**Table S5: Genes shared by SAFR-032 and ATCC-7061, but absent in FO-36b.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Unique to** **SAFR-032****and ATCC-7061** | **Gene** | **Locus tag** | **Protein length** | **% identity** |
| **CHP** | **178** | **99** | **NH** |
| **CHP** | **888** | **54** | **NH** |
| **CHP1** | **1299** | **58** | **NH** |
| **CHP** | **1919** | **24** | **NH** |
| **CHP** | **1947** | **70** | **NH** |
| **CHP** | **2482** | **59** | **NH** |
| **CHP** | **2875** | **138** | **NH** |
| **CHP2** | **3109** | **29** | **NH** |
| **CHP** | **3307** | **183** | **NH** |
| **CHP** | **3308** | **134** | **NH** |
| **CHP1** | **3313** | **59** | **NH** |
| **CHP** | **3366** | **58** | **NH** |
| **CHP** | **3609** | **136** | **NH** |
| **ECF family DNA-directed RNA polymerase sigma factor SigV3** | **588** | **181** | **NH** |
| **flagellin4 *hag2***  | **1149** | **300** | **NH** |
| **flagellin4 *hag3*** | **1150** | **305** | **NH** |
| **Hypotheticals** | **CHP1** | **359** | **124** | **45** |
| **CHP2** | **373****374****375** | **130****79****97** | **64****51****35** |
| **CHP** | **457** | **264** | **84** |
| **CHP** | **589** | **482** | **46** |
| **CHP** | **634** | **89** | **54** |
| **CHP** | **177** | **71** | **64** |
| **CHP** | **179** | **315** | **54** |
| **CHP** | **187** | **69** | **64** |
| **CHP** | **254** | **112** | **48** |
| **CHP** | **749** | **163** | **61** |
| **CHP** | **864** | **132** | **33** |
| **CHP** | **889** | **288** | **58** |
| **CHP** | **1128** | **62** | **75** |
| **CHP** | **1228** | **123** | **82** |
| **CHP** | **1311** | **140** | **41** |
| **CHP** | **1728** | **115** | **78** |
| **CHP** | **1732** | **303** | **66** |
| **CHP** | **1733** | **105** | **71** |
| **CHP** | **2110** | **90** | **71** |
| **CHP** | **2338** | **217** | **32** |
| **CHP** | **2483** | **62** | **90** |
| **CHP** | **2728** | **211** | **58** |
| **CHP** | **2746** | **57** | **57** |
| **CHP** | **2747** | **109** | **58** |
| **CHP** | **2748** | **292** | **68** |
| **CHP** | **2898** | **76** | **65** |
| **CHP** | **3100** | **101** | **82** |
| **CHP** | **3304** | **176** | **26**  |
| **CHP** | **3305** | **185** | **31** |
| **CHP** | **3362** | **167** | **54** |
| **CHP** | **3363** | **204** | **44** |
| **CHP** | **3364** | **176** | **40** |
| **CHP** | **3365** | **377** | **54** |
| **CHP** | **3367** | **71** | **60** |
| **CHP** | **3369** | **63** | **51** |
| **CHP YozM** | **3382** | **92** | **39** |
| **CHP** | **3477** | **222** | **24** |
| **CHP** | **3481** | **112** | **46** |
| **CHP** | **3605** | **160** | **46** |
| **CHP** | **3608** | **496** | **24** |
| **CHP** | **3664** | **336** | **73** |
| **CHP** | **3665** | **703** | **43** |
| **CHP** | **3672** | **86** | **47** |
| **Transcription** **regulation** | **LysR family transcriptional regulator** | **494** | **329** | **72** |
| **Xre family transcriptional regulator** | **550** | **128** | **40** |
| **LysR family transcriptional regulator**  | **1227** | **287** | **85** |
| **MarR family transcriptional regulator**  | **1729** | **141** | **77** |
| **TetR family transcriptional regulator**  | **1730** | **189** | **62** |
| **transcriptional regulator**  | **1740** | **132** | **78** |
| **transcriptional regulator** | **2598** | **148** | **43** |
| **TetR family transcriptional regulator** | **3694** | **203** | **53** |
| **sporulation** | **spore transcriptional regulator YopK5** | **549** | **372** | **36** |
| **FtsW/RodA/SpoVE family cell division protein** | **2729** | **384** | **74** |
| **DNA repair** | **DNA (cytosine-5-)-methyltransferase YdiP5** | **561** | **261** | **72** |
| **Transport** | **MFS family major facilitator transporter, macrolide:cation transporter YfmI** | **628** | **410** | **33** |
| **oligopeptide ABC transporter substrate-binding protein OppAB & OppF4** | **1070** **1071****1074** | **552** **309** **309** | **48** **70** **84** |
|  |  |  |  |
| **MFS family major facilitator transporter** | **2065** | **419** | **68** |
| **ABC transporter ATP-binding prfotein YgaD** | **3306** | **603** | **41** |
| **MFS family major facilitator transporter** | **3417** | **386** | **55** |
| **Biochemical pathways** | **Metal-dependent hydrolase** | **139** | **248** | **79** |
| **aldo/keto dehydrogenase**  | **495** | **262** | **85** |
| **thioesterase BacT** | **631** | **236** | **62** |
| **3-hydroxybutyryl-CoA dehydrogenase** | **632** | **285** | **56** |
| **methoxymalonyl-ACP biosynthesis protein** | **633** | **351** | **64** |
| **acyl-CoA dehydrogenase (NADP(+))** | **635** | **380** | **58** |
| **alkaline phosphatase PhoB** | **641** | **468** | **52** |
| **alanine racemase**  | **979** | **368** | **70** |
| **acetyltransferase**  | **1269** | **174** | **62** |
| **GNAT family acetyltransferase** | **1657** | **180** | **72** |
| **cytidine deaminase** | **1737** | **140** | **80** |
| **esterase1** | **1739** | **308** | **68** |
| **NAD(P)H dehydrogenase (quinone)1** | **2597** | **195** | **65** |
| **purine nucleosidase** | **3604** | **311** | **62** |
| **Competence** | **competence pheromone precursor ComX** | **2839** | **56** | **51** |
| **Other functions** | **glutamate rich protein GrpB6** | **458** | **168** | **64** |
| **cytochrome P450 protein** | **3695** | **401** | **65** |
| **Antibiotic resistance** | **nonribosomal peptide synthetase subunit** | **629** | **1470** | **40** |
| **beta-lactamase PbpX** | **630** | **513** | **39** |
| **nonribosomal peptide synthetase subunit**  | **636** | **889** | **33** |
| **polyketide synthase subunit**  | **637** | **1501** | **40** |
| **polyketide synthase subunit** | **638** | **2416** | **43** |
| **polyketide synthase subunit** | **639** | **2136** | **40** |
| **kanamycin kinase**  | **1575** | **307** | **39** |
| **Translation** | **threonyl-tRNA synthetase ThrZ** | **761** | **643** | **70** |
| **Recombination** | **integrase YdcL** | **580** | **425** | **80** |

|  |  |  |
| --- | --- | --- |
|  |  |  |

**CHP – conserved hypothetical protein; NH – no homolog**

**1 - Portion of the open reading frame is present without stop codons in FO-36b;**

**2 - In FO36b, flanking genes terminate contigs;**

**3 - Extra gene copy;**

**4 - First half of the open reading frame is present without stop codons in FO-36b; second half is replete with base changes resulting in a pseudogene;**

**5 – A portion of the open reading frame is present without stop codons in ATCC-7061;**

**6 - Genome location not conserved.**