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Supplementary tables

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52		

53 **Table S0: Statistics of Illumina HiSeq2000 sequencing output data for *B. licheniformis***
54 **strains G-1, F1-1 and F2-1**

Statistic	Strain G-1	Strain F1-1	Strain F2-1
Number of produced paired reads	78,947,464	65,238,978	91,092,216
Read length (bp)	101	101	101
Q20 (%)	94.82	93.74	94.73
Q30 (%)	87.92	85.99	87.85
N%	0.01	0.01	0.01

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67 **Table S1: Comparison of genes among strains G-1, F1-1 and F2-1 as determined by RAST, TBLASTN and raw read mapping.**

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Gene/ Function	Strain G-1		Strain F1-1		Strain F2-1		Presence/absence in		Highest scoring NCBI database sequence and organism using blastp
	Presence / Absence ¹	Contig (coordinates)	Presence / absence	Contig (coordinates)	Presence / absence	Contig (coordinates)	<i>B. licheniformis</i> ATCC 14580	<i>B. subtilis</i> 168	
Eukaryotic-type low-affinity urea transporter	Y	31 (407355-408293)	N	-	N	-	N	N	<i>Bacillus</i> sp. 10403023 (ZP_10915670.1)
4-amino, 4-deoxyprephenate dehydrogenase	Y	8 (97182-98096)	N	-	N	-	N	N	<i>Saccharopolyspora spinosa</i> NRRL 18395 (ZP_08878928.1)
Para-aminobenzoate	Y	8 (95089-	N	-	N	-	N	N	<i>S. spinosa</i> NRRL 18395

synthase, amidotransferase component		97182)							(ZP_08878927.1)
Fructose-1,6- biphosphatase, <i>Bacillus</i> type	Y	15 (70491- 72413)	N	-	N	-	N	Y	<i>Bacillus atrophaeus</i> C89 (ZP_14344679.1)
Endo-beta-1,3-1,4 glucanase (Licheninase)	Y	30 (201004- 201732)	N	-	N	-	N	Y	<i>B. atrophaeus</i> 1942 (YP_003973210.1)
Low-specificity D- threonine aldolase	Y	30 (497417- 498520)	Y	1 (1100939- 1102042)	N	-	Y	N	<i>B. licheniformis</i> ATCC 14580 (YP_079923.1)
2-methyloaconitate isomerase	Y	30 (488023- 489174)	N	-	N	-	N	N	<i>Bacillus sonorensis</i> L12 (ZP_22899089.1)
Poly(glycerol-phosphate) alpha-glucosyltransferase	Y	15 (579317- 581356)	N	-	N	-	N	Y	<i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> AS43.3 (YP_007188047.1)
Thymidylate synthase (ThyX)	Y	30 (31580- 32392)	N	-	N	-	N	N	<i>B. sonorensis</i> L12 (ZP_22898135.1)

ATP-dependent ligase	DNA	Y	14 (11244- 12038)	N	-	Y	23 (2068 to 2862)	N	Y	<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. SC-8 (ZP_12671269.1)
ATP-dependent ligase	DNA	Y	8 (45668- 46057)	N	-	N	-	Y	Y	<i>B. licheniformis</i> ATCC 14580 (YP_078721.1)
ATP-dependent ligase	DNA	Y	32 (502933- 503742)	N	-	Y	Raw reads ²	Y	Y	<i>B. licheniformis</i> ATCC 14580 (YP_078721.1)
DNA-cytosine methyltransferase		Y	25 (244- 1809)	N	-	N	-	N	N	<i>Bacillus cereus</i> AH1134 (ZP_03233286.1)
DNA-cytosine methyltransferase		Y	30 (34721- 36070)	N	-	N	-	N	N	<i>Bacillus</i> <i>amyloliquefaciens</i> DSM 7 (YP_003919517.1)
Crossover endodeoxyribonuclease RuvC	junction	Y	30 (23809- 24333)	N	-	N	-	N	N	<i>Brevibacillus</i> <i>borstelensis</i> AK1 (EMT54751.1)
Type I restriction- modification system, subunit M		Y	32 (467190- 468656)	N	-	N	-	Y	N	<i>Enterococcus</i> <i>faecium</i> E980 (ZP_06681840.1)
Type I restriction-		Y	32 (468697-	N	-	N	-	Y	N	<i>E. faecium</i> E980 (ZP_06681839.1)

modification system, subunit R		471072)							
Type I restriction- modification system, subunit S	Y	32 (465752- 467185)	N	-	N	-	Y	N	<i>Capnocytophaga ochracea</i> str. Holt 25 (ZP_14667284.1)
Putative peptidoglycan hydrolase (YvbX)	Y	12 (154529- 155560)	N	-	N	-	N	Y	<i>B. atrophaeus</i> 1942 (YP_003974852.1)
Spore germination protein (GerHB/GerIB)	Y	32 (203381- 204496)	N	-	N	-	N	N	<i>B. licheniformis</i> WX-02 (ZP_17656399.1)
Nickel transporter (UreH)	Y	31 (413565- 414254)	N	-	N	-	N	N	<i>Bacillus</i> sp. 10403023 (ZP_10915662.1)
Biphenyl-2,3-diol 1,2- dioxygenase III-related protein	Y	15 (638813- 639202)	Y	Raw reads	Y	Raw reads	Y	N	<i>Rhizobium etli</i> IE4771 (ZP_03515769.1)
Deoxyuridine 5'- triphosphate nucleotidohydrolase	Y	30 (30553- 31095)	N	-	N	-	N	N	<i>B. sonorensis</i> L12 (ZP_22898133.1)

Potassium-transporting ATPase A chain	Y	30 (418208-419878)	N	-	N	-	N	N	<i>B. sonorensis</i> L12 (ZP_22899191.1)
Potassium-transporting ATPase B chain	Y	30 (419895-421964)	N	-	N	-	N	N	<i>B. sonorensis</i> L12 (ZP_22899190.1)
Potassium-transporting ATPase C chain	Y	30 (421980-422537)	N	-	N	-	N	N	<i>B. sonorensis</i> L12 (ZP_22899189.1)
Alanyl-tRNA synthetase family protein	Y	30 (498547-499785)	Y	1 (1099683 to 1100912)	N	-	Y	N	<i>B. licheniformis</i> ATCC 14580 (YP_079922.1)
Urease accessory protein UreD	Y	31 (412669-413490)	N	-	N	-	N	N	<i>Bacillus</i> sp. 10403023 (ZP_10915663.1)
Urease accessory protein UreE	Y	31 (410904-411356)	N	-	N	-	N	N	<i>Bacillus</i> sp. 10403023 (ZP_10915666.1)
Urease accessory protein UreF	Y	31 (411352-412032)	N	-	N	-	N	N	<i>Bacillus</i> sp. 10403023 (ZP_10915665.1)
Urease accessory protein UreG	Y	31 (412107-412664)	N	-	N	-	N	N	<i>Bacillus</i> sp. 10403023 (ZP_10915664.1)
Urease subunit alpha	Y	31 (409181-	N	-	N	-	N	Y	<i>Bacillus</i> sp. 10403023 (ZP_10915667.1)

		410890)							
Urease subunit beta	Y	31 (408858-409181)	N	-	N	-	N	N	<i>Bacillus</i> sp. 10403023 (ZP_10915668.1)
Urease subunit gamma	Y	31 (408567-408833)	N	-	N	-	N	N	<i>Paenibacillus alvei</i> DSM 29 (ZP_10862792.1)
Xylose ABC transporter, periplasmic xylose-binding protein (XylF)	N	-	Y	4 (152214-153275)	Y	2 (152189-153250)	Y	N	<i>Bacillus</i> sp. BT1B_CT2 (ZP_08003205.1)
Cell-division initiation protein	Y	Raw reads	Y	14 (34320-34694)	Y	4 (21007-21381)	Y	Y	<i>B. licheniformis</i> ATCC 14580 (YP_077348.1)
Recombinational DNA repair protein RecT (prophage associated)	Y	Raw reads	Y	Raw reads	Y	1 (137935-138666)	Y	Y	<i>Bacillus vallismortis</i> DV1-F-3 (ZP_10509695.1)
Competence protein F homolog, phosphoribosyltransferase domain	Y	Raw reads	Y	25 (178363-179094)	Y	24 (33244-34152)	Y	Y	<i>B. licheniformis</i> ATCC 14580 (YP_080871.1)

69 ¹Y=Presence of gene, N=Absence of gene or only a few reads (1-6) were aligned with the coverage depth of 1 when raw reads corresponding to the gene were
70 mapped to the contigs of another strain having this gene in order to see its presence or absence.¹Raw reads with significant coverage were seen in the strain
71 when the former were mapped to the contigs of another strain.

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73 **Table S2A: The ‘Mobility and chemotaxis’ genes in *B. subtilis* 168 and the regions of**
 74 **their homologs in *B. licheniformis* strains G-1, F1-1, and F2-1**

<i>B. subtilis</i> gene ¹	Contigs and coordinates in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>cheC</i>	31 (275479-276105)	75	1 (181644-182270)	75	27 (181708-182334)	75
<i>cheD</i>	31 (276123-276608)	77	1 (182288-182773)	77	27 (182352-182837)	77
<i>cheR</i>	30 (875740-876501)	75	1 (712109-712870)	73	35 (551559-552320)	74
<i>cheV</i>	31 (37609-38520)	75	8 (604621-605532)	74	48 (587865-588776)	74
<i>cheW</i>	31 (274992-275453)	71	1 (181157-181609)	73	27 (181221-181673)	73
<i>flgB</i>	31 (251403-251789)	71	1 (157592-157972)	71	27 (157584-157964)	69
<i>flgC</i>	31 (251792-252241)	77	1 (157975-158424)	77	27 (157967-158416)	77
<i>flgE</i>	31 (260274-261071)	61	1 (166451-167236)	62	27 (166443-167228)	62
<i>flgK</i>	15 (609980-611488)	68	25 (180444-181952)	68	1 (135077-136585)	68

<i>flgL</i>	15 (611502-612410)	75	25 (181966-182874)	75	1 (134155-135063)	75
<i>flgM</i>	NSH ²	-	NSH	-	NSH	-
<i>flhA</i>	31 (267836-269866)	90	1 (174001-176031)	90	27 (174065-176095)	90
<i>flhB</i>	31 (266723-267799)	75	1 (172888-173964)	75	27 (172952-174028)	75
<i>flhF</i>	31 (269869-270972)	58	1 (176034-177137)	58	27 (176098-177201)	58
<i>flhO</i>	15 (498498-499331)	71	25 (86777-87610)	71	1 (229412-230245)	71
<i>flhP</i>	15 (499381-500205)	62	25 (87660-88484)	62	1 (228538-229362)	62
<i>fliD</i>	15 (615911-617389)	65	25 (185664-187121)	66	1 (129908-131365)	66
<i>fliE</i>	NSH	-	NSH	-	NSH	-
<i>fliF</i>	31 (252626-254224)	69	1 (158809-160407)	69	27 (158801-160399)	69
<i>fliG</i>	31 (254241-255254)	89	1 (160424-161437)	88	27 (160416-161429)	88
<i>fliH</i>	31 (255379-255945)	53	1 (161562-162128)	53	27 (161554-162120)	53
<i>fliI</i>	31 (256044-257318)	85	1 (162227-163501)	85	27 (162219-163493)	85
<i>fliJ</i>	31 (257324-	75	1 (163507-	76	27 (163499-	76

	257761)		163944)		163936)	
<i>fliK</i>	31 (258916- 259734)	46	1 (164874- 165911)	41	27 (164866- 165903)	41
<i>fliL</i>	NSH	-	NSH	-	NSH	-
<i>fliM</i>	31 (261796- 262791)	88	1 (167964- 168959)	88	27 (167956- 169023)	77
<i>fliP</i>	31 (264989- 265651)	90	1 (171154- 171816)	90	27 (171218- 171880)	90
<i>fliQ</i>	31 (265671- 265936)	79	1 (171836- 172101)	79	31 (171900- 172165)	79
<i>fliR</i>	31 (265950- 266720)	74	1 (172115- 172885)	74	27 (172179- 172949)	74
<i>fliS</i>	15 (617411- 617809)	71	25 (187167- 187565)	71	1 (129464- 129862)	71
<i>fliT</i>	NSH	-	NSH	-	NSH	-
<i>fliY</i>	31 (262793- 263917)	71	1 (168961- 170082)	71	27 (169025- 170146)	71
<i>fliZ</i>	31 (264328- 264993)	60	1 (170493- 171158)	57	27 (170557- 171222)	57
<i>hag</i>	15 (613835- 614749)	81	25 (184298- 185116)	74	1 (131913- 132731)	74
<i>hemAT</i>	32 (279077- 280303)	67	8 (181170- 182396)	67	48 (157726- 158952)	67
<i>mcpA</i>	4 (38696- 40678)	65	15 (35843- 37825)	65	13 (36925- 38907)	65

	4 (36580-36559)	64	15 (33728-35707)	64	13 (34810-36789)	64
	4 (40825-42804)	61	15 (37974-39953)	61	13 (39397-41037)	59
	30 (1086640-1088604)	60	1 (507608-509587)	60	27 (507649-509628)	60
<i>mcpB</i>	31 (25113-26858)	31	8 (592243-593907)	33	48 (575487-577151)	32
	4 (38696-40678)	62	15 (35843-37825)	62	13 (36925-38907)	62
	4 (36580-38559)	61	15 (33728-35707)	61	13 (34810-36789)	61
	4 (40825-42804)	61	15 (37974-39953)	61	13 (39397-41037)	59
	30 (1086640-1088604)	61	1 (507608-509587)	61	27 (507649-509628)	61
<i>mcpC</i>	31 (24894-26858)	60	8 (591943-593907)	59	48 (575187-577151)	59
	4 (36583-38151)	31	15 (33731-35299)	31	13 (34813-36381)	31
	4 (38699-40270)	30	15 (35846-37417)	31	13 (36928-38499)	30
	4 (40825-42396)	32	15 (39545-37974)	32	13 (39310-40629)	35
	30 (1086652-	33	1 (508025-	33	27 (508066-	33

	1088187)		50581)		509622)	
<i>motA</i>	11 (19330-20148)	75	8 (560954-561772)	75	48 (500438-501256)	75
<i>motB</i>	11 (18579-19310)	67	8 (560203-560934)	67	48 (499687-500418)	67
<i>tlpA</i>	31 (25056-26858)	32	8 (592090-593907)	32	48 (575334-577151)	32
	4 (38696-40600)	60	15 (35843-37747)	60	13 (36925-38829)	60
	4 (40825-42726)	59	15 (37974-39875)	59	13 (39397-40959)	57
	4 (36580-38481)	59	15 (33728-35629)	58	13 (34810-36711)	58
	30 (1086640-1088526)	56	1 (507686-509587)	57	27 (507727-509628)	57
	8 (159300-160427)	39	-	-	-	-
<i>tlpB</i>	4 (38696-40678)	61	15 (35843-37825)	61	13 (36925-38907)	61
	4 (40825-42804)	59	15 (37974-39953)	60	13 (39394-41037)	58
	4 (36580-38559)	59	15 (33728-35707)	59	13 (34810-36789)	58
	30 (1086640-1088604)	60	1 (507608-509587)	61	27 (507649-509628)	60

<i>tlpC</i>	1 (15596-17215)	25	4 (17515-19203)	54	2 (17491-18606)	53
<i>yfmS</i>	12 (115896-116678)	84	30 (144375-145157)	85	29 (132903-133685)	85
<i>ylqH</i>	NSH	-	NSH	-	NSH	-
<i>ylxG</i>	31 (259854-260243)	59	1 (166031-166420)	59	27 (166023-166412)	59
<i>ylxH</i>	31 (270987-271856)	59	1 (177152-178021)	59	27 (177216-178085)	59
<i>yoaH</i>	15 (105746-107347)	80	16 (32490-34091)	79	8 (24904-26505)	79
<i>ytxD</i>	30 (148194-149009)	79	28 (111216-112031)	79	49 (112884-113699)	79
<i>ytxE</i>	30 (149002-149688)	63	28 (112024-112707)	63	49 (113692-114375)	63
<i>yvaQ</i>	8 (158931-160358)	31	4 (153388-154458)	40	12 (144640-146067)	31
	-	-	-	-	2(153363-154433)	40
<i>yvyC</i>	NSH	-	NSH	-	NSH	-
<i>yvyF</i>	15 (608692-609105)	66	25 (179156-179569)	63	1 (137460-137873)	63
<i>yvyG</i>	NSH	-	NSH	-	NSH	-
<i>yvzB</i>	15 (614177-614749)	63	25 (184640-185116)	78	1 (131913-132389)	78

75 ¹Homology for the proteins encoded by these genes were first searched with TBLASTN
76 using BLOSUM62 matrix in the three target strains, and if the region of significant homology
77 was not achieved using this matrix, BLOSUM45 matrix was used. If the protein sequences
78 did not show homology, discontinuous megablast with corresponding nucleotide sequences
79 as queries (instead of amino acid sequenced) were used (homologous regions found in such a
80 way are shown green). ²NSH means 'no significant homology'. The contigs and coordinates
81 for the genes for which query coverage was 95% or less are coloured brown. The percentage
82 identity in black and brown fonts represents amino acid identity and that in green represents
83 nucleotide identity.

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95 **Table S2B: The ‘Mobility and chemotaxis’ genes in *B. licheniformis* ATCC 14580 and**
 96 **the regions of their homologs in *B. licheniformis* strains G-1, F1-1, and F2-1¹**

<i>B. licheniformis</i> ATCC 14580 gene ²	and coordinates in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1	% identity	F1-1	% identity	F2-1	% identity
<i>flgM</i>	15 (609191- 609457)	98	25 (179655- 179921)	100	1 (137108- 137374)	100
<i>fliE</i>	31 (252258- 252572)	96	1 (158441- 158755)	100	27 (158433- 158747)	100
<i>fliL</i>	31 (261329- 261757)	97	1 (167497- 167925)	100	27 (167489- 167917)	100
<i>fliT</i>	15 (617812- 618150)	93	25 (187568- 187906)	100	1 (129123- 129461)	100
<i>ylqH</i>	31 (240057- 240341)	97	1 (146239- 146520)	99	27 (146231- 146512)	100
<i>yvyC</i>	15 (615550 -615891)	94	25 (185304 - 185645)	99	1 (131384 -131725)	98
<i>yvyG</i>	15 (609476-	97	25 (179940-	99	1 (136616- 137089)	99

	609949)		180413)			
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97 ¹If no homologous region is found for any amino acid sequence or gene by using the
 98 sequence from *B. subtilis*, the corresponding amino acid or gene sequence was obtained from
 99 *B. licheniformis* ATCC 14580 (NC_006322.1) and homology search was performed similar
 100 to that for the genes in table S2A. ²These genes, when extracted from *B. subtilis* genome, had
 101 shown no significant homology in table S2A. The colour codes are same as that used in the
 102 above table S2A.

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116 **Table S3A: The genes involved in the protein secretion in *B. subtilis* 168 and the regions**
 117 **of their homologs in *B. licheniformis* strains G-1, F1-1, and F2-1**

<i>B. subtilis</i> gene ¹	Contig and coordinates in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>csaA</i>	NSH ²	-	NSH	-	NSH	-
<i>ffh</i>	31 (232295-233632)	91	1 (138486-139823)	92	27 (138478-139815)	92
<i>ftsY</i>	31 (230836-231813)	83	1 (137027-138004)	83	27 (137019-137996)	83
<i>lspA</i>	31 (177085-177534)	83	1 (83290-83739)	82	27 (83277-83726)	82
<i>lytA</i>	NSH	-	NSH	-	NSH	-
<i>prsA</i>	32 (320033-320791)	68	8 (140967-141725)	68	48 (117520-118278)	68
<i>secA</i>	15 (619493-622015)	90	25 (189244-191766)	91	1 (125263-127785)	91
<i>secDF</i>	30 (357233-359431)	84	1 (1218290-1220488)	85	35 (109945-112143)	85
<i>secE</i>	NSH	-	NSH	-	NSH	-
<i>secG</i>	NSH	-	NSH	-	NSH	-
<i>secY</i>	13 (42448-43740)	84	10 (14426-15718)	84	7 (14422-15714)	84

<i>sipS</i>	31 (72942-73493)	68	8 (640162-640713)	68	48 (623406-623957)	68
<i>sipT</i>	31 (72975-73490)	79	8 (640195-640710)	79	48 (623439-623954)	79
<i>sipU</i>	NSH	-	NSH	-	NSH	-
<i>sipV</i>	32 (273598-274098)	67	8 (187372-187872)	68	48 (163928-164428)	68
<i>sipW</i>	30 (626911-627477)	65	1 (985867-986433)	63	35 (352645-353211)	63
<i>tatAC</i>	NSH	-	NSH	-	NSH	-
<i>tatAD</i>	NSH	-	NSH	-	NSH	-
<i>tatAY</i>	NSH	-	NSH	-	NSH	-
<i>tatCD</i>	19 (140627-141352)	70	4 (128234-128959)	71	2 (128210-128935)	71
<i>tatCY</i>	28 (3327-4073)	76	30 (7800-8552)	76	24 (45617-46369)	76
<i>tepA</i>	31 (319047-319715)	89	1 (225194-225862)	90	27 (225258-225926)	90
<i>yacD</i>	2 (8851-9735)	70	14 (45981-46865)	70	4 (8835-9719)	69
<i>yobE</i>	33 (24505-25143)	71	30 (17256-17894)	71	29 (5608-6246)	71
<i>yoqW</i>	33 (24505-25167)	73	30 (17232-17894)	73	29 (5584-6246)	73

<i>yvmB</i>	30 (1083040-1083516)	65	1 (512736-513212)	65	27 (512777-513253)	65
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118 ¹Homology for the proteins encoded by these genes were first searched with TBLASTN
119 using BLOSUM62 matrix in the three target strains, and if the region of significant homology
120 was not achieved using this matrix, BLOSUM45 matrix was used. ²NSH means ‘no
121 significant homology’. The contigs and coordinates of genes for which query coverage was
122 95% or less are coloured brown. The percentage represents amino acid identity.

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136 **Table S3B: The genes involved in the protein secretion in *B. licheniformis* ATCC 14580**
 137 **and the regions of their homologs in *B. licheniformis* strains G-1, F1-1, and F2-1¹**

<i>B. licheniformis</i> ATCC 14580 Gene ²	Contig, coordinates and % identity in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>csaA</i>	30 (1086242-1086571)	95	1 (509642-509971)	100	27 (509683-510012)	100
<i>lytA</i>	NSH ³	-	25 (155617-155937)	100	1 (161092-161412)	100
<i>secE</i>	13 (16335-16514)	99	10 (41684-41863)	100	7 (41680-41859)	100
<i>secG</i>	15 (744214-744444)	98	25 (312561-312791)	100	1 (4315-4545)	100
<i>sipU</i>	31 (72936-73493)	98	8 (640156-640713)	99	48 (623400-623957)	99
<i>tatAC</i>	-	-	-	-	-	-
<i>tatAD</i>	19 (141434-141640)	95	4 (129030-129242)	100	2 (129006-129218)	100
<i>tatAY</i>	28 (4080-4249)	97	30 (7614-7793)	100	24 (46376-46555)	100

138 ¹If no homologous region is found for any amino acid sequence or gene by using the
 139 sequence from *B. subtilis*, the corresponding amino acid or gene sequence was obtained from

140 *B. licheniformis* ATCC 14580 (NC_006322.1). ²These genes, when extracted from *B.*
141 *subtilis* genome, had shown no significant homology in table S3A. The way of performing
142 homology search and colour codes are same as that used in table S3A. Additionally, if the
143 protein sequences did not show homology, discontinuous megablast with corresponding
144 nucleotide sequences as queries (instead of amino acid sequences) were used (homologous
145 regions found in such a way are shown green). The percentage identity in black font
146 represents amino acid identity and that in green represents nucleotide identity. ³NSH means
147 either ‘no significant homology’ or a few reads (1-6) with the coverage depth of 1 could be
148 aligned when the raw reads from the strain were mapped onto the genome of another strain in
149 which the related gene is present.

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161 **Table S4: The genes involved in the metabolism of phosphate in *B. subtilis* 168 and the**
 162 **regions of their homologs in *B. licheniformis* strains G-1, F1-1, and F2-1**

<i>B. subtilis</i> gene ¹	Contig, coordinates and % identity in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>phoA</i>	30 (694901-696289)	36	1 (842971-844359)	35	35 (420452-421840)	35
<i>phoB</i>	30 (694982-696301)	37	1 (842959-844278)	37	35 (420533-421852)	37
<i>phoD</i>	19 (141894-143414)	81	4 (129495-131015)	81	2 (129471-130991)	81
	30 (229072-230424)	51	1(1358730-1360082)	50	15 (65390-66742)	50
<i>phoH</i>	30 (553247-554197)	84	1 (1055764-1056714)	84	35 (282368-283318)	84
<i>ppaC</i>	15 (493163-494083)	75	25 (81444-82364)	74	1 (234658-235578)	74
<i>xpaC</i>	2 (54572-55183)	55	14 (597-1208)	55	4 (54493-55104)	55
<i>ybfM</i>	4 (73468-73947)	63	1 (956179-956658)	62	13 (71975-72454)	62
<i>ykoX</i>	35 (6885-7541)	71	8 (534405-535061)	71	48 (473889-474545)	71

<i>ylaK</i>	31 (108469-109764)	82	1 (14680-15975)	81	27 (14674-15969)	81
<i>yngC</i>	32 (102724-103284)	79	8 (350458-351018)	79	48 (330053-330613)	79

163 ¹Homology for the proteins encoded by these genes were searched with TBLASTN using
164 BLOSUM62 matrix in the three target strains, and if the region of significant homology was
165 not achieved using this matrix, BLOSUM45 matrix was used. The contigs and coordinates of
166 genes for which query coverage was 95% or less are coloured brown. The percentage identity
167 represents amino acid identity.

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179 **Table S5: The genes involved in the metabolism of sulphur in *B. subtilis* 168 and the**
 180 **regions of their homologs in *B. licheniformis* strains G-1, F1-1, and F2-1**

<i>B. subtilis</i> gene ¹	Contig, coordinates and % identity in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>sat</i>	31 (192696-193814)	82	1 (98912-100030)	81	27 (98899-100017)	81
<i>ssuD</i>	32 (452435-453535)	78	8 (10245-11345)	77	34 (11648-12748)	77
<i>yisZ</i>	31 (193852-194373)	63	1 (1000068-100589)	63	27 (100055-100576)	63
<i>yitA</i>	31 (192708-193814)	67	1 (98924-100030)	67	27 (98911-100017)	67
<i>yitB</i>	31 (190896-191591)	59	1 (97112-97807)	59	27 (97099-97794)	59
	30 (1131772-1132473)	67	1 (463775-464476)	68	27 (463817-464518)	68
<i>yuiH</i>	4 (114199-114789)	70	1 (915705-916295)	69	13 (112339-112929)	69
<i>yvgQ</i>	32 (76788-78503)	88	8 (370576-372291)	88	48 (350175-351890)	88
<i>yvgR</i>	30 (406375-408072)	28	1 (1169722-1171419)	29	35 (159028-160725)	29

	32 (78534-80360)	76	8 (368719-370545)	76	48 (348318-350144)	76
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181 Homology for the proteins encoded by these genes were searched with TBLASTN using
182 BLOSUM62 matrix in the three target strains, and if the region of significant homology was
183 not achieved using this matrix, BLOSUM45 matrix was used. The contigs and coordinates of
184 genes for which query coverage was 95% or less are coloured brown. The percentage identity
185 represents amino acid identity.

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199 **Table S6A: The genes involved in transformation/ competence in *B. subtilis* 168 and the**
 200 **regions of their homologs in *B. licheniformis* strains G-1, F1-1, and F2-1**

<i>B. subtilis</i> gene ¹	Contig, coordinates and % identity in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>cinA</i>	31 (331075-332322)	76	1 (237220-238467)	76	27 (237284-238531)	76
<i>comC</i>	30 (322072-322764)	47	1 (1254975-1255667)	47	35 (74766-75458)	46
<i>comEA</i>	NSH ²	-	NSH	-	NSH	-
<i>comEB</i>	30 (525006-525572)	84	1 (1082121-1082687)	84	35 (256395-256961)	84
<i>comEC</i>	30 (525709-527889)	50	1 (1079805-1081985)	49	35 (257097-259277)	50
<i>comER</i>	30 (523407-524225)	71	1 (1083469-1084287)	71	35 (254795-255613)	71
<i>comFA</i>	15 (606209-607582)	57	25 (176676-178049)	56	1 (138980-140353)	56
<i>comFB</i>	15 (607655-60792)	59	25 (178122-178394)	63	1 (138635-138907)	63
<i>comFC</i>	15 (607947-608630)	54	25 (178414-179094)	52	1 (137935-138615)	52
<i>comGA</i>	30 (621338-	68	1 (990984-	67	35 (347078-	67

	622390)		992000)		348130)	
<i>comGB</i>	30 (622449- 623417)	57	1 (989921- 990889)	57	35 (348189- 349157)	57
<i>comGC</i>	30 (623434- 623724)	70	1 (989614- 989904)	67	35 (349174- 349464)	67
<i>comGD</i>	NSH	-	NSH	-	NSH	-
<i>comGE</i>	NSH	-	NSH	-	NSH	-
<i>comGF</i>	NSH	-	NSH	-	NSH	-
<i>comGG</i>	NSH	-	NSH	-	NSH	-
<i>comS</i>	NSH	-	NSH	-	NSH	-
<i>comP</i>	4 (86188- 83876)	53	1 (943944- 946247)	52	13 (82386- 84689)	52
<i>comX³</i>	4 (86236- 86379)	42	1 (943757- 943852)	56	13 (84781- 84876)	56
<i>comZ</i>	32 (160686- 160865)	73	8 (295423- 295602)	73	48 (274150- 274329)	73
<i>mecA</i>	32 (137167- 137802)	82	8 (317690- 318325)	83	48 (297404- 298039)	83
<i>med</i>	32 (160891- 161832)	68	8 (294456- 295397)	68	48 (273183- 274124)	68
<i>rok</i>	31 (55210- 54698)	81	8 (621703- 622218)	81	48 (604947- 605462)	81
<i>smf</i>	31 (242711- 243607)	57	1 (148892- 149788)	58	27 (148884- 149780)	58

<i>ylbF</i>	31 (127732-128124)	82	1 (33907-34299)	82	27 (33901-34293)	82
<i>ypbH</i>	30 (852347-852928)	81	1 (735681-736262)	80	35 (528167-528748)	80

201 ¹Homology for the proteins encoded by these genes were first searched with TBLASTN
202 using BLOSUM62 matrix in the contigs of three target strains, and if the region of significant
203 homology was not achieved using this matrix, BLOSUM45 matrix was used. ²NSH means
204 ‘no significant homology’. ³This is a gene of small size and hence the score below 50 was
205 used to determine its presence. The genes for which query coverage was 95% or less are
206 coloured brown. The percentage identity represents amino acid identity.

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217 **Table S6B: The genes involved in transformation/ competence in *B. licheniformis* ATCC**
 218 **14580 and the regions of their homologs in *B. licheniformis* strains G-1, F1-1, and F2-1¹**

<i>B. licheniformis</i> ATCC 14580 Gene ²	Contig, coordinates and % identity in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>comEA</i>	30 (524308-524934)	89	1 (1082759-1083385)	99	35 (255697-256323)	99
<i>comGD</i>	30 (623733-624167)	90	1 (989171-989605)	100	35 (349473-349907)	100
<i>comGE</i>	30 (624154-624498)	90	1 (988840-989184)	100	35 (349894-350238)	100
<i>comGF</i>	30 (624410-624895)	83	1 (988443-988928)	100	35 (350150-350635)	99
<i>comGG</i>	30 (624910-625272)	85	1 (988065-988427)	99	35 (350651-351013)	99
<i>ComS</i>	19 (5043-5276)	87	11 (4282-4516)	99	10 (4664-4897)	99

219 ¹If no homologous region is found for any amino acid sequence or gene by using the
 220 sequence from *B. subtilis*, the corresponding amino acid or gene sequence was obtained from
 221 *B. licheniformis* ATCC 14580 (NC_006322.1) and homology search was performed similar
 222 to those for the genes in table S6A. ²These genes, when extracted from *B. subtilis* genome,
 223 showed no significant homology in table S6A.

224 **Table S7A: The genes involved in the sporulation in *B. subtilis* 168 and the regions of**
 225 **their homologs in *B. licheniformis* strains G-1, F1-1, and F2-1**

<i>B. subtilis</i> gene ¹	Contig, coordinates and % identity in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>bofA</i>	NSH ²	-	NSH	-	NSH	-
<i>bofC</i>	30 (348867-349322)	63	1 (1228414-1228806)	68	35 (101627-102019)	68
<i>cgeA</i>	NSH	-	NSH	-	NSH	-
<i>cgeB</i>	NSH	-	NSH	-	NSH	-
<i>cgeC</i>	NSH	-	NSH	-	NSH	-
<i>cgeD</i>	NSH	-	NSH	-	NSH	-
<i>cgeE</i>	30 (971390-972139)	49	1 (616732-617484)	48	35 (646943-647695)	48
<i>cotA</i>	12 (22497-24023)	66	30 (64813-66339)	66	29 (53165-54691)	66
<i>cotB</i>	NSH	-	NSH	-	NSH	-
<i>cotC</i>	NSH	-	NSH	-	NSH	-
<i>cotD</i>	NSH	-	NSH	-	NSH	-
<i>cotE</i>	31 (342521-343066)	91	1 (248663-249208)	91	27 (248727-249272)	91
<i>cotF</i>	15 (29361-29825)	64	7 (29566-29102)	65	14 (15493-15963)	65

<i>cotG</i>	NSH	-	NSH	-	NSH	-
<i>cotH</i>	32 (219185- 220270)	45	8 (241045- 242115)	46	48 (219985- 221055)	45
<i>cotJA</i>	NSH	-	NSH	-	NSH	-
<i>cotJB</i>	NSH	-	NSH	-	NSH	-
<i>cotJC</i>	32 (245479- 246045)	89	8 (217608- 218174)	89	48 (194158- 194724)	89
<i>cotM</i>	NSH	-	NSH	-	NSH	-
<i>cotP</i>	NSH	-	NSH	-	NSH	-
<i>cotS</i>	NSH	-	NSH	-	NSH	-
<i>cotSA</i>	NSH	-	NSH	-	NSH	-
<i>cotT</i>	NSH	-	NSH	-	NSH	-
<i>cotV</i>	NSH	-	NSH	-	NSH	-
<i>cotW</i>	NSH	-	NSH	-	NSH	-
<i>cotX</i>	NSH	-	NSH		NSH	-
<i>cotY</i>	32 (109138- 109614)	82	8 (344100- 344558)	82	48 (323683- 324141)	
<i>cotZ</i>	32 (109786- 110217)	70	8 (343473- 343898)	70	48 (323056- 323481)	
<i>coxA</i>	NSH	-	NSH	-	NSH	-
<i>csgA</i>	NSH	-	NSH	-	NSH	-
<i>jag</i>	15 (11829- 12449)	60	7 (11573- 12193)	60	14 (32872- 33492)	60
<i>kapB</i>	NSH	-	NSH	-	NSH	-

<i>kapD</i>	4 (64801-65415)	77	1 (964743-965357)	77	13 (63277-63891)	77
<i>kbaA</i>	13 (79313-79906)	73	10 (1176-1769)	74	7 (1172-1765)	74
<i>kipA</i>	8 (113843-114844)	55	17 (99641-100642)	56	12 (99577-100578)	55
<i>kipI</i>	8 (114859-115548)	67	17 (100657-101346)	67	12 (100593-101282)	67
<i>obg</i>	30 (334109-335392)	89	1 (1242358-1243641)	89	35 (86792-88075)	89
<i>phrA</i>	NSH	-	NSH	-	NSH	-
<i>phrC</i>	NSH	-	NSH	-	NSH	-
<i>phrE</i>	NSH	-	NSH	-	NSH	-
<i>phrF</i>	NSH	-	NSH	-	NSH	-
<i>phrG</i>	NSH	-	NSH	-	NSH	-
<i>phrI</i>	NSH	-	NSH	-	NSH	-
<i>phrK</i>	NSH	-	NSH	-	NSH	-
<i>rapA</i>	11 (27088-27774)	46	8 (387-1499)	48	48 (550895-551707)	50
	30 (813891-815006)	54	1 (774210-775325)	54	35 (489102-490217)	54
	32 (329446-330561)	42	8 (131188-132303)	42	48 (107741-108856)	42
	7 (5759-6868)	45	-	-	-	-

	14 (3684-4796)	36	19 (35058-36164)	37	-	-
	5 (20294-21388)	35	-	-	-	-
	31 (404884-406002)	41	-	-	-	-
	31 (350340-351455)	51	-	-	-	-
<i>rapB</i>	30 (813888-815006)	50	1 (774210-775328)	51	35 (489099-490217)	51
	14 (3687-4796)	37	-	-	36 (597-1706)	37
	31 (350340-351455)	41	8 (393-1499)	40	-	-
	32 (329446-330549)	37	8 (131200-132303)	37	48 (107753-108856)	37
	7 (5759-6862)	40	-	-	-	-
	5 (20294-21385)	38	-	-	-	-
	31 (404893-406002)	38	-	-	-	-
<i>rapC</i>	31 (350340-351455)	41	8 (390-1499)	38	48 (550877-551698)	41
	30 (813891-815006)	47	1 (774210-775325)	48	35 (489102-490217)	48

	7 (5759-6865)	39	19 (35058-36167)	33	36 (594-1706)	33
	31 (404887-406002)	37	8 (131203-132303)	37	48 (107756-108856)	37
<i>rapD</i>	4 (4814-5797)	37	15 (4804-5820)	36	13 (4800-5816)	36
<i>rapE</i>	7 (5759-6865)	47	1 (774210-775331)	47	35 (489096-490217)	47
	30 (813885-815006)	48	8 (390-1499)	48	48 (550862-551695)	41
	31 (404908-406002)	35	19 (35058-36146)	35	13 (166366-167454)	35
	31 (350331-351455)	75	-	-	48 (107756-108856)	38
<i>rapF</i>	14 (3678-4784)	33	19 (35058-36170)	34	36 (588-1694)	33
	7 (5759-6865)	35	-	-	-	-
	30 (813891-815006)	38	-	-	-	-
	31 (404887-406002)	36	8 (390-1499)	37	-	-
	31 (350340-351455)	45	1 (774210-775325)	45	35 (489102-490217)	45

	5 (20285-21394)	34	8 (131203-132303)	35	-	-
<i>rapG</i>	12 (102920-103969)	42	30 (138738-139736)	42	29 (127279-128277)	42
	32 (253781-254869)	52	8 (206714-207805)	51	48 (183267-184358)	51
<i>rapH</i>	7 (5777-6868)	41	1 (774228-775337)	44	35 (489090-490199)	44
	30 (813879-814988)	45	-	-	-	-
	31 (1-522)	68	-	-	48 (550877-551707)	53
	31 (350340-351446)	40	-	-	-	-
<i>rapI</i>	31 (404860-406005)	45	8 (131194-132306)	42	36 (597-1703)	45
	5 (20279-21385)	45	19 (35052-36161)	44	13 (166360-167469)	44
	4 (132799-133881)	34	1 (899341-900423)	34	13 (128214-129296)	34
	14 (3687-4793)	45	1 (774225-775328)	41	35 (489099-490202)	41
	31 (350355-	36	-	-	-	-

	351452)					
	7 (5762-6868)	33	8 (387-1496)	34	-	-
<i>rapJ</i>	30 (813879-814979)	47	1 (774237-775337)	47	35 (489090-490190)	47
	31 (404884-405978)	40	8 (131191-132279)	41	48 (107744-108832)	41
	14 (3687-4742)	39	8 (393-1487)	38	48 (550862-551695)	39
	5 (20330-21385)	38	19 (35064-36161)	38	36 (597-1652)	38
	31 (350334-351335)	42	-	-	-	-
	7 (5771-6862)	36	-	-	-	-
	31 (329470-330558)	42	-	-	-	-
<i>rapK</i>	12 (102920-104011)	47	30 (138738-139829)	46	29 (127279-128370)	46
	32 (253775-254869)	41	8 (206714-207811)	41	48 (183267-184364)	41
<i>rsfA</i>	15 (386026-386811)	76	5 (65941-66726)	77	6 (23401-24186)	76
<i>safA</i>	30 (342308-	48	1 (1234633-	50	35 (94988-	50

	343126)		1235445)		95800)	
<i>sda</i>	NSH	-	NSH	-	NSH	-
<i>seaA</i>	30 (864117- 865010)	77	1 (723599- 724492)	76	35 (539937- 540830)	76
<i>sinI</i>	NSH	-	NSH	-	NSH	-
<i>soj</i>	15 (19418- 20176)	94	7 (19161- 19919)	94	14 (25146- 25904)	94
<i>splB</i>	31 (23046- 24071)	90	8 (590089- 591114)	90	48 (573333- 574358)	90
<i>spmA</i>	30 (826745- 827870)	88	1 (761386- 761925)	87	35 (502503- 503042)	87
<i>spmB</i>	30 (827337- 827870)	81	1 (760800- 761333)	82	35 (503095- 503628)	82
<i>spo0B</i>	30 (333498- 334064)	57	1 (1243686- 1244252)	58	35 (86181- 86747)	59
<i>spo0E</i>	NSH	-	NSH	-	NSH	-
<i>spo0J</i>	15 (20172- 21017)	82	7 (19915- 20760)	82	14 (24305- 25150)	82
<i>spo0M</i>	NSH	-	NSH	-	NSH	-
<i>spoIIAA</i>	30 (802163- 802510)	83	1 (786703- 787053)	87	35 (477375- 477725)	84
<i>spoIIAB</i>	30 (802513- 802950)	88	1 (786266- 786703)	89	35 (477725- 478162)	89

<i>spoIIB</i>	30 (323042- 324010)	48	1 (1253734- 1254699)	49	35 (75734- 76699)	49
<i>spoIID</i>	15 (448305- 449318)	70	25 (38589- 39602)	71	1 (277424- 278437)	71
<i>spoIIE</i>	2 (17538- 20024)	81	14 (35691- 38177)	82	4 (17524- 20010)	82
<i>spoIIIGA</i>	31 (164235- 165161)	69	1 (70406- 71332)	69	27 (70400- 71326)	69
<i>spoIIIAA</i>	30 (647709- 648629)	66	1 (890437- 891357)	65	35 (373455- 374375)	65
<i>spoIIIBAB</i>	30 (648626- 649093)	72	1 (889970- 890440)	74	35 (374372- 374842)	74
<i>spoIIIBAC</i>	30 (649164- 649367)	82	1 (889699- 889902)	82	35 (374910- 375113)	82
<i>spoIIIBAD</i>	30 (649383- 649775)	92	1 (889291- 889683)	92	35 (375129- 375521)	92
<i>spoIIIBAE</i>	30 (649941- 650951)	84	1 (888115- 889125)	84	35 (375687- 376697)	84
<i>spoIIIBAF</i>	30 (651017- 651643)	64	1 (887423- 888049)	63	35 (376763- 377389)	63
<i>spoIIIBAG</i>	30 (651639- 652331)	70	1 (886735- 887427)	70	35 (377385- 378077)	70
<i>spoIIIBAH</i>	30 (652338- 652967)	59	1 (886099- 886728)	60	35 (378084- 378713)	60
<i>spoIIIBE</i>	30 (140570- 140570)	56	28 (103584- 103584)	57	49 (105240- 105240)	57

	141967)		104981)		106637)	
	31 (320104- 322380)	81	1 (226251- 228524)	82	27 (226315- 228588)	82
<i>spoIIIJ</i>	15 (11062- 11775)	83	7 (10776- 11519)	83	14 (34289- 33546)	83
<i>spoIIM</i>	30 (796068- 796700)	78	1 (792516- 793148)	79	35 (471280- 471912)	79
<i>spoIIP</i>	30 (533424- 534620)	70	1 (1075344- 1076540)	71	35 (262542- 263738)	71
	-	-	-	-	35 (235384- 236370)	48
<i>spoIIQ</i>	15 (482749- 483441)	84	25 (72705- 73397)	85	1 (243625- 244317)	85
<i>spoIIR</i>	15 (430650- 431306)	64	25 (20922- 21584)	66	1 (295448- 296110)	66
<i>spoIISA</i>	32 (34688- 35428)	66	8 (417163- 417903)	66	48 (396891- 397631)	66
<i>spoIISB</i>	NSH	-	NSH	-	NSH	-
<i>spoIVA</i>	30 (869204- 870679)	95	1 (717926- 719401)	95	35 (545028- 546503)	95
<i>spoIVB</i>	30 (665138- 666346)	81	1 (872716- 873987)	80	35 (390825- 392096)	80
<i>spoIVCA</i>	NSH	-	NSH	-	NSH	-
<i>spoIVFA</i>	30 (330504- 331292)	57	1 (124653- 1247241)	57	35 (83192- 83980)	56

<i>spoIVFB</i>	30 (331288-332151)	69	1 (1245594-1246457)	70	35 (83976-84839)	70
<i>spoVAA</i>	30 (803886-804440)	63	1 (784761-785315)	62	35 (479113-479667)	62
<i>spoVAB</i>	NSH	-	NSH	-	NSH	-
<i>spoVAC</i>	30 (804935-805378)	84	1 (783823-784266)	83	35 (480162-480605)	83
<i>spoVAD</i>	30 (805397-806410)	83	1 (782803-783804)	83	35 (480624-481625)	83
<i>spoVAE</i>	30 (806418-807362)	75	1 (781839-782783)	77	35 (481645-482589)	77
<i>spoVAF</i>	30 (807337-808806)	72	1 (780395-781864)	72	35 (482564-484033)	72
	8 (168169-169578)	28	17 (153916-155325)	28	12 (153879-155288)	28
	-	-	1 (1002407-1003846)	45	35 (335233-336672)	45
<i>spoVB</i>	30 (355268-356782)	80	1 (1220939-1222453)	80	35 (107980-109494)	80
<i>spoVC</i>	2 (30529-31092)	82	1 (24635-25198)	84	4 (30503-31066)	84
<i>spoVE</i>	31 (149032-150129)	93	1 (55197-56294)	94	27 (55191-56288)	94
	33 (6384-7397)	42	30 (35020-36039)	42	29 (23372-24391)	42

<i>spoVFA</i>	31 (312196-313080)	76	1 (218341-219225)	76	27 (218405-219289)	76
<i>spoVFB</i>	31 (313098-313682)	80	1 (219243-219827)	81	27 (219307-219891)	81
<i>spoVG</i>	2 (34562-34852)	90	14 (20872-21162)	89	4 (34539-34829)	89
<i>spoVID</i>	NSH	-	NSH	-	NSH	-
<i>spoVK</i>	31 (422741-423694)	89	1 (305170-306123)	89	27 (305234-306187)	89
<i>spoVM</i>	NSH	-	NSH	-	NSH	-
<i>spoVR</i>	32 (390286-391692)	89	8 (72249-73655)	89	48 (45986-47392)	88
<i>spoVS</i>	31 (336527-336784)	84	1 (242670-242927)	84	27 (242734-242991)	84
<i>spsA</i>	NSH	-	NSH	-	NSH	-
<i>spsB</i>	NSH	-	NSH	-	NSH	-
<i>spsC</i>	NSH	-	NSH	-	NSH	-
<i>spsD</i>	NSH	-	NSH	-	NSH	-
<i>spsE</i>	NSH	-	NSH	-	NSH	-
<i>spsF</i>	NSH	-	NSH	-	NSH	-
<i>spsG</i>	NSH	-	NSH	-	NSH	-
<i>spsI</i>	15 (584464-585147)	28	25 (152042-152725)	29	1 (164298-164981)	29
<i>spsJ</i>	9 (100419-	30	3 (2162-3088)	30	9 (2288-3214)	30

	101345)					
	32 (101648- 102604)	29	5 (8525-9481)	28	6 (80643- 81599)	28
	15 (594349- 595245)	29	16 (46846- 47820)	27	8 (11175- 12149)	27
	15 (328611- 329567)	28	25 (164797- 165693)	28	1 (151336- 152232)	28
	15 (92027- 93001)	27	8 (351138- 352094)	28	48 (330737- 331693)	28
<i>spsK</i>	NSH	-	NSH	-	NSH	-
<i>spsL</i>	NSH	-	NSH	-	NSH	-
<i>sspA</i>	NSH	-	NSH	-	NSH	-
<i>sspB</i>	NSH	-	NSH	-	NSH	-
<i>sspC</i>	32 (344208- 344375)	80	8 (117377- 117544)	82	48 (93930- 94097)	82
<i>sspD</i>	NSH	-	NSH	-	NSH	-
<i>sspE</i>	NSH	-	NSH	-	NSH	-
<i>sspF</i>	NSH	-	NSH	-	NSH	-
<i>sspG</i>	NSH	-	NSH	-	NSH	-
<i>sspH</i>	NSH	-	NSH	-	NSH	-
<i>sspI</i>	NSH	-	NSH	-	NSH	-
<i>sspJ</i>	NSH	-	NSH	-	NSH	-
<i>sspK</i>	NSH	-	NSH	-	NSH	-
<i>sspL</i>	NSH	-	NSH	-	NSH	-

<i>sspM</i>	NSH	-	NSH	-	NSH	-
<i>sspN</i>	NSH	-	NSH	-	NSH	-
<i>sspO</i>	NSH	-	NSH	-	NSH	-
<i>sspP</i>	NSH	-	NSH	-	NSH	-
<i>tasA</i>	30 (627556- 628347)	71	1 (984996- 985787)	71	35 (353291- 354082)	71
<i>tgl</i>	4 (42936- 43670)	60	15 (40084- 40818)	61	13 (41168- 41902)	61
<i>tlp</i>	NSH	-	NSH	-	NSH	-
<i>usd</i>	NSH	-	NSH	-	NSH	-
<i>yaaH</i>	23 (13257- 14534)	77	13 (5189- 6466)	76	33 (5184- 6461)	77
	31 (370187- 371335)	35	1 (273629- 274777)	35	27 (274842- 273694)	35
<i>yabG</i>	2 (38384- 39250)	79	14 (16532- 17398)	79	4 (38303- 39169)	79
<i>ydhD</i>	23 (13311- 14540)	33	13 (5183- 6412)	33	33 (5178- 6407)	33
	31 (370172- 371440)	54	1 (273626- 274882)	55	27 (273691- 274947)	55
<i>yknT</i>	31 (55382- 56311)	52	8 (622391- 623332)	52	48 (605635- 606576)	52
<i>ykuD</i>	31 (40557- 41045)	75	8 (607572- 608060)	75	48 (590816- 591304)	75

<i>ykvU</i>	31 (9353-10687)	76	8 (576311-577645)	76	48 (559558-560892)	76
<i>ynzH</i>	NSH	-	NSH	-	NSH	-
<i>yobW</i>	NSH	-	NSH	-	NSH	-
<i>ypeB</i>	30 (858401-859750)	74	1 (728857-730206)	74	35 (534223-535572)	74
<i>yqfD</i>	30 (552054-553247)	71	1 (1056714-1057907)	69	35 (281175-282368)	69
<i>yqgT</i>	30 (615575-616693)	59	1 (996644-997762)	60	35 (341316-342434)	60
<i>yqjG</i>	30 (689879-690673)	66	1 (848586-849380)	66	35 (415431-416225)	66
<i>yraD</i>	31 (369576-369872)	51	1 (273018-273314)	51	27 (273083-273379)	51
<i>yraE</i>	NSH	-	NSH	-	NSH	-
<i>yraF</i>	NSH	-	NSH	-	NSH	-
<i>yraG</i>	NSH	-	NSH	-	NSH	-
<i>yrbC</i>	30 (344293-345006)	74	1 (1232745-1233458)	73	35 (96975-97688)	73
<i>ytaA</i>	NSH	-	NSH	-	NSH	-
<i>ytgP</i>	30 (115621-117237)	75	28 (80546-82162)	76	49 (82203-83819)	76
<i>ytpT</i>	31 (320974-322368)	56	1 (227118-228512)	57	27 (227182-228576)	57

	30 (140411-141958)	82	28 (103404-104972)	81	49 (105060-106628)	81
<i>yyaA</i>	15 (16901-17749)	88	7 (16644-17492)	89	14 (27573-28421)	89

226 ¹Homology for the proteins encoded by these genes were first searched with TBLASTN
227 using BLOSUM62 matrix in the contigs of three target strains, and if the region of significant
228 homology was not achieved using this matrix, BLOSUM45 was used. If the protein
229 sequences did not show homology using this approach, discontinuous megablast with
230 corresponding gene sequences as queries were used (homologous regions found in such a
231 way are shown green). ²NSH means 'no significant homology'. The contigs and coordinates
232 of the genes for which query coverage was 95% or less are coloured brown. The percentage
233 identity in black and brown fonts represents amino acid identity and that in the green
234 represents nucleotide identity.

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243 **Table S7B: The genes involved in the sporulation in *B. licheniformis* ATCC 14580 and**
 244 **the regions of their homologs in *B. licheniformis* strains G-1, F1-1, and F2-1¹**

<i>B. licheniformis</i> ATCC 14580 gene ²	Contig and coordinates in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>bofA</i>	23 (19173-19439)	98	13 (283-549)	100	33 (278-544)	100
<i>cgeA</i>	-	-	-	-	-	-
<i>cgeB</i>	-	-	-	-	-	-
<i>cgeC</i>	-	-	-	-	-	-
<i>cgeD</i>	-	-	-	-	-	-
<i>cotB</i>	-	-	-	-	-	-
<i>cotC</i>	-	-	-	-	-	-
<i>cotD</i>	30 (923998-924267)	96	1 (664326-664595)	100	35 (599833-600102)	100
<i>cotG</i>	-	-	-	-	-	-
<i>cotJA</i>	32 (246336-246569)	97	8 (217084-217317)	99	48 (193634-193867)	100
<i>cotJB</i>	32 (246067-246330)	94	8 (217323-217586)	100	48 (193873-194136)	100
<i>cotM</i>	6 (34041-34445)	90	1 (346002-346406)	100	27 (346039-346443)	100
<i>cotP</i>	-	-	-	-	-	-

<i>cotS</i>	-	-	-		-	-
<i>cotSA</i>	-	-	-		-	-
<i>cotT</i>	-	-	-		-	-
<i>cotV</i>	32 (107643- 108026)	96	8 (345723- 346106)	100	48 (325306- 325689)	100
<i>cotW</i>	NSH ³	-	8 (345276- 345671)	99	48 (324859- 325254)	99
<i>cotX</i>	32 (108499- 109002)	74	8 (344693- 345202)	100	48 (324276- 324785)	100
<i>coxA</i>	30 (343533- 344129)	97	1 (1233624- 1234220)	99	35 (96213- 96809)	99
<i>csgA</i>	19 (185854- 186102)	98	4 (171850- 172098)	100	2 (171826- 172074)	100
<i>kapB</i>	4 (64381- 64767)	95	1 (965391- 965777)	99	13 (62857- 63243)	99
<i>phrA</i>	-	-	-	-	-	-
<i>phrC</i>	-	-	-		-	-
<i>phrE</i>	-	-	-	-	-	-
<i>phrF</i>	-	-	-	-	-	-
<i>phrG</i>	Raw reads present ⁴	-	8 (207814- 207930)	100	48 (184367- 184483)	100
<i>phrI</i>	-	-	-	-	-	-
<i>phrK</i>	12 (104029- 104111)	97	30 (139847- 139977)	100	29 (128388- 128417)	100

	104151)		139969)		128510)	
<i>sda</i>	30 (517799- 517939)	100	1 (1089754- 1089894)	100	35 (249188- 249328)	100
<i>sinI</i>	30 (628824- 629000)	96	1 (984343- 984519)	100	35 (354559- 354735)	100
<i>spo0E</i>	11 (16043- 16285)	95	8 (557664- 557906)	100	48 (497148- 497390)	100
<i>spo0M</i>	-	-	-	-	-	-
<i>spoIISB</i>	32 (35434- 35607)	98	8 (416984- 417157)	99	48 (396712- 396885)	99
<i>spoIVCA</i>	NSH	-	NSH	-	NSH	-
<i>spoVAB</i>	30 (804496- 804918)	99	1 (784283- 784705)	100	35 (479723- 480145)	100
<i>spoVID</i>	30 (314531- 315301)	90	1 (1261606- 1262976)	99	35 (67415- 68173)	99
	30 (315647- 316126)	94	-	-	35 (68336- 68827)	100
<i>spoVM</i>	NSH	-	NSH	-	NSH	-
<i>spsA</i>	-	-	-	-	-	-
<i>spsB</i>	-	-	-	-	-	-
<i>spsC</i>	9 (94062- 95147)	95	3 (8363- 9469)	100	9 (8489- 9595)	100
<i>spsD</i>	-	-	-	-	-	-

<i>spsE</i>	-	-	-	-	-	-
<i>spsF</i>	-	-	-	-	-	-
<i>spsG</i>	-	-	-	-	-	-
<i>spsI</i>	-	-	-	-	-	-
<i>spsJ</i>	-	-	-	-	-	-
<i>spsK</i>	-	-	-	-	-	-
<i>spsL</i>	-	-	-	-	-	-
<i>sspA</i>	30 (168453- 168665)	100	1 (1421105- 1421317)	100	15 (4159- 4371)	100
<i>sspB</i>	32 (344181- 344384)	98	8 (117368- 117571)	100	48 (93921- 94124)	100
<i>sspC</i>	-	-	-	-	-	-
<i>sspD</i>	35 (3491- 3688)	96	8 (538255- 538452)	100	48 (477739- 477936)	100
<i>sspE</i>	9 (14226- 14390)	100	3 (88391- 88555)	100	9 (88518- 88682)	100
<i>sspF</i>	2 (37542- 37727)	96	14 (18055- 18240)	100	4 (37461- 37646)	100
<i>sspG</i>	-	-	-	-	-	-
<i>sspH</i>	30 (347509- 347687)	96	1 (1230067- 1230246)	100	35 (100187- 100366)	100
<i>sspI</i>	30 (251604- 251816)	96	1 (1339979- 1340191)	100	15 (85281- 85493)	100
<i>sspJ</i>	5 (98676- 98688)	98	19 (110107- 110126)	100	13 (241415- 241428)	100

	98816)		110247)		241555)	
<i>sspK</i>	9 (22861- 23010)	99	3 (79798- 79947)	100	9 (79925- 80074)	100
<i>sspL</i>	30 (941705- 941851)	98	1 (646852- 646998)	100	35 (617429- 617575)	100
<i>sspM</i>	NSH	-	NSH	-	NSH	-
<i>sspN</i>	6 (38718- 38861)	97	1 (350681- 350824)	100	27 (350718- 350861)	100
<i>sspO</i>	6 (34769- 34915)	95	1 (346730- 346876)	99	27 (346767- 346913)	100
<i>sspP</i>	6 (34581- 34727)	97	1 (346542- 346688)	100	27 (346579- 346725)	100
<i>tlp</i>	6 (38887- 39123)	95	1 (350850- 351086)	100	27 (350887- 351123)	100
<i>usd</i>	15 (496704- 496814)	100	25 (84981- 85091)	100	1 (231931- 232041)	100
<i>ynzH</i>	32 (296163- 296360)	98	8 (165393- 165587)	98	48 (141943- 142140)	100
<i>yobW</i>	30 (1074482- 1074895)	95	1 (521360- 521773)	100	27 (521401- 521814)	100
<i>yraE</i>	31 (369869- 370069)	94	1 (273311- 273511)	100	27 (273376- 273379)	100
<i>yraF</i>	-	-	-	-	-	-
<i>yraG</i>	4 (134680- 134680)	92	1 (898286- 898286)	100	13 (130086- 130086)	100

	134946)		898552)		130352)	
<i>ytaA</i>	-	-	-	-	-	-

245 ¹If no homologous region is found for any amino acid sequence or gene by using the
246 sequence from *B. subtilis*, the corresponding amino acid or gene sequence was obtained from
247 *B. licheniformis* ATCC 14580 (NC_006322.1). The colour codes are same as that used in the
248 above table. ²These genes, when extracted from *B. subtilis* genome, showed no significant
249 homology in table S7A. Rows with '-' in all boxes means genes were not found in *B.*
250 *licheniformis* ATCC 14580 (NC_006322.1) for further comparison with strains G-1, F1-1,
251 and F2-1. ³NSH means either no significant homology or a few raw reads (1-6) were mapped
252 with the coverage depth of 1 with the genomic region of another strain possessing this gene.
253 ⁴Raw reads from the strain were aligned to the gene of another strain with significant coverage
254 depth.

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264 **Table S8A: The genes involved in germination in *B. subtilis* 168 and the regions of their**
 265 **homologs in *B. licheniformis* strains G-1, F1-1, and F2-1**

<i>B. subtilis</i> gene ¹	Contig, coordinates and % identity in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>gerAA</i>	8 (168229-169590)	38	17 (153976-155355)	38	12 (153939-155318)	38
	5(58709-60088)	67	19 (72571-73950)	68	13 (203879-205258)	68
	30 (1091279-1092577)	44	-	-	27 (503686-504858)	46
	32 (202040-203296)	34	-	-	-	-
<i>gerAB</i>	5 (60120-61139)	61	19 (73982-75001)	61	13 (205290-206309)	61
	30 (1092684-1093676)	39	1 (502546-503538)	39	27 (502587-503579)	40
	30 (1093820-1094812)	35	1 (499093-500088)	35	27 (499136-500131)	35
	30 (1096140-1097018)	39	-	-	-	-
<i>gerAC</i>	5 (61265-62329)	47	19 (75127-76191)	47	13 (206435-207499)	47

<i>gerBA</i>	5 (58721-60094)	43	19 (72775-73956)	48	13 (203891-205264)	43
	8 (168169-169614)	38	17 (153916-155361)	37	12 (153879-155324)	37
	30 (1091171-1092637)	42	-	-	27 (503626-505083)	42
	32 (202031-203326)	34	-	-	-	-
<i>gerBB</i>	30 (1093802-1094881)	34	1 (501347-502426)	34	27 (501390-502469)	34
	30 (1092672-1093676)	35	1 (499027-500106)	34	27 (499070-500149)	34
	30 (1096122-1097120)	34	1 (502546-503556)	34	27 (502587-503597)	34
	5 (60129-61205)	33	19 (73991-75067)	33	13 (205299-206375)	32
<i>gerBC</i>	5 (61268-62320)	33	19 (75130-76182)	32	13 (206438-207490)	33
	30 (1094943-1096073)	29	-	-	-	-
<i>gerD</i>	13 (78651-79199)	74	10 (1884-2432)	74	7 (1880-2428)	73
<i>gerKA</i>	8 (168091-169725)	61	17 (153838-155472)	62	12 (153801-155435)	62
	5 (58835-)	40	19 (72697-)	41	13 (204005-)	41

	60133)		73995)		205303)	
	32 (202049- 203365)	35	-	-	27 (503626- 505065)	41
<i>gerKB</i>	8 (165828- 166850)	59	17 (151575- 152597)	59	12 (151538- 152560)	59
<i>gerKC</i>	8 (166908- 168044)	52	17 (152655- 153791)	52	12 (152618- 153791)	52
<i>gerM</i>	30 (281909- 283015)	72	1 (1305394- 1306500)	74	35 (24711- 25817)	74
<i>gerPA</i>	NSH ²	-	NSH	-	NSH	-
<i>gerPB</i>	32 (221414- 221641)	67	8 (239679- 239909)	68	48 (218619- 218843)	68
<i>gerPC</i>	32 (221684- 222283)	63	8 (239044- 239622)	62	48 (217984- 218562)	62
<i>gerPD</i>	32 (222289- 222462)	74	8 (238865- 239038)	74	48 (217805- 217978)	74
<i>gerPE</i>	NSH	-	NSH	-	NSH	-
<i>gerPF</i>	NSH	-	NSH	-	NSH	-
<i>gpr</i>	30 (532200- 533303)	76	1 (1076662- 1077765)	76	35 (261317- 262420)	77
<i>sleB</i>	30 (857507- 858380)	71	1 (730227- 731100)	71	35 (533241- 534203)	70
<i>yfkQ</i>	5 (168139- 169572)	45	17 (153895- 155319)	45	12 (153858- 155282)	45

	30 (1091228-1092652)	43	1 (503570-504994)	42	27 (503611-505035)	42
	5 (58784-60148)	38	19 (72646-74010)	39	13 (203954-205318)	39
	32 (201986-203368)	31	1 (1002428-1003711)	31	-	-
<i>yfkR</i>	8 (166920-168044)	23	17 (152724-153791)	23	12 (152687-153754)	23
<i>yfkT</i>	NSH	-	NSH	-	NSH	-
<i>ykvT</i>	31 (8565-9170)	51	8 (575510-576118)	51	48 (558757-559365)	51
<i>yndD</i>	30 (1091072-1092634)	64	1 (503588-505150)	63	27 (503629-505191)	63
	8 (168172-169605)	43	17 (153919-155352)	42	12 (153882-155315)	42
	5 (58658-60091)	42	19 (72520-73953)	42	13 (203828-205261)	41
	32 (202244-203356)	35	1 (1002398-1003822)	31	-	-
<i>yndE</i>	30 (1092720-1093751)	57	1 (502471-503502)	56	27 (502512-503543)	57
	30 (1093802-1094881)	54	1 (501347-502372)	56	27 (501390-502469)	55
	30 (1096176-1097135)	58	1 (499027-500052)	60	27 (499070-500095)	60

	5 (60186-61205)	36	19 (74048-75067)	36	13 (205356-206375)	36
<i>yndF</i>	30 (1094943-1096079)	55	1 (500149-501285)	55	27 (500192-501328)	55
	-	-	1 (550263-551429)	51	27 (550304-551470)	51

266 ¹Homology for the proteins encoded by these genes were first searched with TBLASTN
267 using BLOSUM62 matrix in the contigs of three target strains, and if the region of significant
268 homology be not achieved using this matrix, BLOSUM45 matrix was used. If the protein
269 sequences did not show homology, discontinuous megablast with corresponding gene
270 sequences as queries were used (homologous regions found in such a way are shown green).

271 ²NSH means ‘no significant homology’. The contigs and coordinates of genes for which
272 query coverage was 95% or less are coloured brown. The percentage identity in black and
273 brown fonts represents amino acid identity and that in the green represents nucleotide
274 identity.

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282 **Table S8B: The genes in *B. licheniformis* ATCC 14580 and the regions of their homologs**
 283 **in *B. licheniformis* strains G-1, F1-1, and F2-1¹**

<i>B. licheniformis</i> ATCC 14580 gene ²	Contig and coordinates in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>gerPA</i>	32 (221180-221400)	94	8 (239915-240136)	100	48 (218855-219076)	100
<i>gerPD</i>	32 (222289-222468)	88	8 (238859-239038)	88	48 (217799-217978)	88
<i>gerPE</i>	32 (222472-222850)	79	8 (238477-238855)	79	48 (217417-217795)	79
<i>gerPF</i>	32 (222907-223125)	98	8 (238202-238420)	98	48 (217142-217360)	99
<i>yfkT</i>	-	-	-	-	-	-

284 ¹If no homologous region is found for any amino acid sequence or gene by using the
 285 sequence from *B. subtilis*, the corresponding amino acid or gene sequence was obtained from
 286 *B. licheniformis* ATCC 14580 (NC_006322.1). The method of homology search and colour
 287 codes is same as that used in table S8A. ²These genes, when extracted from *B. subtilis*
 288 genome, showed no significant homology in table S8A. Rows with ‘-’ in all boxes means
 289 genes were not found in *B. licheniformis* ATCC 14580 (NC_006322.1) for further
 290 comparison with strains G-1, F1-1, and F2-1.

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292 **Table S9: Homology search results for biofilm related genes in *Bacillus licheniformis***
 293 **strains G-1, F2-1, and F1-1¹**

<i>B. licheniformis</i> ATCC 14580 gene	Contig, coordinates and % identity in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1	F2-1		
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>epsA</i>	15 (693863 to 694612)	98	25 (263311 to 264060)	100	1 (52970 to 53719)	100
<i>epsB</i>	15 (694596 to 695294)	97	25 (264044 to 264742)	99	1 (52288 to 52986)	99
<i>epsC</i>	15 (695557 to 697371)	98	25 (265006 to 266820)	99	1 (50210 to 52024)	99
<i>epsD</i>	15 (697385 to 698530)	97	25 (266834 to 267979)	100	1 (49051 to 50196)	100
<i>epsE</i>	15 (698530 to 699369)	96	25 (267979 to 268818)	100	1 (48212 to 49051)	100
<i>epsF</i>	15 (699365 to 700522)	96	25 (268814 to 269971)	100	1 (47059 to 48216)	100
<i>epsG</i>	15 (700530 to 701630)	98	25 (269979 to 271079)	100	1 (45951 to 47051)	100
<i>epsH</i>	15 (701678 to 702706)	96	25 (271142 to 272170)	99	1 (44860 to 45888)	99
<i>epsI</i>	15 (702721 to 703797)	95	25 (272185 to 273261)	100	1 (43769 to 44845)	99

<i>epsJ</i>	15 (703797 to 704813)	97	25 (273261 to 274277)	100	1 (42753 to 43769)	99
<i>epsK</i>	15 (704822 to 706351)	96	25 (274286 to 275815)	99	1 (41215 to 42744)	99
<i>epsL</i>	15 (706390 to 706989)	99	25 (275854 to 276453)	99	1 (40577 to 41176)	99
<i>epsM</i>	15 (706992 to 707615)	96	25 (276456 to 277079)	100	1 (39951 to 40574)	99
<i>epsN</i>	15 (707644 to 708786)	98	25 (277106 to 278248)	100	1 (38782 to 39924)	99
<i>epsO</i>	15 (708800 to 709774)	94	25 (278262 to 279236)	100	1 (37794 to 38768)	100
<i>yqxM</i>	30 (626174 to 626899)	92	1 (986445 to 987170)	99	35 (351908 to 352633)	99
<i>sipW</i>	30 (626899 to 627480)	96	1 (985864 to 986445)	100	35 (352633 to 353214)	100
<i>tasA</i>	30 (627556 to 628347)	99	1 (984996 to 985787)	100	35 (353291 to 354082)	100
<i>sinI</i>	30 (628824 to 629000)	96	1 (984343 to 984519)	100	35 (354559 to 354735)	100
<i>sinR</i>	30 (628458 to 628796)	99	1 (984547 to 984885)	99	35 (354193 to 354531)	99

294 ¹Query sequences for comparison were extracted from *B. licheniformis* ATCC 14580.

295 Homology for the proteins encoded by these genes were first searched with TBLASTN using

296 BLOSUM62 matrix in the contigs of three target strains, and if the region of significant

297 homology be not achieved using this matrix, BLOSUM45 matrix was used. If the protein
298 sequences did not show homology, discontinuous megablast with corresponding gene
299 sequences as queries were used (homologous regions found in such a way are shown green).
300 The percentage identity in normal black font represents amino acid identity and that in the
301 green represents nucleotide identity.

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316 **Table S10A: The genes involved in adaptation to atypical conditions in *B. subtilis* 168**
 317 **and the regions of their homologs in *B. licheniformis* strains G-1, F1-1, and F2-1**

<i>B. subtilis</i> gene ¹	Contig, coordinates and % identity in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>bsaA</i>	30 (950051-950524)	70	1 (638173-638646)	70	35 (625781-626254)	70
<i>clpC</i>	11 (20350-22269)	54	8 (561977-563893)	54	48 (501461-503377)	54
	13 (2381-4810)	96	10 (53383-55812)	96	7 (53379-55808)	96
<i>clpE</i>	11 (20359-22443)	80	8 (561983-564067)	81	48 (501467-503551)	81
	13 (2834-4765)	54	10 (53428-55359)	54	7 (53424-55355)	54
<i>clpP</i>	15 (676774-677358)	93	25 (246542-247132)	92	1 (69897-70487)	92
	15 (484379-484969)	63	25 (74336-74911)	65	1 (242111-242686)	65
<i>clpQ</i>	31 (248268-248810)	90	1 (154449-154991)	90	27 (154441-154983)	90
<i>clpX</i>	30 (301173-302432)	91	1 (1275077-1276336)	91	35 (54056-55315)	91

<i>clpY</i>	31 (248830-250230)	88	1 (155011-156411)	89	27 (155003-156403)	89
<i>csbB</i>	9 (20750-21727)	77	3 (81053-82006)	78	9 (81180-82133)	78
<i>cspB</i>	32 (431021-431216)	95	8 (32580-32775)	95	48 (6512-6707)	95
<i>cspC</i>	8 (41877-42074)	96	17 (33929-34126)	95	12 (33934-34131)	95
<i>cspD</i>	30 (944646-944842)	91	1 (643837-644033)	91	35 (620394-620590)	91
<i>cstA</i>	30 (249776-251569)	89	1 (1340226-1342019)	90	15 (83453-85246)	90
<i>ctc</i>	2 (31296-31835)	68	14 (23892-24431)	68	4 (31270-31809)	68
<i>degQ</i>	NSH ²	-	NSH	-	NSH	-
<i>degR</i>	NSH	-	NSH	-	NSH	-
<i>dnaJ</i>	30 (541971-543095)	90	1 (1066869-1067993)	89	35 (271089-272213)	89
<i>dps</i>	30 (64869-65303)	78	28 (28515-28949)	78	49 (30171-30605)	78
<i>gbsA</i>	6 (99065-100465)	32	1 (407252-408652)	32	27 (407294-408694)	32
	4 (12334-13803)	87	15 (12370-13839)	87	13 (12366-13835)	87
	-	-	17 (128370-	34	12 (128308-	33

			129725)		129663)	
	30 (1019771- 1021195)	44	5 (58382- 59788)	44	27 (567540- 568964)	44
	15 (378469- 379875)	44	1 (567499- 568923)	44	6 (30336- 31742)	44
	19 (138022- 139440)	37	4 (125627- 127045)	38	2 (125603- 127021)	38
	12 (114419- 115804)	36	30 (142898- 144283)	36	29 (131426- 132811)	36
	-	-	16 (8067- 9470)	33	8 (49522- 50925)	33
	8 (142587- 143942)	34	4 (33815- 35200)	34	2 (33796- 35181)	34
<i>gbsB</i>	4 (11108- 12316)	92	15 (11144- 12352)	91	13 (11140- 12348)	91
<i>grpE</i>	30 (539465- 539923)	78	1 (1070041- 1070499)	78	35 (268583- 269041)	78
<i>gsiB</i>	8 (81443- 81811)	92	17 (69156- 69524)	89	12 (69107- 69460)	90
<i>gspA</i>	15 (309949- 310776)	73	6 (9666- 10493)	74	6 (99709- 100536)	74
<i>hit</i>	32 (314106- 314516)	80	8 (147237- 147647)	80	48 (123790- 124200)	80
<i>htpG</i>	15 (123646- 125523)	84	16 (14338- 16215)	84	8 (42778- 44655)	84

<i>htrA</i>	5 (52032-52973)	62	19 (65894-66835)	62	13 (197202-198143)	62
	35 (48808-50100)	61	8 (453423-454709)	61	48 (433141-434427)	61
	15 (51829-52680)	49	9 (6583-7434)	48	11 (6581-7432)	48
<i>lonA</i>	30 (304493-306814)	88	1 (1270693-1273014)	89	35 (57378-59699)	88
<i>lonB</i>	30 (302621-304273)	86	1 (1273236-1274888)	86	35 (55504-57156)	86
<i>mcsA</i>	13 (739-1290)	73	10 (56903-57454)	73	7 (56899-57450)	73
<i>mcsB</i>	13 (1293-2381)	87	10 (55812-56900)	87	7 (55808-56896)	87
<i>mrgA</i>	5 (51253-51708)	64	19 (65376-65831)	63	13 (196684-197139)	63
<i>pspA</i>	33 (15301-15936)	72	30 (26461-27096)	72	29 (14813-15448)	72
<i>rsbP</i>	NSH	-	NSH	-	NSH	-
<i>rsbQ</i>	4 (61195-61935)	26	1 (968200-968940)	26	13 (59672-60412)	26
<i>rsbR</i>	8 (61457-62281)	69	17 (49304-50128)	70	12 (49300-50124)	70
<i>rsbS</i>	8 (61088-61441)	76	17 (48935-49288)	77	12 (48931-49284)	77

<i>rsbT</i>	8 (60684-61082)	85	17 (48531-48929)	85	12 (48527-48925)	85
<i>rsbU</i>	8 (59666-60670)	83	17 (47513-48517)	83	12 (47509-48513)	83
<i>rsbV</i>	NSH	-	NSH	-	NSH	-
<i>rsbW</i>	8 (58799-59278)	82	17 (46643-47125)	80	12 (46639-47121)	80
<i>rsbX</i>	8 (57449-58042)	59	17 (45293-45886)	61	12 (45289-45882)	61
<i>yacC</i>	2 (9794-10657)	85	14 (45059-45922)	84	4 (9778-10641)	84
<i>ydaG</i>	8 (104248-104667)	76	17 (90061-90480)	74	12 (89989-90408)	74
<i>yetI</i>	NSH	-	NSH	-	NSH	-
<i>yezB</i>	30 (620896-621147)	49	1 (992187-992441)	49	35 (346637-346891)	49
<i>yfiQ</i>	15 (112547-113632)	65	16 (26243-27328)	65	8 (31667-32752)	65
<i>ykoB</i>	30 (620356-621120)	35	1 (992217-992981)	36	35 (346097-346861)	36
	8 (61505-62275)	32	17 (49352-50122)	31	12 (49348-50118)	31
<i>ykrL</i>	35 (1609-2499)	80	8 (539444-540334)	81	48 (478928-479818)	81
<i>yloA</i>	31 (196669-	78	1 (102866-	77	27 (102853-	77

	198363)		104581)		104586)	
<i>yloU</i>	31 (216713- 217072)	88	1 (122909- 123268)	89	27 (122901- 123260)	89
<i>ynbA</i>	31 (423897- 424811)	87	1 (306326- 307240)	87	27 (306390- 307304)	87
<i>ynzF</i>	NSH	-	NSH	-	NSH	-
<i>yocK</i>	NSH	-	NSH	-	NSH	-
<i>yocM</i>	NSH	-	NSH	-	NSH	-
<i>yodU</i>	30 (1069447- 1069833)	52	1 (526427- 526822)	51	27 (526468- 526863)	51
<i>yojH</i>	30 (620344- 621126)	36	1 (992211- 992993)	36	35 (346085- 346867)	36
<i>yokG</i>	NSH	-	NSH	-	NSH	-
<i>ypjQ</i>	30 (956596- 957087)	87	1 (631621- 632112)	87	35 (632315- 632806)	87
<i>ypqP</i>	15 (696763- 697203)	42	25 (266212- 266652)	42	1 (50378- 50818)	42
	30 (1069822- 1070421)	37	1 (525839- 526438)	36	27 (525880- 526479)	36
<i>yqhA</i>	30 (620509- 621147)	57	1 (992190- 992798)	60	35 (346280- 340888)	60
<i>yraA</i>	9 (84283- 84792)	61	3 (18717- 19226)	61	9 (18843- 19352)	61
<i>ytvA</i>	5 (52026-	63	Raw reads	-	Raw reads	-

	53384)		present		present	
	35 (48856- 50100)	56	NSH ³	-	NSH	-
	15 (51829- 52674)	49	NSH	-	NSH	-
<i>ytxG</i>	30 (143726- 144132)	71	28 (106739- 107145)	72	49 (108395- 108801)	72
<i>ytxH</i>	NSH	-	NSH	-	NSH	-
<i>ytxJ</i>	NSH	-	NSH	-	NSH	-
<i>yutG</i>	4 (143647- 144090)	71	19 (7935- 8378)	70	13 (139243- 139686)	70
<i>yveK</i>	NSH	-	NSH	-	NSH	-
<i>yveL</i>	15 (694605- 695219)	62	25 (264059- 264667)	62	1 (52363- 52971)	62
<i>yveM</i>	15 (695581- 697353)	68	25 (265030- 266802)	68	1 (50228- 52000)	68
<i>yveN</i>	15 (697385- 698524)	66	25 (266834- 267973)	65	1 (49057- 50196)	65
<i>yveQ</i>	15 (700530- 710630)	72	25 (269979- 271079)	72	1 (45951- 47051)	72
<i>yveR</i>	15 (701678- 702703)	56	25 (271142- 272167)	55	1 (44863- 45888)	56
<i>yvfE</i>	15 (707653- 708765)	72	25 (277115- 278227)	72	1 (38803- 39915)	72

<i>yvtA</i>	5 (52026-53384)	63	19 (65888-67246)	63	13 (197196-198554)	63
	15 (51829-52674)	49	9 (6583-7428)	50	11 (6581-7426)	50
	35 (48856-50100)	27	8 (453423-454661)	56	48 (433141-434379)	56
<i>ywqC</i>	NSH	-	NSH	-	NSH	-
<i>ywqD</i>	15 (694605-695285)	58	25 (264053-264733)	57	1 (52297-52977)	57
<i>ywqE</i>	15 (519146-519868)	56	25 (103989-104711)	56	1 (212311-213033)	56
<i>ywsC</i>	15 (535488-536666)	90	25 (118669-119847)	90	1 (197176-198354)	90
<i>ywtA</i>	15 (536685-537131)	90	25 (119866-120312)	90	1 (196711-197157)	90
<i>ywtB</i>	15 (537154-538296)	67	25 (120335-121474)	67	1 (195546-196688)	67
<i>yxkI</i>	NSH	-	NSH	-	NSH	-
<i>yyxA</i>	15 (51478-52689)	66	9 (6232-7443)	67	11 (6230-7441)	67
	5 (52023-53192)	44	19 (65885-67054)	44	13 (197193-198362)	44
	35 (48796-50076)	41	8 (453447-454721)	42	48 (433165-434439)	42

318 ¹Homology for the proteins encoded by these genes were first searched with TBLASTN
319 using BLOSUM62 matrix in the contigs of three target strains, and if the region of significant
320 homology was not achieved using this matrix, BLOSUM45 matrix was used. If the protein
321 sequences did not show homology, discontinuous megablast with corresponding gene
322 sequences as queries were used (homologous regions found in such a way are shown green).
323 ²NSH means ‘no significant homology’. The contigs and coordinates of genes for which
324 query coverage was 95% or less are coloured brown. The percentage identity in normal black
325 and brown fonts represents amino acid identity and that in green represents nucleotide
326 identity. ³The gene was observed in strains F1-1 and F2-1 only after mapping their raw reads
327 with assembled contigs of strain G-1.

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338 **Table S10B: The genes involved in adaptation to atypical conditions in *B. licheniformis***
339 **ATCC 14580 and the regions of their homologs in *B. licheniformis* strains G-1, F1-1,**
340 **and F2-11**

<i>B. licheniformis</i> ATCC 14580 gene ²	Contig and coordinates in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>degQ</i>	4 (87449-87589)	100	1 (942538-942678)	99	13 (85955-86095)	99
<i>degR</i>	30 (944405-944587)	98	1 (644093-644275)	99	35 (620152-620334)	99
<i>rsbP</i>	-	-	-	-	-	-
<i>rsbV</i>	8 (59281-59604)	97	17 (47128-47451)	99	12 (47124-47447)	99
<i>yetI</i>	-	-	-	-	-	-
<i>ynzF</i>	-	-	-	-	-	-
<i>yocK</i>	30 (1022620-1023105)	68	1 (565623-566108)	96	27 (565664-566149)	96
<i>yocM</i>	-	-	-	-	-	-
<i>yokG</i>	-	-	-	-	-	-
<i>ytxH</i>	30 (144152-144568)	95	28 (107165-107581)	99	49 (108821-109237)	100
<i>ytxJ</i>	30 (144589-	96	28 (107602-	99	49 (109258-	99

	144912)		107925)		109581)	
<i>yveK</i>	15 (693863- 694612)	98	1 (263311- 264060)	100	1 (52970- 53719)	100
<i>ywqC</i>	15 (518397- 519113)	93	25 (103240- 103959)	99	1 (213063- 213782)	100
<i>yxkI</i>	-	-	-	-	-	-

341 ¹If no homologous region is found for any amino acid sequence or gene by using the
342 sequence from *B. subtilis*, the corresponding amino acid or gene sequence was obtained from
343 *B. licheniformis* ATCC 14580 (NC_006322.1). The method of homology search and colour
344 codes is same as that used in the above table. ²These genes, when extracted from *B. subtilis*
345 genome, showed no significant homology in table S10A. ³NSH means ‘no significant
346 homology’. Rows with ‘-’ in all boxes means genes were not found in *B. licheniformis* ATCC
347 14580 (NC_006322.1) for further comparison with strains G-1, F1-1, and F2-1.

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356 **Table S11A. The genes involved in antibiotic production in *B. subtilis* 168 and the**
 357 **regions of their homologs in *B. licheniformis* strains G-1, F2-1, and F1-1**

<i>B. subtilis</i> gene ¹	Contig, coordinates and % identity in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>acpK</i>	NSH ²	-	NSH	-	NSH	-
<i>alba</i>	NSH	-	NSH	-	NSH	-
<i>albB</i>	NSH	-	NSH	-	NSH	-
<i>albC</i>	NSH	-	NSH	-	NSH	-
<i>albD</i>	NSH	-	NSH	-	NSH	-
<i>albE</i>	NSH	-	NSH	-	NSH	-
<i>albF</i>	NSH	-	NSH	-	NSH	-
<i>albG</i>	NSH	-	NSH	-	NSH	-
<i>pksB</i>	NSH	-	NSH	-	NSH	-
<i>pksC</i>	NSH	-	NSH	-	NSH	-
<i>pksD</i>	NSH	-	NSH	-	NSH	-
<i>pksE</i>	NSH	-	NSH	-	NSH	-
<i>pksF</i>	NSH	-	NSH	-	NSH	-
<i>pksG</i>	NSH	-	NSH	-	NSH	-
<i>pksH</i>	NSH	-	NSH	-	NSH	-
<i>pksI</i>	NSH	-	NSH	-	NSH	-
<i>pksJ</i>	NSH	-	NSH	-	NSH	-
<i>pksL</i>	NSH	-	NSH	-	NSH	-

<i>pksM</i>	NSH	-	NSH	-	NSH	-
<i>pksN</i>	NSH	-	NSH	-	NSH	-
<i>pksR</i>	NSH	-	NSH	-	NSH	-
<i>pnbA</i>	33 (17616- 19079)	58	30 (23317- 24765)	59	29 (11669- 13117)	59
<i>ppsA</i> ³	1		4		1	
	15		11		2	
	18		17		10	
	19		25		12	
	30					
<i>ppsB</i>	1		4		1	
	15		11		2	
	18		17		10	
	19		25		12	
	30					
<i>ppsC</i>	1		4		1	
	15		11		2	
	18		17		10	
	19		25		12	
	30					
<i>ppsD</i>	1		4		1	
	15		11		2	
	18		17		10	
	19		25		12	

	30					
<i>ppsE</i>	1		4		1	
	15		11		2	
	18		17		10	
	19		25		12	
	30					
<i>sboA</i>	NSH	-	NSH	-	NSH	-
<i>sboX</i>	NSH	-	NSH	-	NSH	-
<i>sfp</i>	NSH	-	NSH	-	NSH	-
<i>srfAA</i> ⁴	1		4		1	
	15		11		2	
	18		17		10	
	19		25		12	
	30					
<i>srfAB</i>	1		4		1	
	15		11		2	
	18		17		10	
	19		25		12	
	30					
<i>srfAC</i>	1 (2566-6402)	58	4		1	
	15		11		2	
	18		17 (204596- 208432)	58	10	
	19		25		12(204567-	58

					208403)	
	30					
<i>srfAD</i>	1 (6418-7098)	63	17 (203879-204580)	63	12 (203850-204551)	63
<i>sunA</i>	NSH	-	NSH	-	NSH	-

358 ¹Homology for the proteins encoded by these genes were first searched with TBLASTN
359 using BLOSUM62 matrix in the contigs of three target strains, and if the region of significant
360 homology was not achieved using this matrix, BLOSUM45 matrix was used. If the protein
361 sequences did not show homology, discontinuous megablast with corresponding gene
362 sequences as queries were used (homologous regions found in such a way are shown green).
363 ²NSH means ‘no significant homology’. The contigs and coordinates of genes for which
364 query coverage was 95% or less are coloured brown. The percentage identity represents
365 amino acid identity. ^{3, 4} For *pps* and some *srf* genes, only the contig numbers are recorded in
366 the table for clarity because they had too many matches, which might have been partial and
367 overlapping, partial and non-overlapping or full length non-overlapping.

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375 **Table S11B. The genes involved in antibiotic production in *B. licheniformis* ATCC**
 376 **14580 and the regions of their homologs in *B. licheniformis* strains G-1, F2-1, and F1-1¹**

<i>B. licheniformis</i> ATCC 14580 gene ²	Contig and coordinates in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>acpK</i>	-	-	-	-	-	-
<i>alba</i>	-	-	-	-	-	-
<i>albB</i>	-	-	-	-	-	-
<i>albC</i>	-	-	-	-	-	-
<i>albD</i>	-	-	-	-	-	-
<i>albE</i>	-	-	-	-	-	-
<i>albF</i>	-	-	-	-	-	-
<i>albG</i>	-	-	-	-	-	-
<i>pksB</i>	-	-	-	-	-	-
<i>pksC</i>	-	-	-	-	-	-
<i>pksD</i>	-	-	-	-	-	-
<i>pksE</i>	-	-	-	-	-	-
<i>pksF</i>	-	-	-	-	-	-
<i>pksG</i>	-	-	-	-	-	-
<i>pksH</i>	-	-	-	-	-	-
<i>pksI</i>	-	-	-	-	-	-
<i>pksJ</i>	-	-	-	-	-	-
<i>pksL</i>	-	-	-	-	-	-

<i>pksM</i>	-	-	-	-	-	-
<i>pksN</i>	-	-	-	-	-	-
<i>pksR</i>	-	-	-	-	-	-
<i>pnbA</i>	-	-	-	-	-	-
<i>ppsA</i>	-	-	-	-	-	-
<i>ppsB</i>	-	-	-	-	-	-
<i>ppsC</i>	-	-	-	-	-	-
<i>ppsD</i>	-	-	-	-	-	-
<i>ppsE</i>	-	-	-	-	-	-
<i>sboA</i>	-	-	-	-	-	-
<i>sboX</i>	-	-	-	-	-	-
<i>sfp</i>	1 (9618- 10295)	96	17 (200705- 201382)	100	12 (200676- 201353)	100
<i>srfAA</i>	-	-	-	-	-	-
<i>srfAB</i>	-	-	-	-	-	-
<i>srfAC</i>	-	-	-	-	-	-
<i>srfAD</i>	-	-	-	-	-	-
<i>sunA</i>	-	-	-	-	-	-

377 ¹If no homologous region is found for any amino acid sequence or gene by using the
378 sequence from *B. subtilis*, the corresponding amino acid or gene sequence was obtained from
379 *B. licheniformis* ATCC 14580 (NC_006322.1). The colour codes are same as that used in the
380 above table. ²These genes, when extracted from *B. subtilis* genome, showed no significant
381 homology in table S11A. Rows with '-' in all boxes means genes were not found in *B.*
382 *licheniformis* ATCC 14580 (NC_006322.1) for further comparison with strains G-1, F1-1,
383 and F2-1.

384 **Table S12A: The genes involved in detoxification in *B. subtilis* 168 and the regions of**
 385 **their homologs in *B. licheniformis* strains G-1, F1-1, and F2-1**

<i>B. subtilis</i> gene ¹	Contig, coordinates and % identity in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>aadK</i>	19 (192401-193189)	51	4 (184753-185541)	50	2 (184729-185538)	49
<i>ahpC</i>	15 (78931-79491)	92	9 (28341-28901)	91	11 (28341-28901)	91
<i>ahpF</i>	15 (77388-78914)	91	9 (26798-28324)	92	9 (26798-28324)	92
<i>arsC</i>	18 (34769-35185)	86	1 (430292-430708)	87	27(430334-430750)	87
<i>bmrU</i>	30 (681736-682617)	60	1 (856664-857545)	60	35 (407266-408147)	60
<i>cah</i>	19 (37227-38174)	77	4 (27855-28802)	77	2 (27836-28783)	77
<i>cypA</i>	12 (134522-135667)	36	30 (159237-160382)	36	29 (147685-148830)	36
	12 (52329-53384)	36	30 (94118-95173)	37	29 (82470-83525)	37
	30 (1107296-1108165)	39	1 (488029-488904)	40	27 (488071-488946)	40

	30 (440503-441735)	76	1 (1144990-1146222)	75	35 (184245-185477)	75
<i>cypX</i>	15 (767314-768522)	77	19 (156596-157807)	77	13 (287904-289115)	77
<i>katA</i>	15 (260933-262384)	87	6 (57494-58945)	86	6 (147548-148999)	86
	15 (262620-264056)	50	6 (55820-57268)	49	6 (145874-147322)	49
	15 (191719-193188)	44	6 (148884-150353)	44	8 (113029-114498)	44
<i>katE</i>	15 (191638-193710)	78	6 (148362-150434)	78	8 (112948-115020)	78
	15 (260939-262363)	44	6 (57515-58939)	44	6 (147569-148993)	44
	15 (262569-264086)	40	6(55790-57313)	40	6 (145844-147367)	40
<i>katX</i>	15 (262554-264164)	75	6 (55712-57295)	77	6 (145766-147349)	77
	15 (260954-262375)	51	6 (57503-58924)	51	6 (147557-148978)	51
	15 (191722-193164)	41	6 (148908-150350)	42	8 (113032-114474)	42
<i>ksgA</i>	2 (39413-40288)	85	14 (15494-16369)	85	4 (39332-40207)	85
<i>mmr</i>	32 (435420-	24	8 (27113-	24	48 (1045-	24

	436676)		28369)		2301)	
	32 (71188- 72429)	24	8 (376643- 377884)	24	48 (356242- 357483)	24
	30 (1097528- 1098745)	27	NSH ²	-	NSH	-
	30 (1101828- 1103033)	23	NSH	-	NSH	-
	15 (478397- 479275)	31	NSH	-	NSH	-
	15 (646130- 647320)	26	NSH	-	NSH	-
	15 (101682- 102917)	22	NSH	-	NSH	-
	8 (151750- 152973)	24	NSH	-	NSH	-
<i>mrpB</i>	4 (79353- 79766)	73	1 (950360- 950773)	73	13 (77860- 78273)	73
<i>mrpC</i>	4 (79769- 80107)	81	1 (950019- 950357)	74	13 (78276- 78614)	74
<i>mrpD</i>	4 (80103- 81578)	75	1 (948548- 950023)	75	13 (78610- 80085)	76
<i>mrpE</i>	4 (81587- 82060)	68	1 (948066- 948539)	68	13 (80094- 80567)	68
<i>mrpF</i>	4 (82063- 82344)	80	1 (947782- 9480630)	80	13 (80570- 80851)	80

<i>mrpG</i>	¹ NSH	-	NSH	-	NSH	-
<i>msrA</i>	30 (970057- 970587)	79	1 (618071- 618601)	80	35 (645826- 646356)	80
<i>nap</i>	5 (106919- 107812)	79	NSH	-	NSH	-
<i>padC</i>	4 (134172- 134651)	87	1 (898571- 899050)	88	13 (129588- 130067)	88
<i>penP</i>	19 (143775- 144659)	53	4 (131378- 132262)	54	2 (131354- 132238)	54
<i>pksS</i>	12 (134531- 135589)	36	1 (487876- 488883)	34	27 (487918- 488925)	34
	12 (52284- 53375)	34	30 (94073- 95164)	34	29 (82425- 83516)	34
	30 (440566- 441630)	45	1 (1145098- 1146159)	44	35 (184308- 185369)	45
	30 (1107311- 1108318)	35	30 (159246- 160289)	35	29 (147694- 148737)	35
<i>sodA</i>	30 (589195- 589800)	88	1 (1017689- 1018294)	88	35 (320786- 321391)	88
<i>sodF</i>	30 (1014366- 1015196)	68	1 (573598- 574440)	66	27 (573639- 574481)	66
<i>tetL</i>	NSH	-	NSH	-	NSH	-
<i>thdF</i>	15 (12788- 14164)	88	7 (12531- 13907)	88	14 (31158- 32534)	88
<i>tmrB</i>	NSH	-	NSH	-	NSH	-

<i>tpx</i>	30 (175068-175568)	86	1 (1412005-1412505)	86	15 (12969-13469)	86
<i>yaaD</i>	23 (4333-5214)	96	13 (14504-15385)	96	33 (14498-15379)	96
<i>yaaJ</i>	23 (15235-15672)	86	13 (4044-4487)	86	33 (4039-4482)	86
<i>yaaN</i>	2 (53377-54528)	69	14 (1251-2402)	70	4 (53299-54450)	70
<i>ybbE</i>	19 (218310-219614)	62	4 (207338-208660)	62	2 (207339-208661)	62
<i>ybfK</i>	5 (106934-107776)	60	NSH	-	NSH	-
<i>ybfO</i>	19 (193771-194823)	27	NSH	-	NSH	-
<i>ybxI</i>	19 (146534-147226)	36	4 (134054-134881)	36	2 (134030-134857)	36
<i>ycbJ</i>	19 (121339-122241)	60	4 (112310-113215)	61	2 (112292-113197)	62
<i>ycbR</i>	NSH	-	NSH	-	NSH	-
<i>yceC</i>	19 (62701-63297)	73	4 (54623-55219)	73	2 (54604-55200)	73
<i>yceD</i>	19 (62089-62667)	81	4 (54010-54588)	81	2 (53991-54569)	81
	19 (61431-62006)	64	4 (53356-53931)	65	2 (53337-53912)	65

<i>yceE</i>	19 (61431-62006)	89	4 (53356-53931)	90	2 (53337-53912)	90
	19 (62092-62667)	65	4 (54013-54588)	66	2 (53994-54569)	66
<i>yceF</i>	19 (60592-61362)	85	4 (52517-53287)	85	2 (52498-53268)	85
<i>yceH</i>	19 (56232-57317)	82	4 (48161-49246)	83	2 (48142-49227)	83
<i>ycsF</i>	8 (117697-118452)	78	17 (103493-104248)	78	12 (103429-104184)	78
<i>ydbD</i>	6 (15039-15851)	69	1 (326587-327399)	70	27 (326630-327442)	70
	15 (492211-493014)	77	25 (80488-81291)	79	1 (235731-236534)	79
<i>yddN</i>	15 (722037-723011)	41	25 (291338-292312)	41	1 (24718-25692)	41
	19 (70845-71822)	34	4 (62765-63742)	33	2 (62746-63723)	33
<i>ydfB</i>	NSH	-	NSH	-	NSH	-
<i>ydhE</i>	8 (85495-86634)	34	17 (73206-74345)	33	12 (73134-74273)	33
	9 (64768-65907)	69	3 (37651-38787)	69	9 (37778-38914)	69
<i>ydhU</i>	6 (310-762)	91	NSH	-	NSH	-
<i>ydjP</i>	Raw reads		1 (555747-	28	27 (555788-	28

	present ³		556514)		556555)	
	NSH	-	1 (968200- 968955)	22	NSH	-
<i>yerP</i>	12 (83053- 86262)	86	30 (124879- 128046)	87	29 (113232- 116399)	87
<i>yetM</i>	NSH	-	NSH	-	NSH	-
<i>yetO</i>	30 (404902- 408078)	63	1 (1169716- 1172892)	62	35 (157555- 160731)	62
	32 (78534- 80165)	31	8 (368914- 370545)	31	48 (348513- 350144)	31
<i>yflM</i>	12 (153509- 154501)	74	30 (174058- 175050)	73	29 (162506- 163498)	73
<i>yfnC</i>	NSH	-	NSH	-	NSH	-
<i>ygaF</i>	9 (2442-2909)	85	3 (99872- 100339)	85	9 (99999- 100466)	85
<i>yhdA</i>	32 (394542- 395045)	70	8 (68690- 69193)	71	48 (42633- 43136)	71
<i>yhjG</i>	31 (105768- 107240)	55	1 (11979- 13451)	55	27 (11973- 13445)	55
<i>yisY</i>	30 (1036015- 1036788)	44	1 (555750- 556523)	44	27 (555791- 556564)	44
<i>yjiB</i>	12 (52305- 53450)	63	30 (94094- 95239)	62	29 (82446- 83591)	62
	30 (1107206- 1107206)	44	1 (487855- 487855)	44	27 (487897- 487897)	44

	1108333)		488988)		489030)	
	12 (134546- 135652)	33	30 (159261- 160367)	32	29 (147709- 148815)	32
	30 (440569- 441660)	40	1 (1145068- 1146156)	40	35 (184311- 185399)	40
<i>yjiC</i>	8 (85612- 86670)	34	17 (73323- 74381)	33	12 (73251- 74309)	33
	31 (366632- 367753)	58	1 (270074- 271195)	57	27 (270139- 271260)	57
<i>yjqC</i>	6 (15039- 15851)	66	1 (327399- 326587)	66	27 (326630- 327442)	66
	15 (492211- 493014)	62	25 (80488- 81291)	65	1 (235731- 236534)	65
<i>ykfA</i>	35 (41187- 41888)	68	8 (461629- 462303)	72	48 (441347- 442021)	72
<i>ykkB</i>	NSH	-	NSH	-	NSH	-
<i>ykoY</i>	35 (5843- 6679)	76	8 (535267- 536103)	76	48 (474751- 475587)	76
<i>ykvJ</i>	11 (23966- 24622)	88	8 (565596- 566252)	88	48 (505080- 505736)	88
<i>ykzA</i>	35 (23947- 24351)	79	8 (477473- 477877)	77	48 (457184- 457588)	77
	35 (25019- 25423)	49	8 (476400- 476804)	50	48 (456111- 456515)	50
<i>ynbB</i>	31 (425091- 425091)	86	1 (307520- 307520)	86	27 (307584- 307584)	86

	426353)		308782)		308846)	
<i>yndN</i>	11 (15092- 15505)	62	8 (556701- 557117)	62	Raw reads present	
<i>yocD</i>	30 (1063045- 1064007)	56	8 (461398- 462291)	31	48 (441116- 442009)	31
<i>yojK</i>	8 (85480- 86676)	55	17 (73278- 74387)	57	12 (73206- 74315)	57
	9 (64843- 65949)	33	3 (37609- 38715)	33	9 (37736- 38842)	33
<i>yojM</i>	30 (1002458- 1003000)	58	1 (585797- 586339)	59	27 (585838- 586380)	59
<i>yokD</i>	NSH	-	NSH	-	NSH	-
<i>yqfP</i>	30 (577120- 578061)	90	1 (1029426- 1030367)	90	35 (308713- 309654)	90
<i>yrhJ</i>	30 (404902- 408078)	65	1 (1169716- 1172892)	65	35 (157555- 160731)	65
	32 (78534- 80150)	23	8 (368929- 370545)	30	48 (348528- 350144)	30
<i>yrpB</i>	4 (43674- 44708)	61	15 (40822- 41856)	61	13 (41906- 42940)	61
<i>ytmO</i>	15 (350732- 351721)	42	5 (30651- 31640)	41	6 (58484- 59473)	41
<i>ytnJ</i>	NSH	-	NSH	-	NSH	-
<i>yubB</i>	4 (32658- 33449)	81	15 (29811- 30602)	81	13 (30893- 31684)	81

<i>yusI</i>	5 (34614-34964)	84	19 (48751-49101)	85	13 (180059-180409)	85
<i>yvaK</i>	15 (744585-745322)	87	25 (312932-313669)	88	1 (3437-4174)	88
<i>yvbT</i>	15 (722019-723020)	84	25 (291320-292321)	83	1 (24709-25710)	83
	15 (350726-351724)	36	5 (30645-31643)	36	6 (58481-59479)	36
	19 (70845-71825)	37	4 (62765-63745)	37	2 (62746-63726)	37
<i>yvdP</i>	NSH	-	NSH	-	NSH	-
<i>ywcH</i>	15 (350732-351724)	71	5 (30651-31643)	72	6 (58481-59473)	72
	19 (70836-71825)	47	4 (62756-63745)	46	2 (62737-63726)	46
<i>ywnH</i>	15 (482067-482555)	73	25 (72024-72512)	72	1 (244511-244999)	72
<i>yxeI</i>	15 (166682-167662)	61	6 (174356-175336)	63	8 (88060-89040)	63
<i>yxeK</i>	NSH	-	NSH	-	NSH	-
<i>yyaR</i>	NSH	-	NSH	-	NSH	-

386 ¹Homology for the proteins encoded by these genes were first searched with TBLASTN
387 using BLOSUM62 matrix in the contigs of three target strains, and if the region of significant
388 homology was not achieved using this matrix, BLOSUM45 matrix was used. If the protein
389 sequences did not show homology, discontinuous megablast with corresponding gene

390 sequences as queries were used (homologous regions found in such a way are shown green).

391 ²NSH means ‘no significant homology’ or few (1-6) reads was aligned with the depth of

392 coverage 1 when the raw reads from the strain were mapped with the genomic region of

393 another strain containing the gene. The contigs and coordinates of genes for which query

394 coverage was 95% or less are coloured brown. The percentage identity in black and brown

395 fonts represents amino acid identity and that in the green represents nucleotide identity. ³Raw

396 reads were mapped to the genomic region of another strain.

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410 **Table S12B: The genes involved in detoxification in *B. licheniformis* ATCC 14580 and**
 411 **the regions of their homologs in *B. licheniformis* strains G-1, F1-1, and F2-1¹**

<i>B. licheniformis</i> ATCC 14580 Gene ²	Contig, coordinates and % identity in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>mrpG</i>	4 (82400-82702)	97	1 (947424-947726)	100	13 (80907-81209)	100
<i>tetL</i>	-	-	-	-	-	-
<i>tmrB</i>	-	-	-	-	-	-
<i>ycbR</i>	-	-	-	-	-	-
<i>ydfB</i>	30 (515811-516572)	87	1 (1091122-1091883)	99	35 (247199-247960)	99
<i>yetM</i>	-	-	-	-	-	-
<i>yfnC</i>	-	-	-	-	-	-
<i>ykkB</i>	6 (79967-80470)	95	1 (392250-392753)	100	27 (392259-392762)	100
<i>yokD</i>	-	-	-	-	-	-
<i>ytnJ</i>	-	-	-	-	-	-
<i>yvdP</i>	-	-	-	-	-	-
<i>yxeK</i>	-	-	-	-	-	-
<i>yyaR</i>	-	-	-	-	-	-

412 ¹If no homologous region is found for any amino acid sequence or gene by using the

413 sequence from *B. subtilis*, the corresponding amino acid or gene sequence was obtained from

414 *B. licheniformis* ATCC 14580 (NC_006322.1). The method of homology search and colour
415 codes is same as that used in table S12A. These genes, when extracted from *B. subtilis*
416 genome, showed no significant homology in table S12A. Rows with '-' in all boxes means
417 genes were not found in *B. licheniformis* ATCC 14580 (NC_006322.1) for further
418 comparison with strains G-1, F1-1, and F2-1.

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434 **Table S13: Selected genes involved in metabolism of carbohydrate and related**
435 **molecules in *B. subtilis* 168 and the regions of their homologs in *B. licheniformis* strains**
436 **G-1, F1-1, and F2-1**

<i>B. subtilis</i> gene ¹	Contig, coordinates and % identity in strains of <i>B. licheniformis</i> where the homologous sequence is found					
	G-1		F1-1		F2-1	
	Contig and coordinates	% identity	Contig and coordinates	% identity	Contig and coordinates	% identity
<i>abnA</i>	30 (235583-236470)	68	1 (1352689-1353573)	70	15 (71899-72783)	70
	32 (88427-89287)	72	1 (364067-364927)	73	48 (343666-344526)	72
<i>amyE</i>	NSH ²	-	NSH	-	NSH	-
<i>bglC</i>	6 (78037-79578)	76	1 (390323-391861)	77	27 (390359-391900)	77
<i>bglH</i>	19 (30802-32217)	44	6 (151201-152592)	44	8 (110790-112181)	44
	30 (698770-700140)	36	1 (839118-840488)	36	35 (424323-425693)	36
	15 (170447-171853)	87	6 (170166-171572)	87	8 (91825-93231)	87
	15 (189469-190860)	44	4 (21412-22827)	44	2 (21389-22804)	44
	NSH	-	30 (136143-137606)	54	29 (124684-126147)	54

<i>bglS</i>	30 (201004- 201669)	92	NSH	-	NSH	-
<i>csn</i>	NSH	-	NSH	-	NSH	-
<i>glgA</i>	30 (43292- 44713)	68	28 (6935- 8386)	66	49 (8591- 10042)	67
<i>lacA</i>	1 (45576- 47597)	52	17 (160995- 163028)	51	12 (160965- 162998)	51
	15 (99036- 101087)	78	16 (38749- 40794)	77	8 (18201- 20246)	77
	32 (9046- 11007)	24	8 (441599- 443560)	24	48 (421317- 423278)	24
<i>lctE</i>	19 (52437 to 53390)	80	4 (43062 to 44015)	80	2 (43043 to 43996)	80
	30 (204963 to 205889)	35	1 (1383055 to 1383981)	36	15 (41492 to 42418)	36
<i>yckE</i>	19 (30802- 32235)	86	4 (21412- 22845)	86	2 (21389- 22822)	86
	15 (189448- 190860)	49	6 (151201- 152613)	49	8 (110769- 112181)	49
	NSH	-	6 (170166- 171572)	43	8 (91825- 93231)	43
	30 (698773- 700140)	38	1 (839118- 840485)	38	35 (424326- 42693)	38
	NSH	-	30 (136158- 137606)	39	29 (124699- 126147)	39

<i>ydaM</i>	15 (149270-150529)	92	6 (193349-194563)	93	8 (68423-69682)	93
<i>ydhP</i>	15 (219606-221006)	46	6 (117919-119319)	44	8 (138372-139772)	44
	15 (170450-171844)	35	4 (21421-22845)	35	2 (21398-22822)	35
	19 (30811-32235)	35	6 (170175-171569)	35	8 (91828-93222)	35
	15 (189448-190851)	37	6 (151210-152613)	37	8 (110769-112172)	37
	30 (698764-700143)	76	1 (839115-840494)	77	35 (424317-425696)	77
	NSH	-	30 (136149-137597)	31	29 (124690-126138)	31
<i>yesZ</i>	32 (9043-11010)	69	8 (441596-443557)	70	48 (421314-423275)	70
	1 (45585-47600)	26	17 (161004-163019)	26	12 (160974-162989)	26
<i>fbp</i>	15 (70491-72437)	96	NSH	-	NSH	-

437 ¹Homology for the proteins encoded by these genes were first searched with TBLASTN
438 using BLOSUM62 matrix in the target strains, and if the region of significant homology was
439 not achieved using this matrix, BLOSUM45 matrix was used. If the protein sequences did not
440 show homology, discontinuous megablast with corresponding DNA sequences as queries
441 were used (homologous regions found in such a way are shown green). ²NSH means ‘no

442 significant homology using these matrices and algorithm'. The genes for which query
443 coverage was 95% or less are coloured brown.

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460 **Table S14: Contigs, coordinates, and completeness of phage or related regions in strains**
 461 **G-1, F2-1, and F1-1¹**

Strain	Contig	Length in Kb (coordinates within the contig)	G+C content (%)	Phage related regions	Related phage
G-1	30	18.3 (17,702-36,073)	49.16	Incomplete prophage	<i>Bacillus</i> phage SP10
	32	35.7 (33,580-69,333)	47.23	Questionable prophage	<i>Streptococcus</i> phage Cp_1
	32	34 (465,547-499,568)	44.34	Incomplete prophage	<i>Bacillus</i> phage phBC6A51
F1-1	1	13 (1,291,440- 1,304,503)	41.10	Questionable prophage	<i>Bacillus</i> phage SPBc2
	2	42 (1- 42, 012)	40.82	Questionable prophage	<i>Bacillus</i> phage phi105
	8	35.2 (380,132- 415,370)	47.09	Intact phage	<i>Streptococcus</i> phage Cp_1
	8	39.9 (487,865- 527,841)	43.31	Questionable phage	<i>Bacillus</i> phage SPP1
	24	0.34 (2,054- 2,394)	47.8	² Phage terminase large and small subunits	-
F2-1	17	30.1 (541- 30,730)	41.68	Questionable prophage	<i>Bacillus</i> phage phi105
	24	44.1 (198- 44,396)	43.67	Incomplete prophage	<i>Bacillus</i>

					phage SPP1
	48	35.3 (359,731-395,098)	46.92	Intact phage	<i>Streptococcus</i> phage Cp_1
	48	40 (519,448-559,496)	44.10	Incomplete prophage	<i>Bacillus</i> phage phBC6A51

462 ¹Data were obtained using the software called PHAST (Phage search tool); ²found using

463 BLAST

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