Strain	Sequences Analyzed	All genes		Core genes	
		% Leading	% Lagging	# Genes Leading	# Genes Lagging
B. subtilis subsp. subtilis str. 168	4176	73	27	627	132
B. subtilis BSn5	4145	74	26		
B. subtilis subsp. subtilis str. RO-NN-1	4101	71	29		
B. subtilis subsp. spizizenii TU-B-10	4297	73	27		
B. subtilis subsp. spizizenii str. W23	4062	73	27		

Supplementary Table 1. Distribution of genes between leading and lagging strand in the 5 *Bacillus subtilis* strains used in the bioinformatics analysis.

Leading strand genes			
Name	**CDS-region**	**Product**	**Length (AA)**
dnaA	410-1750	chromosome replication initiator DnaA	446
yaaA	3206-3421	RNA binding protein	71
recF	3437-4549	recombination protein F	370
yaaB	4567-4812	hypothetical protein	81
dacA	17534-18865	D-alanyl-D-alanine carboxypeptidase	443
yaaD	19062-19946	pyridoxal biosynthesis lyase PdxS	294
recR	28867-29463	recombination protein RecR	198
yaaL	29481-29705	hypothetical protein	74
yaaQ	39871-40200	hypothetical protein	109
holB	40665-41654	DNA polymerase III subunit delta'	329
yaaT	41657-42484	hypothetical protein	275
yabA	42499-42858	DNA replication intiation control protein YabA	119
yabE	48629-49942	cell wall shaping enzyme	437
veg	52763-53023	hypothetical protein	86
sspF	53183-53368	small acid-soluble spore protein	61
ipk	53516-54385	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	289
purR	54441-55298	pur operon repressor	285
spoVG	55866-56159	regulatory protein SpoVG	97
prs	57745-58698	ribose-phosphate pyrophosphokinase	317
pth	59504-60070	peptidyl-tRNA hydrolase	188
yabK	60130-60360	hypothetical protein	76
yabP	68216-68518	spore protein involved in the shaping of the spore coat	100
yabQ	68515-69150	membrane protein of the forespore	211
divIC	69168-69545	cell-division initiation protein	125
yabR	69626-70012	hypothetical protein	128
yabS	73106-73843	hypothetical protein	245
tilS	74929-76347	tRNAile lysidine synthetase	472
hprT	76344-76886	hypoxanthine-guanine phosphoribosyltransferase	180
ftsH	76984-78897	cell-division protein and general stress protein	637
coaX	79092-79868	pantothenate kinase	258
hslO	79880-80755	heat shock protein 33	291
cysK	81771-82697	cysteine synthase	308
yazB	87401-87610	transcriptional regulator	69
lysS	88727-90226	lysyl-tRNA synthetase	499
ctsR	101449-101913	transcriptional regulator	154
mcsA	101927-102484	activator of protein kinase McsB	185
mcsB	102484-103575	ATPguanido phosphotransferase	363
yacK	107476-108558	DNA integrity scanning protein DisA	360

yacL	108674-109774	hypothetical protein	366
gltX	111047-112498	glutamyl-tRNA synthetase	483
cysE	112800-113453	serine acetyltransferase	217
rlmB	115269-116018	23S rRNA methyltransferase	249
yacP	116025-116537	ribonuclease with PIN and NYN domains	170
sigH	116600-117256	RNA polymerase factor sigma-70	218
rpmG	117349-117498	50S ribosomal protein L33	49
secE	117532-117711	preprotein translocase subunit SecE	59
nusG	117890-118423	transcription antitermination protein NusG	177
rplK	118591-119016	50S ribosomal protein L11	141
rplA	119111-119809	50S ribosomal protein L1	232
rplL	120607-120978	50S ribosomal protein L7/L12	123
ybxB	121068-121673	ribosomal RNA methyltransferase	201
rpoB	121919-125500	DNA-directed RNA polymerase subunit beta	1193
rpoC	125562-129161	DNA-directed RNA polymerase subunit beta'	1199
ybxF	129340-129588	ribosomal protein L7Ae-like	82
rpsL	129702-130118	30S ribosomal protein S12	138
rpsG	130160-130630	30S ribosomal protein S7	156
fusA	130684-132762	elongation factor G	692
tufA	132882-134072	elongation factor Tu	396
rpsJ	135364-135672	30S ribosomal protein S10	102
rplC	135712-136341	50S ribosomal protein L3	209
rplD	136369-136992	50S ribosomal protein L4	207
rplW	136992-137279	50S ribosomal protein L23	95
rplB	137311-138144	50S ribosomal protein L2	277
rpsS	138202-138480	30S ribosomal protein S19	92
rplV	138497-138838	50S ribosomal protein L22	113
rpsC	138842-139498	30S ribosomal protein S3	218
rplP	139500-139934	50S ribosomal protein L16	144
rpmC	139924-140124	50S ribosomal protein L29	66
rpsQ	140147-140410	30S ribosomal protein S17	87
rplX	140857-141168	50S ribosomal protein L24	103
rplE	141195-141734	50S ribosomal protein L5	179
rpsH	141974-142372	30S ribosomal protein S8	132
rplF	142402-142941	50S ribosomal protein L6	179
rplR	142974-143336	50S ribosomal protein L18	120
rpsE	143361-143861	30S ribosomal protein S5	166
rpmD	143875-144054	50S ribosomal protein L30	59
rplO	144085-144525	50S ribosomal protein L15	146
secY	144527-145822	preprotein translocase subunit SecY	431
adk	145877-146530	adenylate kinase	217

mapA	146527-147273	methionine aminopeptidase	248
infA	147585-147803	translation initiation factor IF-1	72
rpsM	147973-148338	30S ribosomal protein S13	121
rpsK	148359-148754	30S ribosomal protein S11	131
rpoA	148931-149875	DNA-directed RNA polymerase subunit alpha	314
rplQ	149953-150315	50S ribosomal protein L17	120
cbiO	150443-151288	cobalt transporter ATP-binding subunit	281
truA	152937-153680	tRNA pseudouridine synthase A	247
rplM	153842-154279	50S ribosomal protein L13	145
rpsI	154300-154692	30S ribosomal protein S9	130
ybaK	156109-156552	alkylated deoxynucleotide triphosphohydrolase	147
kbaA	159182-159778	hypothetical protein	198
sigW	194849-195412	RNA polymerase sigma factor SigW	187
rsiW	195426-196052	anti-sigma(W) factor	208
ybbP	196213-197034	hypothetical protein	273
glmS	200277-202079	glucosamine--fructose-6-phosphate aminotransferase	600
csgA	228066-228314	sporulation-specific SASP protein	82
ybxH	228331-228522	hypothetical protein	63
ybfQ	252514-253482	hypothetical protein	322
tatAD	285775-285987	twin-arginine pre-protein translocation pathway protein	70
yceE	313396-313974	stress adaptation protein	192
opuAB	322271-323119	glycine betaine ABC transporter permease	282
aroK	340025-340585	shikimate kinase	186
ycgM	344551-345462	proline oxidase	303
ycgP	348724-349959	transcriptional regulator	411
hxlR	376032-376394	positive regulator of hxlAB expression	120
comS	390880-391020	regulator of genetic competence	46
rapC	428831-429979	response regulator aspartate phosphatase	382
phrC	429963-430085	secreted regulator of the activity of phosphatase RapC	40
yclN	432372-433322	iron-siderophore ABC transporter permease	316
yclO	433315-434262	iron-siderophore ABC transporter permease	315
ydaG	473803-474225	general stress protein	140
gsiB	494506-494877	general stress protein	123
dctP	500166-501431	C4-dicarboxylate transporter DctA	421
ydbL	504689-505024	hypothetical protein	111
ddl	508248-509312	D-alanyl-alanine synthetase A	354
cshA	511106-512641	ATP-dependent RNA helicase; cold shock	511
ndoA	518943-519293	endoribonuclease toxin	116
rsbU	521019-522026	serine phosphatase	335

cspC	559264-559464	cold-shock protein	66
rimI	642810-643265	ribosomal protein S18 alanine N-acetyltransferase	151
moaC	646582-647094	molybdenum cofactor biosynthesis protein MoaC	170
ydiH	647091-647738	redox-sensing transcriptional repressor Rex	215
tatAY	647760-647933	twin-arginine pre-protein translocation pathway protein	57
groES	649903-650187	co-chaperonin GroES	94
groEL	650234-651868	molecular chaperone GroEL	544
ydjM	679390-679761	hypothetical protein	123
guaA	692740-694281	GMP synthase	513
yebE	697538-698092	hypothetical protein	184
yebG	698092-698289	hypothetical protein	65
purE	698612-699100	phosphoribosylaminoimidazole carboxylase I	162
purB	700232-701527	adenylosuccinate lyase	431
purS	702319-702573	phosphoribosylformylglycinamidine synthase subunit PurS	84
purQ	702570-703253	phosphoribosylformylglycinamidine synthase I	227
yerC	716431-716745	hypothetical protein	104
gatC	728732-729022	aspartyl/glutamyl-tRNA amidotransferase subunit C	96
gatA	729038-730495	aspartyl/glutamyl-tRNA amidotransferase subunit A	485
gatB	730509-731939	aspartyl/glutamyl-tRNA amidotransferase subunit B	476
yerQ	736436-737347	lipid kinase	303
cotJA	755907-756155	inner spore coat protein	82
cotJC	756417-756986	inner spore coat protein	189
yesY	774138-774791	rhamnogalacturonan acetylesterase	217
lplA	779529-781037	lipoprotein	502
yfnH	798469-799233	sugar-phosphate cytidylyltransferase	254
yfmP	812140-812562	MerR family transcriptional regulator	140
yflS	829382-830818	2-oxoglutarate/malate transporter	478
citM	834383-835684	transporter of divalent metal ions/citrate complexes	433
yfjT	869273-869458	hypothetical protein	61
sspE	937900-938154	small acid-soluble spore protein	84
ygaC	938731-939261	hypothetical protein	176
perR	944487-944924	Fur family transcriptional regulator	145
rpsN	965909-966178	30S ribosomal protein S14	89
cspR	970135-970617	rRNA methylase	160
yhcC	979939-980313	hypothetical protein	124
yhcU	996643-997038	hypothetical protein	131
yhcV	997175-997597	oxidoreductase	140
plsC	1031395-1031994	1-acylglycerol-3-phosphate O-acyltransferase	199
yhdX	1038653-1038760	hypothetical protein	35
yheA	1054746-1055099	hypothetical protein	117

yhzE	1071402-1071488	hypothetical protein	28
yhaI	1072768-1073109	hypothetical protein	113
yhzF	1074381-1074572	hypothetical protein	63
ecsA	1077440-1078183	ABC transporter ATP-binding protein	247
yhjE	1121550-1122173	hypothetical protein	207
sipV	1122175-1122681	type I signal peptidase	168
yhjM	1129715-1130704	transcriptional regulator of the ntd operon; (LacI family)	329
yisL	1153265-1153621	hypothetical protein	118
yisR	1162267-1163130	AraC family transcriptional regulator	287
yitT	1188689-1189531	hypothetical protein	280
comZ	1207597-1207788	late competence gene	63
appD	1211477-1212463	oligopeptide ABC transporter ATP-binding protein	328
yjbA	1217326-1218078	nucleic acid binding protein	250
oppC	1222533-1223450	oligopeptide ABC transporter permease	305
yjbC	1226938-1227516	thiol oxidation management factor; acetyltransferase	192
spxA	1227697-1228092	transcriptional regulator Spx	131
mecA	1229068-1229724	adaptor protein	218
yjbL	1236609-1236977	phosphatase	122
rex	1298612-1299034	transcriptional repressor of the rex ndh operon	140
ndh	1299074-1300252	NADH dehydrogenase	392
exuM	1301939-1303318	Na+altronate/mannonate symporter	459
yjoB	1314453-1315724	ATPase possibly involved in protein degradation	423
rapA	1315869-1317005	response regulator aspartate phosphatase	378
xkdF	1328702-1329529	hypothetical protein	275
xkdG	1329555-1330490	capsid protein of PBSX prophage	311
dppB	1361242-1362168	dipeptide ABC transporter permease	308
ykzD	1395371-1395508	hypothetical protein	45
ykzB	1397938-1398093	hypothetical protein	51
ykoM	1398496-1398960	MarR family transcriptional regulator	154
sigI	1411892-1412647	RNA polymerase sigma factor SigI	251
spo0E	1430684-1430941	negative regulatory phosphatase acting on Spo0A-P	85
mhqR	1433199-1433636	MarR family transcriptional regulator	145
queD	1440100-1440549	6-pyruvoyl tetrahydrobiopterin synthase	149
ykzS	1448013-1448207	hypothetical protein	64
glcT	1456092-1456958	transcriptional antiterminator BglG family	288
ptsH	1459384-1459650	phosphocarrier protein HPr	88
ptsI	1459650-1461362	phosphotransferase system (PTS) enzyme I	570
kinA	1470026-1471846	sporulation-specific ATP-dependent protein histidine kinase	606
ykuJ	1484117-1484356	hypothetical protein	79
ykuK	1484466-1484984	RNAse	172

ykzF	1485118-1485315	hypothetical protein	65
dapH	1488973-1489683	tetrahydrodipicolinate N-acetyltransferase	236
ykuS	1490939-1491184	hypothetical protein	81
rok	1493787-1494362	repressor of comK	191
fruR	1507578-1508333	DeoR family transcriptional regulator	251
sipT	1511308-1511889	type I signal peptidase	193
pdhA	1528326-1529441	pyruvate dehydrogenase (E1 alpha subunit)	371
pdhB	1529445-1530422	pyruvate dehydrogenase (E1 beta subunit)	325
pdhC	1530537-1531865	branched-chain alpha-keto acid dehydrogenase subunit E2	442
pdhD	1531870-1533282	dihydrolipoamide dehydrogenase	470
ykzW	1534120-1534239	hypothetical protein	39
ykzI	1537113-1537301	hypothetical protein	62
bipA	1546121-1547959	GTPase	612
ylaH	1548016-1548333	hypothetical protein	105
ylaN	1552412-1552693	hypothetical protein	93
ctaB	1559309-1560226	protoheme IX farnesyltransferase	305
ylbD	1567651-1568049	hypothetical protein	132
ylbE	1568065-1568304	hypothetical protein	79
ylbF	1568420-1568869	regulatory protein	149
ylbG	1568924-1569196	hypothetical protein	90
ylbH	1569519-1570073	hypothetical protein	184
ylbL	1572765-1573790	degradative enzyme	341
ylbN	1575264-1575782	hypothetical protein	172
rpmF	1575804-1575983	50S ribosomal protein L32	59
ylbO	1576129-1576710	spore coat protein regulator protein YlbO	193
yllB	1580121-1580552	cell division protein MraZ	143
ftsL	1581597-1581950	cell-division protein	117
mraY	1587926-1588900	phospho-N-acetylmuramoyl-pentapeptide-transferase	324
spoVE	1590317-1591417	factor for spore cortex peptidoglycan synthesis (stage V sporulation)	366
murB	1592663-1593574	UDP-N-acetylenolpyruvoylglucosamine reductase	303
divIB	1593704-1594495	cell-division initiation protein	263
sbp	1595935-1596300	hypothetical protein	121
ftsA	1596474-1597796	cell-division protein essential fo Z-ring assembly	440
ftsZ	1597832-1598980	cell division protein FtsZ	382
sigG	1605630-1606412	sporulation sigma factor SigG	260
ylmC	1608919-1609164	hypothetical protein	81
ylmE	1610170-1610862	hypothetical protein	230
ylmG	1611321-1611593	factor involved in shape determination	90
ylmH	1611654-1612427	factor involved in shape determination, RNA-	257

		binding fold	
divIVA	1612521-1613015	cell-division initiation protein	164
lspA	1616744-1617208	lipoprotein signal peptidase	154
cysH	1630382-1631083	(phospho)adenosine phosphosulfate reductase	233
sumT	1634061-1634834	uroporphyrinogen III and precorrin-1 C-methyltransferase	257
yloC	1640720-1641595	hypothetical protein	291
ylzA	1641672-1641941	hypothetical protein	89
gmk	1641949-1642563	guanylate kinase	204
rpoZ	1642567-1642770	DNA-directed RNA polymerase subunit omega	67
prpC	1650384-1651148	phosphorylated protein phosphatase	254
yloQ	1653103-1653999	ribosome-associated GTPase	298
yloU	1656064-1656426	hypothetical protein	120
sdaAB	1658242-1658904	L-serine dehydratase subunit beta	220
ylpC	1661967-1662533	fatty acid biosynthesis transcriptional regulator	188
plsX	1662547-1663548	glycerol-3-phosphate acyltransferase PlsX	333
acpP	1665337-1665570	acyl carrier protein	77
rnc	1665710-1666459	ribonuclease III	249
ylxM	1671828-1672160	DNA-binding protein	110
ffh	1672174-1673514	signal recognition particle-like (SRP) GTPase	446
rpsP	1673620-1673892	30S ribosomal protein S16	90
ylqC	1673892-1674137	RNA binding protein	81
ylqD	1674259-1674645	hypothetical protein	128
rplS	1676033-1676389	50S ribosomal protein L19	118
sucC	1680431-1681588	succinyl-CoA synthetase subunit beta	385
sucD	1681617-1682519	succinyl-CoA synthetase subunit alpha	300
xerC	1687187-1688101	site-specific tyrosine recombinase XerC	304
clpQ	1688114-1688659	ATP-dependent protease peptidase subunit	181
codY	1690119-1690898	transcriptional repressor CodY	259
flgB	1691278-1691667	flagellar basal-body rod protein FlgB	129
flgC	1691667-1692119	flagellar basal body rod protein FlgC	150
fliE	1692130-1692450	flagellar hook-basal body protein FliE	106
fliG	1694119-1695135	flagellar motor switch protein G	338
fliJ	1697196-1697639	flagellar biosynthesis chaperone	147
ylxF	1697651-1698265	kinesin-like protein	204
ylzI	1701016-1701231	flagellar protein	71
fliL	1701228-1701650	flagellar basal body protein FliL	140
fliM	1701684-1702682	flagellar motor switch protein FliM	332
fliZ	1704211-1704870	flagella biosynthesis protein FliZ	219
fliP	1704863-1705528	flagellar biosynthesis protein FliP	221
cheW	1714855-1715325	modulation of CheA activity in response to attractants (chemotaxis)	156

cheC	1715344-1715973	signal terminating phosphatase	209
cheD	1715970-1716470	sequence specific deamidase	166
sigD	1716493-1717257	RNA polymerase sigma factor SigD	254
rpsB	1717933-1718673	30S ribosomal protein S2	246
tsf	1718775-1719656	elongation factor Ts	293
pyrH	1719802-1720524	uridylate kinase	240
frr	1720526-1721083	ribosome recycling factor	185
uppS	1721214-1721996	undecaprenyl pyrophosphate synthase	260
cdsA	1722000-1722809	phosphatidate cytidylyltransferase	269
dxr	1722871-1724022	1-deoxy-D-xylulose 5-phosphate reductoisomerase	383
rseP	1724029-1725297	inner membrane zinc metalloprotease	422
ylxS	1731776-1732246	hypothetical protein	156
nusA	1732281-1733396	transcription elongation factor NusA	371
ylxR	1733410-1733685	RNA binding protein; new fold	91
ylxQ	1733687-1733989	hypothetical protein	100
infB	1734009-1736159	translation initiation factor IF-2	716
ylxP	1736156-1736434	hypothetical protein	92
rbfA	1736451-1736804	ribosome-binding factor A	117
rpsO	1738941-1739210	30S ribosomal protein S15	89
spoVFA	1744367-1745260	dipicolinate synthase subunit A	297
asd	1745991-1747031	aspartate-semialdehyde dehydrogenase	346
rnjB	1749418-1751085	ribonuclease J2	555
ymfJ	1760464-1760721	hypothetical protein	85
recA	1764645-1765691	recombinase A	348
ymdA	1767310-1768872	phosphodiesterase	520
spoVS	1769935-1770195	stage V sporulation protein	86
ymcB	1772843-1774372	(dimethylallyl)adenosine tRNA methylthiotransferase	509
ymcA	1774374-1774805	master regulator for biofilm formation	143
hfq	1867373-1867594	RNA-binding protein Hfq	73
ymzA	1868144-1868374	hypothetical protein	76
nrdI	1868617-1869009	ribonucleotide reductase stimulatory protein	130
spoVK	1874203-1875171	mother cell sporulation ATPase	322
glnR	1877959-1878366	nitrogen metabolism transcriptional regulator	135
glnA	1878425-1879759	glutamine synthetase	444
xylA	1891908-1893245	xylose isomerase	445
yneF	1922549-1922767	hypothetical protein	72
yneJ	1924471-1924962	hypothetical protein	163
ynzL	1930074-1930199	hypothetical protein	41
sspN	1930264-1930410	acid-soluble spore protein N	48
gltC	2014779-2015681	LysR family transcriptional regulator	300

yocJ	2096350-2096976	azoreductase	208
yozO	2099446-2099790	hypothetical protein	114
yojG	2121641-2122306	deacetylase	221
yoyC	2122672-2122950	hypothetical protein	92
yodJ	2134566-2135387	D-alanyl-D-alanine carboxypeptidase	273
deoD	2135470-2136171	purine nucleoside phosphorylase	233
yozD	2137602-2137778	hypothetical protein	58
yodN	2138037-2138717	hypothetical protein	226
ypmP	2292432-2292683	hypothetical protein	83
ilvA	2292769-2294037	threonine dehydratase	422
ypeQ	2308792-2308974	hypothetical protein	60
ypzF	2311986-2312132	hypothetical protein	48
ypsB	2331779-2332075	cell division protein GpsB	98
cotD	2332784-2333011	spore coat protein	75
asnC	2346224-2347516	asparaginyl-tRNA synthetase	430
ypmB	2348864-2349349	hypothetical protein	161
panD	2352592-2352975	aspartate alpha-decarboxylase	127
panB	2353839-2354672	3-methyl-2-oxobutanoate hydroxymethyltransferase	277
mgsA	2358911-2359324	methylglyoxal synthase	137
ypjD	2360155-2360490	nucleotide phosphohydrolase	111
qcrB	2363913-2364587	cytochrome b6	224
qcrA	2364589-2365092	menaquinolcytochrome c oxidoreductase iron-sulfur subunit	167
ndk	2381354-2381803	nucleoside diphosphate kinase	149
hepT	2381919-2382965	heptaprenyl diphosphate synthase component II	348
ubiE	2382907-2383608	ubiquinone/menaquinone biosynthesis methyltransferase	233
hepS	2383615-2384370	heptaprenyl diphosphate synthase component I	251
mtrB	2384534-2384761	transcription attenuation protein MtrB	75
folE	2384783-2385355	GTP cyclohydrolase I	190
hbs	2385543-2385821	non-specific DNA-binding protein HBsu; signal recognition particle-like (SRP) component	92
spoIVA	2386195-2387673	morphogenetic stage IV sporulation protein	492
yphE	2388610-2388813	hypothetical protein	67
rpsA	2394664-2395812	30S ribosomal protein S1	382
ypfB	2396798-2396974	hypothetical protein	58
gudB	2402067-2403350	cryptic glutamate dehydrogenase	427
ypbH	2403506-2404090	adaptor protein	194
sigX	2414627-2415211	RNA polymerase sigma factor SigX	194
resA	2420804-2421343	thiol-disulfide oxidoreductase	179
ypuI	2424654-2425193	hypothetical protein	179
scpA	2425831-2426586	segregation and condensation protein A	251

ypzK	2427405-2427779	acetyltransferase	124
ribH	2427892-2428356	6,7-dimethyl-8-ribityllumazine synthase	154
ribE	2429600-2430247	riboflavin synthase subunit alpha	215
ypuD	2431737-2432081	hypothetical protein	114
sigF	2443429-2444196	sporulation sigma factor SigF	255
spoIIAA	2444645-2444998	anti-anti-sigma factor (antagonist of SpoIIAB)	117
yqzK	2449489-2449716	hypothetical protein	75
ansA	2455819-2456808	exported L-asparaginase	329
yqkB	2461873-2462196	hypothetical protein	107
yqjI	2480750-2482159	6-phosphogluconate dehydrogenase	469
artP	2492029-2492796	High affinity arginine ABC transporter binding lipoprotein	255
spo0A	2518023-2518826	response regulator	267
xseB	2526669-2526923	exodeoxyribonuclease VII small subunit	84
folD	2528404-2529255	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase	283
nusB	2529267-2529662	transcription antitermination protein NusB	131
yqhY	2529926-2530333	hypothetical protein	135
accC	2530354-2531706	acetyl-CoA carboxylase biotin carboxylase subunit	450
accB	2531718-2532197	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	159
spoIIIAG	2533010-2533699	stage III sporulation engulfment assembly protein	229
spoIIIAF	2533692-2534312	stage III sporulation protein	206
spoIIIAD	2535544-2535945	stage III sporulation protein	133
spoIIIAC	2535952-2536158	stage III sporulation protein	68
efp	2538115-2538672	elongation factor P	185
yqhO	2542439-2543314	hypothetical protein	291
mntR	2543440-2543868	manganese transport transcriptional regulator	142
mgsR	2564026-2564406	transcriptional regulator of stress	126
pstS	2580715-2581617	phosphate ABC transporter binding lipoprotein	300
sodA	2585434-2586042	superoxide dismutase	202
sigA	2600214-2601329	RNA polymerase sigma factor RpoD	371
dnaG	2601528-2603339	DNA primase	603
yqxD	2603373-2603867	hypothetical protein	164
yqfL	2604121-2604933	hypothetical protein	270
ccpN	2604959-2605597	negative regulator of gluconeogenesis	212
yqzL	2609750-2609893	hypothetical protein	47
era	2610041-2610946	GTP-binding protein Era	301
cdd	2610927-2611337	cytidine/deoxycytidine deaminase	136
phoH	2614496-2615455	phosphate starvation-induced protein	319
yqfD	2615452-2616648	stage IV sporulation protein	398

yqfC	2616667-2616948	hypothetical protein	93
yqeY	2619910-2620356	hypothetical protein	148
rpsU	2620371-2620544	30S ribosomal protein S21	57
yqeU	2623032-2623802	16S ribosomal RNA methyltransferase RsmE	256
dnaK	2626112-2627947	molecular chaperone DnaK	611
grpE	2627971-2628534	heat shock protein GrpE	187
hrcA	2628606-2629637	heat-inducible transcription repressor	343
holA	2636096-2637139	DNA polymerase III subunit delta	347
nadD	2643765-2644334	nicotinic acid mononucleotide adenylyltransferase	189
yqeI	2644346-2644636	RNA-binding protein	96
yqeG	2646594-2647112	hydrolase	172
levD	2762395-2762835	phosphotransferase system (PTS) fructose-specific enzyme IIA component	146
yrzI	2778923-2779072	hypothetical protein	49
greA	2791494-2791967	transcription elongation factor GreA	157
udk	2792218-2792853	uridine kinase	211
yrrN	2794147-2795076	hydrolase	309
yrrM	2795082-2795735	acyl-CoA O-methyltransferase	217
yrzB	2797100-2797381	hypothetical protein	93
yrrK	2797399-2797815	Holliday junction resolvase-like protein	138
yrzL	2797823-2798089	hypothetical protein	88
yrzQ	2805348-2805479	hypothetical protein	43
yrzR	2805501-2805692	hypothetical protein	63
yrrD	2805704-2806228	hypothetical protein	174
mnmA	2809413-2810528	tRNA-specific 2-thiouridylase MnmA	371
cymR	2811717-2812133	transcriptional regulator of cysteine biosynthesis	138
yrzK	2818191-2818361	hypothetical protein	56
yrvI	2820077-2820475	D-tyrosyl-tRNA(Tyr) deacylase	132
relA	2820529-2822733	GTP pyrophosphokinase	734
apt	2822901-2823413	adenine phosphoribosyltransferase	170
comN	2829152-2829448	post-transcriptional regulator	98
yajC	2832424-2832690	preprotein translocase subunit YajC	88
yrzS	2834957-2835157	hypothetical protein	66
pheB	2852157-2852600	hypothetical protein	147
obgE	2852661-2853947	GTPase ObgE	428
spo0B	2853981-2854559	sporulation initiation phosphotransferase	192
rpmA	2854880-2855164	50S ribosomal protein L27	94
rplU	2855518-2855826	50S ribosomal protein L21	102
minD	2857776-2858582	ATPase activator of MinC	268
minC	2858584-2859264	septum formation inhibitor	226
mreC	2859832-2860704	rod shape-determining protein MreC	290

mreB	2860735-2861748	rod shape-determining protein MreB	337
maf	2862572-2863141	Maf-like protein	189
hemX	2876928-2877758	negative effector of the concentration of glutamyl-tRNA reductase HemA	276
hemA	2877766-2879133	glutamyl-tRNA reductase	455
clpX	2884781-2886043	ATP-dependent protease ATP-binding subunit ClpX	420
tig	2886315-2887589	trigger factor	424
leuC	2889552-2890970	isopropylmalate isomerase large subunit	472
ysmB	2904043-2904483	MarR family transcriptional regulator	146
gerE	2904727-2904951	transcriptional regulator	74
sdhA	2906335-2908095	succinate dehydrogenase flavoprotein subunit	586
sdhC	2908129-2908737	succinate dehydrogenase (cytochrome b558 subunit)	202
etfB	2916378-2917151	electron transfer flavoprotein subunit beta	257
yshE	2920517-2920921	hypothetical protein	134
yshB	2925100-2925633	hypothetical protein	177
yshA	2925640-2925897	cell division protein ZapA	85
pheS	2929438-2930472	phenylalanyl-tRNA synthetase subunit alpha	344
araQ	2939851-2940696	arabinose/arabinan permease	281
araP	2940697-2941638	arabinose/arabinan permease	313
rplT	2952224-2952583	50S ribosomal protein L20	119
rpmI	2952615-2952815	50S ribosomal protein L35	66
infC	2952828-2953349	translation initiation factor IF-3	173
thrS	2959257-2961188	threonyl-tRNA synthetase	643
nrdR	2965681-2966139	transcriptional regulator NrdR	152
speD	2966413-2966793	S-adenosylmethionine decarboxylase	126
ytaF	2971531-2972163	hypothetical protein	210
phoP	2977800-2978522	two-component response regulator	240
mdh	2978734-2979672	malate dehydrogenase	312
icd	2979716-2980987	isocitrate dehydrogenase	423
citZ	2981151-2982269	citrate synthase	372
pfkA	2986588-2987547	6-phosphofructokinase	319
accA	2987731-2988708	acetyl-CoA carboxylase carboxyltransferase subunit alpha	325
accD	2988693-2989565	acetyl-CoA carboxylase subunit beta	290
nrnA	2995908-2996849	3',5'-bisphosphate nucleotidase	313
fabG	3010661-3011428	3-ketoacyl-ACP reductase	255
argG	3013133-3014344	argininosuccinate synthase	403
ackA	3015111-3016298	acetate kinase	395
tpx	3017696-3018199	thiol peroxidase	167
ytfJ	3018309-3018764	hypothetical protein	151
sspA	3025445-3025654	small acid-soluble spore protein	69
yttP	3032417-3033040	transcriptional regulator	207

ytzK	3038060-3038203	hypothetical protein	47
ccpA	3044165-3045169	Lacl family transcriptional regulator	334
aroA	3045445-3046521	bifunctional 3-deoxy-7-phosphoheptulonate synthase/chorismate mutase	358
ytpQ	3053364-3054173	hypothetical protein	269
ytmP	3060674-3061288	kinase/phosphotransferase	204
yteP	3082260-3083225	permease	321
ytcP	3087321-3088181	ABC transporter permease	286
ytwF	3102201-3102512	sulfur transferase	103
leuS	3102629-3105043	leucyl-tRNA synthetase	804
ytvB	3105470-3105799	hypothetical protein	109
ytrA	3118847-3119239	GntR family transcriptional regulator	130
asnB	3125777-3127675	asparagine synthetase	632
metK	3127825-3129027	S-adenosylmethionine synthetase	400
ytmB	3131152-3131394	hypothetical protein	80
ytkD	3134983-3135459	nucleoside triphosphate phosphohydrolase	158
ytkC	3135668-3136072	autolytic amidase	134
dps	3136238-3136675	DNA-protecting protein, ferritin	145
luxS	3137495-3137968	S-ribosylhomocysteinase	157
rpmE2	3138978-3139226	50S ribosomal protein L31	82
yubF	3190462-3190725	hypothetical protein	87
yugP	3217496-3218173	metal-dependent protease/peptidase	225
yugI	3225178-3225570	general stress protein 13	130
yugG	3226933-3227433	Lrp/AsnC family transcriptional regulator	166
yufK	3236422-3236979	hypothetical protein	185
comA	3252804-3253448	two-component response regulator	214
degQ	3257092-3257232	pleiotropic regulator	46
pncA	3260891-3261442	nicotinamidase	183
yuzF	3264265-3264501	hypothetical protein	78
yukD	3275832-3276071	bacteriocin	79
yukE	3276141-3276434	hypothetical protein	97
ybdZ	3280294-3280503	hypothetical protein	69
yuiB	3299344-3299664	hypothetical protein	106
yuiA	3299718-3299861	hypothetical protein	47
yuzB	3308368-3308604	hypothetical protein	78
yuzD	3309960-3310286	sulfur oxido-reduction management enzyme	108
yutD	3319286-3319561	hypothetical protein	91
lipA	3320324-3321220	lipoyl synthase	298
yunB	3322463-3323227	spore formation protein	254
yunF	3325917-3326765	hypothetical protein	282
frlM	3347919-3348821	fructose-amino acid permease	300

frlN	3348825-3349703	fructose-amino acid permease	292
frlB	3351110-3352096	fructoselysine-6-P-deglycase	328
sufB	3355593-3356990	FeS cluster formation protein	465
iscU	3357011-3357454	iron-sulfur cluster assembly scaffold protein	147
sufS	3357444-3358664	cysteine desulfurase	406
sufD	3358664-3359977	FeS assembly protein SufD	437
sufC	3359995-3360780	sulfur mobilizing ABC protein, ATPase	261
metN	3361767-3362591	methionine ABC transporter, substrate binding lipoprotein	274
metQ	3363266-3364291	methionine ABC transporter ATP-binding protein	341
yusG	3365831-3366067	hypothetical protein	78
yusH	3366123-3366506	glycine cleavage system protein H	127
yusI	3366573-3366929	oxidoreductase	118
yusU	3378800-3379087	hypothetical protein	95
yusV	3379112-3379939	iron(III)-siderophore transporter ATP binding protein	275
yuzO	3387781-3387945	hypothetical protein	54
fumC	3389024-3390412	fumarate hydratase	462
yvzF	3390479-3390664	hypothetical protein	61
sspJ	3421465-3421605	small acid-soluble spore protein	46
yvaG	3449732-3450526	oxidoreductase	264
smpB	3451248-3451718	SsrA-binding protein	156
rnr	3451863-3454202	ribonuclease R	779
yvaK	3454221-3454967	carboxylesterase	248
secG	3455093-3455323	preprotein translocase subunit SecG	76
yvzC	3456282-3456515	transcriptional regulator	77
eno	3476555-3477847	phosphopyruvate hydratase	430
pgm	3477877-3479412	phosphoglyceromutase	511
tpiA	3479405-3480166	triosephosphate isomerase	253
pgk	3480197-3481381	phosphoglycerate kinase	394
gapA	3481698-3482705	glyceraldehyde-3-phosphate dehydrogenase	335
cggR	3482752-3483774	transcriptional regulator of gapA	340
epsB	3528462-3529145	protein tyrosine kinase	227
epsA	3529151-3529855	modulator of protein tyrosine kinase EpsB	234
padC	3532325-3532810	phenolic acid decarboxylase	161
crh	3569292-3569549	phosphocarrier protein Chr	85
whiA	3569573-3570523	morphogen	316
yvcK	3570546-3571499	gluconeogenesis factor	317
csbA	3615116-3615346	hypothetical protein	76
ftsX	3623938-3624828	cell-division ABC transporter	296
ftsE	3624821-3625507	cell-division ABC transporter ATP-binding protein	228
yvyD	3631003-3631572	ribosome-associated sigma 54 modulation protein	189

csrA	3636046-3636270	carbon storage regulator	74
yviF	3636264-3636695	flagellar assembly protein FliW	143
flgM	3640285-3640551	anti-sigma factor repressor of sigma(D)-dependent transcription	88
degU	3644607-3645296	two-component response regulator	229
degS	3645379-3646536	two-component sensor histidine kinase	385
pgsC	3698982-3699431	capsular polyglutamate amide ligase/translocase subunit	149
pgsB	3699446-3700627	capsular polyglutamate synthetase	393
alsD	3708799-3709566	alpha-acetolactate decarboxylase	255
ywzD	3733505-3733648	hypothetical protein	47
ssbB	3740206-3740547	single-strand DNA-binding protein	113
mbl	3747254-3748255	rod shape-determining protein Mbl	333
spoIIID	3748421-3748702	transcriptional regulator	93
usd	3748717-3748827	required for translation of spoIIID	36
murAA	3777949-3779259	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	436
ywmB	3779293-3780033	hypothetical protein	246
atpC	3781069-3781467	ATP synthase F0F1 subunit epsilon	132
atpD	3781491-3782912	ATP synthase F0F1 subunit beta	473
atpG	3782938-3783801	ATP synthase F0F1 subunit gamma	287
atpA	3783878-3785386	ATP synthase F0F1 subunit alpha	502
atpH	3785403-3785948	ATP synthase F0F1 subunit delta	181
atpF	3785945-3786457	ATP synthase F0F1 subunit B	170
atpE	3786620-3786832	ATP synthase F0F1 subunit C	70
atpB	3786878-3787612	ATP synthase F0F1 subunit A	244
atpI	3787620-3788003	ATP synthase subunit i	127
glyA	3789190-3790437	serine hydroxymethyltransferase	415
prfA	3797085-3798155	peptide chain release factor 1	356
rpmE	3803081-3803281	50S ribosomal protein L31	66
rho	3803400-3804683	transcription termination factor Rho	427
murAB	3806086-3807375	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	429
ywjH	3807754-3808392	translaldolase	212
fbaA	3808512-3809369	fructose-bisphosphate aldolase	285
ywiB	3835317-3835745	hypothetical protein	142
ywgA	3858999-3859499	hypothetical protein	166
ywfO	3859535-3860836	metal-dependent phosphohydrolase	433
ywzC	3860998-3861222	hypothetical protein	74
eutD	3865355-3866326	phosphotransacetylase	323
spsA	3892351-3893121	spore coat dTDP-glycosyltransferase	256
ywcI	3907012-3907314	hypothetical protein	100

qoxD	3914315-3914689	cytochrome aa3-600 quinol oxidase subunit IV	124
qoxC	3914691-3915305	cytochrome aa3-600 quinol oxidase subunit III	204
qoxB	3915319-3917268	cytochrome aa3-600 quinol oxidase subunit I	649
qoxA	3917296-3918261	cytochrome aa3-600 quinol oxidase subunit II	321
menA	3950726-3951661	1,4-dihydroxy-2-naphthoate octaprenyltransferase	311
licB	3961566-3961874	phosphotransferase system (PTS) lichenan-specific enzyme IIB component	102
cydB	3976791-3977807	cytochrome bd ubiquinol oxidase subunit II	338
yxzJ	4019005-4019136	hypothetical protein	43
yxeO	4058029-4058778	ABC transporter ATP-binding protein	249
yxeN	4058791-4059465	ABC transporter permease	224
yxeH	4063684-4064496	hydrolase	270
yxeC	4066607-4067005	hypothetical protein	132
yxeA	4068189-4068536	hypothetical protein	115
yxdM	4068550-4070418	cationic peptides ABC transporter permease	622
iolJ	4073081-4073953	2-deoxy-5-keto-D-gluconic acid 6-phosphate aldolase	290
iolH	4074896-4075765	sugar-phosphate epimerase/isomerase	289
iolC	4081029-4082006	2-deoxy-5-keto-D-gluconic acid kinase	325
yxaF	4107352-4107927	transcriptional regulator	191
yyzF	4134996-4135166	hypothetical protein	56
walR	4153696-4154403	two-component response regulator YycG	235
purA	4155433-4156725	adenylosuccinate synthetase	430
dnaC	4157471-4158835	replicative DNA helicase	454
yybT	4163643-4165622	phosphodiesterase	659
yybS	4165659-4166588	hypothetical protein	309
yyzH	4166815-4166964	hypothetical protein	49
rpsR	4198603-4198842	30S ribosomal protein S18	79
ssbA	4198886-4199404	single-strand DNA-binding protein	172
rpsF	4199445-4199732	30S ribosomal protein S6	95
yyzM	4203124-4203330	hypothetical protein	68
noc	4207897-4208748	DNA-binding protein Spo0J-like	283
gidB	4208870-4209589	16S rRNA methyltransferase GidB	239
gidA	4209603-4211489	tRNA uridine 5-carboxymethylaminomethyl modification protein GidA	628
trmE	4211510-4212889	tRNA modification GTPase TrmE	459
spoIIIJ	4213823-4214608	OxaA-like protein precursor	261
rnpA	4214753-4215103	ribonuclease P	116
rpmH	4215255-4215389	50S ribosomal protein L34	44

Lagging strand genes			
Name	**CDS-region**	**Product**	**Length (AA)**
abrB	44848-45138	transcriptional regulator for transition state genes	96
gerD	158515-159072	lipoprotein	185
ycbP	281769-282155	inner integral membrane protein	128
ycgQ	349996-350853	hypothetical protein	285
nasE	355412-355732	assimilatory nitrite reductase subunit	106
tcyC	409208-409951	cystine ABC transporter ATP-binding protein	247
tcyB	409965-410669	cystine ABC transporter permease	234
ycnC	437474-438352	TetR family transcriptional regulator	292
ycnE	439282-439569	hypothetical protein	95
yczJ	463496-463783	hypothetical protein	95
ydbN	506322-506501	hypothetical protein	59
ydbP	507753-508073	thioredoxin	106
ydgJ	612836-613330	MarR family transcriptional regulator	164
pbuE	625125-626291	hypoxanthine efflux transporter	388
ydiK	648742-648933	hypothetical protein	63
yflI	839077-839232	hypothetical protein	51
yflG	839735-840484	methionine aminopeptidase	249
yflE	842047-843996	exported enzyme and anion transporter	649
sspK	928112-928264	acid-soluble spore protein K	50
yfhP	934457-935440	membrane hydrolase	327
yfhS	936773-936997	hypothetical protein	74
ygaE	941168-942229	hypothetical protein	353
katA	959535-960986	vegetative catalase 1	483
ygzD	966671-966871	HTH-type transcriptional regulator	66
yhdK	1028233-1028523	negative regulator of the activity of sigma-M	96
sigM	1029577-1030068	RNA polymerase sigma factor SigM	163
yhdP	1032063-1033397	transporter or sensor	444
cueR	1033458-1033889	copper efflux transcriptional regulator	143
sspB	1050031-1050234	small acid-soluble spore protein	67
yheE	1050443-1050661	hypothetical protein	72
hpr	1073106-1073717	transcriptional regulator Hpr	203
yhaH	1073895-1074251	hypothetical protein	118
yhfH	1098120-1098260	hypothetical protein	46
yhzC	1116583-1116816	hypothetical protein	77
yhjC	1120628-1120828	hypothetical protein	66
ntdC	1126400-1127452	neotrehalosadiamine biosynthesis dehydrogenase	350
gerPF	1148494-1148721	spore germination protein	75
yjzD	1204731-1204916	hypothetical protein	61

yjbI	1234510-1234908	thiol management oxidoreductase component	132
yjoA	1313840-1314304	hypothetical protein	154
spoIISB	1348442-1348612	two-component apoptotic control system component B	56
tnrA	1397411-1397743	nitrogen sensing transcriptional regulator	110
sspD	1413800-1413994	small acid-soluble spore protein	64
motB	1433676-1434461	flagellar motor protein MotB	261
ykvS	1447662-1447847	hypothetical protein	61
ykzT	1473240-1473401	hypothetical protein	53
ykyB	1474560-1475024	hypothetical protein	154
ykpC	1516339-1516473	hypothetical protein	44
ykzG	1524791-1525000	hypothetical protein	69
def	1526195-1526749	peptide deformylase	184
slp	1533327-1533701	small peptidoglycan-associated lipoprotein	124
ylaF	1545820-1546008	hypothetical protein	62
ylaI	1548389-1548598	hypothetical protein	69
lexA	1917639-1918256	LexA repressor	205
ynzD	1922841-1923014	Spo0A-P phosphatase	57
cotM	1925655-1926047	spore coat protein	130
sspO	1926306-1926452	acid-soluble spore protein O	48
yoeD	2004262-2004492	excisionase	76
yocA	2085303-2085980	transposon-related lytic enzyme	225
yodC	2127813-2128421	oxidoreductase	202
yoyF	2137897-2138040	hypothetical protein	47
ypoP	2288194-2288619	MarR family transcriptional regulator	141
metA	2305378-2306283	homoserine O-succinyltransferase	301
cspD	2307905-2308105	cold-shock protein	66
ypdP	2309730-2310419	hypothetical protein	229
sspL	2310859-2310987	small acid-soluble spore protein	42
ypzG	2329870-2330022	hypothetical protein	50
yppF	2338582-2338770	site-specific integrase	62
sspM	2339670-2339774	small acid-soluble spore protein	34
recU	2340802-2341422	Holliday junction-specific endonuclease	206
ypzI	2393422-2393559	hypothetical protein	45
fer	2409729-2409977	ferredoxin	82
yqzJ	2483586-2483873	hypothetical protein	95
yqhP	2542047-2542442	hypothetical protein	131
sinI	2552446-2552619	antagonist of SinR	57
sinR	2552653-2552988	transcriptional regulator for post-exponential-phase response	111
yqgY	2564638-2564883	hypothetical protein	81
yqzD	2576367-2576720	hypothetical protein	117

ispG	2589123-2590256	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	377
antE	2602979-2603275	hypothetical protein	98
rpsT	2635815-2636081	30S ribosomal protein S20	88
yqzM	2637369-2637503	hypothetical protein	44
sda	2647456-2647614	chemotaxis protein CheC	52
sigV	2769850-2770350	RNA polymerase ECF(extracytoplasmic function)-type sigma factor (sigma(V))	166
yrzA	2788680-2788883	hypothetical protein	67
yslB	2909030-2909476	hypothetical protein	148
sspI	2931692-2931907	small acid-soluble spore protein SspI	71
ysdB	2951490-2951882	hypothetical protein	130
ytrI	2995067-2995597	sporulation protein	176
ytzJ	2995699-2995890	hypothetical protein	63
ytpI	2996980-2997282	hypothetical protein	100
rpsD	3035730-3036332	30S ribosomal protein S4	200
acuA	3040092-3040724	protein acetyltransferase	210
acuB	3040751-3041395	acetoin degradation regulation pathway protein	214
ytzH	3060395-3060673	hypothetical protein	92
ytzE	3072401-3072622	DeoR family transcriptional regulator	73
ytzL	3141900-3142058	hypothetical protein	52
yuzA	3224864-3225100	hypothetical protein	78
yuxJ	3232640-3233818	exporter	392
mrpB	3248996-3249427	monovalent cation/H+ antiporter subunit B	143
mrpC	3249427-3249768	monovalent cation/H+ antiporter subunit C	113
mrpF	3251724-3252008	monovalent cation/H+ antiporter subunit F	94
yutJ	3308867-3309934	NADH dehydrogenase	355
yutI	3310386-3310721	(Fe-S)-binding protein	111
yutG	3317502-3318002	phosphatidylglycerophosphatase A	166
yuzL	3372569-3372715	hypothetical protein	48
yuzM	3373743-3373988	hypothetical protein	81
yusN	3374001-3374333	hypothetical protein	110
mrgA	3383565-3384026	metalloregulation DNA-binding stress protein	153
yuxN	3388113-3388988	transcriptional regulator	291
yvfG	3513887-3514105	hypothetical protein	72
sacB	3536012-3537433	levansucrase	473
clpP	3546234-3546827	ATP-dependent Clp protease proteolytic subunit	197
yvdC	3559632-3559952	pyrophosphohydrolase	106
ywpF	3741182-3741592	hypothetical protein	136
ywoH	3749052-3749465	MarR family transcriptional regulator	137
sboA	3836058-3836189	subtilosin A	43
albB	3837682-3837843	hypothetical protein	53

ywhB	3853486-3853674	4-oxalocrotonate tautomerase	62
thiD	3900963-3901778	pyridoxal kinase	271
ywcE	3914009-3914272	protein required for proper spore morphogenesis and germination	87
ywbH	3933209-3933595	holin-like protein	128
lrgB	3933577-3934254	anti-holin factor controlling activity of murein hydrolases	225
sacY	3943667-3944509	transcriptional antiterminator	280
ywzH	3952108-3952257	hypothetical protein	49
dltB	3953783-3954970	D-alanine esterase for lipoteichoic acid and wall teichoic acid	395
dltC	3954987-3955223	D-alanine--poly(phosphoribitol) ligase subunit 2	78
ywaA	3957391-3958482	branched-chain amino acid aminotransferase	363
yxjG	3999350-4000486	methyltetrahydrofolate methyltransferase	378
yxeD	4066210-4066563	hypothetical protein	117
ahpC	4118950-4119513	alkyl hydroperoxide reductase	187
ahpF	4119527-4121056	alkyl hydroperoxide reductase	509

Supplementary Table 2. List of core *Bacillus subtilis* genes analyzed on both leading and lagging strand. Essential genes are highlighted in gray.

Strand		**# of Genes**	**Mean Pi**	**Mean dS**	**Mean dN**
Lead	Mean	2086	0.017082	0.060589	0.00549
	Standard deviation		0.008668	0.036492	0.005119
	Standard error		0.00019	0.000799	0.000112
Lag	Mean	856	0.017353	0.058889	0.006205
	Standard deviation		0.008729	0.034128	0.005741
	Standard error		0.000298	0.001166	0.000196
z value			0.7668	1.202696	3.16732
p value			0.4432	0.2291	0.0015

Supplementary Table 3. The mean values for all, non-core, genes in relation to diversity are presented. This analysis included the genes of leading and lagging strands which are mosaic in nature, i.e. at least present in two strains but not in all five (we used *B. subtilis* subsp. subtilis str. 168 as the reference genome and extracted homologs from other 4 strains with nucleotide sequence identity and length coverage values of $\geq$ 95%). The π (Pi), dS and dN values are listed for the leading and lagging strands. A statistically significant difference in dN between the two strands is detected with a $p<0.005$. Analysis of statistical significance was performed using the z-test for π, dS and dN values (see methods).

List of 34 leading strand genes under positive selection

Name	CDS-region	Product	Length (AA)
spoIIIAF	2533695-2534312	stage III sporulation protein	206
yabQ	68515-69147	membrane protein of the forespore	211
yesY	774138-774788	rhamnogalacturonan acetylesterase	217
epsB	3528465-3529145	protein tyrosine kinase	227
ywmB	3779296-3780033	hypothetical protein	246
ylmH	1611654-1612424	factor involved in shape determination,RNA-binding fold	257
sumT	1634061-1634831	uroporphyrinogen III and precorrin-1C-methyltransferase	257
uppS	1721214-1721993	undecaprenyl pyrophosphate synthase	260
xkdF	1328702-1329526	hypothetical protein	275
yloC	1640720-1641592	hypothetical protein	291
spoVFA	1744367-1745257	dipicolinate synthase subunit A	297
yybS	4165662-4166588	hypothetical protein	309
nrnA	2995911-2996849	3',5'-bisphosphate nucleotidase	313
yteP	3082263-3083225	permease	321
eutD	3865358-3866326	phosphotransacetylase	323
frlB	3351113-3352096	fructoselysine-6-P-deglycase	328
yhjM	1129715-1130701	transcriptional regulator of the ntd operon;(LacI family)	329
ylbL	1572765-1573787	degradative enzyme	341
holA	2636099-2637139	DNA polymerase III subunit delta	347
dxr	1722871-1724019	1-deoxy-D-xylulose 5-phosphate reductoisomerase	383
rseP	1724029-1725294	inner membrane zinc metalloprotease	422
yabE	48629-49939	cell wall shaping enzyme	437
sufD	3358667-3359977	FeS assembly protein SufD	437
dacA	17534-18862	D-alanyl-D-alanine carboxypeptidase	443
xylA	1891908-1893242	xylose isomerase	445
hemA	2877769-2879133	glutamyl-tRNA reductase	455
tilS	74929-76344	tRNAile lysidine synthetase	472
leuC	2889555-2890970	isopropylmalate isomerase large subunit	472
atpA	3783881-3785386	ATP synthase F0F1 subunit alpha	502
guaA	692740-694278	GMP synthase	513
yxdM	4068553-4070418	cationic peptides ABC transporter permease	622
asnB	3125780-3127675	asparagine synthetase	632
infB	1734009-1736156	translation initiation factor IF-2	716
leuS	3102632-3105043	leucyl-tRNA synthetase	804

List of 8 lagging strand genes under positive selection			
Name	**CDS-region**	**Product**	**Length (AA)**
yodC	2127813-2128418	oxidoreductase	202
lrgB	3933577-3934251	anti-holin factor controlling activity of mureinhydrolases	225
ycgQ	349999-350853	hypothetical protein	285
ycnC	437477-438352	TetR family transcriptional regulator	292
ntdC	1126403-1127452	neotrehalosadiamine biosynthesis dehydrogenase	350
yuxJ	3232640-3233815	exporter	392
dltB	3953783-3954967	D-alanine esterase for lipoteichoic acid and wall teichoic acid	395
sacB	3536012-3537430	levansucrase	473

Supplementary Table 4. List of core *Bacillus subtilis* genes identified to have convergent amino acid mutations (i.e. repeated phylogenetic changes at same amino acid positions).

Strand	**Lower part of dN**		**Higher part of dN**	
	Median dN	Median transformed Log Ratio	Median dN	Median transformed Log Ratio
Lead	0.00133	1.23310	1.03039	1.03039
Lag	0.00296	0.78541	0.00701	2.35645

Supplementary Table 5. Comparison of gene expression median values to dN. The transformed Log Ratio value is 3 times higher for high dN genes than low dN genes, whereas for leading strand the Log Ratio value for high dN genes are smaller or nearly equal to the low dN genes.

IPTG+					No IPTG			
Co-directional		Head-On			Co-Directional		Head-On	
Revertants	**Cells**	**Revertants**	**Cells**		**Revertants**	**Cells**	**Revertants**	**Cells**
5	7.5E+07	7	6.8E+08		1	2.7E+08	0	2.6E+08
6	8.1E+08	10	3.5E+08		1	5.3E+08	0	2.7E+08
6	1.4E+08	10	3.2E+08		1	2.6E+08	0	6.0E+08
6	7.5E+07	11	4.5E+08		1	3.3E+08	1	3.8E+08
6	9.0E+07	12	3.2E+08		1	5.3E+08	1	3.9E+08
7	4.7E+08	12	2.1E+08		1	2.4E+08	1	2.4E+08
7	1.5E+08	13	3.8E+08		2	3.0E+08	1	3.6E+08
7	2.4E+08	14	1.5E+08		2	4.8E+08	1	4.5E+08
9	1.2E+08	14	1.1E+08		2	1.2E+08	1	1.8E+08
9	6.0E+07	15	1.4E+08		2	2.1E+08	1	5.7E+08
9	5.0E+08	16	2.7E+08		2	2.1E+08	1	6.9E+08
10	1.4E+08	18	3.0E+08		2	1.2E+08	1	3.8E+08
10	3.0E+07	20	1.4E+08		2	4.4E+08	2	4.2E+08
10	7.5E+07	25	1.5E+08		2	2.3E+08	2	3.2E+08
10	1.5E+08	25	2.6E+08		2	5.1E+08	2	3.5E+08
12	6.2E+08	29	4.4E+08		2	4.1E+08	2	5.7E+08
13	8.0E+08	29	7.7E+08		3	1.8E+08	3	5.4E+08
13	3.5E+09	31	3.3E+08		3	4.7E+08	3	1.5E+08
13	3.9E+08	35	2.9E+08		3	3.6E+08	3	2.6E+08
13	1.5E+07	36	5.3E+08		3	4.8E+08	3	6.0E+08
14	2.1E+08	38	3.0E+08		4	3.3E+08	4	6.5E+08
15	2.3E+08	38	5.3E+08		4	4.8E+08	4	1.1E+08
16	1.2E+09	39	4.1E+08		4	2.3E+08	4	1.5E+08
16	5.9E+08	41	4.5E+08		4	2.4E+08	5	6.8E+08
20	5.7E+08	43	6.0E+08		5	1.8E+08	6	3.8E+08
21	2.8E+09	43	3.8E+08		5	3.5E+08	6	7.2E+08
26	8.0E+08	43	5.0E+08		5	5.3E+08	6	1.4E+08
29	6.8E+08	47	6.5E+08		5	5.0E+08	7	1.5E+07
29	4.4E+08	48	5.7E+08		7	3.2E+08	8	4.2E+08
32	7.2E+08	50	3.9E+08		8	5.6E+08	11	4.5E+08
36	5.6E+08	57	2.4E+08		13	9.6E+08	15	4.7E+08
46	5.3E+08	57	6.2E+08					
158	5.0E+08							

Supplementary Table 6. Raw data from reversion assays. Colonies arising after 48 hours growth on medium lacking histidine were counted for each condition and are indicated as the number of revertants. The number of viable cells per culture at the time of plating is indicated in columns labeled “cells”.

Strain	**Genotype**	**Reference**
YB955	*hisC952 metB5 leuC427* xin-1 SPβ^{SENS}	[1]
HM419	*hisC952 metB5 leuC427* xin-1 SPβ^{SENS} *amyE*::{ P$_{spank(hy)}$-*hisC952* Head-On *spc*})$^{\cdot}$	This Study
HM420	*hisC952 metB5 leuC427* xin-1 SPβ^{SENS} *amyE*::{ P$_{spank(hy)}$-*hisC952* Co-Directional *spc*})$^{\cdot}$	This Study

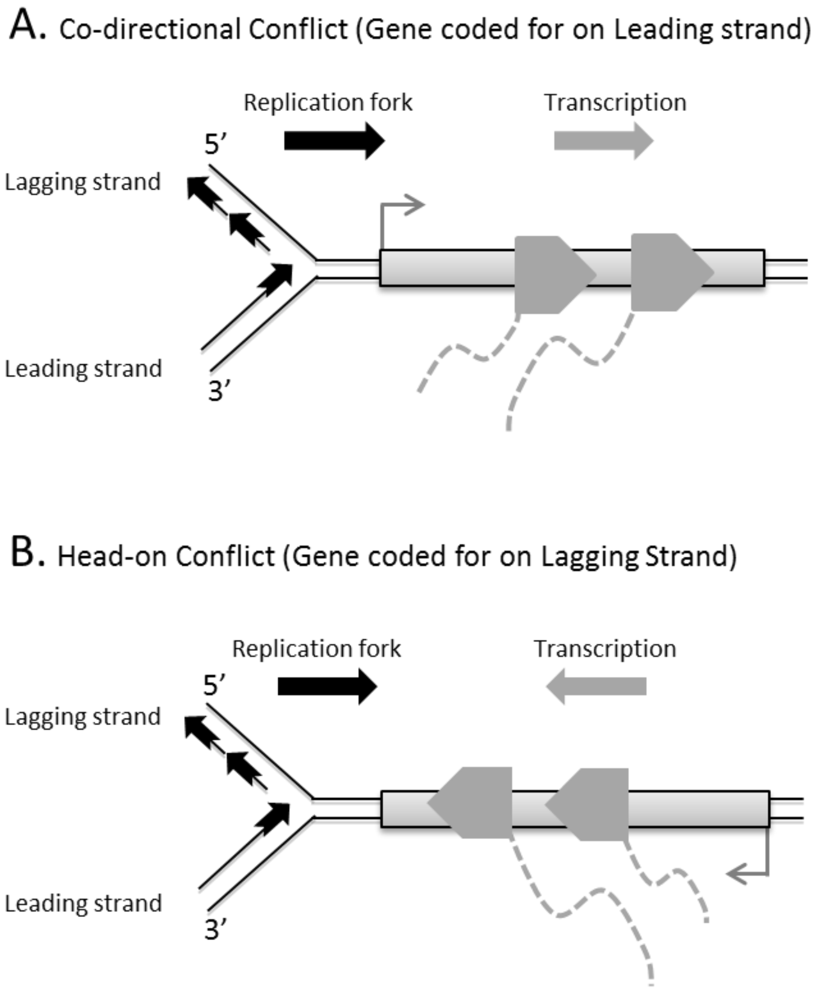
Supplementary Table 7. Strains used in this study. HM419 and HM420 were constructed as described.

Plasmid	**Genotype**	**Reference**
pHM392	*amyE::* P$_{spank(hy)}$-*hisC952* Head-On *spc lacI*	This Study
pHM394	*amyE::* P$_{spank(hy)}$-*hisC952* Co-Directional *spc lacI*	This Study

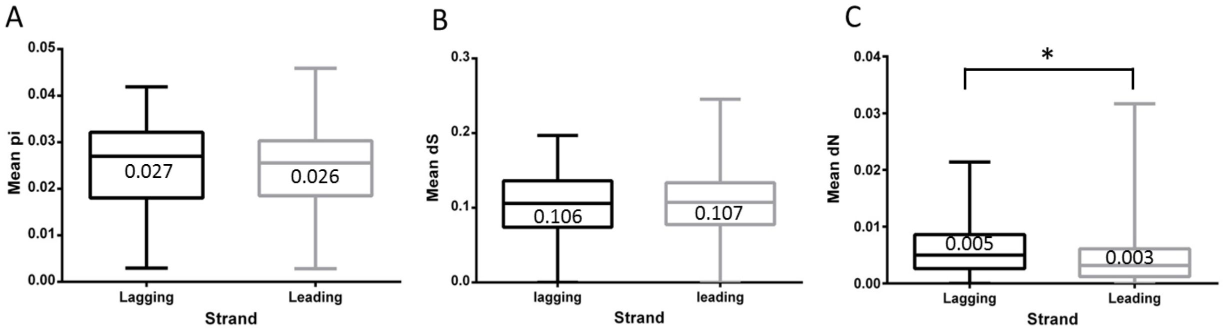
Supplementary Table 8. Plasmids used in this study. pHM392 and pHM394 were constructed as described.

Position	**Nucleotide Change**	**Amino Acid Change**	**Total Number**	**Number Head-on**	**Number Co-directional**
952	T==>C	Stop==>Gln	18	17	1
	T==>A	Stop==>Lys			
	T==>G	Stop==>Glu	6	4	2
953	A==>T	Stop==>Leu			
	A==>C	Stop==>Ser	1	1	
	A==>G	Stop==>Trp	1		1
954	G==>T	Stop==>Tyr			
	G==>C	Stop==>Tyr			

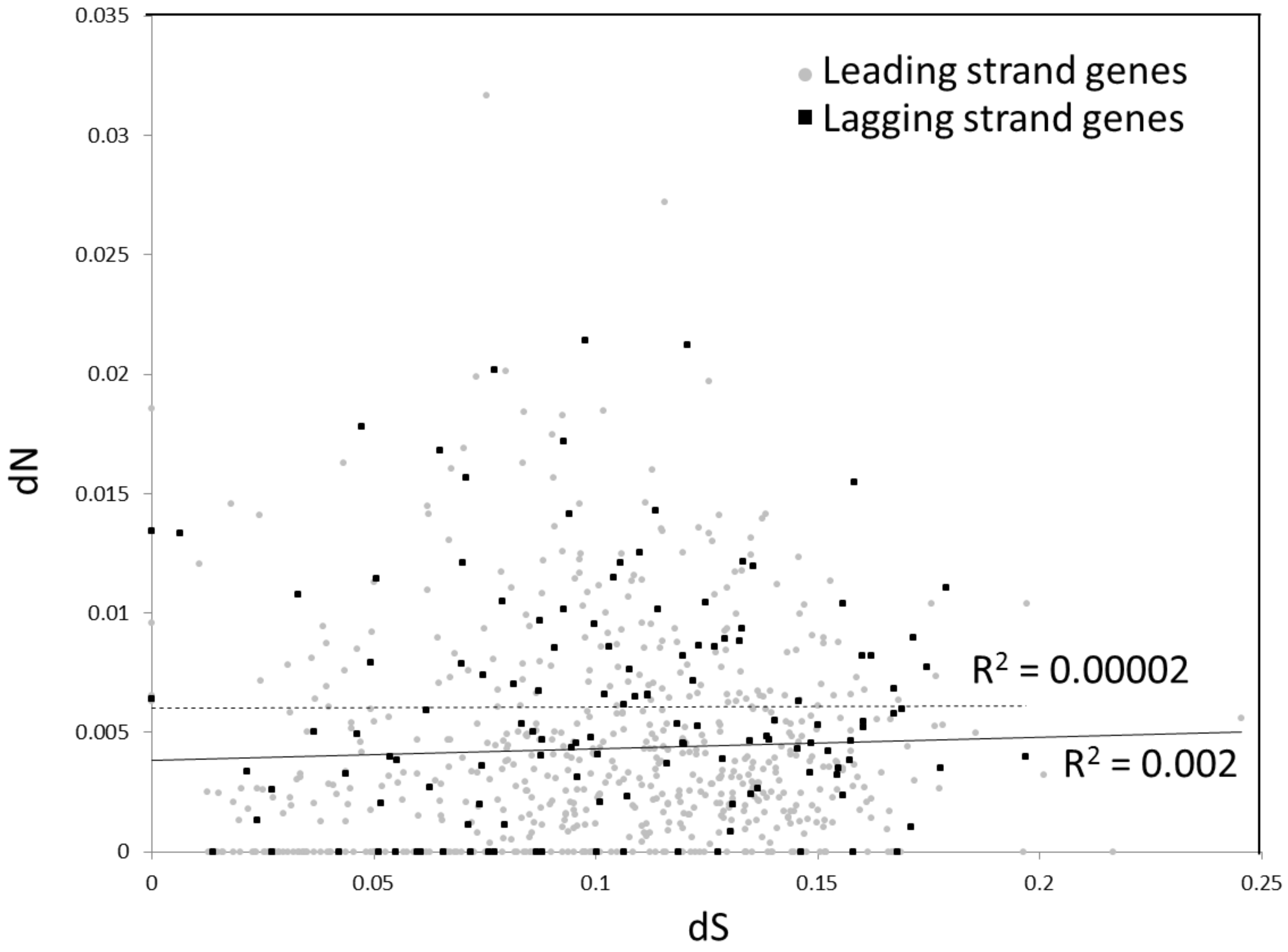
Supplementary Table 9. Table Outlining all the possible ways hisC952 *could* revert and the reversions mapped from the reporter experiments. WT *hisC* gene codon 318 is a CAG (Glutamine): the *hisC*952 allele has a TAG Stop codon at position 952 (C➔T mutation). Twenty-four revertants from head-on and four co-directional reporter constructs were sequenced. The number for each type of reversion that was found in the *hisC* allele at *amyE* is shown.



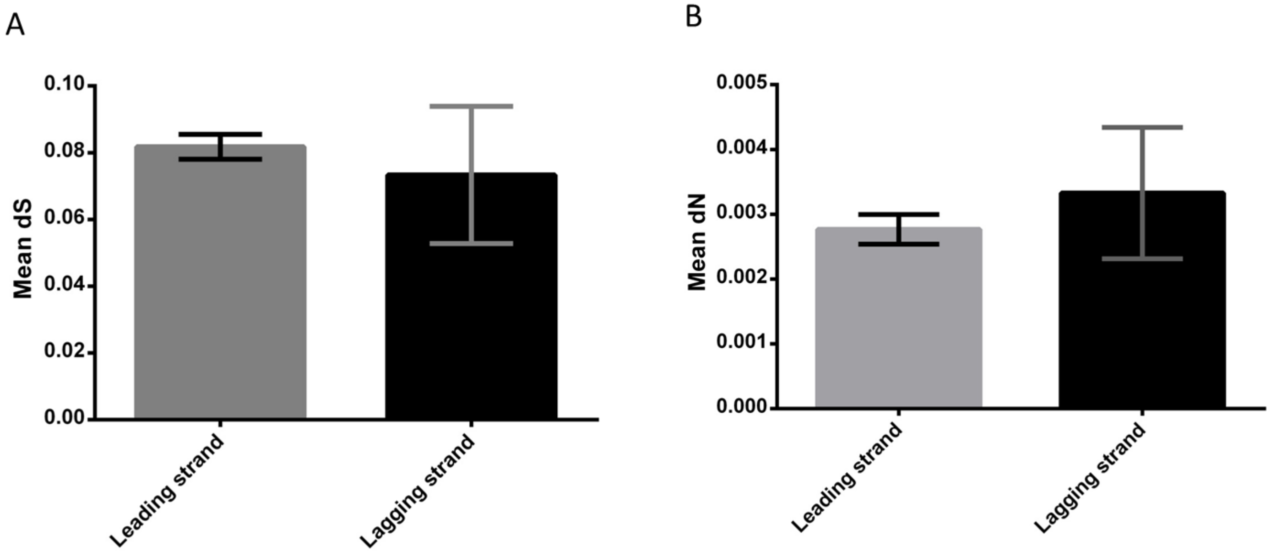
Supplementary Figure 1. Cartoon schematic of conflicts in the two orientations. The replication fork is indicated in black arrows, RNA polymerases are indicated as gray pentagons, mRNA is indicated as dashed lines, and the promoter and the direction of the gene is indicated as a gray arrow, pointing in the same direction as the gene and the movement of RNA polymerases. **A.** Co-directional conflicts between the replication and transcription machineries occur when a gene is encoded on the leading strand. In these conflicts, transcription occurs in the same direction as leading-strand replication. **B.** Head-on conflicts between the replication and transcription machineries occur when a gene is encoded on the lagging strand. In these conflicts, transcription occurs in the opposite direction to leading-strand replication.



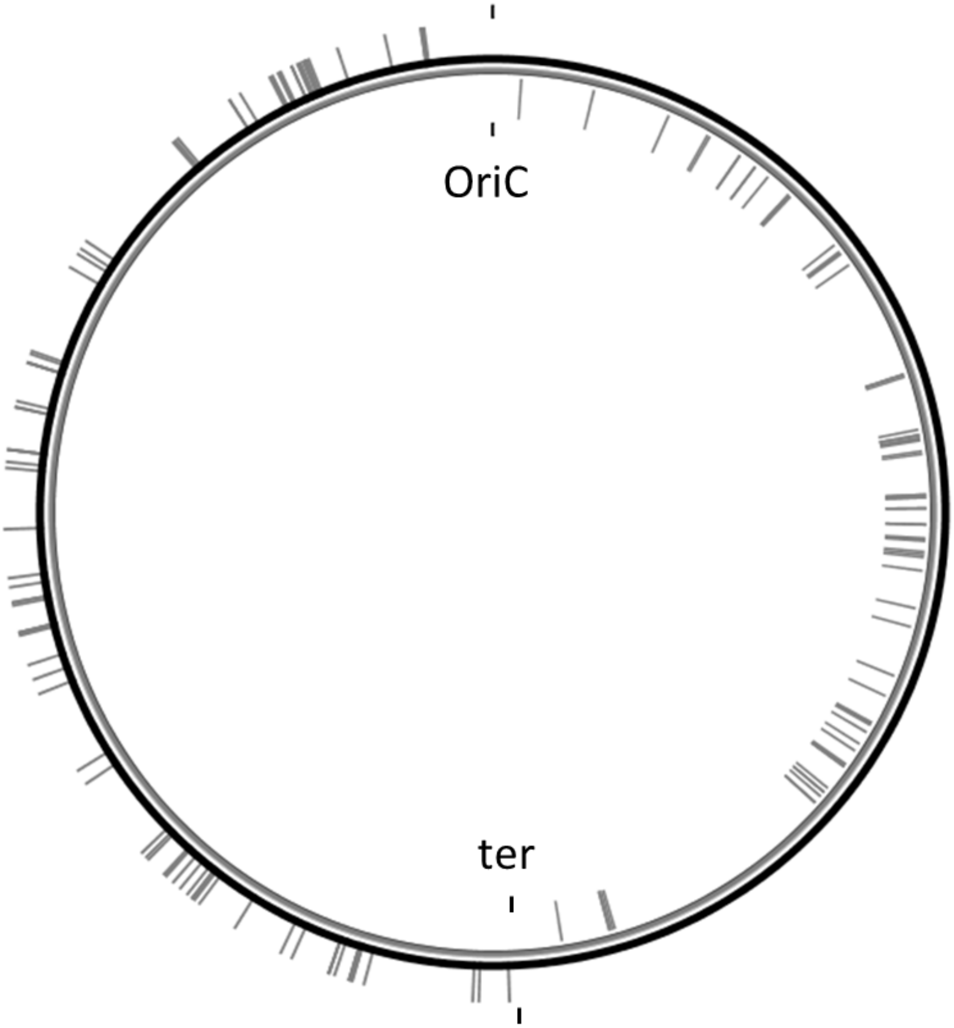
Supplementary Figure 2. Box and whisker plot of the mean values for π **(A)**, dS **(B)** and dN **(C)** are plotted for the leading (gray) and lagging (black) strands. The ranges of the original data are represented by bars (min and max values) and boxes (25-75%). The line in the box represents the median and the median values are mentioned. Values for dN in the two strands are significantly different ($p<0.0001$, indicated by *) by Mann Whitney test (two tailed).



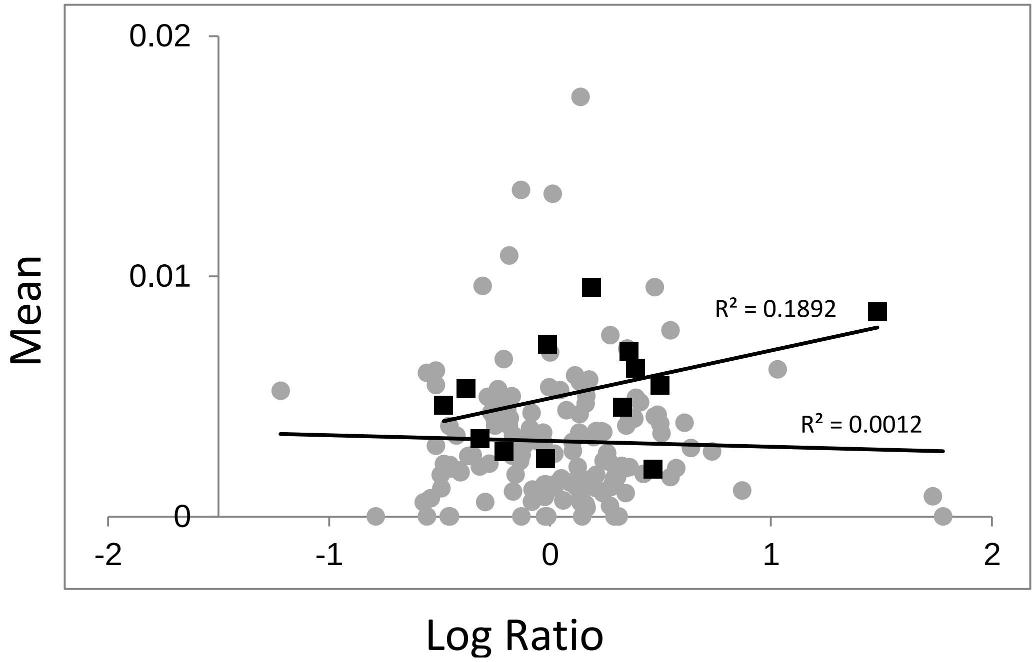
Supplementary Figure 3. Plot of mean dS vs mean dN values for 627 and 132 gene-set analyzed from leading (gray dots) and lagging (black square) stand of replication respectively. The trend lines showing no correlation between the dS and dN values (dotted lines for lagging strand genes and black line for leading strand genes).



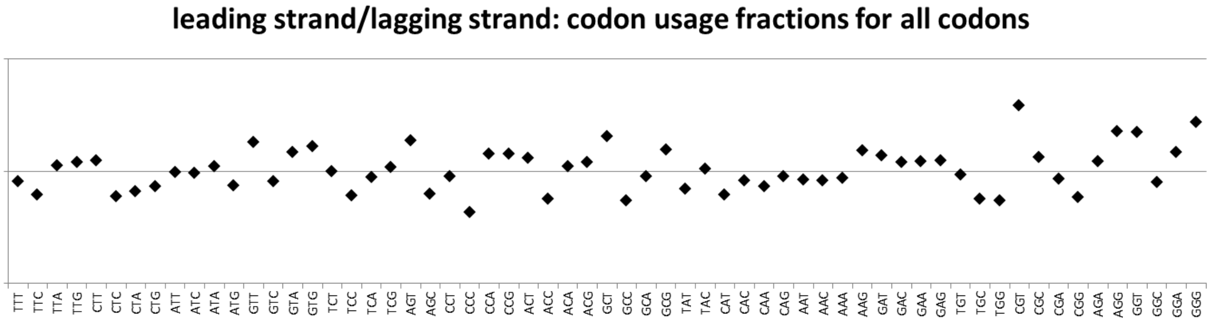
Supplementary Figure 4. Average rate of accumulation of **(A)** synonymous (dS) and **(B)** non-synonymous changes (dN) and standard error of mean for core essential genes on the leading (142 genes) and lagging (6 genes) strand.



Supplementary Figure 5. Schematic view of circular maps of *B. subtilis* str. 168 genome showing distribution of 132 lagging strand genes under study. This plot was generated by using CG view software[2].



Supplementary Figure 6. Plot of gene expression data (Log Ratio (635/532)) with the mean dN of any gene for leading strand (gray) and lagging strand (black). The comparison of regression lines of leading and lagging strand population show that the two slopes are significantly (p=0.0076) different. See supplementary methods.



Supplementary Figure 7. Codon usage bias of the genes in the two strands. The codon usage fraction for all codons, except for the stop codons, TAA, TAG and TGA, were analyzed in the core genes in both the leading and the lagging strands. The codon fraction was found by dividing the number of each codon with total number of codons in that gene, for each strand. The average fraction of usage was determined for each codon, for all five strains analyzed, and the ratio between the leading and the lagging strand usage fractions is plotted per codon. A ratio of 1 indicates no difference between usage fractions in the two strands. See supplementary methods.

Supplementary Methods:

Gene expression analysis and correlative comparisons to dN. We used the GEO accession GSM978786 dataset for *B. subtilis* to pull out the expression value of each gene. We analyzed genes only with 300 or more amino acid lengths from leading (142) and lagging (13) strand. When we plotted the expression in terms of Log Ratio (635/532) versus mean nonsynonymous substitution rate (dN) we found a positive correlation between them for lagging strand genes whereas there was a negative correlation for leading strand genes. We divided the leading and lagging strand values into two parts, according to the median value of their dN distribution (0.00256 for leading and 0.00532 for lagging), and calculated the median of transformed Log Ratio values for each parts corresponding to low or high dN values.

Calculation of codon usage fractions. In order to calculate the codon usage fraction of individual protein coding genes, we used an in-house software which finds the number of each of the 64 codons of any given gene and then calculates the codon usage fraction by dividing the number of each codon with the total number of codons in that gene. We have gene sequence data for 627 leading strand genes and 132 lagging strand genes for the five *B. subtilis* strains used in this study. Using this software, we calculated the codon usage frequency of the 627 leading strand and 132 lagging strand genes.

Supplementary References:

1 Yasbin, R. E., R. Miehl-Lester, and P. E. Love. *Mutagenesis in Bacillus subtilis*. Vol. 86 73-84 (1987).

2 Stothard, P. & Wishart, D. S. Circular genome visualization and exploration using CGView. *Bioinformatics* **21**, 537-539, doi:10.1093/bioinformatics/bti054 (2005).