



Fig. S1. An example image of a read depth change.

The positions showing drastic change of depth were regarded as transcriptional start sites (TSSs).

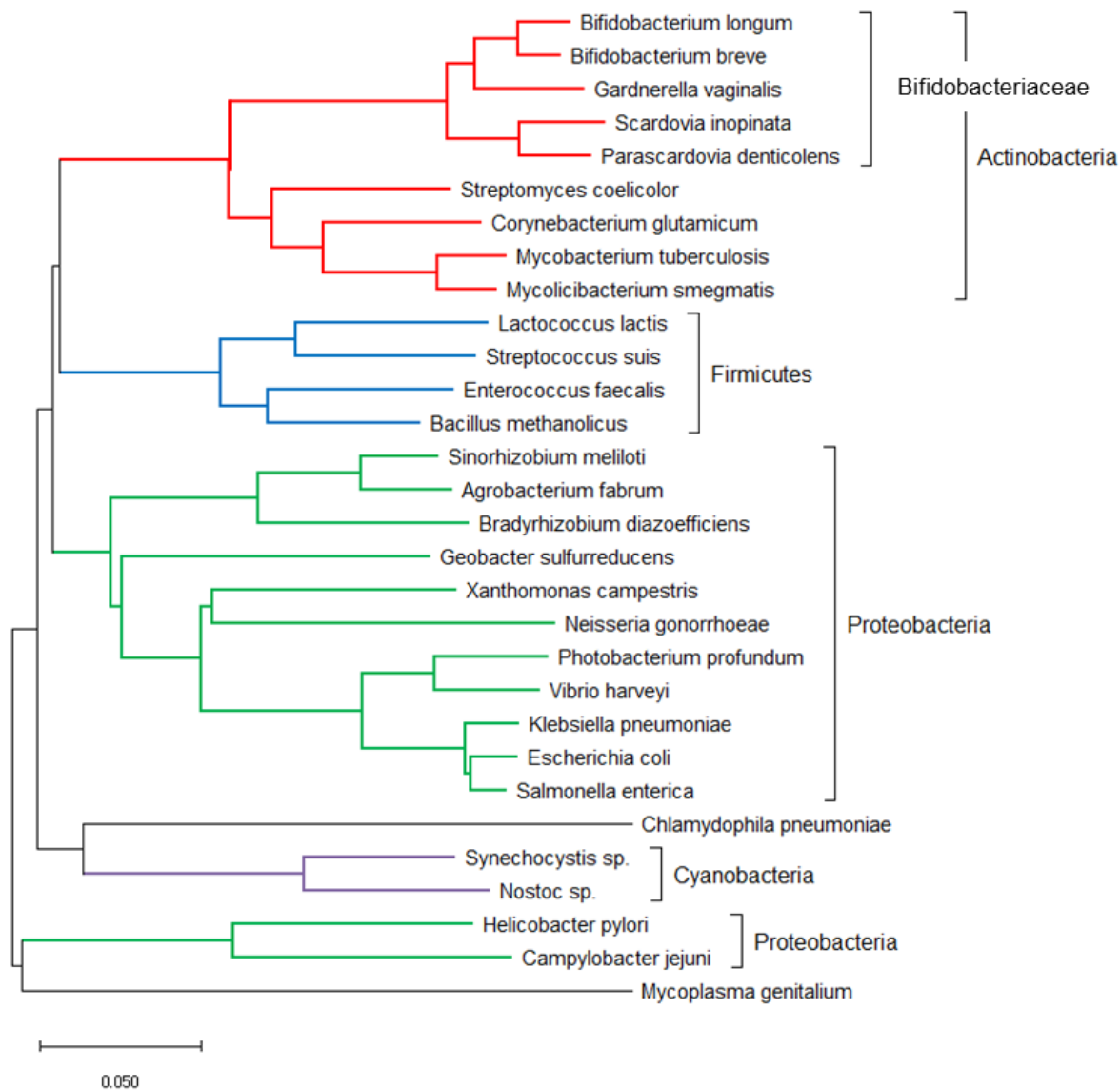


Fig. S2. The phylogenetic tree based on 16S ribosomal RNA gene sequences.

The phylogenetic classification of bacteria utilized in Table 1. Four bacteria in the phylum Actinobacteria; *C. glutamicum* ATCC 13032, *M. smegmatis* MC² 155, *M. tuberculosis* H37Rv, and *S. coelicolor* A3(2). Four bacteria in the phylum Firmicutes; *B. methanolicus* MGA3, *E. faecalis* V583, *S. suis* P1/7, and *L. lactis subsp. cremoris* MG1363. Two bacteria in the phylum Cyanobacteria; *Nostoc* sp. PCC 7120 and *Synechocystis* sp. PCC 6803. Thirteen bacteria in the phylum Proteobacteria; *G. sulfurreducens* PCA, *C. jejuni subsp. jejuni* NCTC 11168, *H. pylori* 26695, *B. japonicum* USDA110, *A. fabrum* C58, *S. meliloti* 1021, *S. enterica* serovar Typhimurium str. SL1344, *K. pneumoniae subsp. pneumoniae* MGH 78578, *E. coli* K-12 MG1655, *V. harveyi* FDAARGOS_107, *P. profundum* SS9, *X. campestris pv. vesicatoria* 85-10, and *N. gonorrhoeae* MS11. One bacterium in the phylum Chlamydiae; *C. pneumoniae* CWL029.

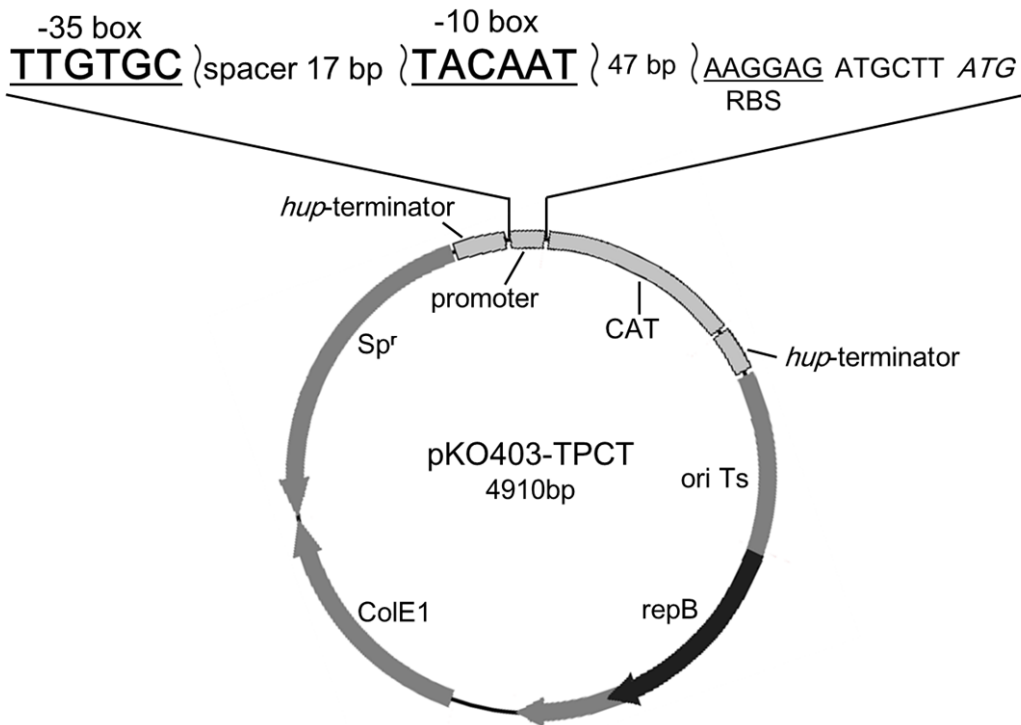
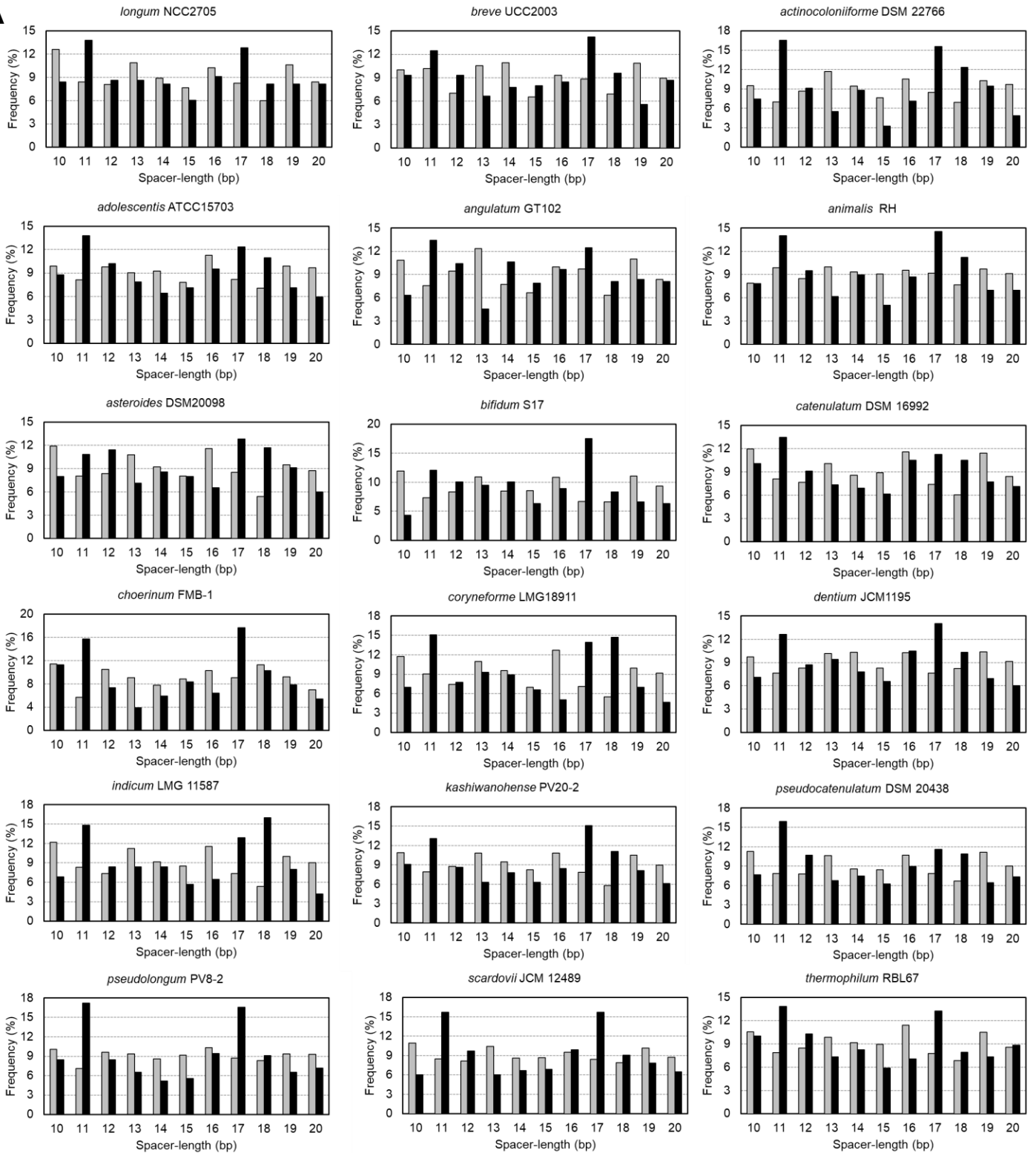


Fig. S3. The plasmid map of the pKO403-TPCTcon.

The spacer sequence between the -35 and -10 boxes is in the upstream region of the *CAT* gene. AAGGAG was designed as the RBS and the 17 bp-long sequences as the spacers between the -35 and -10 boxes. *hup*-terminator; terminator of a *hup* gene in *Bifidobacterium longum* NCC2705 strain. *Spr^r*; a resistance gene of spectinomycin. *ColE1*; a replication origin for *Escherichia coli*. *repB*; a replication origin for *B. longum*. *ori Ts*; a temperature-sensitive replication origin. *CAT*; a gene coding region of chloramphenicol acetyltransferase.

A

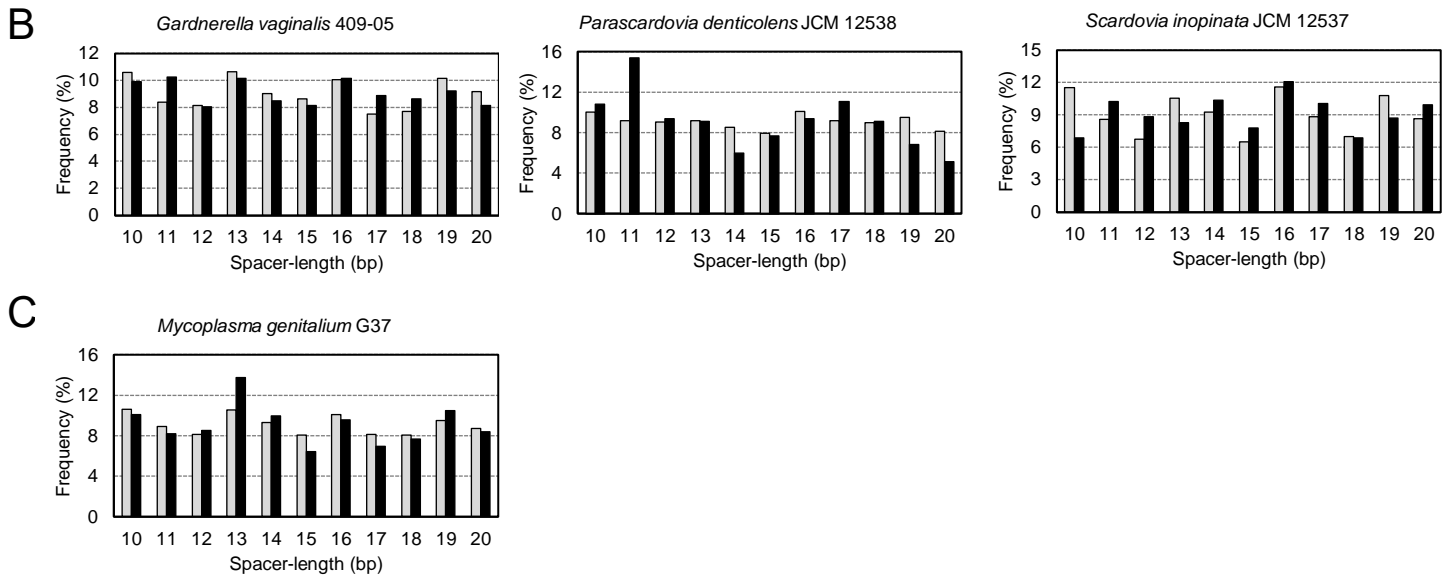


Fig. S4. Comparison of the frequency of spacer-lengths among bacteria.

A; Comparison among the genus *Bifidobacterium*. Two peaks of 11 and 17 bp was shown in the genus *Bifidobacterium*. Fig. 2D is based on these values. B; Comparison among the family Bifidobacteriaceae. Two peaks of 11 and 17 bp was shown in *Gardnerella*, *Parascardovia*, and *Scardovia*. C; the frequency of spacer-length in *Mycoplasma*, showing a specific peak in 13 bp. Gray and black bars represent frequencies in other regions and regions 150 bp upstream of genes.

Domain 2_Alternative sigma	K R A R F E Q L A M P A V N A L Y R Q A M R L T N D P D D A Q D L V Q D T - - - F E R G F K A F D S F Q P G S N F E A W
Domain 2_primary sigma	- - K A K D H L L E A N L R L V V S L A K R Y T G R G M L F L D L I Q E G N L G L I R A V E K F D - W K K G F K F S T Y
	: : * . . : . : * * * . * * : * : : * . . : * * : : * : * . : :
Domain 2_Alternative sigma	M T T I E R N A Y F N Q Y A K A K R R P Q R A N D S T G E Y D D W D I Y D A A E H
Domain 2_primary sigma	A T W W I R Q A I T R A M A D Q A R - T I R V P V H M V E V I - - - - - - - - - -
	* * * : * . * . * . * . * . *
<hr/>	
Domain 4_Alternative sigma	T S D G L K S A E E E Y L D A F A P E E I M A A L A K L S P E R R Q V F I D A A I D G K S Y Q Q - V A D E Q G V K I G T
Domain 4_primary sigma	P S D A V A F S - - - - - L L Q E Q F K Q V L E T L S P - R E A G V I K M R Y G L E D G Q P K T L D D I G R V Y G V
	. * * . : : : : * : : . * . * * * * . * . . : . * . * : * * * .
Domain 4_Alternative sigma	V M S R L N R A R T Q L K R E L A S Y A K
Domain 4_primary sigma	T R E R I R - - - Q I E S K T M S K L R
	. . * : . * : : : * : :

Fig. S5. The alignment of sigma factors of the genus *Bifidobacterium*.

Alternative sigma; alternative sigma factor in *B. longum* NCC2705 (BL1357). Primary sigma; primary sigma factor in *B. longum* NCC2705 (BL1428), corresponding to sigma 70 in *E. coli*. Domain 2 and 4 relate to the recognition of -10 and -35 boxes.

longum - - - - - M A T K E T T A T K Q T A E S S - - - - - E E T E T K K K A S S T T T A R K T S A K K
breve - - - - - M A T K E T T A T K Q T A E S S - - - - - E E T E T K K K A S S - T T A R K T S A K K
catenulatum - - - - - M A T K E T T A S M E - - - - - Q A D L T E K T T S T K K A A T R K A S T K
kashiwanohense - - - - - M A T K E T T A S M E - - - - - Q A D L T E K T T S T K K A A T R K A S T K
pseudocatenulatum - - - - - M A T K E T T A S M E - - - - - Q A D L T E K T T S T K K A A T R K A S T K
dentium - - - - - M A T K E T T A S T E - - - - - Q A D L T D K T T S T K K A P S R K A S T K
adolescentis M V Y A S G G I N R R I S L A T K E T T V N T E - - - - - Q T D L T E K T T S G K K A S T R K P A A K
thermophilum - - - - - M A - K E T T A S K K - - - - - D A D Q T E K T T S T R K S A A K K A A T P
bifidum - - - - - M A T K D T M A T T V P D D T D A K T K S E K K G T A A R T A S T A D K K T A A G R K S A A G
scardovii - - - - - M A K K D A K A T T D - - - - - N A E Q L D K A T S T K R K A A S A
angulatum - - - - - M A T K S T T A A E N - - - - - T E Q V Q D E A K A V S A K K A S A T R
animalis - - - - - M V A K E T T S T E K A A K K K A - - - - - S E S A H D E A A V E E K G K T T R R R A S S K
choerinum - - - - - M A T K R T A N T K D K S E D K D - - - - - T S T V E G A S A T K E T S A K P A K R T R - K
pseudolongum - - - - - M W R R N S L V T K Q T S N A A K K S E G K T - - - - - S S T K A D E A Q Q E D E T T A K K P A K - -
indicum - - - - - M A T K D T K S V K T A E V D A E - - - - - E A K T P S T S G K D R S Q K G D K A K
coryneforme - - - - - M A T K D T K S V K T A E V D A E - - - - - E A K T P S T S G K D R S Q K G D K A K
asteroides - - - - - M A T K D T K S A K T A A V D T G - - - - - K G R T S S T A G - - - - - K T K
actinocoloniiforme - - - - - M A A P A K T K A R K V P S K G G A - - - - - K S S S S S T R K A K G S S K S A A S S

longum S K S A E - - P S K K T T R K S A A K K T A K K A K D D E L V K D E D T Q V D D E L D D D A E V - - - - -
breve T K D T K G T T A A K T G E K T S R K T S A K K V K K E E E L P Q N D I S Q S D D P E D - - - - -
catenulatum K S A A K K T P A T K T P R K T T A K K S A P A K K - E E E Q I E D D V L D D E D A Q - - - - -
kashiwanohense K S A A K K T P A T K T P R K T T A K K S A P A K K - E E E Q I E N D A L D D E D A Q - - - - -
pseudocatenulatum K S A A K K T T A T K T P R K T T A K K S A P A K K - E E P - L E D D A L D D E D A Q - - - - -
dentium K A A D K K T P A T K T P R K T T A K K K A P A K R Q E I T A N D P D V G E D V L D D E - - - - -
adolescentis K S E S S K T - A T K T S R K T A A K K T S A A K K S K K A E E E E E N L I E Q D A P E D - - - - -
thermophilum A K A T K R S A T S A S A K K T A A A K S A K T S K A A K A S G G E S A A P K A K K K A S R T A T A T K T - - - - -
bifidum K K T S S R S A A S K S T V R E S S A K A A A P A K P T R K R A A S K S A K A V K D E T E E M A - - - - -
scardovii G R K P S R K G A T K K A S D T A R K V T A K E D P I T A N D P D V G E D V L D D E - - - - -
angulatum K T A A A K K T T A K K T A K S G E G T G S V R K K S A A T K S T K N S K T K K R S E E D - - - - -
animalis A S S A K K G S A G K T T K R A T A R K K K D A A E S E S T P A R K T R A A S K T G A K K A I S - - - - -
choerinum S T S A K S G - - - - A R K G T A K K S S A S A Q A E A T K Q P R K S T A K K K T A K K E T T G - - - - -
pseudolongum - - - - - R T T R K S T A K K T A K A A S - - - - - Q T K A P K K T T A R K S A S K - - - - -
indicum T G T R A K G K T A T P T K K S A A K K T A A A K A S S N K S G A T A E K E S V E G S S T G K S K S T G A R K S S A K K
coryneforme T G T R A K G K T A T P T K K S A A K K T A A A K A S S N K S G A T A E K E S V E G S S T G K S K S T G A R K S S A K K
asteroides T A T R S K T S S S K A S H K T S S R K T A T A S T S T A K - - - - -
actinocoloniiforme S K A R S S K T T T K A T V K T K A S K - - - - -

longum - - - - - N D D D L D V D D L D E D L D D V D E D - - - - - D
breve - - - - - L D V D N L D E D L D D V E S E - - - - - D
catenulatum - - - - - V D D P D L D D F D D D L D D V D S - - - - -
kashiwanohense - - - - - V D D P L D D F D D D L D D V D S - - - - -
pseudocatenulatum - - - - - V D D A D L D D F D A D L D D V D S - - - - -
dentium - - - - - V D E A D L D D F D D D L D D V D A E - - - - -
adolescentis - - - - - D P V E D A D L D D F D D D L D D V D D E - - - - -
thermophilum - - - - - P R K R T A K R T E P A A A E H D E T Q L D D E D E D I N D E D I E N - - - - F D D L D E
bifidum - - - - - K T E E L A N E D S S D D L D D V Q V D E D G L E N L D D D L D D V D D G G L
scardovii - - - - - D Q D G E A D L D D L E D D E S G L D - - - - -
angulatum - - - - - L D E V D E F D E D A D L D D A K D E D - - - - - L D
animalis - - - - - K S E E I D D E D M I G - - - - - E D V I D E E - - - - - D L D L D E D
choerinum - - - - - H A A Q P E D D E D V M L D D D D E Q I D E D - - - - - S L D L D E D
pseudolongum - - - - - P K D D E P V D D D E V M I D E E D I D L D D - - - - - D L E D V D D
indicum S A A K T G T T K K T S G K S T S T K A G K T T D - K P V D D A I L E D Q T G E D E F D V T D I D E N G T P E S D E L D
coryneforme S A A K T G T T K K T S G K S T S T K A G K T T D N K P V D D A I L E D Q T G E D E F D V T D I D E N G T P E S D E L D
asteroides - - - - - T N R R P A S K T S K K V E E E P I L Q Q E E Q E P D E D L L E D Q E D - - - - - D D Q L D
actinocoloniiforme - - - - - S S E H D E A L E D K A P E E L E E D Q E L D I D D L E E G - - - - -

longum A D - - - - D E D L D E D D A D D D D V E D D E D E E E A K S K A P E Q - - - - P K E K G A Y V V S D T D D E E E - N
breve V D D L E D A D A E S D D E D I D D E D D E D E D E G K A A S K A P E Q - - - - P K E K G A Y V V S D T D D E E E - N
catenulatum - D D D D L D D D E E S E P E D D - - - - D D E - - E E R K K P E E - - - - - P K E K G A F V V R D D D D D E - - N
kashiwanohense - D D D D L D D D E E S E P E D D - - - - D D E D E E E R K K P E E - - - - - P K E K G A F V V R D D D D D E - - N
pseudocatenulatum - D D E D L D D D E E S E P E D D - - - - D D E D E E E R K K P E E - - - - - P K E K G A F V V R D D D D D E - - N
dentium - D E A D L D D E D E S E P E D D - - - - E D E D D E E R K K P E E - - - - - P K E K G A F V V R D D D D D E - - N
adolescentis - G E D D L D E D N I D E D D D S E L - - - - D D D E D K R K K P E E - - - - - P K E K G A F V V R D D D D D E - - N
thermophilum G D D P D N L D D D I D S D D E D D E E G E D D S E D D E E N K P K H R E P E V L P K A K G A F V M R D D D D D - - N
bifidum D G D D D I D D E S G E D D D V P E D E D D E G T E P G R K E P E Q - - - - - P K E K G A F V V R D D D D D E - - N
scardovii - - D E D E G D E L D E D S D I A D D E D - - - - - E V K R K E P E T - - - - - P K E K G A F V V R D D D D D E - - N
angulatum V D D V D L D G I N G E S D A P D I S K Q K G A F V V S D D D D D D E - D
animalis L - D A D E N D D D L E D E E S E D E P E P E E D D - D E E P Q A P K E - - - - - P K E K G A F V V S D N D E D D E A L
choerinum L G D V D G Q D V D A D D E D D E S E P E P E E D D E D E E K K P E E - - - - - P K E K G A F V V R D D D D D E - - T
pseudolongum V D D H D H M D D E D D E H D T D D D A V E D D E D D E D P K P E E - - - - - P K A K G A F V V R D D D D D E - - T
indicum K D Q D Q L E D E P G S D D E E E H E A R E V S E E A E E D R K A A H E L A - - - - - A K V K G A F V V D D S E D D E - - S
coryneforme K D Q D Q L E D E P G S D D E E E H E A R E V S E E A E E D R K A A H E L A - - - - - A K V K G A F V V D D S E D D E - - S
asteroides K S E D Q L E D E P D E D D Q E E D E V S R V E D E A E E D R K A A H A L A - - - - - A K V K G A F V V D S D D E - - N
actinocoloniiforme - Q E D Q V E D E E P D G E V D - - - - - G N E D E E E S P K P V V T P - - - - - P D I K G A F V V S D S D D D E - - N

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	4.1																		4.2																																									
<i>longum</i>	I	A	P	S	D	A	V	A	F	S	L	L	Q	E	Q	F	K	Q	V	L	E	T	L	S	P	R	E	A	G	V	I	K	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R
<i>breve</i>	I	A	P	S	D	A	V	A	F	S	L	L	Q	E	Q	F	K	Q	V	L	E	T	L	S	P	R	E	A	G	V	I	K	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R
<i>catenulatum</i>	I	A	P	S	D	A	V	A	F	S	L	L	Q	E	Q	F	R	Q	V	L	E	T	L	S	P	R	E	A	G	V	I	K	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R
<i>kashiwanohense</i>	I	A	P	S	D	A	V	A	F	S	L	L	Q	E	Q	F	R	Q	V	L	E	T	L	S	P	R	E	A	G	V	I	K	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R
<i>pseudocatenulatum</i>	I	A	P	S	D	A	V	A	F	S	L	L	Q	E	Q	F	R	Q	V	L	E	T	L	S	P	R	E	A	G	V	I	K	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R
<i>dentium</i>	I	A	P	S	D	A	V	A	F	S	L	L	Q	E	Q	F	K	Q	V	L	E	T	L	S	P	R	E	A	G	V	I	K	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R
<i>adolescentis</i>	I	A	P	S	D	A	V	A	F	S	L	L	Q	E	Q	F	K	Q	V	L	E	T	L	S	P	R	E	A	G	V	I	K	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R
<i>thermophilum</i>	I	A	P	S	D	A	V	A	F	S	L	L	Q	E	Q	F	K	Q	V	L	E	T	L	S	P	R	E	A	G	V	I	K	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R
<i>bifidum</i>	I	A	P	S	D	A	V	A	F	S	L	L	Q	E	Q	F	K	Q	V	L	E	T	L	S	P	R	E	A	G	V	I	K	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R
<i>scardovii</i>	I	A	P	S	D	A	V	A	F	S	L	L	Q	E	Q	F	K	Q	V	L	E	T	L	S	P	R	E	A	G	V	I	R	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R
<i>angulatum</i>	I	A	P	S	D	A	V	A	F	S	L	L	Q	D	Q	F	K	Q	V	L	E	T	L	S	P	R	E	S	G	V	I	K	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R
<i>animalis</i>	I	A	P	S	E	A	V	A	F	S	L	L	Q	E	Q	F	R	Q	V	L	E	T	L	S	P	R	E	A	G	V	I	K	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R
<i>choerinum</i>	I	A	P	S	D	A	V	A	F	S	L	L	Q	E	Q	F	R	Q	V	L	E	T	L	S	P	R	E	A	G	V	I	K	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R
<i>pseudolongum</i>	I	A	P	S	D	A	V	A	F	S	L	L	Q	E	Q	F	K	Q	V	L	E	T	L	S	P	R	E	A	G	V	I	K	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R
<i>indicum</i>	I	A	P	S	D	A	V	A	F	S	L	L	Q	E	Q	F	K	Q	V	L	E	T	L	S	P	R	E	A	G	V	I	K	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R
<i>coryneforme</i>	I	A	P	S	D	A	V	A	F	S	L	L	Q	E	Q	F	K	Q	V	L	E	T	L	S	P	R	E	A	G	V	I	K	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R
<i>asteroides</i>	I	A	P	S	D	A	V	A	F	S	L	L	Q	E	Q	F	R	Q	V	L	E	T	L	S	P	R	E	A	G	V	I	K	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R
<i>actinocoloniiforme</i>	I	A	P	S	D	A	V	A	F	S	L	L	Q	E	Q	F	K	Q	V	L	E	T	L	S	P	R	E	A	G	V	I	K	M	R	Y	G	L	E	D	G	Q	P	K	T	L	D	D	I	G	R	V	Y	G	V	T	R	E	R	I	R

<i>longum</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	R	D	F	L	D	Q
<i>breve</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	R	D	F	L	D	Q
<i>catenulatum</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	R	D	F	L	D	Q
<i>kashiwanohense</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	R	D	F	L	D	Q
<i>pseudocatenulatum</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	R	D	F	L	D	Q
<i>dentium</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	R	D	F	L	D	Q
<i>adolescentis</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	R	D	F	L	D	Q
<i>thermophilum</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	R	D	F	L	D	Q
<i>bifidum</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	R	D	F	L	D	Q
<i>scardovii</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	S	D	F	L	D	Q
<i>angulatum</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	R	D	F	L	D	Q
<i>animalis</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	R	D	F	L	D	Q
<i>choerinum</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	R	D	F	L	D	Q
<i>pseudolongum</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	R	D	F	L	D	Q
<i>indicum</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	R	D	F	L	D	Q
<i>coryneforme</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	R	D	F	L	D	Q
<i>asteroides</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	R	D	S	L	D	Q
<i>actinocoloniiforme</i>	Q	I	E	S	K	T	M	S	K	L	R	H	P	S	R	S	Q	T	L	R	D	F	L	D	Q

Fig. S6. The alignment of sigma factors of the genus *Bifidobacterium*.

The alignment of primary sigma factors of the 18 bacteria belonging to the genus *Bifidobacterium*. Amino acids in N-terminal regions are colored as the positively charged amino acids K, R, H (blue), the negatively charged amino acids D, E (red), and the non-charged polar amino acids N, S, T, and Q (yellow).

<i>Bifidobacterium longum</i>	1 M A T K E T T A T K Q T A E S S E E T E T K K K A S S T T T A R K T S A K K S K S A E S K K T T R K S A A K K T A K K	60
	61 A K D D E L V K D E D T Q V D D E L D D D A E V N D D D L D V D D L D E D L D D V D E D D A D D E D L D E D D A D D D D	120
	121 V E D D E E E A K S A P E Q P K E K	141
<i>Bifidobacterium breve</i>	1 M A T K E T T A T K Q T A E S S E E T E T K K K A S S T T A R K T S A K K T K D T K G T T A A K T G E K T S R K T S A K	60
	61 K V K K E E E L P Q N D I S Q S D D P E D L D V D N L D E D L D D V E S E D V D D L E D A D A E S D D E D I D D E D D E	120
	121 D E D E G K A A S K A P E Q P K E K	139
<i>Gardnerella vaginalis</i>	1 M T S E V G L T V D S D E M Q D D T K P V K T R K A S V A R K T S T R T S S A D S K T R S S R S K K T E D N K I D T E S	60
	61 V S A D A E H D E T E D S V D I E S Q D Q L S I D D P L D D S H L D V G D E H L N L D D L D D I Q P E D I S D V D D L	120
	121 S D I V A D D L D D E E S E D L D E I D D H D E I K H D A P Q V P Q A K	157
<i>Scardovia inopinata</i>	1 M V A A K K T D A G I G E E P V S S G T T V S K T G K K V K S S A K K S S A K T G A Q K S T A K T S S A K K S T A K T	60
	61 A S T K K T S A K K T A S T R K T V K K K P A V E D D Q K K T S Q S T S A H S A E G K S S Q K T A S K S K K A A S K K	120
	121 S S A I K S A N E E P Q T S S R K T H K K Q D D L S H V P E K G S E S Q T G T H D E D I R S L D S L D A G N Q T D T D I	180
	181 P V E D D D I D E G I G P G D E R S N A L D H I D D S V E L D E N G D P I S P D D S D I L A D A E E K D L E E E E D	240
	241 E G R A E E K Q P V E E	252
<i>Parascardovia denticolens</i>	1 M A T K K T V T D A N P T V V S E I D A S V K G S E V K I S R T K T K K A T G K K A T A S K K T T V K K P S S K A	60
	61 A S A K A T S A K A K S D K T E S G V E P V A E K D V A S T Q K P A K A K K S V A S D K A E K S A E S N K G K S A K T	120
	121 V K S D K T E A E D S A K T V K S T S A T A K A P T K A S R S S T S A K A S S T E A K E A Q S K A A E P T	180
	181 A A K T G K S R K T D E T E K E E G K A S A K K T T S K A S A K K V A A K T S E K T G K S S A K S A E K T E D E D L	240
	241 P A E E A S A E E G K V E E D K V D E S T A S D E D D Q S L N D D D M D G D L G P G S H A V N A L D H I D D S V E L	300
	301 D E N G D P I Q E D D E N I V T D S E E K D L E D E G D E E E A P V E K K P L E E	342
<i>Mycobacterium tuberculosis</i>	1 M A T K A S T A T D E P V K R T A T K S P A A S A G A K T G A K R T A A K S A S G S P P A K R A T K P A A R S V K P	60
	61 A S A P Q D T T S T I P K R K T R A A A K S A A K A P S A R G H A T K P R A P K D A Q H E A A T D P E D A L D S V E	120
	121 E L D A E P D L D V E P G E D L D L A A L N L D D L E D D V A P D A D D L D S G D D E D H E D L E A E A V A P G	180
	181 Q T A D D D E E I A E P T E K D K A S	199
<i>Mycobacterium smegmatis</i>	1 M A T K A S P A T E E P V K R T A T K T P A K K A P A K R A A K S A A A K A G G K A P A K K A P A K R A A K G T A A K	60
	61 P E D G V T D D L E V T D D L E A E P G E D L D V E D T L E L D D L D S D D D T A V E D E E E A D A A T P A V A T A	120
	121 K A A D D D I D E P S E K D K A S	137
<i>Corynebacterium glutamicum</i>	1 M E S S M V E N N V A K K T V A K K T A R K A A P R V A T P L G V A S E S P I S A T P A R S I D G T S T P V E A	60
	61 A D T I E T T A P A A K A P A A K A P A K K T A R K A P A K K T V A K K A T T A K A A P A T A K D E N A P V D D	120
	121 D E E N L A Q D E Q D F D G D D F V D G I E D E E D E D G V E A L G E E S E D D E E D	163
<i>Streptomyces coelicolor</i>	1 M S A S T S R T L P P E I A E S S V M A L I E R G K A E G Q I A G D D V R R A F E A D Q I P A T Q W K N V L R S L N Q	60
	61 I L E E E G V T L M V S A A E P K R T R K S V A A K S P A K R T A T K A V A A K P V T S R K A T A P A A P A P A T E P	120
	121 A A V E E E A P A K K A A A K K T T A K K A T A K K A A A K K T T A K K E D G E L L E D E A T E E P K A A T E	180
	181 E P E G T E N	187

Fig. S7. The amino acid sequences of N-terminal regions of sigma factors of the phylum Actinobacteria.

Alignment of N-terminal sequences of primary sigma factors of the nine bacteria belonging to the phylum Actinobacteria. Amino acids in N-terminal regions are colored as the positively charged amino acids K, R, H (blue), the negatively charged amino acid D, E (red), and the non-charged polar amino acids N, S, T, and Q (yellow).

Table S1. The plasmids and primers.

	Type	Properties	Reference	
Plasmids	pKO403- <i>lacZ</i>	4,473 bp, Ori ^{ts} , <i>lacZ</i> , Sp ^r	(1)	
	pKO403-TPCTcon	4,913 bp, Ori ^{ts} , Sp ^r , Cm ^r , TTGTGC-spacer (17 bp)-TACAAT	This study	
	pKO403-TPCT1-3	4,913 bp, Ori ^{ts} , Sp ^r , Cm ^r , vTTGTGC-spacer (17 bp)-TACAAT	This study	
	pKO403-TPCT4-6	4,913 bp, Ori ^{ts} , Sp ^r , Cm ^r , TvTTGTGC-spacer (17 bp)-TACAAT	This study	
	pKO403-TPCT7-9	4,913 bp, Ori ^{ts} , Sp ^r , Cm ^r , TThTGC-spacer (17 bp)-TACAAT	This study	
	pKO403-TPCT10-12	4,913 bp, Ori ^{ts} , Sp ^r , Cm ^r , TTGvGC-spacer (17 bp)-TACAAT	This study	
	pKO403-TPCT13-15	4,913 bp, Ori ^{ts} , Sp ^r , Cm ^r , TTGTThC-spacer (17 bp)-TACAAT	This study	
	pKO403-TPCT16-18	4,913 bp, Ori ^{ts} , Sp ^r , Cm ^r , TTGTGd-spacer (17 bp)-TACAAT	This study	
	pKO403-TPCT19-21	4,913 bp, Ori ^{ts} , Sp ^r , Cm ^r , TTGTGC-spacer (17 bp)-vACAAT	This study	
	pKO403-TPCT22-24	4,913 bp, Ori ^{ts} , Sp ^r , Cm ^r , TTGTGC-spacer (17 bp)-TbCAAT	This study	
	pKO403-TPCT25-27	4,913 bp, Ori ^{ts} , Sp ^r , Cm ^r , TTGTGC-spacer (17 bp)-TAvAAT	This study	
	pKO403-TPCT28-30	4,913 bp, Ori ^{ts} , Sp ^r , Cm ^r , TTGTGC-spacer (17 bp)-TACbAT	This study	
	pKO403-TPCT31-33	4,913 bp, Ori ^{ts} , Sp ^r , Cm ^r , TTGTGC-spacer (17 bp)-TACAbT	This study	
	pKO403-TPCT34-36	4,913 bp, Ori ^{ts} , Sp ^r , Cm ^r , TTGTGC-spacer (17 bp)-TACAAv	This study	
	pK0403-TPCT-10bp	4,906 bp, Ori ^{ts} , Sp ^r , Cm ^r , TTGTGC-spacer (10 bp)-TATAAT	This study	
	pK0403-TPCT-11bp	4,907 bp, Ori ^{ts} , Sp ^r , Cm ^r , TTGTGC-spacer (11 bp)-TATAAT	This study	
	pK0403-TPCT-12bp	4,908 bp, Ori ^{ts} , Sp ^r , Cm ^r , TTGTGC-spacer (12 bp)-TATAAT	This study	
	pK0403-TPCT-15bp	4,911 bp, Ori ^{ts} , Sp ^r , Cm ^r , TTGTGC-spacer (15 bp)-TATAAT	This study	
	pK0403-TPCT-16bp	4,912 bp, Ori ^{ts} , Sp ^r , Cm ^r , TTGTGC-spacer (16 bp)-TATAAT	This study	
	pK0403-TPCT-18bp	4,914 bp, Ori ^{ts} , Sp ^r , Cm ^r , TTGTGC-spacer (18 bp)-TATAAT	This study	
pK0403-TPCT-19bp	4,915 bp, Ori ^{ts} , Sp ^r , Cm ^r , TTGTGC-spacer (19 bp)-TATAAT	This study		
Primers	Fw_-35	TCACTACAGAGTCGGACTACAATCA	This study	
	(5' → 3')	Rv_-35_mu1-3	GCACAbTGCCCGCGTTTTATA	This study
	Rv_-35_mu4-6	GCACbATGCCCGCGTTTTATA	This study	
	Rv_-35_mu7-9	GCAdAATGCCCGCGTTTTATA	This study	
	Rv_-35_mu10-12	GCbCAATGCCCGCGTTTTATA	This study	
	Rv_-35_mu13-15	GdACAATGCCCGCGTTTTATA	This study	
	Rv_-35_mu16-18	hCACAATGCCCGCGTTTTATA	This study	
	Rv_-10	GAGCACAATGCCCGCGTTTTA	This study	
	Fw_-10_mu1-3	ACTACAGAGTCGGACvACAATCATTGA	This study	
	Fw_-10_mu4-6	ACTACAGAGTCGGACTbCAATCATTGA	This study	
	Fw_-10_mu7-9	ACTACAGAGTCGGACTAdAATCATTGA	This study	
	Fw_-10_mu10-12	ACTACAGAGTCGGACTACbATCATTGA	This study	
	Fw_-10_mu13-15	ACTACAGAGTCGGACTACAbTCATTGA	This study	
	Fw_-10_mu16-18	ACTACAGAGTCGGACTACAAvCATTGA	This study	
	Fw_-10	ACTACAGAGTCGGACTACAATCATTGA	This study	

Fw_spacer19	GTACCGGACTATAATCATTGATG	This study
Fw_spacer18	GTACGGACTATAATCATTGATG	This study
Fw_spacer16	GCGGACTATAATCATTGATG	This study
Fw_spacer15	CGGACTATAATCATTGATG	This study
Rv_spacer15-19	TCTGTAGTGAGCACAATG	This study
Fw_spacer10-12	CGGACTATAATCATTGATGACAACA	This study
Rv_spacer12	GTAGTGAGCACAATGCCC	This study
Rv_spacer11	TAGTGAGCACAATGCCCG	This study
Rv_spacer10	AGTGAGCACAATGCCCG	This study

Table S2. The bacterial strains of the genus *Bifidobacterium*.

	Type	Properties	GenBank
<i>Bifidobacterium</i>	<i>longum</i> NCC2705	RNA-Seq sample, Transformation host, Informatics analysis	Nantes Culture Collection, AE014295.3
	<i>actinocoloniiforme</i> DSM 22766 ^T	Informatics analysis	CP011786
	<i>adolescentis</i> ATCC 15703	Informatics analysis	AP009256
	<i>angulatum</i> JCM 1194 ^T	Informatics analysis	AP012322
	<i>animalis</i> strain RH	Informatics analysis	CP007755
	<i>asteroides</i> PRL 2011	Informatics analysis	CP003325
	<i>bifidum</i> S17	Informatics analysis	CP002220
	<i>breve</i> UCC 2003	Informatics analysis	CP000303
	<i>catenulatum</i> JCM 1194 ^T	Informatics analysis	AP012325
	<i>choerinum</i> FMB-1	Informatics analysis	CP018044
	<i>coryneform</i> strain LMG 18911 ^T	Informatics analysis	CP007287
	<i>dentium</i> JCM 1195 ^T	Informatics analysis	AP012326
	<i>indicum</i> LMG 11587 ^T	Informatics analysis	CP006018
	<i>kashiwanohense</i> PV20-2	Informatics analysis	CP007456
	<i>pseudocatenulatum</i> JCM 1200 ^T	Informatics analysis	AP012330
	<i>pseudolongum</i> PV8-2	Informatics analysis	CP007457
	<i>scardovii</i> JCM 12489 ^T	Informatics analysis	AP012331
	<i>thermophilum</i> RBL67	Informatics analysis	CP004346

Table S3. The genes with 11 bp type spacer in the upstream regions.

Gene	Function
<i>BL0001</i>	cold-shock protein
<i>BL0004</i>	hypothetical protein
<i>BL0017</i>	histidyl-tRNA synthetase
<i>BL0047</i>	polyphosphate glucokinase
<i>BL0060</i>	trans-aconitate 2-methyltransferase
<i>BL0065</i>	elongation factor P
<i>BL1292</i>	morphine 6-dehydrogenase
<i>BL1422</i>	anthranilate phosphoribosyltransferase
<i>BL1431</i>	ribokinase
<i>BL1432</i>	ATP-dependent helicase II
<i>BL1444</i>	EamA-like transporter family
<i>BL0702</i>	excinuclease ABC subunit A
<i>BL0712</i>	lanine-synthesizing transaminase
<i>BL0724</i>	threonyl-tRNA synthetase
<i>BL0739</i>	UTP-glucose-1-phosphate uridylyltransferase
<i>BL0745</i>	hypothetical protein
<i>BL0766</i>	hypothetical protein
<i>BL0815</i>	hypothetical protein
<i>BL0854</i>	hypothetical protein
<i>BL0872</i>	ABC transporter
<i>BL0969</i>	acetate kinase
<i>BL0992</i>	30S ribosomal protein S1
<i>BL0993</i>	methenyltetrahydrofolate cyclohydrolase
<i>BL1026</i>	peptidyl-tRNA hydrolase
<i>BL1107</i>	phosphoribosylaminoimidazole-succinocarboxamide synthase
<i>BL1118</i>	amino acid ABC transporter substrate-binding protein
<i>BL1151</i>	hypothetical protein
<i>BL1164</i>	sugar ABC transporter solute-binding protein
<i>BL1175</i>	glucosamine--fructose-6-phosphate aminotransferase
<i>BL1194</i>	4-hydroxy-tetrahydrodipicolinate reductase
<i>BL1229</i>	tyrosine kinase
<i>BL0294</i>	50S ribosomal protein L32
<i>BL0319</i>	phospho-2-dehydro-3-deoxyheptonate aldolase
<i>BL0330</i>	50S ribosomal protein L28
<i>BL0458</i>	hypothetical protein
<i>BL0477</i>	hypothetical protein

BL0492 aspartate-semialdehyde dehydrogenase
BL0525 LacI-type transcriptional regulator
BL0557 hypothetical protein
BL0564 modification methylase Sau3AI
BL0600 tryptophanyl-tRNA synthetase
BL0617 putative hemolysin
BL0681 transporter
BL0145 hypothetical protein
BL0160 MarR-type transcriptional regulator
BL0181 alpha-arabinofuranosidase I
BL0202 hypothetical protein
BL1530 IclR-type transcriptional regulator
BL1567 hypothetical protein
BL1609 hypothetical protein
BL1652 arabinose polymer utilization protein
BL1657 two-component system response regulator
BL1661 hypothetical protein
BL1694 sugar ABC transporter substrate-binding protein
BL1723 oligoribonuclease
BL1728 prolyl-tRNA synthetase
BL1732 methionine aminopeptidase
BL1745 hypothetical protein
BL1765 MarR-type transcriptional regulator

Perl script for spacer analysis

open (IN,"<genome.txt"); #genome.txt is FASTA format file of bacterium whole-genome.

open (OUT,">A_total-genome.txt");

open (OUT2,">B_total-genome_rev.txt");

while (<IN>) {

 s/^>.+\n/\n/;

 print OUT;

 tr/TAGC/ATCG/;

 print OUT2;

}

close(IN);

close(OUT);

close(OUT2);

open (IN, "<cds_GB.txt"); #cds_GB.txt is GB format file of bacterium.

open (OUT, ">C_gene_locus.txt");

while (\$file = <IN>) {

 if(\$file =~ /^ +CDS +complement\{([0-9]+\.\{([0-9]+\)\})\}{

 \$cds_comp = \$1;

 print OUT "gene\t";

 print OUT \$cds_comp;

 print OUT "\t-\n";

 }

 elsif(\$file =~ /^ +CDS +\{([0-9]+\.\{([0-9]+\)\})\}{

 \$cds_comp = \$1;

 print OUT "gene\t";

 print OUT \$cds_comp;

 print OUT "\t+\n";

 }

}

close(IN);

close(OUT);

\$X = 150; #\$X is the length of upstream regions you extract.

open (IN,"<A_total-genome.txt");

open (IN2,"<B_total-genome_rev.txt");

open (IN3,"<C_gene_locus.txt");

open (OUT,">D_up_150_region.txt");

@genome = <IN>;

chomp @genome;


```

$genome = join("",@genome);
@genome_rev = <IN2>;
chomp @genome_rev;
$genome_rev = join("",@genome_rev);
@line = <IN3>;
chomp @line;
for($i=0;$i<@line;$i++){
    if(@line[$i] =~ /(gene\t)(\d+)(\t)/){
        $start = $2 - $X - 1;
        $sequence = substr($genome,$start,$X);
        print OUT $sequence;
        print OUT "\n";
    }
    if(@line[$i] =~ /(gene\t)(\d+)(\t-)/){
        $start = $2 ;
        $sequence =reverse substr($genome_rev,$start,$X);
        print OUT $sequence;
        print OUT "\n";
    }
}
}
close(IN);
close(IN2);
close(IN3);
close(OUT);

```

```

open(OUT, '> F_spacer-count_upstream.txt');
print OUT "Seq\tNo\n";
open(IN, '< D_up_150_region.txt') or die;
while (<IN>){
$Zero++ while (/TTG[A-Z]{3}TA[A-Z]{3}T/g);
$One++ while (/TTG[A-Z]{4}TA[A-Z]{3}T/g);
$Two++ while (/TTG[A-Z]{5}TA[A-Z]{3}T/g);
$Three++ while (/TTG[A-Z]{6}TA[A-Z]{3}T/g);
$Four++ while (/TTG[A-Z]{7}TA[A-Z]{3}T/g);
$Five++ while (/TTG[A-Z]{8}TA[A-Z]{3}T/g);
$Six++ while (/TTG[A-Z]{9}TA[A-Z]{3}T/g);
$Seven++ while (/TTG[A-Z]{10}TA[A-Z]{3}T/g);
$Eight++ while (/TTG[A-Z]{11}TA[A-Z]{3}T/g);
$Nine++ while (/TTG[A-Z]{12}TA[A-Z]{3}T/g);
$Ten++ while (/TTG[A-Z]{13}TA[A-Z]{3}T/g);

```

```
$Eleven++ while (/TTG[A-Z]{14}TA[A-Z]{3}T/g);
$Twelve++ while (/TTG[A-Z]{15}TA[A-Z]{3}T/g);
$Thirteen++ while (/TTG[A-Z]{16}TA[A-Z]{3}T/g);
$Fourteen++ while (/TTG[A-Z]{17}TA[A-Z]{3}T/g);
$Fifteen++ while (/TTG[A-Z]{18}TA[A-Z]{3}T/g);
$Sixteen++ while (/TTG[A-Z]{19}TA[A-Z]{3}T/g);
$Seventeen++ while (/TTG[A-Z]{20}TA[A-Z]{3}T/g);
$Eighteen++ while (/TTG[A-Z]{21}TA[A-Z]{3}T/g);
$Nineteen++ while (/TTG[A-Z]{22}TA[A-Z]{3}T/g);
$Twenty++ while (/TTG[A-Z]{23}TA[A-Z]{3}T/g);
$Twe1++ while (/TTG[A-Z]{24}TA[A-Z]{3}T/g);
$Twe2++ while (/TTG[A-Z]{25}TA[A-Z]{3}T/g);
$Twe3++ while (/TTG[A-Z]{26}TA[A-Z]{3}T/g);
$Twe4++ while (/TTG[A-Z]{27}TA[A-Z]{3}T/g);
$Twe5++ while (/TTG[A-Z]{28}TA[A-Z]{3}T/g);
}
print OUT "0bp¥t$Zero¥n";
print OUT "1bp¥t$One¥n";
print OUT "2bp¥t$Two¥n";
print OUT "3bp¥t$Three¥n";
print OUT "4bp¥t$Four¥n";
print OUT "5bp¥t$Five¥n";
print OUT "6bp¥t$Six¥n";
print OUT "7bp¥t$Seven¥n";
print OUT "8bp¥t$Eight¥n";
print OUT "9bp¥t$Nine¥n";
print OUT "10bp¥t$Ten¥n";
print OUT "11bp¥t$Eleven¥n";
print OUT "12bp¥t$Twelve¥n";
print OUT "13bp¥t$Thirteen¥n";
print OUT "14bp¥t$Fourteen¥n";
print OUT "15bp¥t$Fifteen¥n";
print OUT "16bp¥t$Sixteen¥n";
print OUT "17bp¥t$Seventeen¥n";
print OUT "18bp¥t$Eighteen¥n";
print OUT "19bp¥t$Nineteen¥n";
print OUT "20bp¥t$Twenty¥n";
print OUT "21bp¥t$Twe1¥n";
print OUT "22bp¥t$Twe2¥n";
print OUT "23bp¥t$Twe3¥n";
```

```
print OUT "24bp\t$Twe4\n";
print OUT "25bp\t$Twe5\n";
close(IN);
close(OUT);
```

```
open (IN,"< A_total-genome.txt");
open (IN2,"< B_total-genome_rev.txt");
open (OUT,"> E_total-genome_both.txt");
@genome = <IN>;
chomp @genome;
$genome = join("",@genome);
@genome_rev = <IN2>;
chomp @genome_rev;
$genome_rev = join("",@genome_rev);
$genome_rev = reverse($genome_rev);
print OUT "$genome\n$genome_rev";
close(IN);
close(IN2);
close(OUT);
```

```
open(OUT, '> G_spacer-count-whole.txt');
print OUT "Seq\tNo\n";
open(IN, '< E_total-genome_both.txt') or die;
while (<IN>){
$Zero++ while (/TTG[A-Z]{3}TA[A-Z]{3}T/g);
$One++ while (/TTG[A-Z]{4}TA[A-Z]{3}T/g);
$Two++ while (/TTG[A-Z]{5}TA[A-Z]{3}T/g);
$Three++ while (/TTG[A-Z]{6}TA[A-Z]{3}T/g);
$Four++ while (/TTG[A-Z]{7}TA[A-Z]{3}T/g);
$Five++ while (/TTG[A-Z]{8}TA[A-Z]{3}T/g);
$Six++ while (/TTG[A-Z]{9}TA[A-Z]{3}T/g);
$Seven++ while (/TTG[A-Z]{10}TA[A-Z]{3}T/g);
$Eight++ while (/TTG[A-Z]{11}TA[A-Z]{3}T/g);
$Nine++ while (/TTG[A-Z]{12}TA[A-Z]{3}T/g);
$Ten++ while (/TTG[A-Z]{13}TA[A-Z]{3}T/g);
$Eleven++ while (/TTG[A-Z]{14}TA[A-Z]{3}T/g);
$Twelve++ while (/TTG[A-Z]{15}TA[A-Z]{3}T/g);
$Thirteen++ while (/TTG[A-Z]{16}TA[A-Z]{3}T/g);
$Fourteen++ while (/TTG[A-Z]{17}TA[A-Z]{3}T/g);
$Fifteen++ while (/TTG[A-Z]{18}TA[A-Z]{3}T/g);
```

```
$Sixteen++ while (/TTG[A-Z]{19}TA[A-Z]{3}T/g);
$Seventeen++ while (/TTG[A-Z]{20}TA[A-Z]{3}T/g);
$Eighteen++ while (/TTG[A-Z]{21}TA[A-Z]{3}T/g);
$Nineteen++ while (/TTG[A-Z]{22}TA[A-Z]{3}T/g);
$Twenty++ while (/TTG[A-Z]{23}TA[A-Z]{3}T/g);
$Twe1++ while (/TTG[A-Z]{24}TA[A-Z]{3}T/g);
$Twe2++ while (/TTG[A-Z]{25}TA[A-Z]{3}T/g);
$Twe3++ while (/TTG[A-Z]{26}TA[A-Z]{3}T/g);
$Twe4++ while (/TTG[A-Z]{27}TA[A-Z]{3}T/g);
$Twe5++ while (/TTG[A-Z]{28}TA[A-Z]{3}T/g);
}
print OUT "0bp\t$Zero\n";
print OUT "1bp\t$One\n";
print OUT "2bp\t$Two\n";
print OUT "3bp\t$Three\n";
print OUT "4bp\t$Four\n";
print OUT "5bp\t$Five\n";
print OUT "6bp\t$Six\n";
print OUT "7bp\t$Seven\n";
print OUT "8bp\t$Eight\n";
print OUT "9bp\t$Nine\n";
print OUT "10bp\t$Ten\n";
print OUT "11bp\t$Eleven\n";
print OUT "12bp\t$Twelve\n";
print OUT "13bp\t$Thirteen\n";
print OUT "14bp\t$Fourteen\n";
print OUT "15bp\t$Fifteen\n";
print OUT "16bp\t$Sixteen\n";
print OUT "17bp\t$Seventeen\n";
print OUT "18bp\t$Eighteen\n";
print OUT "19bp\t$Nineteen\n";
print OUT "20bp\t$Twenty\n";
print OUT "21bp\t$Twe1\n";
print OUT "22bp\t$Twe2\n";
print OUT "23bp\t$Twe3\n";
print OUT "24bp\t$Twe4\n";
print OUT "25bp\t$Twe5\n";
close(IN);
close(OUT);
```

REFERENCE

1. Sakaguchi K, He J, Tani S, Kano Y, Suzuki T. 2012. A targeted gene knockout method using a newly constructed temperature-sensitive plasmid mediated homologous recombination in *Bifidobacterium longum*. Appl Microbiol Biotechnol 95:499–509.