SUPPLEMENTARY MATERIALS

Histidine-Triad Hydrolases Provide Resistance to Peptide-Nucleotide Antibiotics

Eldar Yagmurov[1], Darya Tsibulskaya[1,2], Alexey Livenskyi[2,3] Marina Serebryakova[2,4], Yury I. Wolf[5], Sergei Borukhov[6], Konstantin Severinov[1,7,8 *], and Svetlana Dubiley[1,2 *]

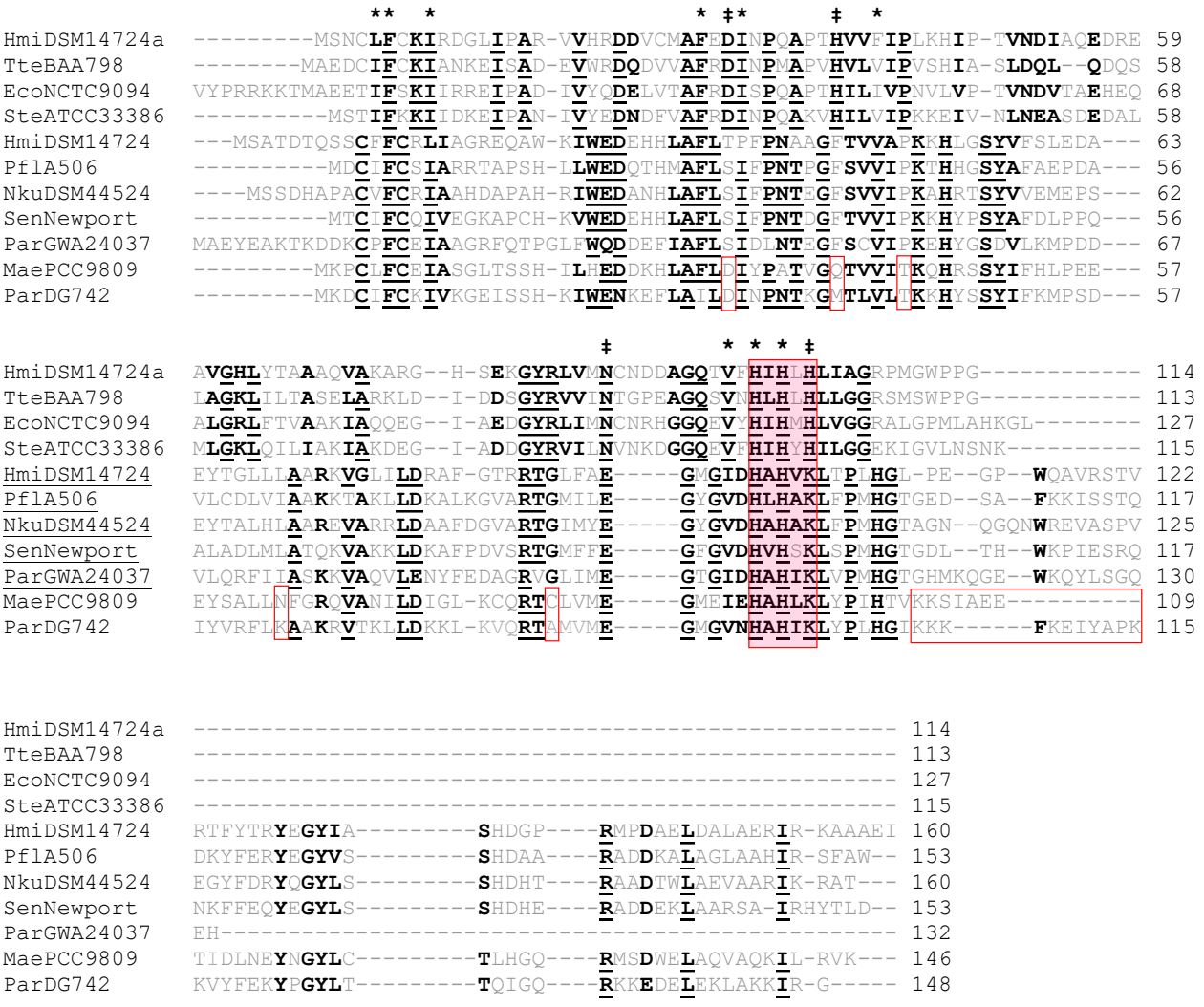

Figure S4. Conservation of the amino acid sequence in the Protein Kinase C Interacting protein-related clade of HIT proteins. Sequence alignment of HinT clade of HIT proteins (HmiDSM14724a, WP_044187632.1 of *Hyalangium minutum* DSM 14724; TteBAA798, ACZ41971.1, of *Thermobaculum terrenum* ATCC BAA-798; EcoNCTC9094, WP_096759427.1

of *Escherichia coli* NCTC 9094; SteATCC33386, ACZ09064.1 of *Sebaldella termitidis* ATCC 33386) and MccH clade of HIT proteins (HmiDSM14724, WP_044187428.1 of *Hyalangium minutum* DSM 14724; PflA506, AFJ55311.1 of *Pseudomonas fluorescens* A506; NkuDSM44524, WP_017574753.1 of *Nocardiopsis kunsanensis* DSM 44524; SenNewport, ECU0367860.1 of *Salmonella enterica* subsp. *enterica* serovar Newport; ParGWA24037, KKR61370.1 of *Parcubacteria bacterium* GW2011_GWA2_40_37; MaePCC9809, CCI22782.1 of *Microcystis aeruginosa* PCC 9809; ParDG742, KPJ57467.1 of *Parcubacteria bacterium* DG_74_2). Residues conserved in either of the two groups are shown in bold and underlined. Histidine-triad active site region is indicated by a red-shaded box. Conserved and partially conserved hydrophobic and polar residues forming the nucleotide-binding pocket of HIT proteins are indicated by an asterisk (*). Substitutions of the active site residues in MccH clade proteins are indicated by (‡). Red boxes mark residues of "inactive" MaePCC9809 and ParDG742 MccH-like proteins, that differ considerably from the MccH consensus.