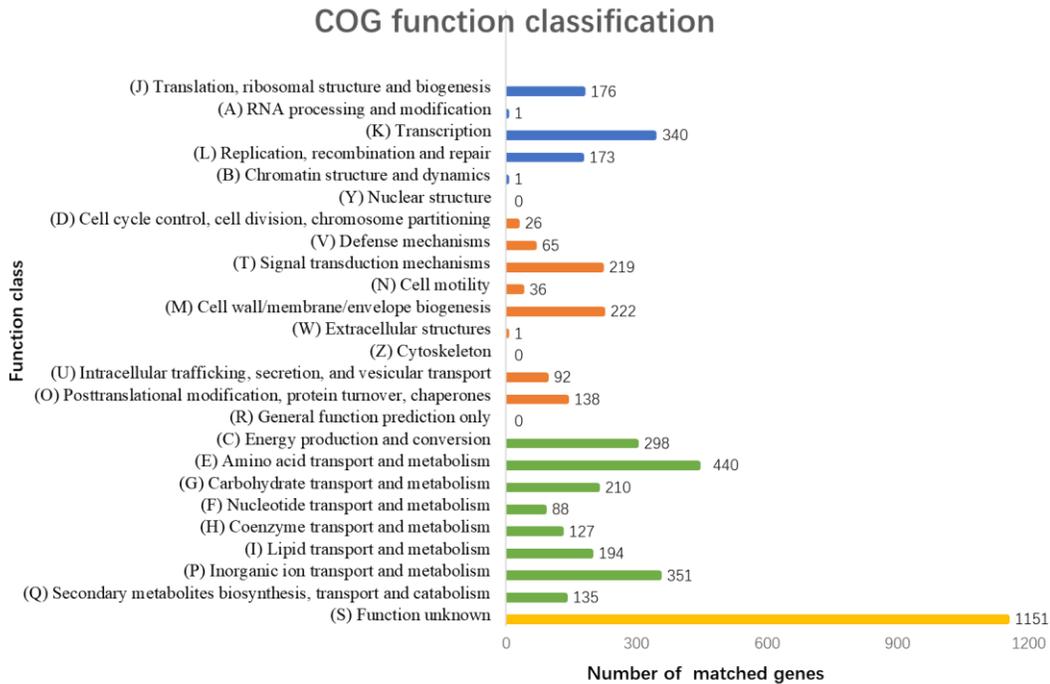
## Supplementary material:



**Figure S1. The dissimilarity of phenanthrene-consuming bacterial community structures by NMDS analysis.** Stress < 0.2 indicates that the result of NMDS analysis is reliable. Each colored solid symbol on the plot represents the microbial community structure derived from different treatments. The solid line ellipse indicates 95% confidence. RT0, phenanthrene-consuming enrichment culture. RT1–RT5, phenanthrene-consuming subcultures.



**Figure S2. Circular view of the genome of *Variovorax* sp. strain N23 visualized using CGViewer.** From outside to center, the tracks display CDSs on positive and negative chains, GC Skew, GC content, non-coding RNA (including rRNA and tRNA), and CRISPRs. The innermost track denotes the genome size.



**Figure S3. COGs present in *Variovorax* sp. strain N23.** Y-axis indicates the COG function classification of 25 categories. X-axis indicates the number of matched genes. The COG function was further divided into information storage and processing (blue), cellular processes and signaling (orange), metabolism (green), and poorly characterized (yellow).

**Table S1 Analysis of similarities (ANOSIM) between bacterial community structures from different treatments.**

<b>Treatments</b>	<b><i>R</i> value</b>	<b><i>P</i> value</b>	<b>Significant</b>
RT0/RT1	0.82	0.020	*
RT0/RT2	0.63	0.027	*
RT0/RT3	0.65	0.029	*
RT0/RT4	0.57	0.037	*
RT0/RT5	0.48	0.032	*
RT1/RT2	-0.20	0.946	
RT1/RT3	-0.01	0.457	
RT1/RT4	0.06	0.272	
RT1/RT5	0.20	0.165	
RT2/RT3	-0.11	0.690	
RT2/RT4	-0.09	0.703	
RT2/RT5	0.11	0.241	
RT3/RT4	-0.17	0.722	
RT3/RT5	0.00	0.369	
RT4/RT5	-0.03	0.359	

The treatment explanation is the same as that in the caption of Fig. S1.