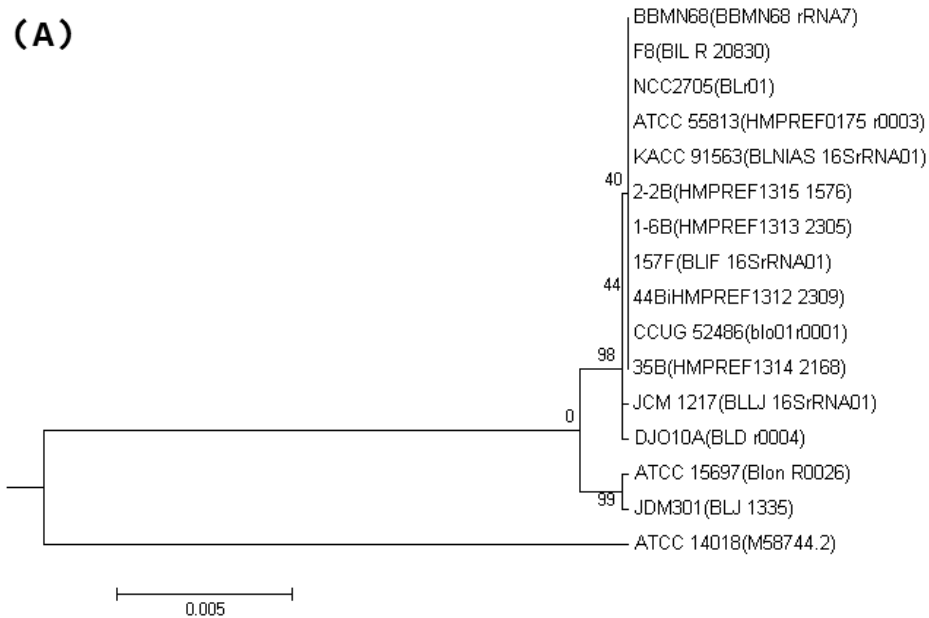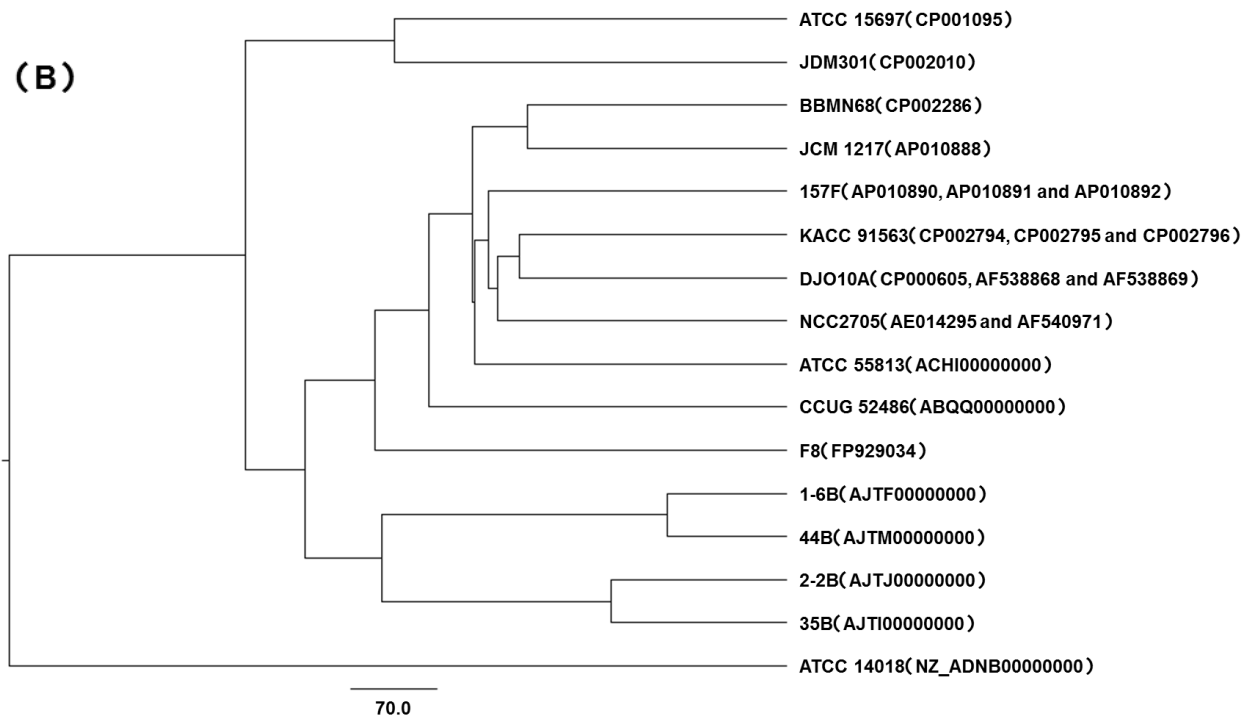1 **Supplementary file 1 – Phylogenetic tree based on (a) 16S rRNA gene sequences**
2 **and (b) whole genes of *B. longum***
3 Each phylogenetic tree was constructed using (a) the ClustalW program and (b) the

4 PGAP pipeline [21] via the neighbour-joining method. The numbers in parentheses

5 indicate the (A) locus_tag and (B) accession number

(A)

BBMN68(BBMN68 rRNA7)
F8(BIL R 20830)
NCC2705(BLr01)
ATCC 55813(HMPREF0175 r0003)
KACC 91563(BLNIAS 16SrRNA01)
40
2-2B(HMPREF1315 1576)
1-6B(HMPREF1313 2305)
157F(BLIF 16SrRNA01)
44
44BiHMPREF1312 2309)
CCUG 52486(blo01r0001)
98
35B(HMPREF1314 2168)
JCM 1217(BLLJ 16SrRNA01)
0
DJO10A(BLD r0004)
ATCC 15697(Blon R0026)
99
JDM301(BLJ 1335)
ATCC 14018(M58744.2)

0.005

6

(B)

ATCC 15697(CP001095)
JDM301(CP002010)
BBMN68(CP002286)
JCM 1217(AP010888)
157F(AP010890, AP010891 and AP010892)
KACC 91563(CP002794, CP002795 and CP002796)
DJO10A(CP000605, AF538868 and AF538869)
NCC2705(AE014295 and AF540971)
ATCC 55813(ACHI00000000)
CCUG 52486(ABQQ00000000)
F8(FP929034)
1-6B(AJTF00000000)
44B(AJTM00000000)
2-2B(AJTJ00000000)
35B(AJTI00000000)
ATCC 14018(NZ_ADNB00000000)

70.0

7

8 **Supplementary file 2 – Phylogenetic tree based on (a) 16S rRNA gene sequences**
9 **and (b) whole genes of _B. breve_**
10 Each phylogenetic tree was constructed using (A) the ClustalW program and (B) the

11 PGAP pipeline [21] via the neighbour-joining method. The numbers in parentheses

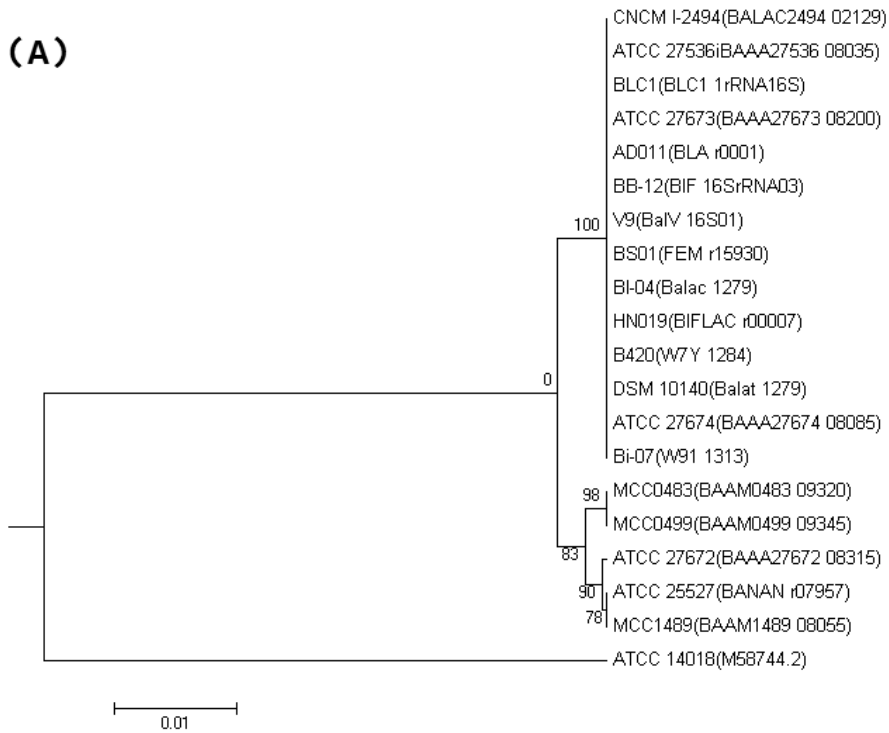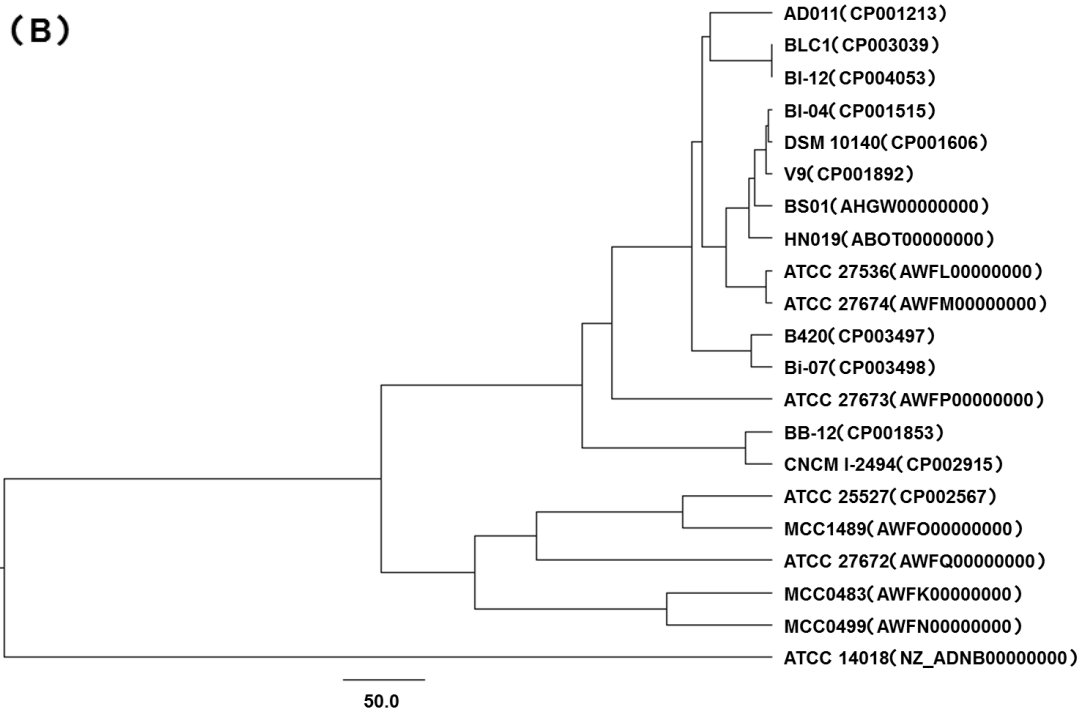12 indicate the (A) locus_tag and (B) accession number.

13

14
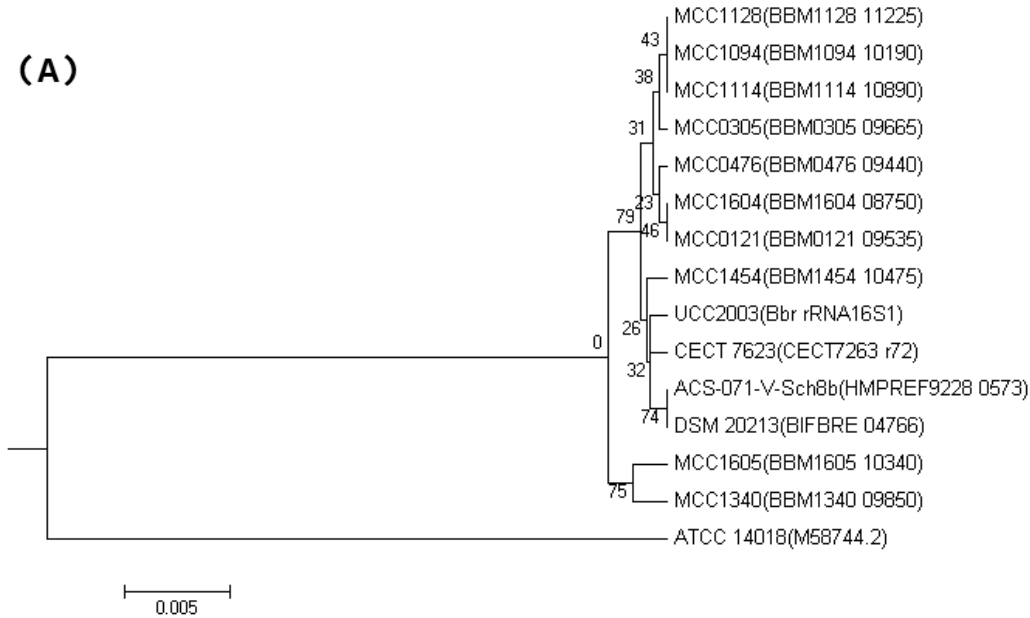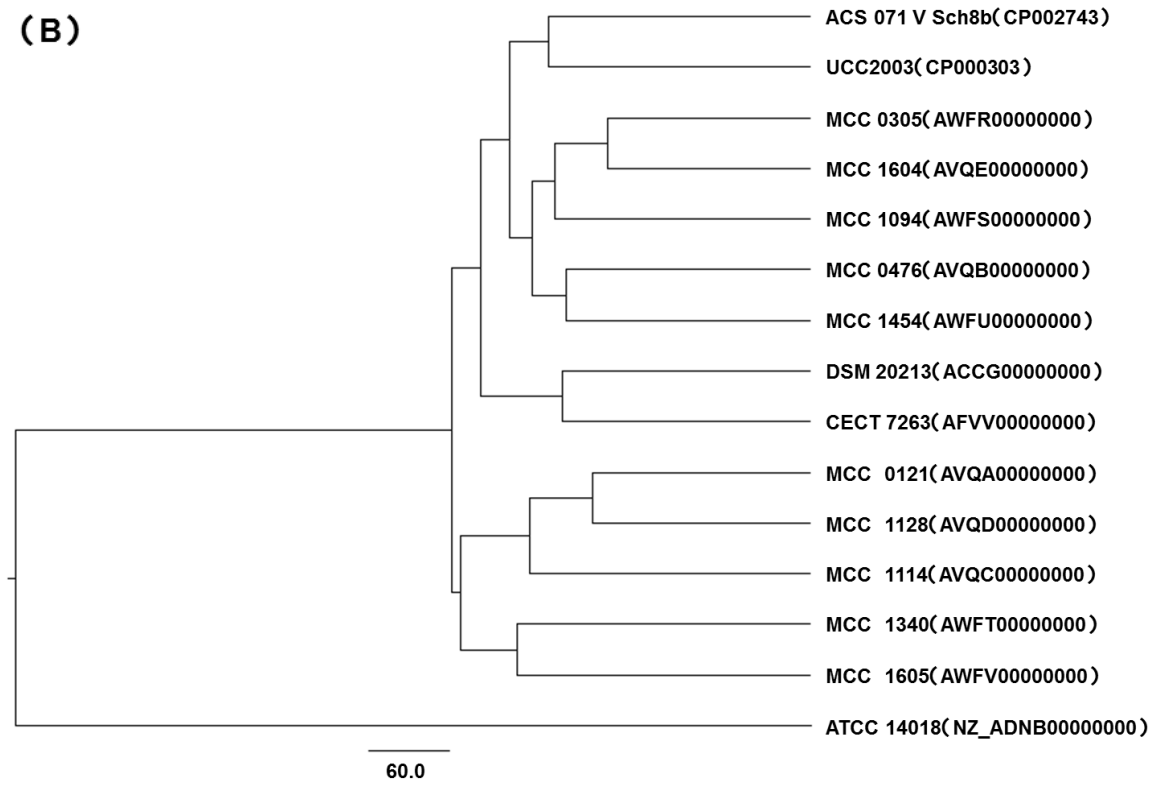
Supplementary file 3 – Phylogenetic tree based on (a) 16S rRNA gene sequences and (b) whole genes of *B. animalis*

Each phylogenetic tree was constructed using (A) the ClustalW program and (B) the

PGAP pipeline [21] via the neighbour-joining method. The numbers in parentheses

indicate the (A) locus_tag and (B) accession number.

(A)

CNCM I-2494(BALAC2494 02129)
ATCC 27536iBAAA27536 08035)
BLC1(BLC1 1rRNA16S)
ATCC 27673(BAAA27673 08200)
AD011(BLA r0001)
BB-12(BIF 16SrRNA03)
V9(BalV 16S01)
BS01(FEM r15930)
BI-04(Balac 1279)
HN019(BIFLAC r00007)
B420(W7Y 1284)
DSM 10140(Balat 1279)
ATCC 27674(BAAA27674 08085)
Bi-07(W91 1313)
MCC0483(BAAM0483 09320)
MCC0499(BAAM0499 09345)
ATCC 27672(BAAA27672 08315)
ATCC 25527(BANAN r07957)
MCC1489(BAAM1489 08055)
ATCC 14018(M58744.2)

100
0
98
83
90
78

0.01

(B)

AD011(CP001213)
BLC1(CP003039)
BI-12(CP004053)
BI-04(CP001515)
DSM 10140(CP001606)
V9(CP001892)
BS01(AHGW00000000)
HN019(ABOT00000000)
ATCC 27536(AWFL00000000)
ATCC 27674(AWFM00000000)
B420(CP003497)
Bi-07(CP003498)
ATCC 27673(AWFP00000000)
BB-12(CP001853)
CNCM I-2494(CP002915)
ATCC 25527(CP002567)
MCC1489(AWFO00000000)
ATCC 27672(AWFQ00000000)
MCC0483(AWFK00000000)
MCC0499(AWFN00000000)
ATCC 14018(NZ_ADNB00000000)

50.0
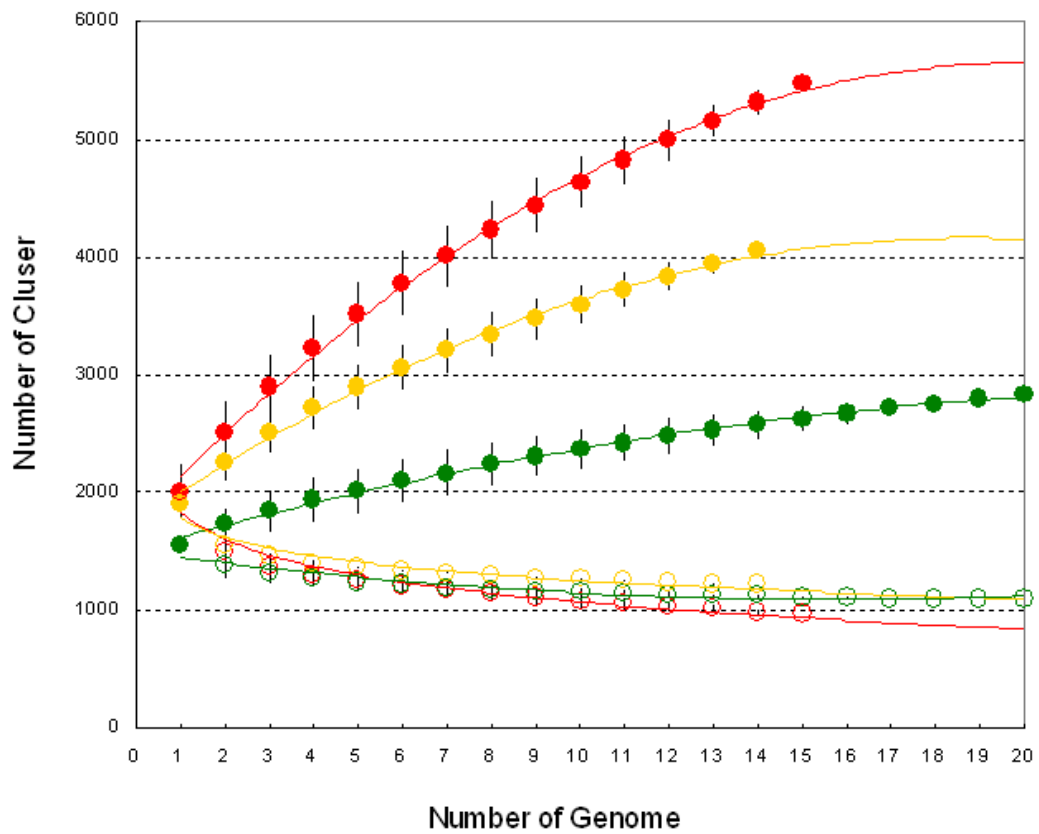
23 **Supplementary file 4 – Pan- and core genome plots for the three analysed species**
24 Solid and open symbols indicate the numbers of pan-genomes and core genomes,

25 respectively. Each colour indicates a different species: red, *B. longum*; orange, *B.*

26 *breve*; green, *B. animalis.*

27

28

29 **Supplementary file 5 - Ability of bifidobacteria in the assimilation of human milk**
30 **oligsaccharide, lacto-N-tetraose (LNT)**
31

Species	Strain	24 h		48 h	
		Mean	SD	Mean	SD
B. longum subsp. *longum*	JCM 1217[T]	1.3	0.03	1.6	0.19
B. longum subsp. *infantis*	ATCC 15697 [T]	1.7	0.03	2.0	0.03
B. breve	DSM 20213[T]	1.5	0.03	2.0	0.14
B. animalis subsp. *animalis*	ATCC 25527[T]	0.0	0.00	0.0	0.00
B. animalis subsp. *lactis*	DSM 10140[T]	0.0	0.00	0.0	0.00

32 OD600 after cultivation at 37ºC under anaerobic conditions for 24 to 48 h in a

33 medium containing 2% of LNT as the sole carbohydrate