**Table S3 SAFR-032 characteristic genes**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Type 1** | **Gene class** | **Name** | **Locus tag** | **Protein length** | **% identity**  |
| **DNA repair** | **Helicase1** | **608** | **1015** | **25** |
| **ATP-binding protein** | **652** | **496** | **48** |
| **Endonuclease** | **653** | **936** | **52** |
| **DNA (cytosine-5-) methyltransferase1** | **656** | **548** | **43** |
| **DNA helicase**  | **3674** | **815** | **45** |
| **Peroxide resistance** | **NADH-dependent flavin oxidoreductase1**  | **1716** | **344** | **74** |
| **Sporulation** | **FtsK/SpoIIIE family protein YdcQ** | **554** | **444** | **63** |
| ***spoIIIC* (C-terminal half of *sigK*)2** | **2315** | **NA** | **NA** |
| **Structural integrity** | **C40 family peptidase YddH (CwlT)** | **576** | **325** | **71** |
| **cell wall-associated protein WapA** | **2339** | **2340** | **74** |
| **Lipoprotein** | **2314** | **219** | **37** |
| **Hypotheticals** | **CHP** | **211** | **245** | **29** |
| **CHP** | **212** | **105** | **44** |
| **CHP** | **334** | **128** | **35** |
| **CHP** | **335** | **326** | **29** |
| **CHP** | **552** | **80** | **54** |
| **CHP** | **553** | **321** | **35** |
| **CHP** | **556** | **75** | **60** |
| **CHP YddA** | **557** | **92** | **54** |
| **CHP** | **559** | **847** | **39** |
| **CHP** | **564** | **130** | **31** |
| **CHP** | **565** | **409** | **49** |
| **CHP** | **566** | **270** | **36** |
| **CHP** | **567** | **253** | **34** |
| **CHP** | **568** | **119** | **47** |
| **CHP YddB** | **571** | **331** | **48** |
| **CHP YddC** | **572** | **86** | **41** |
| **CHP YddD** | **573** | **155** | **61** |
| **CHP YddG** | **575** | **793** | **38** |
| **CHP YddI** | **577** | **163** | **50** |
| **CHP3**  | **578** | **69** | **90** |
| **CHP3** | **654** | **342** | **83** |
| **CHP** | **655** | **589** | **49** |
| **CHP** | **1069** | **119** | **31** |
| **CHP** | **1127** | **131** | **36** |
| **CHP** | **1143** | **96** | **30** |
| **CHP** | **1661** | **114** | **56** |
| **CHP** | **2269** | **349** | **34** |
| **CHP** | **2312** | **171** | **64** |
| **CHP** | **2337** | **56** | **41** |
| **CHP**  | **2485** | **111** | **66** |
| **CHP** | **2487** | **65** | **52** |
| **CHP** | **2919** | **667** | **32** |
| **CHP** | **2946** | **287** | **26** |
| **CHP** | **2947** | **87** | **29** |
| **CHP** | **3028** | **183** | **32** |
| **CHP** | **3029** | **276** | **24** |
| **CHP** | **3098** | **183** | **47** |
| **CHP3** | **3402** | **105** | **82** |
| **CHP** | **3403** | **91** | **54** |
| **CHP** | **3405** | **131** | **50** |
| **CHP** | **3406** | **108** | **51** |
| **CHP**  | **3607** | **165** | **39** |
| **CHP4** | **3625** | **173** | **35**  |
| **CHP** | **3626** | **174** | **28** |
| **CHP** | **3627** | **73** | **54** |
| **CHP** | **3628** | **94** | **64** |
| **CHP** | **3639** | **247** | **28** |
| **CHP4,5** | **3640** | **62** | **80**  |
| **CHP** | **3658** | **204** | **47** |
| **CHP** | **3661** | **326** | **71** |
| **CHP** | **3671** | **88** | **48** |
| **CHP** | **3675** | **253** | **53** |
| **Transporters** | **ABC transporter ATP-binding protein**  | **336** | **428** | **35** |
| **ABC transporter ATP-binding protein**  | **337** | **224** | **50** |
| **DASS family divalent anion:sodium (Na+) symporter**  | **684** | **471** | **72** |
| **PTS family glucose/glucoside (glc) porter component IIBCA6** | **1742** | **630** | **60** |
| **AGCS family alanine or glycine:sodium (Na+) or proton (H+) symporter** | **2351** | **483** | **64** |
| **ABC transporter ATP-binding protein MglA** | **3564** | **217** | **37** |
| **major facilitator transporter YdeG3** | **3591** | **423** | **78** |
| **ABC transporter ATP-binding protein** | **3622** | **306** | **29** |
| **ABC transporter ATP-binding protein**  | **3623** | **297** | **43** |
| **Transcriptional regulator** | **transcriptional regulator YdcR** | **555** | **366** | **59** |
| **AraC family transcriptional regulator YddE** | **584** | **290** | **65** |
| **TetR family transcriptional regulator** | **1148** | **204** | **38** |
| **MarR family transcriptional regulator**  | **1717** | **143** | **44** |
| **BglG family transcriptional antiterminator LicT6** | **1743** | **280** | **57** |
| **LysR family transcriptional regulator YwqM** | **2352** | **297** | **56** |
| **Signal transduction** | **response regulator3**  | **353** | **227** | **75** |
| **sensor histidine kinase**  | **354** | **475** | **58** |
| **response regulator** | **3624** | **116** | **47** |
| **Biochemical pathways** | **Acetyltransferase** | **585** | **191** | **75** |
| **Methyltransferase** | **1065** | **250** | **37** |
| **alcohol dehydrogenase**  | **1147** | **370** | **69** |
| **patatin phospholipase**  | **1639** | **355** | **46** |
| **O-methyltransferase3** | **1879** | **304** | **84** |
| **1,3-propanediol dehydrogenase DhaT** | **2350** | **387** | **64** |
| **dehydrogenase3** | **2488** | **326** | **94** |
| **acyltransferase YkrP** | **2739** | **356** | **57** |
| **glycosyltransferase3**  | **3157** | **707** | **57** |
| **glycosyltransferase3**  | **3158** | **330** | **79** |
| **glycosyltransferase**  | **3222** | **610** | **36** |
| **aminotransferase**  | **3223** | **392** | **55** |
| **carbamoylphosphate synthase large subunit6** | **3224** | **426** | **47** |
| **CDP-glycerol glycerophosphotransferase6** | **3225** | **667** | **50** |
| **dTDP-glucose 4,6-dehydratase RfbB** | **3226** | **353** | **68** |
| **glucose-1-phosphate thymidylyltransferase**  | **3227** | **294** | **72** |
| **glycosyltransferase TagFA** | **3234** | **1204** | **62** |
| **Genome recombination** | **Transposase** | **352** | **451** | **84** |
| **Transposase** | **814** | **451** | **83** |
| **Transposase** | **841** | **477** | **84** |
| **transposase OrfX3** | **898** | **107** | **83** |
| **integrase3** | **899** | **269** | **85** |
| **Transposase** | **1287** | **451** | **84** |
| **Transposase** | **1820** | **451** | **84** |
| **Integrase** | **1948** | **266** | **91** |
| **Transposase** | **1949** | **110** | **97** |
| **Transposase** | **2310** | **451** | **84** |
| **Transposase** | **2368** | **451** | **83** |
| **Transposase** | **2484** | **513** | **48** |
| **Transposase** | **3568** | **451** | **83** |
| **Translation** | **ribosomal-protein-alanine N-acetyltransferase YjcK** | **1821** | **186** | **71** |

**Type 1: SAFR-032 characteristic genes completely deleted while the same flanking regions/genes seen in SAFR-032 are still present in FO-36b and ATCC-7061; % identity - with the nearest homolog (from PSI-BLAST results); CHP – Conserved hypothetical protein; HP – Hypothetical protein; NH = No homolog (SAFR-032 unique genes); NA = not applicable;**

**1 - genes were reported in the previous study[10]; their uniqueness to SAFR-032 is confirmed with their absence from the two closest relatives of SAFR-032, namely the JPL isolate *Bacillus safensis* F036B and the *Bacillus pumilus* type strain ATCC-7061; 2 - in SAFR-032, unfused *spoIIIC* occurs as a separate gene; the fused *sigK* containing *spoIVCB (N-terminal half of SigK)* and *spoIIIC (C-terminal half of SigK)* occur as a single fused gene, a feature shared by ATCC-7061, F-036b and several other *Bacillus* sp.; 3 - eleven type 1 genes share > 75% identity with their respective non FO-36b and ATCC-7061 homologs; 4 – one homolog only; 5 - shares homolog with another recently isolated *B. pumilus* strain; 6 - extra gene copy;**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Type 2** | **Name** | **Locus tag**  | **Protein length** | **ATCC-7061** | **F-036b** | **% identity**  |
| **CHP** | **469** | **122** | **A1** | **A** | **76** |
| **CHP**  | **832** | **144** | **A1** | **A** | **66** |
| **CHP**  | **1662** | **345** | **A1** | **A** | **70** |
| **CHP** | **3606** | **160** | **A1** | **A** | **45** |
| **flagellin *hag1*** | **150** | **322** | **Ps** | **A1** | **81** |
| **YddE (ConE)** | **574** | **818** | **A** | **A1** | **68** |
| **MFS family major facilitator transporter5** | **1066** | **414** | **A1** | **A1** | **37** |
| **glycosyl hydrolase**  | **1741** | **488** | **A1** | **A** | **97** |

**Type 2: genes in which a portion of the open reading frame is present without stop codons in either FO-36b or ATCC-7061 (A1); in the case of FO-36b these genes may be partial because they terminate a contig; A = completely absent; Ps = pseudogene; A2 = non-homologous sequence without an ORF; 3 = gene misannotated as ‘*yfiS*’**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Type 3** | **Name** | **Locus Tag**  | **Protein length** | **ATCC-7061** | **F-036b** | **% identity**  |
| **CHP** | **328** | **196** | **A1** | **A** | **46** |
| **CHP**  | **330** | **32** | **A2** | **A2** | **50** |
| **CHP** | **341** | **194** | **A** | **Ps** | **45** |
| **CHP**  | **836** | **107** | **A1** | **Ps** | **40** |
| **CHP5** | **1016** | **91** | **A2** | **A** | **62** |
| **CHP**  | **1660** | **222** | **Ps** | **A** | **40** |
| **CHP** | **1736** | **255** | **Ps** | **A** | **30** |
| **CHP** | **2313** | **67** | **A** | **Ps** | **54** |
| **CHP** | **2611** | **202** | **A** | **A2** | **37** |
| **transposase** | **1812** | **451** | **Ps** | **A** | **84** |

**Type 3: genes with homologs in either FO-36b or ATCC-7061, or both, with stop codons**

**Ps = pseudogene; A1 = sequence analog without an ORF; A2 = corresponding homolog has base deletion(s)/insertions, causing in-frame stop codons, possibly due to sequencing errors; A3 = gene with the corresponding locations in FO-36b or ATCC-7061 showing patches of significant similarity with SAFR-032, but both lacking an ORF; 4 = extra gene copy.**