

Supplementary Materials

SUPPLEMENTARY TABLES

Supplementary Table 1. Primer sequences of different genes for RT-qPCR

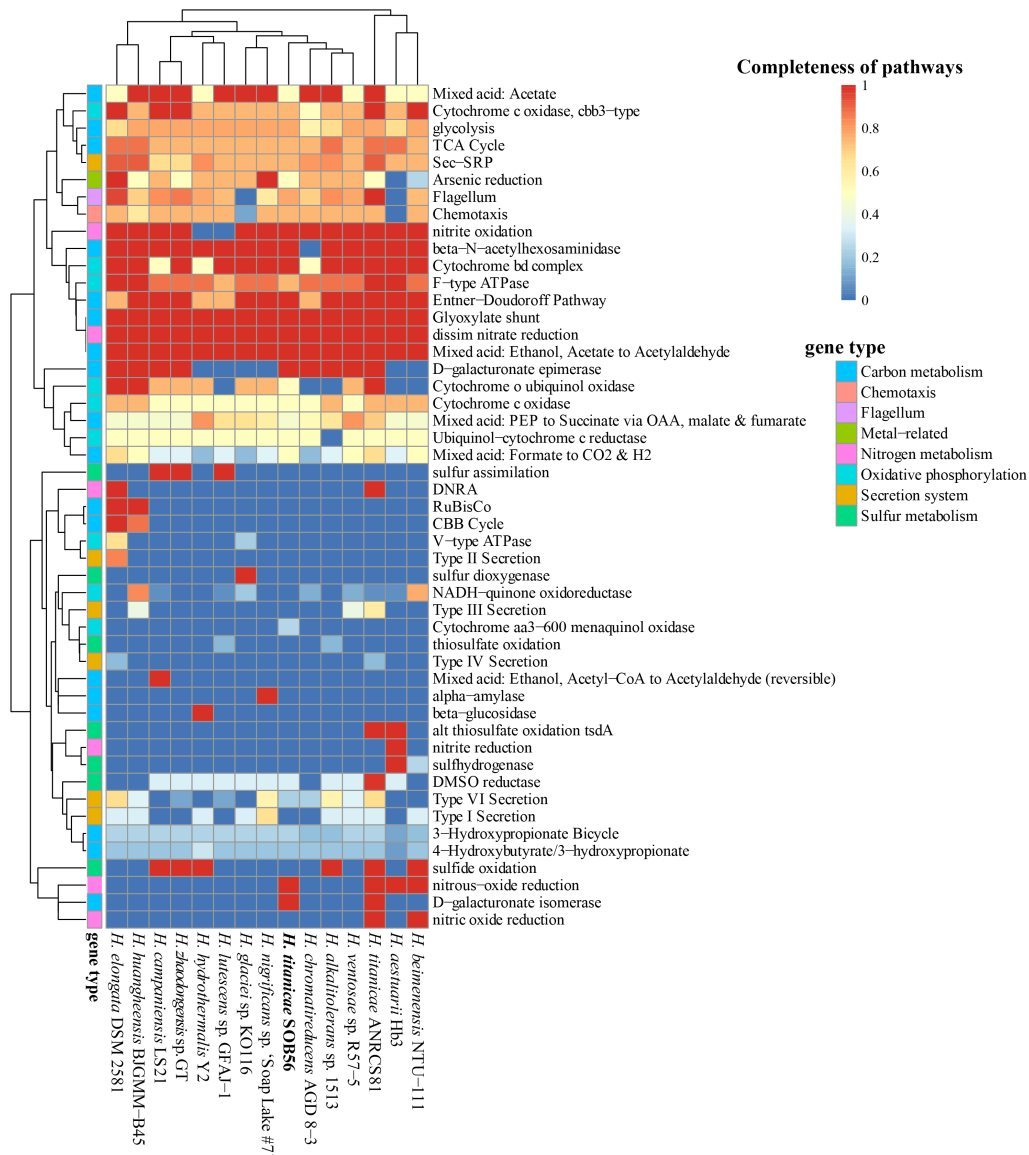
Name	Primer sequences
Q4151-F	GTATCGCAGGTTGCTTTGCTTATT
Q4151-R	GAACAGTTTTTCCTGGTAAGCCG
Q4152-F	ATGATGACGTTTGCCAATATGCT
Q4152-R	TGATGCGTGTCTCGTTTTTCCA
RecA-F	TGAAGTTCTATGCCAGCGTGCG
RecA-R	TGGCTTTACCTTGACCGATTTTCTT

Supplementary Table 4. Genes related to metal ion metabolism in *H. titanicae* SOB56 (CP059082)

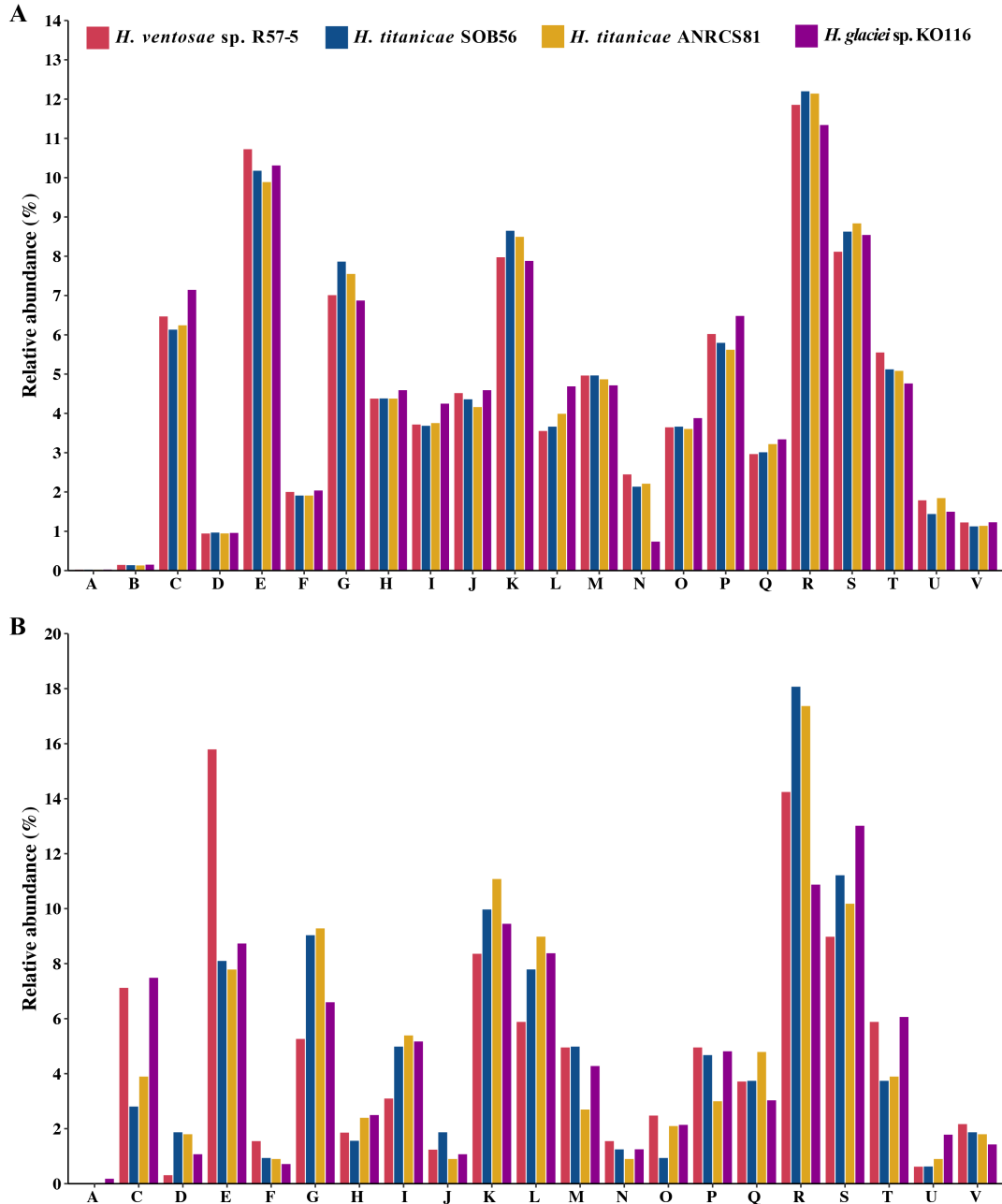
Metal Element	Encoded gene product
Cu	Copper homeostasis protein CutE Copper resistance protein CopC Copper resistance protein CopD Copper resistance protein CopB Multicopper oxidase
Fe	Iron (III) dicitrate transport system permease protein FecD ABC transporter (iron), permease component Iron-chelator utilization protein Iron-regulated protein A precursor Iron-uptake factor PiuB Ferric iron ABC transporter, ATP-binding protein Ferric iron ABC transporter, permease protein Ferroxidase ABC-type Fe ³⁺ -siderophore transport system, periplasmic iron-binding component
Mn	Manganese ABC transporter, periplasmic-binding protein SitA Manganese ABC transporter, ATP-binding protein SitB Manganese ABC transporter, inner membrane permease protein SitC Manganese ABC transporter, inner membrane permease protein SitD Manganese superoxide dismutase (EC 1.15.1.1)
As	Arsenical-resistance protein ACR3 Arsenical resistance operon repressor Arsenic resistance protein ArsH Arsenic efflux pump protein
Ni	Nickel responsive regulator NikR
Zn	Lead, cadmium, zinc and mercury transporting ATPase Zinc uptake regulation protein ZUR Zinc ABC transporter, periplasmic-binding protein ZnuA Zinc ABC transporter, inner membrane permease protein ZnuB Zinc ABC transporter, ATP-binding protein ZnuC Exported zinc metalloprotease YfgC precursor Membrane-associated zinc metalloprotease
Mg/Co	Magnesium and cobalt transport protein CorA Magnesium and cobalt efflux protein CorC Cobalt ABC transporter, ATP-binding component CbtL
Co-Zn-Cd	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA Cobalt-zinc-cadmium resistance protein CzcD

Pb/Cd/Zn/Hg	Lead, cadmium, zinc and mercury transporting ATPase
Hg	Mercuric transport protein, MerE Mercuric resistance operon coregulator Mercuric ion reductase (EC 1.16.1.1) Mercuric transport protein, MerC Periplasmic mercury (+2) binding protein Mercuric transport protein, MerT Mercuric resistance operon regulatory protein
Mo	Molybdenum ABC transporter, periplasmic molybdenum-binding protein ModA (TC 3.A.1.8.1) Molybdenum transport system permease protein ModB (TC 3.A.1.8.1) Molybdenum transport ATP-binding protein ModC (TC 3.A.1.8.1) Putative molybdenum transport ATP-binding protein modF
Others	Metal transporter, ZIP family Heavy metal sensor histidine kinase

SUPPLEMENTARY FIGURES

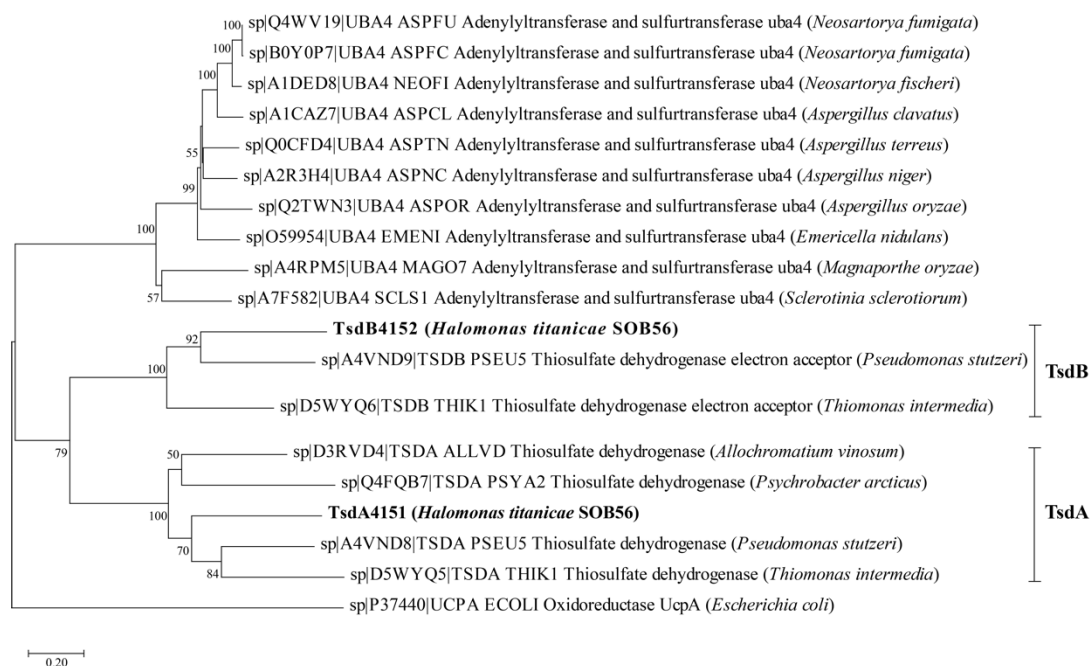


Supplementary Figure 1. KEGG annotation results for fifteen *Halomonas* genomes. Categories of pathways are presented at left side of heatmap by different colors. Color of each cell refers to completeness of enzymes involved in each pathway.

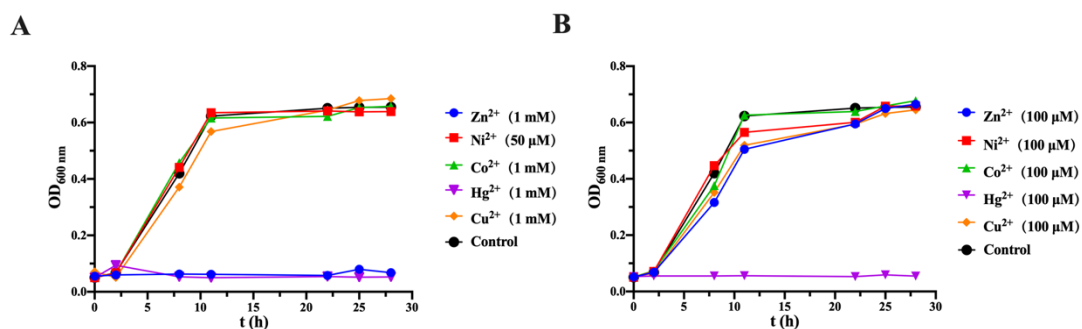


Supplementary Figure 2. Comparison of functional genes in four *Halomonas* genomes. **A** Total gene annotation. **B** Species-specific genes annotation of each strain. Designations of functional categories: A, RNA processing and modification; B, chromatin structure and dynamics; C, energy production and conversion; D, cell cycle control, cell division, chromosome partitioning; E, amino acid transport and metabolism; F, nucleotide transport and metabolism; G, carbohydrate transport and metabolism; H, coenzyme transport and metabolism; I, lipid transport and metabolism; J, translation, ribosomal structure and biogenesis; K, transcription; L, replication, recombination and repair; M, cell wall/membrane/envelope biogenesis; N, cell motility; O, posttranslational modification, protein turnover, chaperones; P, inorganic ion transport and metabolism; Q, secondary metabolites biosynthesis, transport and catabolism; R, general function prediction only; S, function unknown; T, signal

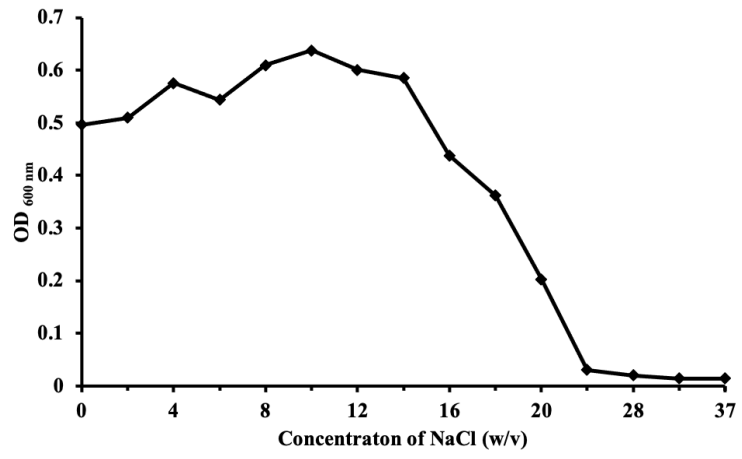
transduction mechanisms; U, intracellular trafficking, secretion, and vesicular transport; V, defense mechanisms; W, extracellular structures.



Supplementary Figure 3. Neighbor-joining phylogenetic tree of TsdA4151, TsdB4152 and homologous proteins. Percentage bootstrap values above 50% (1000 replicates) are shown at branch nodes.



Supplementary Figure 4. The growth course of *H. titanicae* SOB56 under different concentrations of metal ions.



Supplementary Figure 5. Sodium ion tolerance of *H. titanicae* SOB56.