Supplementary Figures



Fig. S1. Distribution of clusters of orthologous groups (COG) between halotolerant genomes of *Chryseobacterium* species isolated from soil and freshwater environments. Annotated genes were categorized into 20 functional categories, excluding poorly characterized categories such as general function prediction only (R) and function unknown (S). The *x*-axis represents the abundance of COG in the halotolerant genomes, while the *y*-axis indicates each COG cluster. As shown in the figure legend, the red and blue bars represent the isolation environments of soil and freshwater, respectively.



Fig. S2. Schematic diagram of one carbon pool by folate (map00670) for the core genome. The diagram shows the distribution of core genes in the tetrahydrofolate biosynthesis pathway. The meanings of all node and edge symbols are described in the legend. The final product of biological pathway is indicated with red text. The locus IDs below the boxes represent the core genes of each species matched with the corresponding KEGG orthologs. Acronyms used for the *Chryseobacterium* species: CCU, *C. cucumeris* GSE06; CHI, *C. hispalense* DSM 25574; CIN, *C. indologenes* PgBE177; COL, *C. oleae* DSM 25575; CPH, *C. phosphatilyticum* ISE14; CSA, *C. salivictor* NBC122; and CSP, *Chryseobacterium* sp. T16E-39.

| Map01110: Biosynthesis of secondary metabolites | | | | | | | | | | | |
|--|---------------------------|-----------------|-----------------|---------------------------------|--|---------------------------------|------------------|-------------------------------|---------------------|--|--|
| | | | | | | | Pathway | | | | |
| Phosphoribosyl- Phosphoribulosyl- Phosphoribosyl- Phosphoribosyl- forminmino- Imidazole- PRPP ATP AMP AICAR-P AICAR-Pglycerol-3P acetol-P L-Histidinol-P | | | | | | | | | | | |
| | | | | | | | | | | | |
| CSA | NBC122_RS12900 | NBC122_RS12865 | NBC122_RS12865 | NBC122_RS12875 | NBC122_RS12870 NBC122_RS12880 | NBC122_RS12885 | NBC122_RS12890 | NBC122_RS12885 | | | |
| CSP | CEY12_RS02890 | CEY12_RS02925 | CEY12_RS02925 | CEY12_RS02915 | CEY12_RS02910 CEY12 RS02920 | CEY12_RS02905 | CEY12_RS02900 | CEY12_RS02905 | | | |
| CIN | DYR29_RS04030 | DYR29_RS04065 | DYR29_RS04065 | DYR29_RS04055 | DYR29_RS04050 DYR29_RS04060 | DYR29_RS04045 | DYR29_RS04040 | DYR29_RS04045 | | | |
| CCU | A1704_RS01460 | A1704_RS01425 | A1704_RS01425 | A1704_RS01435 | A1704_RS01430 A1704_RS01440 | A1704_RS01445 | A1704_RS01450 | A1704_RS01445 | | | |
| CPH | C1631_RS01745 | C1631_RS01780 | C1631_RS01780 | C1631_RS01770 | C1631_RS01765 C1631_RS01775 C1631_RS10455 C1631_RS10460 | C1631_RS01760 | C1631_RS01755 | C1631_RS01760 | | | |
| CHI | AT45_RS02420 | AT45_RS02455 | AT45_RS02455 | AT45_RS02445 | AT45_RS02440 AT45_RS02450 AT45_RS06875 AT45_RS06880 | AT45_RS02435 | AT45_RS02430 | AT45_RS02435 | | | |
| COL | BM143_RS11390 | BM143_RS11355 | BM143_RS11355 | BM143_RS11365 | BM143_RS05555 BM143_RS11360 BM143_RS11370 | BM143_RS11375 | BM143_RS11380 | BM143_RS11375 | | | |
| | | | | | Biinio_nonoro | | | | | | |
| L-Glutamyl- N-Formimino- 4-Imidazolone- tRNA(Glu) L-Glutamate L-glutamate 5-propanoate Urocanate L-Histidine L-Histidinal | | | | | | | | | | | |
| semialdehyde | д € <u></u> К02492 | Оң ко1885 -(| Оң ко1479 -(|)+ ко1468 -(| Оң ко1712 -(| Оң ко1745 -(| Оң кооо13 -(| С кооо13 |) L-Histidinol | | |
| CSA | NBC122_RS04140 | NBC122_RS06680 | NBC122_RS05800 | NBC122_RS06295 | NBC122_RS12205 | NBC122_RS02320 | NBC122_RS12895 | NBC122_RS12895 | | | |
| CIN | DYR29_RS16245 | DYR29_RS13135 | DYR29_RS12675 | DYR29_RS12680 | DYR29_RS07070 | DYR29_RS18690 | DYR29_RS04035 | DYR29_RS04035 | | | |
| CCU | A1704_RS10525 | A1704_RS19545 | A1704_RS20025 | A1704_RS20020 | A1704_RS06965 | A1704_RS19230 | A1704_RS01455 | A1704_RS01455 | | | |
| CPH | C1631_RS17470 | C1631_RS07550 | C1631_RS08025 | C1631_RS08015 | C1631_RS05335 | C1631_RS21295 | C1631_RS01750 | C1631_RS01750 | | | |
| | BM143 RS17760 | BM143 RS16930 | BM143 RS16440 | BM143 RS16455 | BM143 RS01975 | BM143 RS21880 | BM143 RS11385 | BM143 RS11385 | | | |
| GOL | | | | 2 | | | | | | | |
| | i 5-Am | nino- | Hydrox | ymethyl- Uro | por- Copr | opor- Pro | oto- Pro | oto- | | | |
| Glutamate-1- | | | | | | | | унн на)- К01772 +С | Protoheme (heme) | | |
| CSA | NBC122_RS07010 | NBC122_RS01365 | NBC122_RS04145 | NBC122_RS03910 | NBC122_RS04155 | NBC122_RS00810 | NBC122_RS13035 | NBC122_RS07380 | | | |
| CSP | CEY12_RS08850 | CEY12_RS09520 | CEY12_RS15345 | NBC122_RS04150 CEY12_RS15340 | CEY12_RS15335 | NBC122_RS07475 CEY12_RS00310 | CEY12_RS21645 | CEY12_RS10625 | | | |
| CIN | DYR29_RS09670 | DYR29_RS10280 | DYR29_RS16240 | CEY12_RS15730 DYR29_RS16235 | DYR29_RS16230 | DYR29_RS00300 | DYR29_RS22305 | DYR29_RS11470 | | | |
| CCU | A1704_RS13725 | A1704_RS13105 | A1704_RS10520 | DYR29_RS16635 A1704_RS10515 | A1704_RS10510 | DYR29_RS18835 A1704_RS04205 | A1704_RS04940 | A1704_RS22400 | | | |
| CPH | C1631_RS11265 | C1631_RS10615 | C1631_RS17475 | A1704_RS10925 C1631_RS17105 | C1631_RS17485 | A1704_RS19085 C1631_RS14860 | C1631_RS14005 | C1631_RS04765 | | | |
| | AT45 DS07445 | AT45 PS07045 | AT45 PS17240 | C1631_RS17480 | AT45 DS17220 | C1631_RS21150 | AT45 PS14705 | C1631_RS09280 | | | |
| CHI | DM142 DC04720 | DM142 D005400 | DM140_C017310 | AT45_RS17315 | DM140_R017320 | AT45_RS18815 | DM142 D000045 | DM140_D000100 | | | |
| ωL | DIVIT43_N304/30 | Div1143_1300400 | Div(140_NO17/00 | BM143_RS17305 | DIVIT40_NO17700 | BM143_RS21735 | Div1140_1\009040 | BM143 RS11455 | | | |

Fig. S3. Schematic diagram of biosynthesis of secondary metabolites (map01110) for the core genome. The diagram shows the distribution of core genes in the protoheme biosynthesis pathway. The meanings of all node and edge symbols are described in the legend. The final product of biological pathway is indicated with red text. The locus IDs below the boxes represent the core genes of each species matched with the corresponding KEGG orthologs. Acronyms used for the *Chryseobacterium* species: CCU, *C. cucumeris* GSE06; CHI, *C. hispalense* DSM 25574; CIN, *C. indologenes* PgBE177; COL, *C. oleae* DSM 25575; CPH, *C. phosphatilyticum* ISE14; CSA, *C. salivictor* NBC122; and CSP, *Chryseobacterium* sp. T16E-39.

| Map00400: Phenylalanine, tyrosine and tryptophan biosynthesis | | | | | | | | | | |
|---|--|---|---------------------------------|--------------------|----------------|----------------|---|-----------------------|---------------------------------|--|
| | | | | | | | Pathw | icai — — → Cog /ay | nate reaction | |
| | | 2 Dot | audro- | Shikim | 5-O-(1-Car | boxyvinyl)- | | | | |
| Pentose | 3-Dehydr | oquinate shiki | mate Shiki | imate 3-phosp | phate shiki | mate Chorism | Ale K01657 | nthranilate | N-(5-Phospho- | |
| phosphate pathway | <u> </u> |) + _K03786_}►(|) + _K00014_] + (|)⊣_коов91_+(|)+ коовоо ⊧(|)⊣_ко1736_+(| K01658 |)≁_коот66_+С |) β-D-ribosyl)- anthranilate | |
| CSA | NBC122_RS13120 | NBC122_RS02690 | NBC122_RS00530 | NBC122_RS01065 | NBC122_RS02400 | NBC122_RS07330 | NBC122_RS10315 | NBC122_RS10325 | | |
| CSP | CEY12_RS03100 | CEY12_RS16250 | CEY12_RS18155 | CEY12_RS18720 | CEY12_RS12510 | CEY12_RS10800 | CEY12_RS21865 CEY12_RS21870 | CEY12_RS21860 | | |
| CIN | DYR29_RS04255 | DYR29_RS17180 | DYR29_RS19065 | DYR29_RS19610 | DYR29_RS13355 | DYR29_RS11705 | DYR29_RS22475 | DYR29_RS22470 | | |
| CCU | A1704_RS01205 | A1704_RS11490 | A1704_RS18860 | A1704_RS18185 | A1704_RS19350 | A1704_RS22580 | A1704_RS04755 | A1704_RS04765 | | |
| CPH | C1631_RS02055 | C1631_RS16545 | C1631_RS20855 | C1631_RS20215 | C1631_RS07335 | C1631_RS09120 | C1631_RS09555 C1631_RS14200 C1631_RS14205 | C1631_RS14195 | | |
| CHI | AT45_RS03110 | AT45_RS16515 | AT45_RS19050 | AT45_RS18055 | AT45_RS08425 | AT45_RS10130 | AT45_RS05170 | AT45_RS05180 | | |
| COL | BM143_RS11160 | BM143_RS14190 | BM143_RS21510 | BM143_RS20855 | BM143_RS17160 | BM143_RS07065 | BM143_RS10100 | BM143_RS10090 | | |
| Phenyl- Phenyl- Phenyl- Prophenate L-Tryptophan Indolegiycerol Indolegiycerol 1-(2-Carboxyphenylamino)- Indolegiycerol 1-deoxy-D-ribulose 5-phosphate | | | | | | | | | N-(5-Phospho- | |
| alanine | О КООВ17 |)+ K04518 ►(| K04516 ► Chori |) r−−−(smate ! |)+ ко1696 -(| Оң К01695 ┝(|) ∢ K01609 ►(| О◆ К01817 +С |) β-D-ribosyl)- anthranilate | |
| CSA | NBC122_RS06495 NBC122_RS12090 NBC122_RS12260 | NBC122_RS00315 | NBC122_RS12165 | Tryptophan | NBC122_RS10340 | NBC122_RS10345 | NBC122_RS10330 | NBC122_RS10335 | | |
| CSP | NBC122_RS12890 | CEV12 DS22155 | CEV12 DS01035 | metabolism | CEV12 DS21835 | CEV12 DS21830 | CEV12 DS21855 | CEV12 DS21850 | | |
| Cor | CEY12_RS02000 CEY12_RS02900 CEY12_RS04675 CEY12_RS10485 | OET 12_N322133 | | | 02112_0321000 | GET 12_N321000 | 0E112_1021000 | 02112_1021000 | | |
| CIN | DYR29_RS02410 DYR29_RS04040 | DYR29_RS22735 | DYR29_RS02240 | | DYR29_RS22445 | DYR29_RS22440 | DYR29_RS22465 | DYR29_RS22460 | | |
| CCU | A1704_RS01450 A1704_RS02960 | A1704_RS04505 | A1704_RS03120 | | A1704_RS04795 | A1704_RS04770 | A1704_RS04775 | A1704_RS04765 | | |
| CPH | C1631_RS00750 C1631_RS01755 | C1631_RS14515 | C1631_RS00585 | | C1631_RS14175 | C1631_RS14170 | C1631_RS14190 | C1631_RS14185 | | |
| CHI | AT45_RS01645 AT45_RS02430 | AT45_RS04925 | AT45_RS01920 | | AT45_RS05200 | AT45_RS05205 | AT45_RS05185 | AT45_RS05190 | | |
| COL | BM143_RS11380 BM143_RS12360 | BM143_RS10390 | BM143_RS12525 | | BM143_RS10060 | BM143_RS10055 | BM143_RS10085 | BM143_RS10080 | | |
| Tyrosine | 4- K00812 pr K00817 → | Hydrosy- nenylpyruvate)✦ K04517 ✦(| Prephenate | | | | | | | |
| CSA | | NBC122_RS10470 | | | | | | | | |
| CSP | | CEY12_RS20945 | | | | | | | | |
| CIN | | DYR29_RS21525 | | | | | | | | |
| CCU | | A1/04_KS05/45 | | | | | | | | |
| СРП | | AT45 RS05835 | | | | | | | | |
| COL | | BM143_RS09065 | | | | | | | | |

Fig. S4. Schematic diagram of phenylalanine, tyrosine and tryptophan biosynthesis (map00400) for the core genome. The diagram shows the distribution of core genes in the L-tryptophan biosynthesis pathway. The meanings of all node and edge symbols are described in the legend. The final product of biological pathway is indicated with red text. The locus IDs below the boxes represent the core genes of each species matched with the corresponding KEGG orthologs. Acronyms used for the *Chryseobacterium* species: CCU, *C. cucumeris* GSE06; CHI, *C. hispalense* DSM 25574; CIN, *C. indologenes* PgBE177; COL, *C. oleae* DSM 25575; CPH, *C. phosphatilyticum* ISE14; CSA, *C. salivictor* NBC122; and CSP, *Chryseobacterium* sp. T16E-39.



Fig. S5. Effects of *C. salivictor* NBC122 on kinchi cabbage growth under salt stress. (a) Control plants on the left were primed with autoclaved distilled water, while (b) plants on the right were primed with *C. salivictor* NBC122. The plants were grown under 100 mM NaCl conditions, and the photographs were taken 40 days after sowing. (c) Plant growth parameters, including dry weight, root length, leaf length, and leaf count, were measured at the vegetative stage. The bar graphs represent the mean values of 15 replicates, and error bars indicate the standard deviation of the mean. Asterisks represent significant differences between control and NBC122-inoculated plants (Student's *t*-test, *P*-value < 0.05).