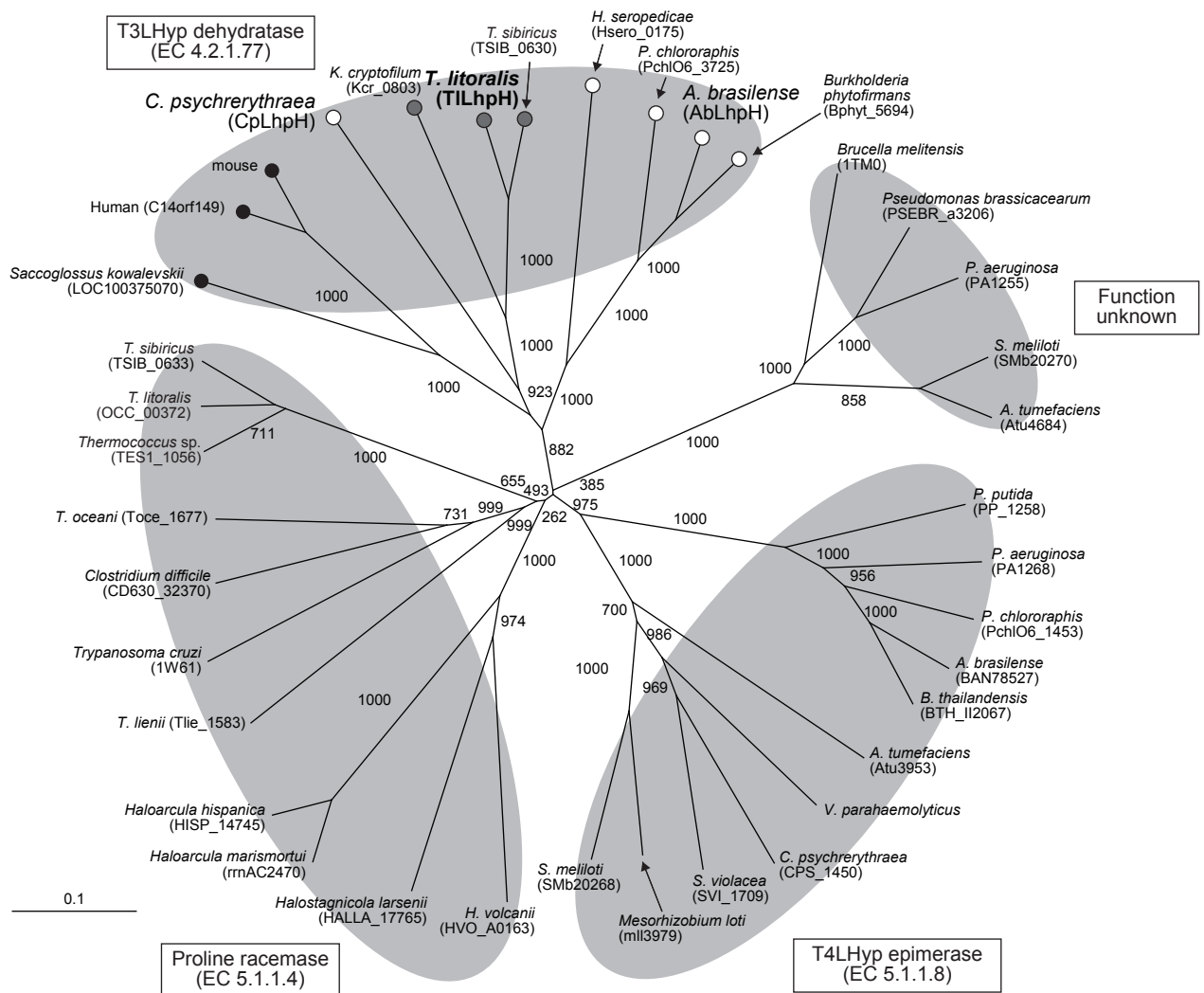


A



B

| | | | | | | | |
|-------------------------------|--------------------------------------|-------|-------|--------|------|--------|----------|
| T3LHyp dehydratase | <i>T. litoralis</i> (OCC_00387) | 99 | GYSTM | CGHATI | 264 | DRSP | EGTGVS |
| | <i>T. sibiricus</i> (TSIB_0630) | 102 | GYSTM | CGHATI | 267 | DRSP | EGTGVSG |
| | <i>K. cryptofilum</i> (kcr_0803) | 98 | GYSTG | CGHAVI | 263 | DRCP | EGTGVS |
| | <i>A. brasilense</i> (BAO2I621) | 86 | GYSDH | CGHGV | 251 | DRSP | EGSGTGG |
| | <i>C. psychrerythraea</i> (CPS_1453) | 106 | GYSSM | CGHAV | 271 | DRSP | EGSGVSG |
| T4LHyp epimerase | Human (C14orf149) | 99 | GYSSM | CGHAVL | 269 | DRSP | EGSGVTA |
| | <i>A. brasilense</i> (AN78527) | 83 | GYLGM | CGHGTI | 232 | DRSP | CGTGTSA |
| | <i>C. psychrerythraea</i> (CPS_1450) | 53 | GCLPM | CGHGTI | 217 | DRSP | CGTGTSA |
| | <i>P. aeruginosa</i> (PA1268) | 83 | GYLGM | CGHGTI | 232 | DRSP | CGTGTSA |
| | <i>P. putida</i> (PP1258) | 83 | GYLNM | CGHGTI | 232 | DRSP | CGTGTSA |
| Proline racemase | <i>S. meliloti</i> (CAC48658) | 85 | GCLPM | CGHGTI | 249 | DRSP | CGTGTSA |
| | <i>T. litoralis</i> (OCC_00372) | 83 | GYLDM | CGHATM | 247 | DRSP | CGTGTSA |
| | <i>T. sibiricus</i> (TSIB_0633) | 83 | GYLDM | CGHATM | 247 | DRSP | CGTGTSA |
| | <i>T. sp.</i> (TES1_1056) | 83 | GYLDM | CGHATM | 247 | DRSP | CGTGTSA |
| | <i>T. lienii</i> (Tlie_1583) | 86 | EGVAM | CGHGST | 251 | DRSP | CGTGTTC |
| Function unknown | <i>T. oceanii</i> (Toce_1677) | 86 | GYLNM | CGHGST | 251 | DRSP | CGTGTTS |
| | <i>T. cruzi</i> (1W61) | 125 | GYLNM | CGHNSI | 296 | DRSP | CGTGTSA |
| | <i>P. aeruginosa</i> (PA1255) | 85 | DTPPM | SGSNSL | 252 | DRSP | CGTGCSSA |
| <i>S. meliloti</i> (SMb20270) | 85 | DTPPM | SGSNS | 252 | DRSP | CGTALS | |

FIGURE S1. Phylogenetic analysis of TILhpH. (A) Phylogenetic tree of proline racemase superfamily. The number on each branch indicates the bootstrap value. Proteins with black, white and gray-colored circles in T3LHyp dehydratase subfamily are from mammals, bacteria, and archaea (discovered in this study), respectively. (B) Partial multiple sequence alignment of deduced amino acid sequences. Catalytic cysteine and/or threonine residues are shown as white letters in black boxes. Gray-shaded letters indicate highly conserved amino acid residues.