

Supplementary material 1

Sequence analysis of SSH fragments from *B. amyloliquefaciens* C06

Clone/ Category	DNA length (bp)	BLASTN/BLASTX sequence homology	Identity/ E-value	Genbank accession number
A18	526	nonribosomal fengycin synthesis FenD [<i>B. amyloliquefaciens</i> FZB42]	98%/4e-95	GQ922452
A25	738	Polyketide synthase BaeR [<i>B. amyloliquefaciens</i> FZB42]	98%/4e-55	GQ922453
A71	60	conserved hypothetical protein YheN [<i>B. amyloliquefaciens</i> FZB42]	100%/1e-24	GQ922454
A93	318	putative Iron-containing alcohol dehydrogenase [<i>B. amyloliquefaciens</i> FZB42]	95%/7e-140	GQ922455
A121	150	difficidin synthesis; modular polyketide synthase of type I, DfnI [<i>B. amyloliquefaciens</i> FZB42]	95%/2e-61	GQ922456
B35	597	extracellular metallorotase Mpr hypothetical protein [<i>B. amyloliquefaciens</i> FZB42]	95%/1e-122	GQ922457
B36	256	cell division protein FtsZ [<i>B. amyloliquefaciens</i> FZB42]	97%/1e-45	GQ922458
B64	393	conserved hypothetical protein B64 [<i>B. amyloliquefaciens</i> FZB42]	96%/0	GQ922459
B65	306	coproporphyrinogen III oxidase TagO [<i>B. amyloliquefaciens</i> FZB42]	97%/4e-66	GQ922460
B84	357	non-ribosomal peptide synthetase B84 [<i>B. amyloliquefaciens</i> FZB42]	98%/5e-146	GQ922461
B96	395	glycerol kinase GlpK [<i>B. amyloliquefaciens</i> FZB42]	98%/0	GQ922462
B96-2	624	conserved hypothetical protein YmcB [<i>B. amyloliquefaciens</i> FZB42]	98%/0	GQ922463
C56	943	putative CDR-glucose 4,6-dehydratase YfnG; PG1	99%/0	GQ922464

		protein [<i>B. amyloliquefaciens</i> FZB42]		
C113	585	probable glucitol transport protein GutA [<i>B. amyloliquefaciens</i> FZB42]	97%/0	GQ922465
CA38	357	YfnG [<i>B. amyloliquefaciens</i> FZB42]	98%/1e-177	GQ922466
CB39	81	phosphate ABC transporter (ATP-binding protein) CB39 [<i>B. amyloliquefaciens</i> FZB42]	97%/3e-30	GQ922467
CB40	760	nonribosomal fengycin synthesis FenE; Protein of unknown function YngL [<i>B. amyloliquefaciens</i> FZB42]	95%/0	GQ922468
D41	356	cell wall-associated hydrolase [<i>Burkholderia multivorans</i> ATCC 17616]	78%/1e-83	GQ922469
D47	349	Hypothetical protein D47 [<i>B. amyloliquefaciens</i> FZB42]	98%/3e-172	GQ922470
D81	159	nonribosomal synthesis of bacillomycin D BmyC [<i>B. amyloliquefaciens</i> FZB42] ;	77%/3e-10	GQ922471
D83	957	putative glycerophosphodiester phosphodiesterase YqiK [<i>B. amyloliquefaciens</i> FZB42]	99%/0	GQ922472
D84	258	non-ribosomal peptide synthetase NrsC [<i>B. amyloliquefaciens</i> FZB42]	97%/5e-144	GQ922473
D103	344	ATP phosphoribosyltransferase regulatory subunit, HisZ [<i>B. amyloliquefaciens</i> FZB42]	97%/0	GQ922474
D104	393	putative antibiotic transport-associated protein YdfJ [<i>B. amyloliquefaciens</i> FZB42]	96%/0	GQ922475
D114	654	uroporphyrin-III C-methyltransferase NasF [<i>B. amyloliquefaciens</i> FZB42]	97%/0	GQ922476
D118	567	conserved hypothetical protein YvdO [<i>B. amyloliquefaciens</i> FZB42]	94%/0	GQ922477
E012	255	conserved hypothetical protein YqfA [<i>B. amyloliquefaciens</i> FZB42]	79%/9e-53	GQ922478
E13	342	flagellar MS-ring protein FliF; flagellar motor switch	99%/1e-	GQ922479

		protein G FliG [<i>B. amyloliquefaciens</i> FZB42]	170	
E16	240	similar to Low-density lipoprotein receptor-related protein 4 precursor E16 [<i>Rattus norvegicus</i>]	74%/6e-149	GQ922480
E63	511	carbamoyl phosphate synthase large subunit CarB [<i>B. amyloliquefaciens</i> FZB42]	95%/4e-167	GQ922481
E64	279	aspartate kinase yclm [<i>B. amyloliquefaciens</i> FZB42]	95%/3e-122	GQ922482
E102	237	conserved hypothetical protein YqfA [<i>B. amyloliquefaciens</i> FZB42]	79%/6e-53	GQ922483
E113	654	flagellar assembly protein FliW [<i>B. amyloliquefaciens</i> FZB42]; conserved hypothetical protein YjbI [<i>B. amyloliquefaciens</i> FZB42]	100%/0	GQ922484
E123	901	pG1 protein [<i>Lactobacillus jensenii</i> 269-3]	99%/0	GQ922485
EA38	195	phage related protein [<i>B. licheniformis</i> ATCC 14580]	79%/2e-14	GQ922486
EB39	263	No significant match		GQ922487
F16	180	putative lipoprotein SpoIIIJ-like protein YqjG [<i>B. amyloliquefaciens</i> FZB42]	97%/4e-79	GQ922488
F101	334	hypothetical protein SPBc2p184 [<i>Bacillus phage</i> SPBc2]	97%/1e-158	GQ922489
F114	387	bacillaene synthesis BaeJ [<i>B. amyloliquefaciens</i> FZB42]	98%/0	GQ922490
FA40	149	putative ABC transporter (ATP-binding protein) YdbJ [<i>B. amyloliquefaciens</i> FZB42]	95%/9e-61	GQ922491
FB38	347	No significant match		GQ922492
FB40	264	Beta-ketoacyl synthase PKSFB40 [<i>B. thuringiensis</i> serovar <i>huazhongensis</i> BGSC 4BD1]	77%/0.002	GQ922493
HB39	315	putative Iron-containing alcohol dehydrogenase HB39 [<i>B. amyloliquefaciens</i> FZB42]	98%/1e-152	GQ922494