

FIG. 1

16s rDNA sequence

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AGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCTGCTTAACACATGCAAGTCCAACGGGATCCATCATGCTTTGCTTGGTGGTG
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CGTTATCCGGAATTATGGGCGTAAAGGGCTCGTAGCGGTTCTGTCGGTCCGGTGTGAAAGTCCATCGCTTAACGGTGGATCCGCG
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ACTGCGTGAAGCGGAGTCGCTAGTAATCGCGAATCAGCAAGTCCGCGTGAATGCGTTCGGGGCTTGTACACACCGCCGCTCAA
GTCATGAAAGTGGGAGCAACCGAAGCGGTGGCTAACCCCTTGTGGGATGGAGCGCTCTAAGGTGAGGCTCGATTGGGACTA
AGTCGTAACAGGTAGCCGTACCGAAGGTGGGCTGGATCACTCCTT

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Sequence distance

		Percent Identity								
Divergence		1	2	3	4	5	6	7		
	1	100	99.1	99.0	92.9	90.8	93.2	1	1	<i>B. longum</i> BG7 (KCTC 12200BP)
15	2	0.9	100	99.8	93.4	90.6	93.7	2	2	<i>B. longum</i> (ATCC15707)
	3	0.9	0.9	100	96.8	90.8	93.0	3	3	<i>B. infantis</i> (ATCC15697)
	4	3.0	3.1	2.3	100	91.4	93.1	4	4	<i>B. breve</i> (ATCC15700)
	5	5.0	5.1	4.6	4.6	100	94.1	5	5	<i>B. bifidum</i> (DSM 20458T)
	6	6.7	7.0	6.9	6.3	7.6	100	6	6	<i>Bifidobacterium lactis</i> (DSM 10140)
20	7	4.9	5.0	5.2	5.1	4.9	6.7	7	7	<i>Bifidobacterium catenulatum</i> (KCTC 3221)
	1	2	3	4	5	6	7			

Phylogenetic tree

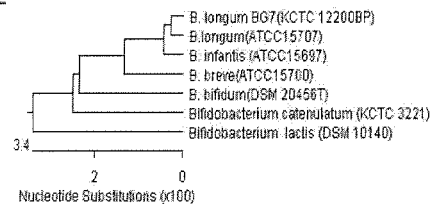


FIG. 2

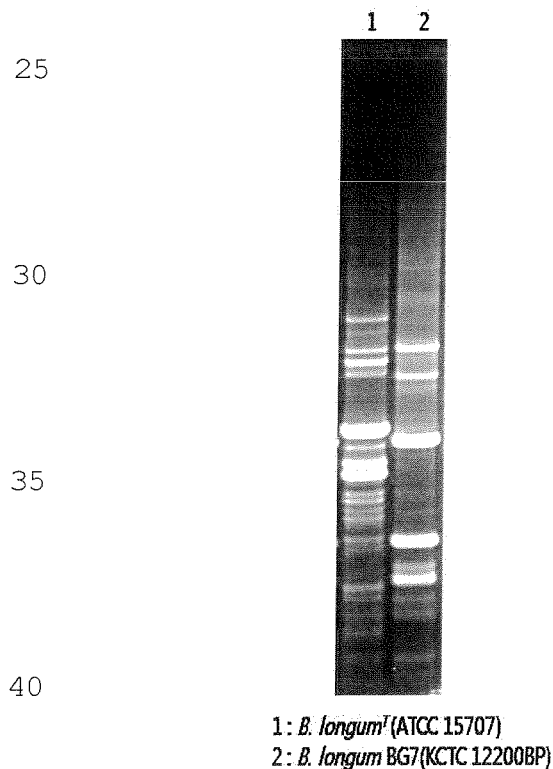


FIG. 3

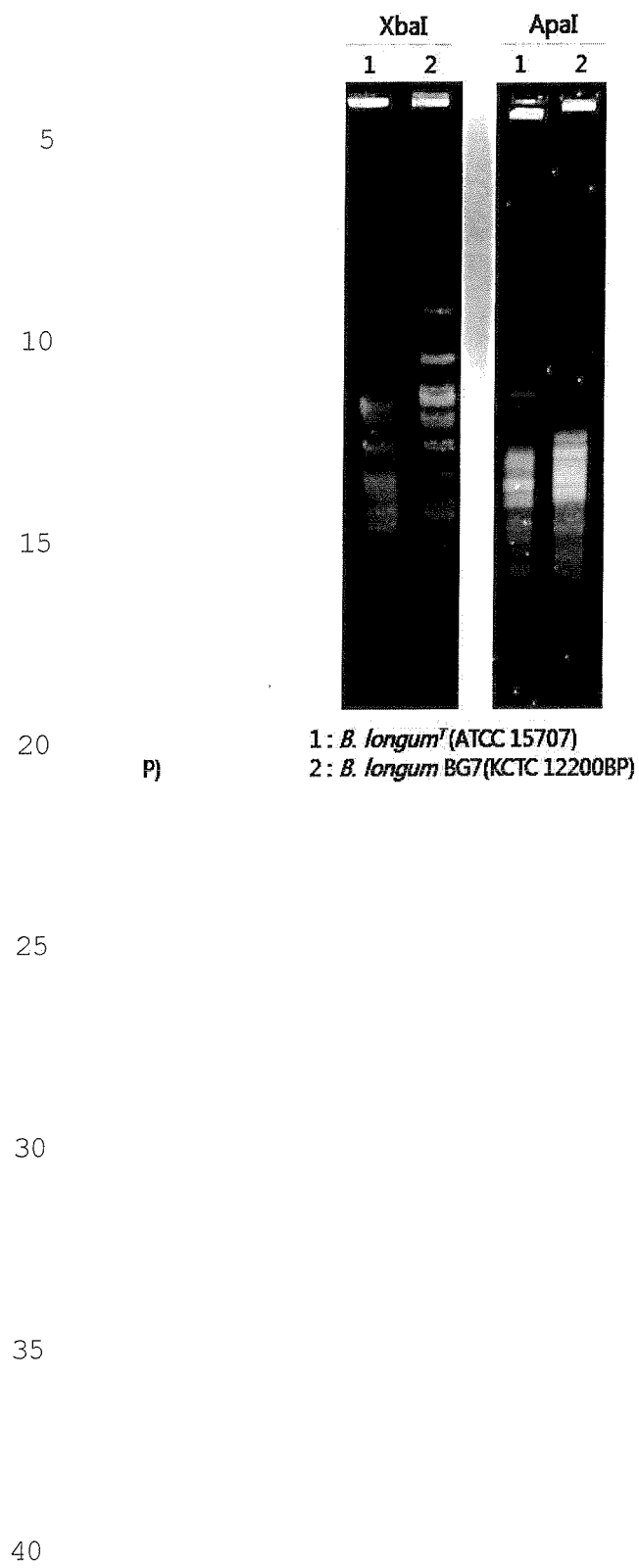


FIG. 4

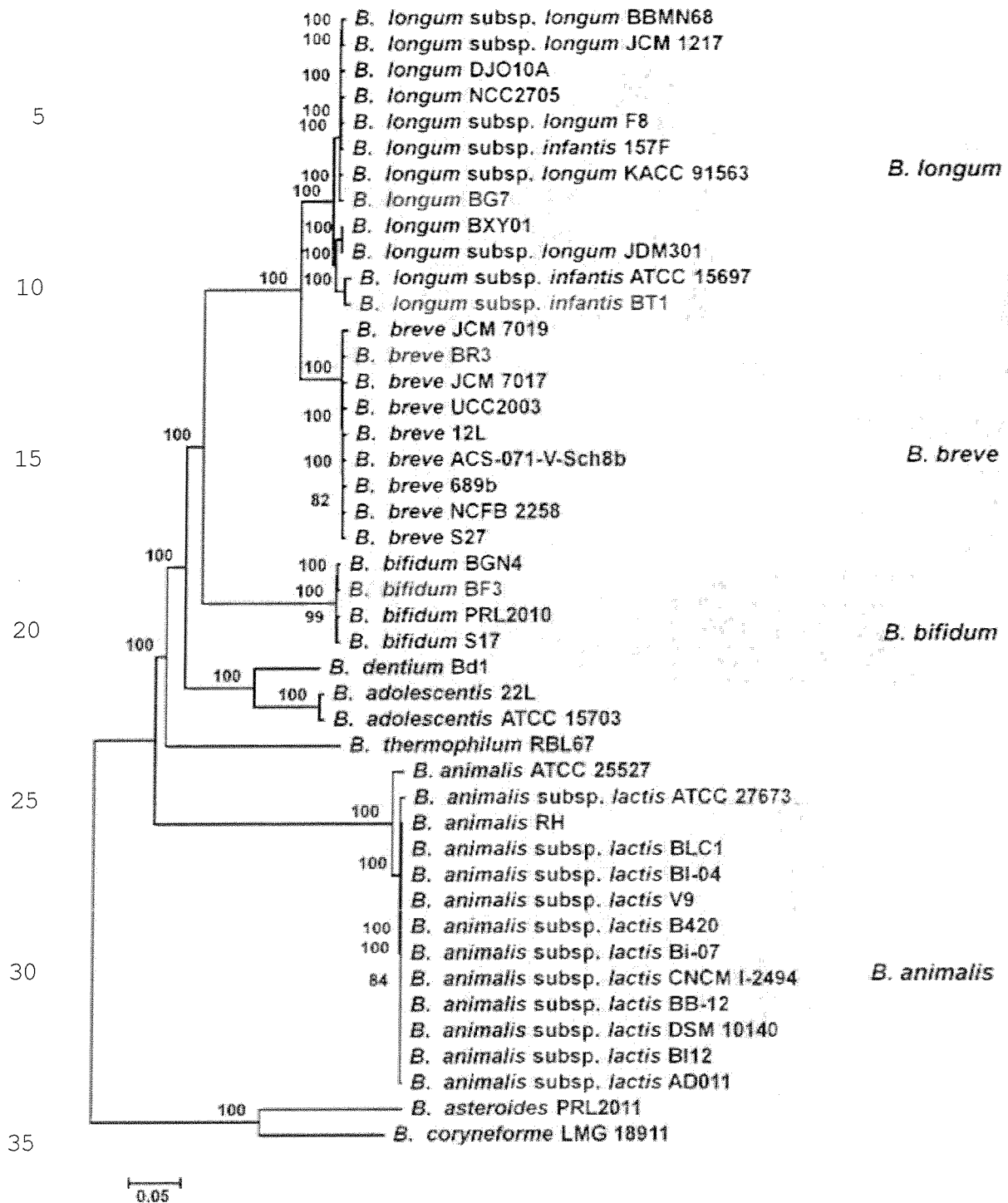


FIG. 5

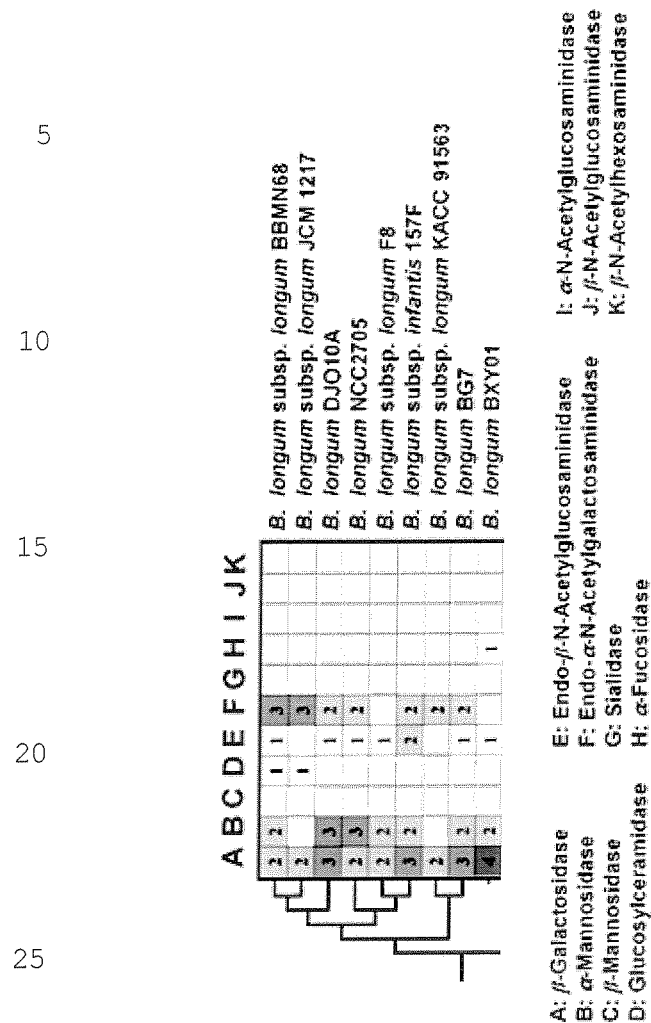


FIG. 6

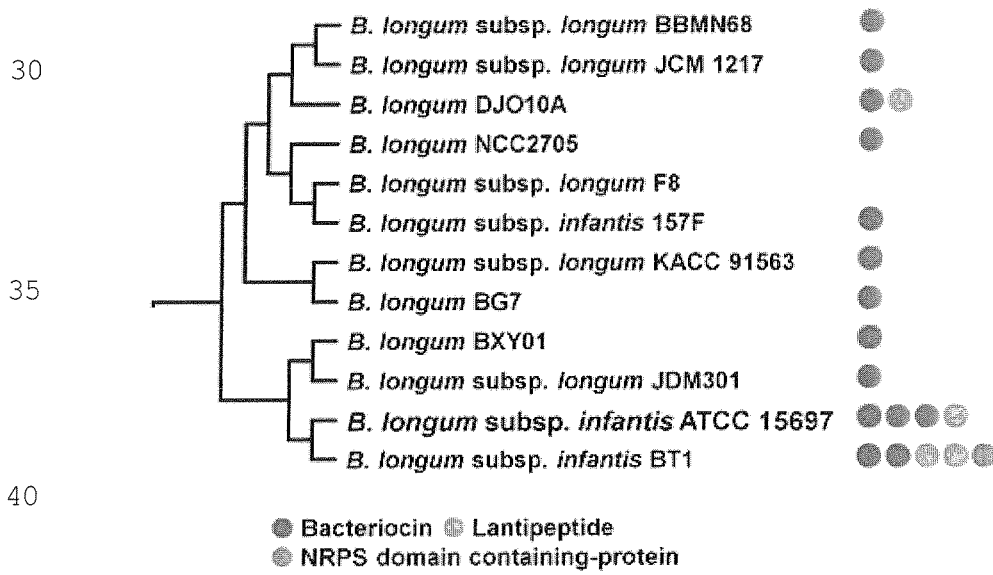


FIG. 7

