Table S1. Primers used for the construction of plasmids used in this study

Primer	Sequence [a]	Location on the genome [b]
dnaA.f	cgcgaattcTTATTACAGATATCACACCG [c]	1215...1234
dnaA.r	gcgcccgggTTTAAGCTGTTCTTTAATTTCTTTTAC	1747...1721
spo0J.f	cgcgaattcAGCGTGAAGATTTATCTCCG	4204583...4204603
spo0J.r	gcgctcgagTGATTCTCGTTCAGACAAAAG	4205088...4205069
1dnaA-HiF	cgcaagcttGATCTAGAAACGAGAATTGC	1238...1257
1dnaA-LinkR	tgcgatcctctcatttcaagTTTAAGCTGTTCTTTAATTTC	1747...1727
2dnaA-HisF	caccaccaccatcatcaccatTAGCAGGACCGGGGATCAATC	1748...1768
2dnaA-BaR	gcgggatccTCGTCAAATACTGATTTTGG	2251...2232
Linker-12His	cttgaaatgagaggatcgcatcaccatcaccatcaccaccaccatcatcaccat	

[a] Capital and lowercase letters indicate sequences derived from *the B. subtilis* genome and others, respectively.
[b] Numbers refer to the SubtiList database (http://genolist.pasteur.fr/SubtiList/index.html).
[c] Underlined sequences represent the recognition sites of restriction enzymes.

Table S2. Genes up- or downregulated by DnaA

gene [a]	x1/5 DnaA [b]	x5 DnaA [c]	ratio	function
downregulated				
dnaA (*dnaAN*) [d]	0.65	0.39	0.13	replication
dnaN (*dnaAN*) [d]	0.48	0.18	0.38	replication
ykuN (*ykuNPO*)	1.58	0.73	0.46	similar to flavodoxin
ykuO (*ykuNPO*)	1.84	0.73	0.40	unknown
ykuP (*ykuNPO*)	2.22	0.89	0.40	similar to flavodoxin
dhbA (*dhbACEB*)	1.04	0.59	0.57	biosynthesis of siderophore group nonribosomal peptides
ywlC	0.70	0.34	0.49	unknown
yydA	0.70	0.45	0.64	unknown
noc (*thdF/gidA/gidB/noc*)	2.78	1.76	0.63	cell division
gidB (*thdF/gidA/gidB/noc*)	3.11	1.70	0.55	translation
gidA (*thdF/gidA/gidB/noc*)	2.10	1.16	0.55	translation
thdF (*thdF/gidA/gidB/noc*)	1.77	1.00	0.56	translation
upregulated				
sda [d]	1.17	3.52	3.00	sporulation
yveL (*yveKL*)	0.19	0.56	2.95	similar to capsular polysaccharide biosynthesis protein
yveK (*yveKL*)	0.24	0.65	2.71	similar to capsular polysaccharide biosynthesis protein
yvdD (*yvdD<>yvdC*)	1.01	2.88	2.85	unknown
yvdC (*yvdD<>yvdC*)	1.28	3.60	2.81	unknown protein with MazG nucleotide pyrophosphohydrolase domain
rocA	0.34	1.97	5.79	arginine catabolism
rocD (*rocCDE*)	0.76	2.06	2.71	arginine and proline metabolism

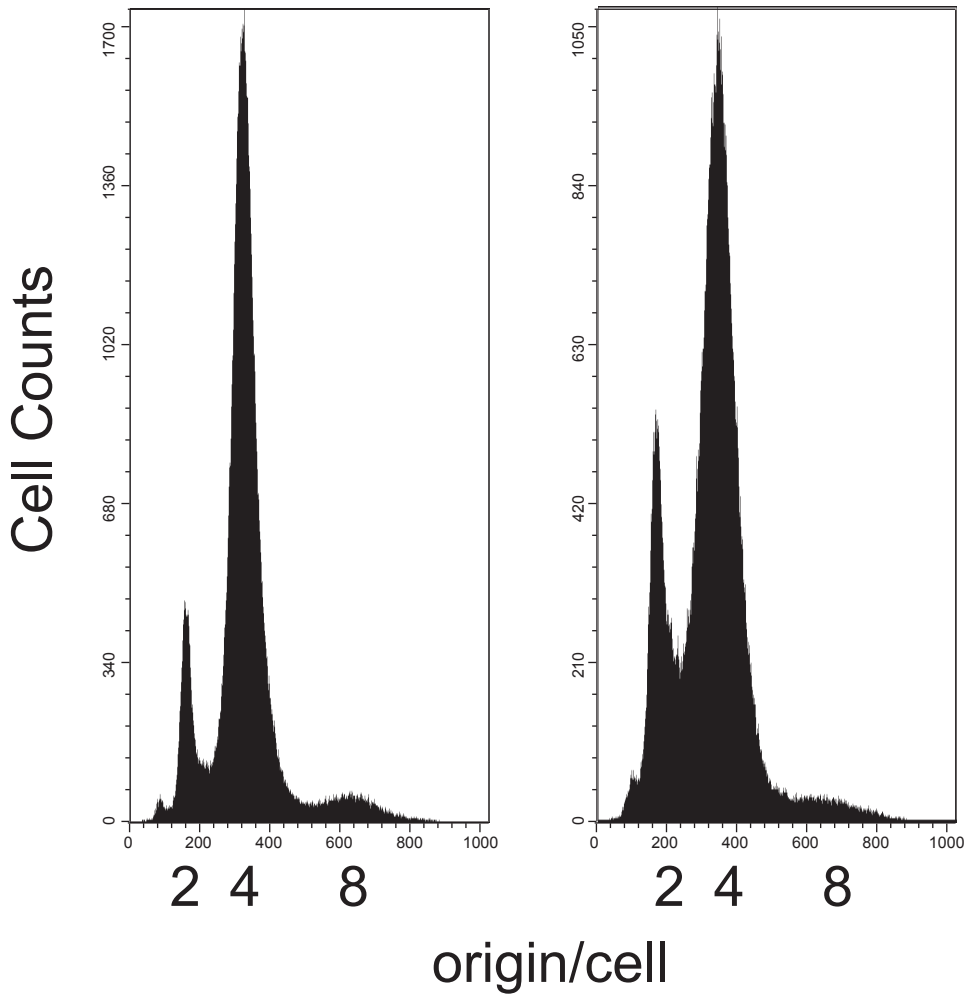
[a] Genes that are downregulated (<0.65) and upregulated (>2.5) in a DnaA-dependent manner in two independent experiments are specified. The operon structure is indicated in parentheses.

[b] Expression levels in NIS2022 cells grown in the absence of IPTG to repress the DnaA level to 1/5 times that in the wild-type strain, CRK6000. Expression level is the average of signal intensities of probes in coding sequences after trimming two of the lowest and highest intensities.

[c] Expression level in NIS2022 cells grown in the presence of 0.1M IPTG to stimulate the DnaA level to 5 times that in the wild-type strain, CRK6000.

[d] Expression levels of *dnaA*, *dnaN* and *sda* were calculated using probes in regions 168..333, 1751..1938, and 2646601..2646849, respectively.

Figure S1



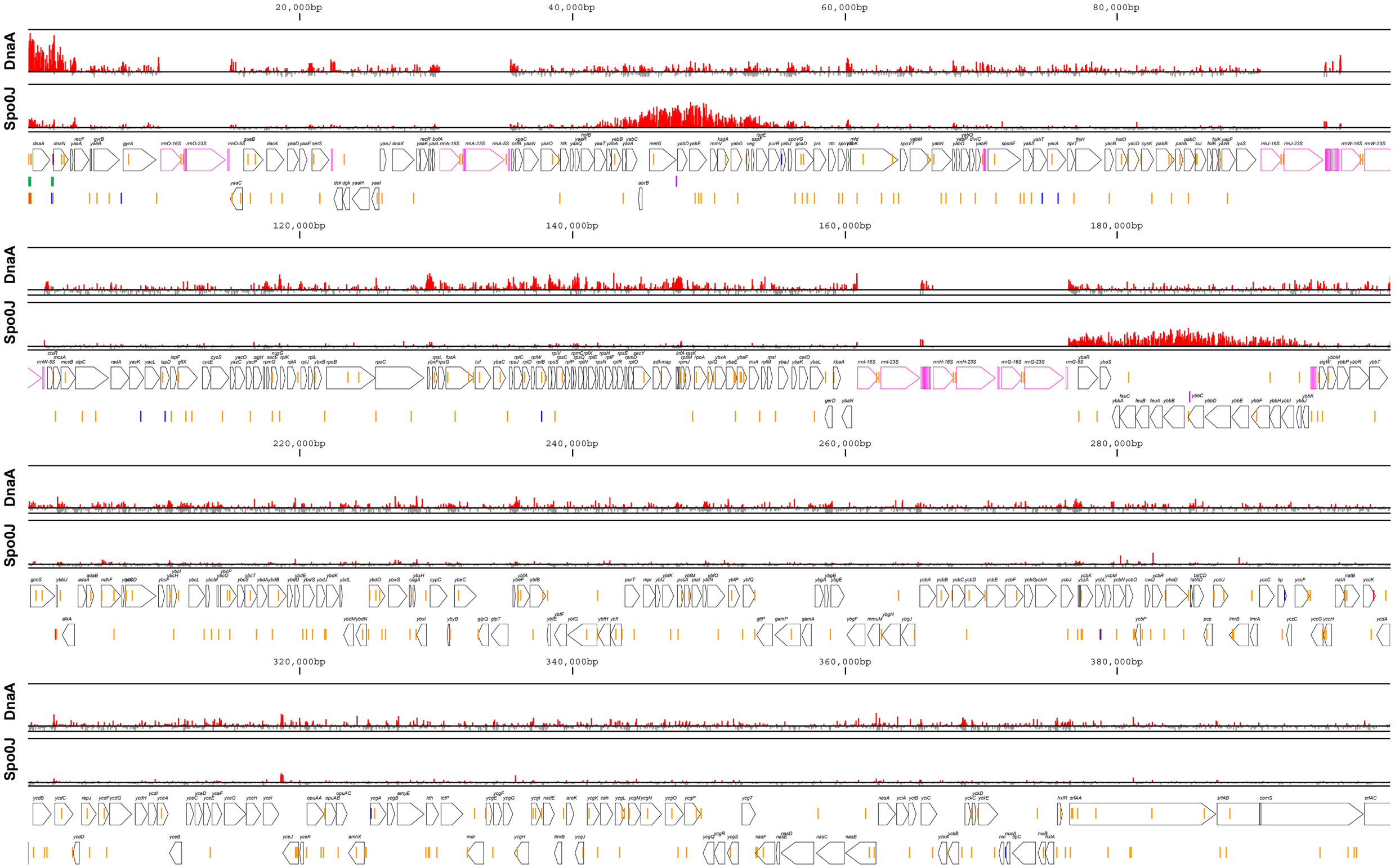
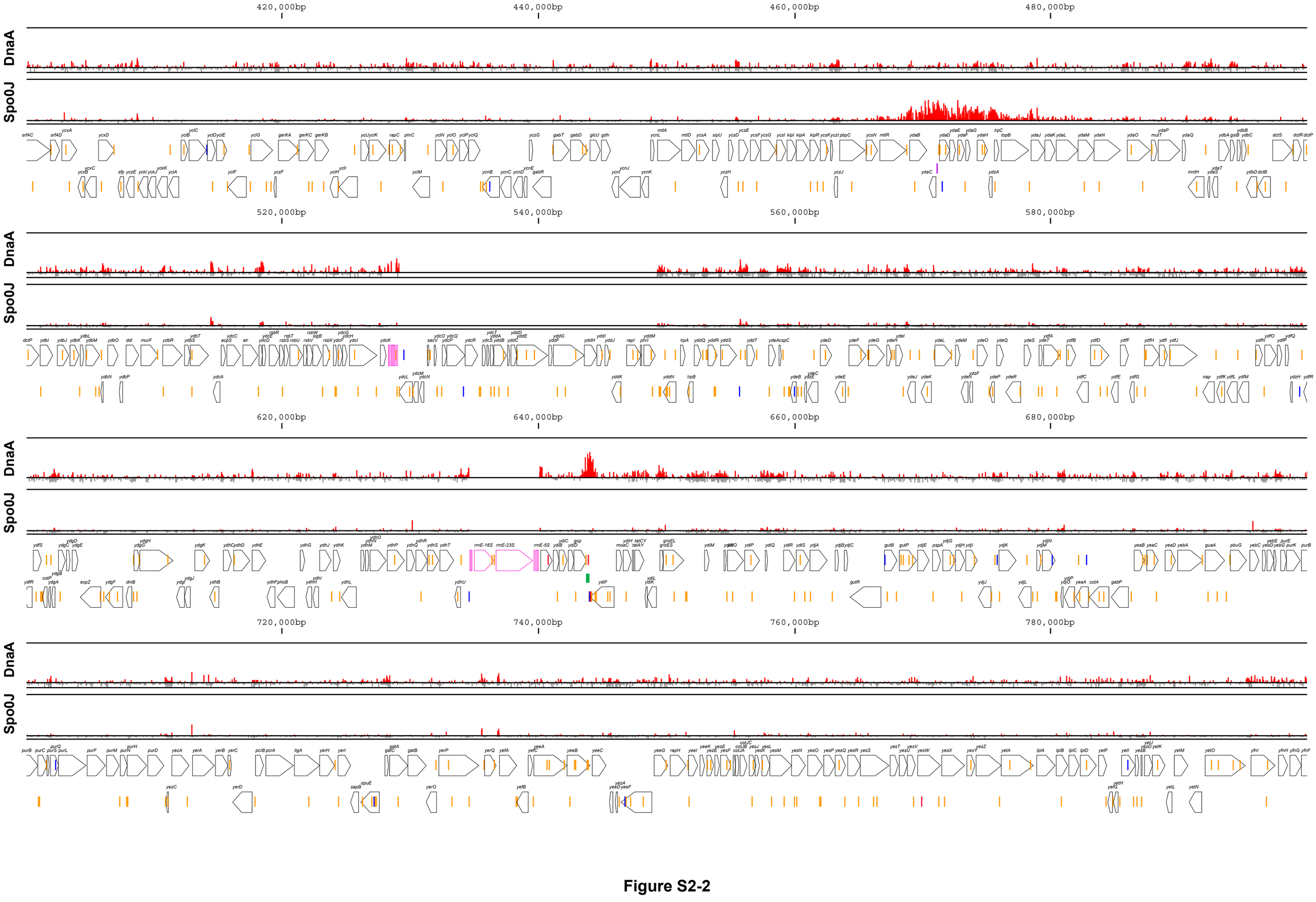

DnaA
Spo0J
20,000bp
40,000bp
60,000bp
80,000bp
120,000bp
140,000bp
160,000bp
180,000bp
220,000bp
240,000bp
260,000bp
280,000bp
320,000bp
340,000bp
360,000bp
380,000bp

Figure S2-1


DnaA
Spo0J
420,000bp
440,000bp
460,000bp
480,000bp
520,000bp
540,000bp
560,000bp
580,000bp
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660,000bp
680,000bp
720,000bp
740,000bp
760,000bp
780,000bp

Figure S2-2

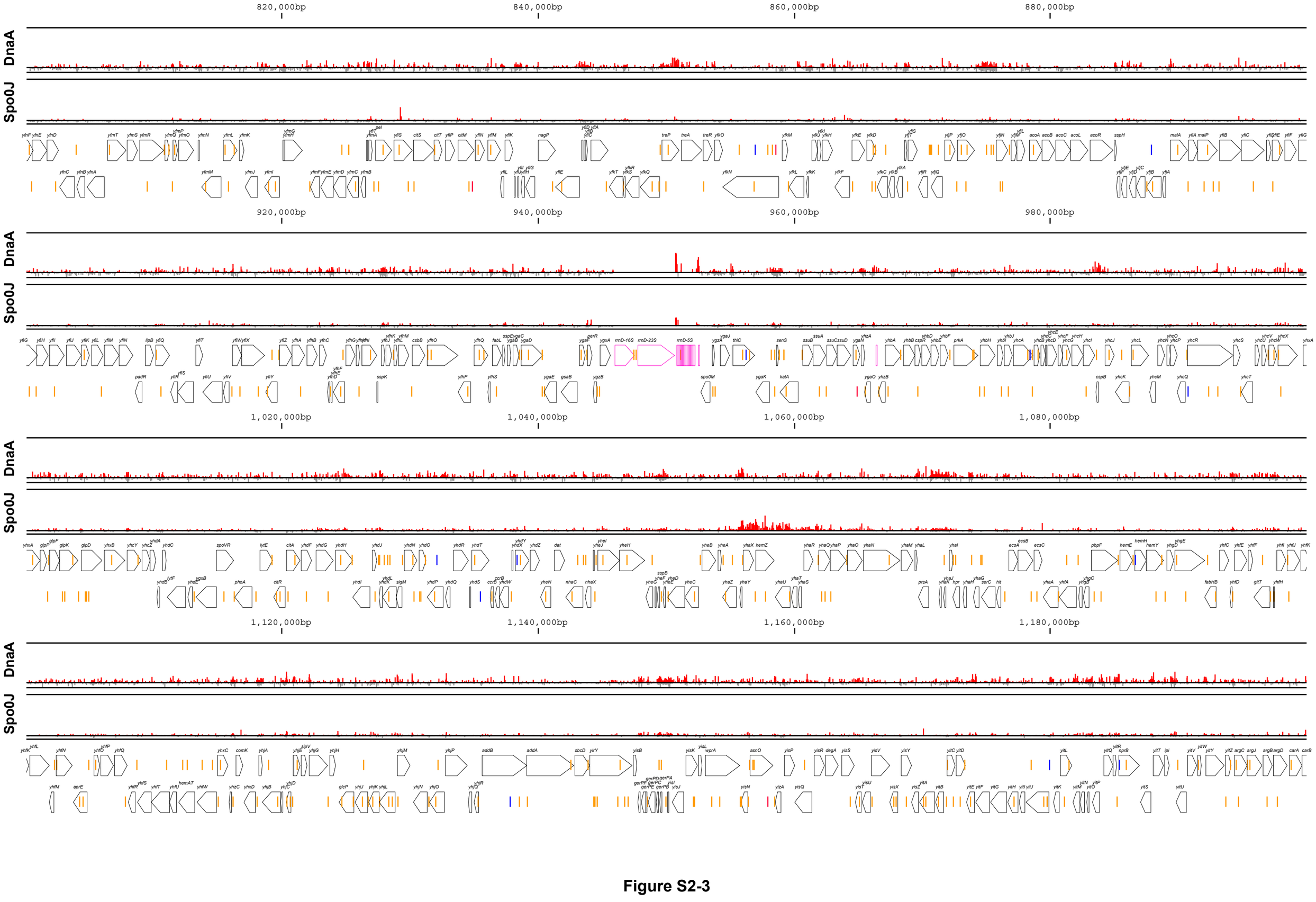
DnaA
Spo0J
820,000bp
840,000bp
860,000bp
880,000bp
920,000bp
940,000bp
960,000bp
980,000bp
1,020,000bp
1,040,000bp
1,060,000bp
1,080,000bp
1,120,000bp
1,140,000bp
1,160,000bp
1,180,000bp

Figure S2-3

DnaA
Spo0J
1,220,000bp
1,240,000bp
1,260,000bp
1,280,000bp
1,320,000bp
1,340,000bp
1,360,000bp
1,380,000bp
1,420,000bp
1,440,000bp
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1,560,000bp
1,580,000bp

Figure S2-4

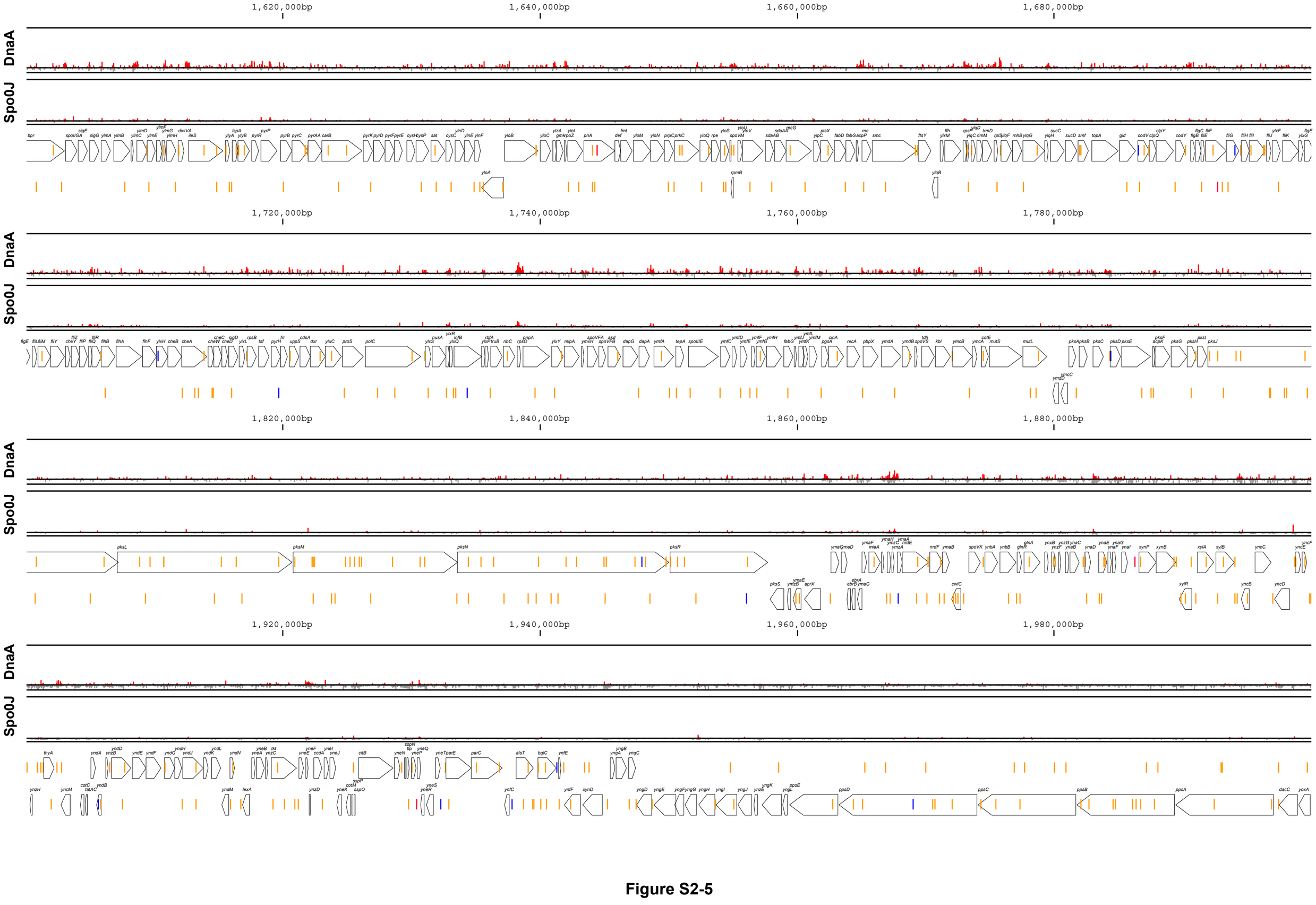
DnaA
Spo0J
1,620,000bp
1,640,000bp
1,660,000bp
1,680,000bp
1,720,000bp
1,740,000bp
1,760,000bp
1,780,000bp
1,820,000bp
1,840,000bp
1,860,000bp
1,880,000bp
1,920,000bp
1,940,000bp
1,960,000bp
1,980,000bp

Figure S2-5

DnaA
Spo0J
2,020,000bp
2,040,000bp
2,060,000bp
2,080,000bp
2,120,000bp
2,140,000bp
2,160,000bp
2,180,000bp
2,220,000bp
2,240,000bp
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2,280,000bp
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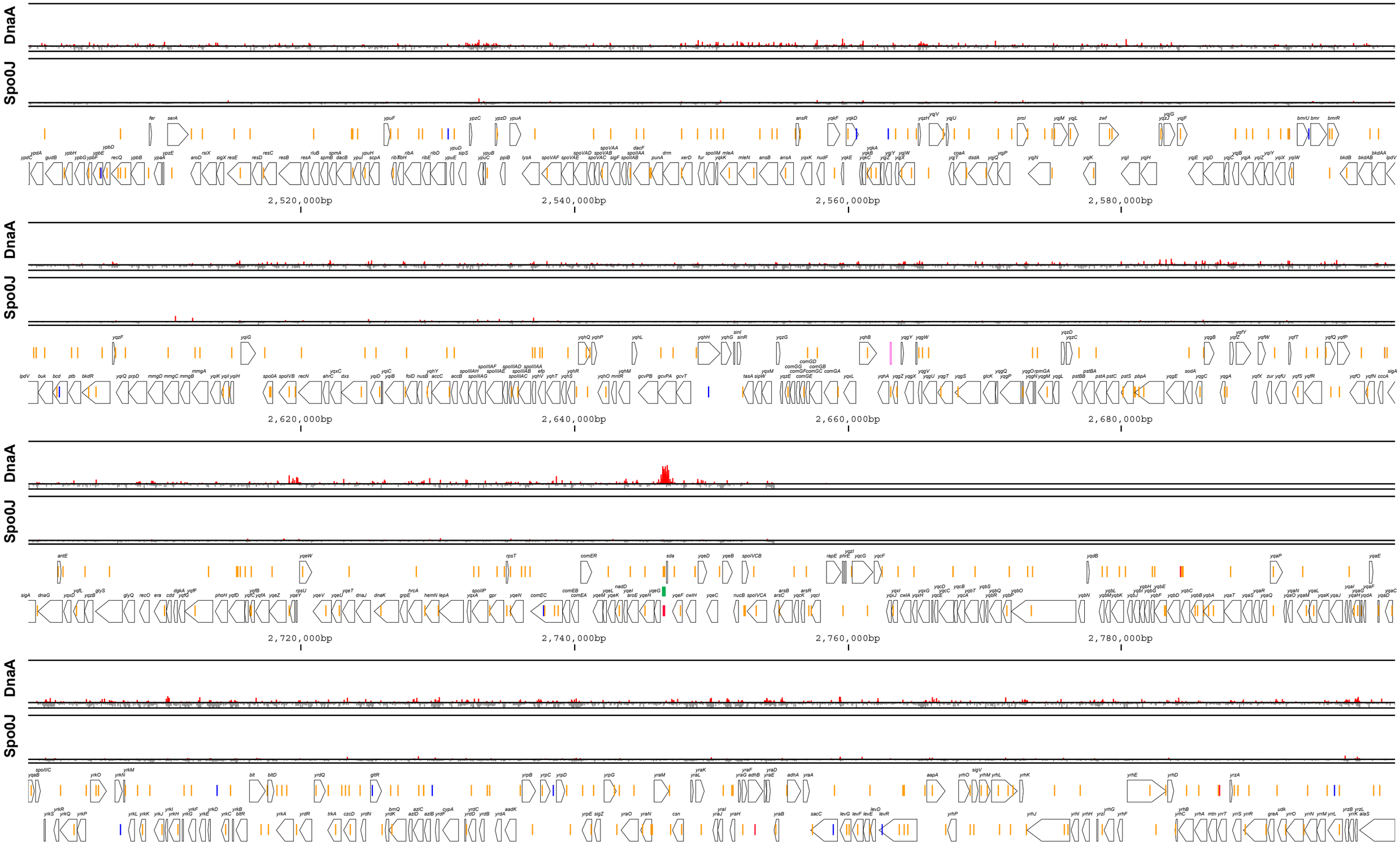
2,340,000bp
2,360,000bp
2,380,000bp

Figure S2-6


DnaA
Spo0J
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2,440,000bp
2,460,000bp
2,480,000bp
2,520,000bp
2,540,000bp
2,560,000bp
2,580,000bp
2,620,000bp
2,640,000bp
2,660,000bp
2,680,000bp
2,720,000bp
2,740,000bp
2,760,000bp
2,780,000bp

Figure S2-7


DnaA
Spo0J
2,820,000bp
2,840,000bp
2,860,000bp
2,880,000bp
2,920,000bp
2,940,000bp
2,960,000bp
2,980,000bp
3,020,000bp
3,040,000bp
3,060,000bp
3,080,000bp
3,120,000bp
3,140,000bp
3,160,000bp
3,180,000bp

Figure S2-8

DnaA
Spo0J
3,220,000bp
3,240,000bp
3,260,000bp
3,280,000bp
3,320,000bp
3,340,000bp
3,360,000bp
3,380,000bp
3,420,000bp
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3,460,000bp
3,480,000bp
3,520,000bp
3,540,000bp
3,560,000bp
3,580,000bp

Figure S2-9

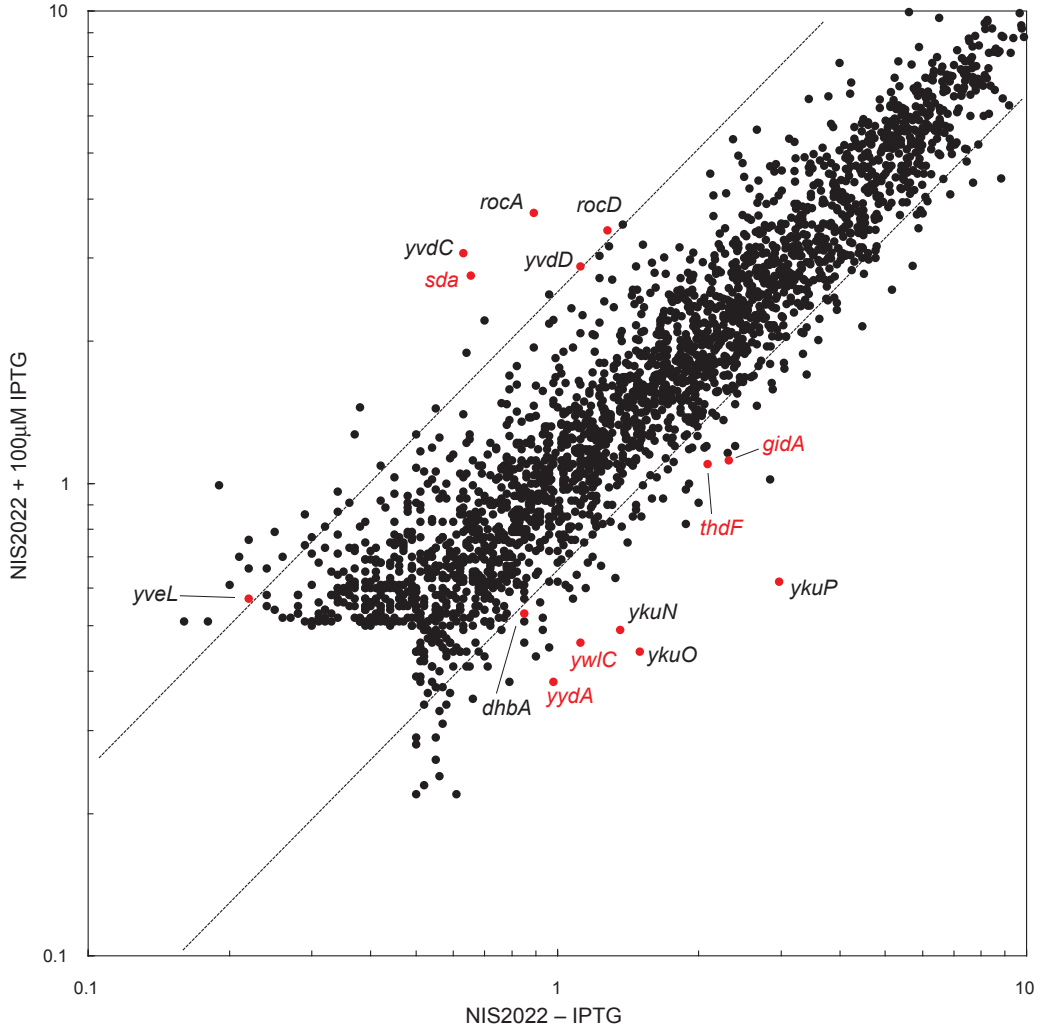
DnaA
Spo0J
3,620,000bp
3,640,000bp
3,660,000bp
3,680,000bp
3,720,000bp
3,740,000bp
3,760,000bp
3,780,000bp
3,820,000bp
3,840,000bp
3,860,000bp
3,880,000bp
3,920,000bp
3,940,000bp
3,960,000bp
3,980,000bp

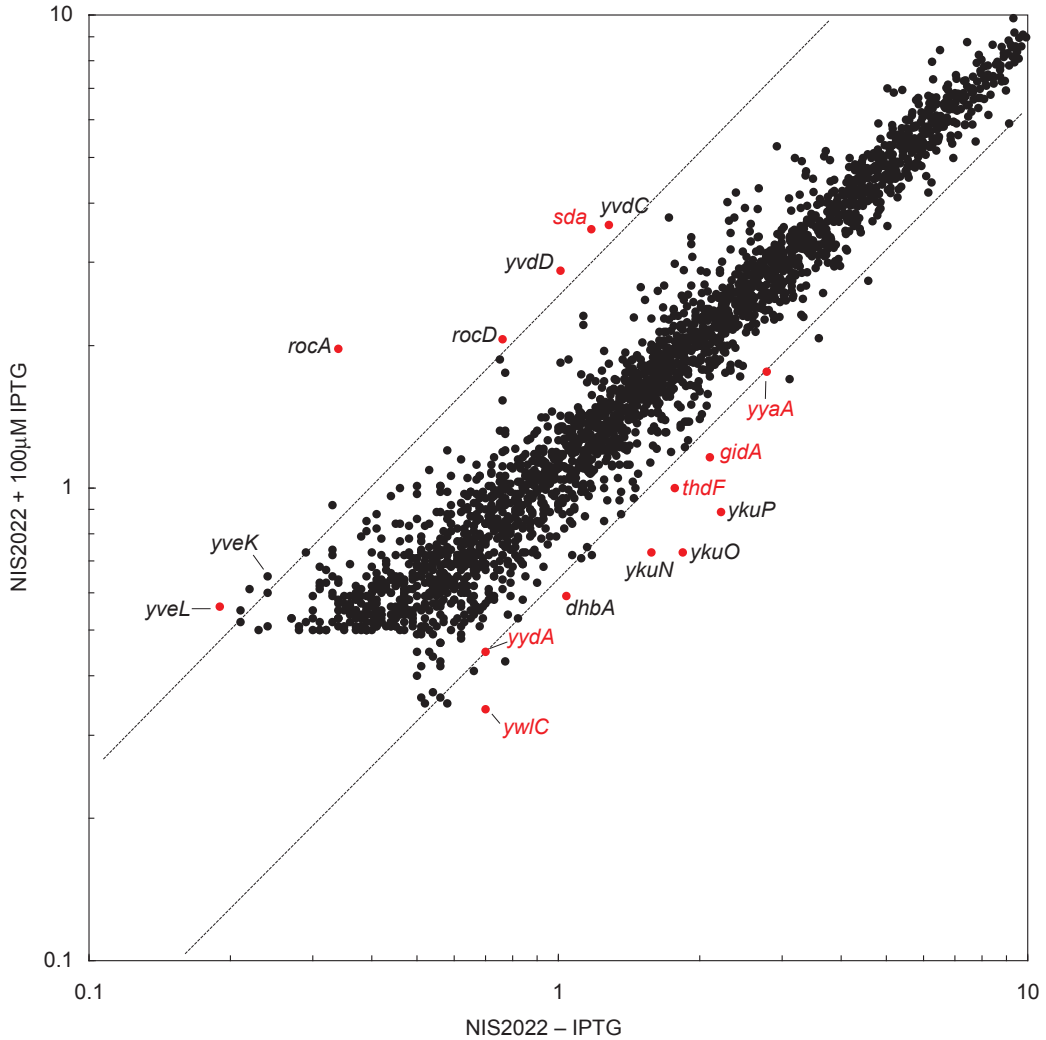
Figure S2-10

DnaA
Spo0J
4,020,000bp
4,040,000bp
4,060,000bp
4,080,000bp
4,120,000bp
4,140,000bp
4,160,000bp
4,180,000bp
yyaC
yyaB
yyaE
yyaD
spo0J
soj
yyaA
gidB
gidA
thdF
spoIIIJ
jag
rpmH
rnpA

Figure S2-11

Figure S3


10
1
0.1
0.1
1
10
NIS2022 + 100µM IPTG
NIS2022 – IPTG
rocA
rocD
yvdC
yvdD
sda
gidA
thdF
ykuP
yveL
ykuN
ykuO
ywlC
yydA
dhbA


10
1
0.1
0.1
1
10
NIS2022 + 100µM IPTG
NIS2022 – IPTG
sda
yvdC
yvdD
rocA
rocD
yyaA
gidA
thdF
ykuP
yveK
yveL
ykuO
ykuN
dhbA
yydA
ywlC