Figure S1. Phylogenetic analysis of Fukushima isolates based on 16S rRNA sequences. The phylogenetic tree included eighteen isolates and reference strains. The tree is based on differences in 1400 bp DNA fragments. The scale bar represents substitutions per nucleotide position, and each genus includes the percentage of the total isolates. Numbers at the nodes indicate the level of bootstrap support (%) based on a neighbor-joining analysis of 1000 re-sampled datasets.
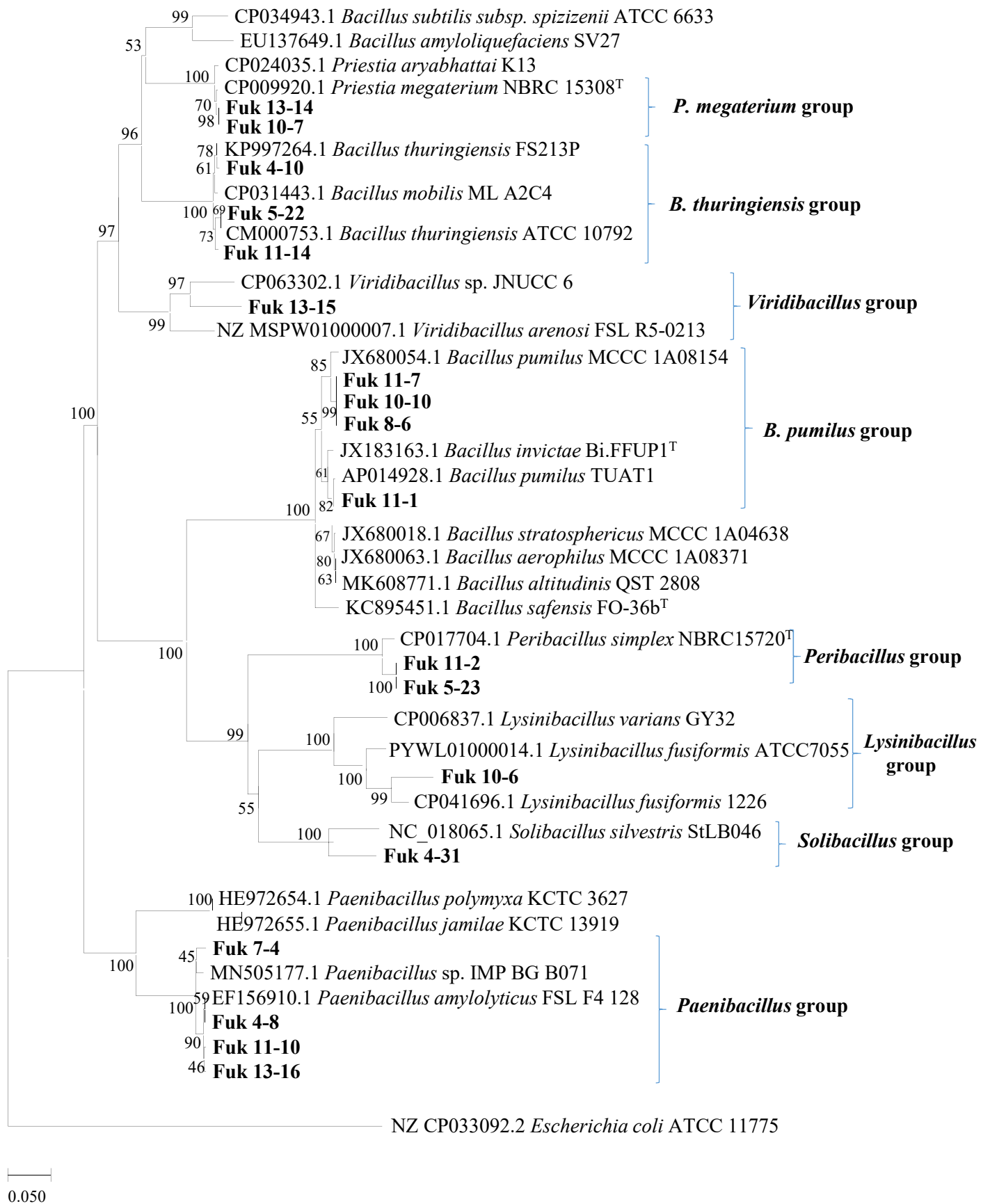
Figure S2. Phylogenetic analysis based on the *rpoB* sequences of Fukushima isolates. The differences are based on a 1300-bp DNA fragment gene. The numbers at the branch nodes indicate bootstrap values (%) based on a neighbor-joining analysis of 1000 re-sampled datasets. The scale bar indicates substitutions per site.
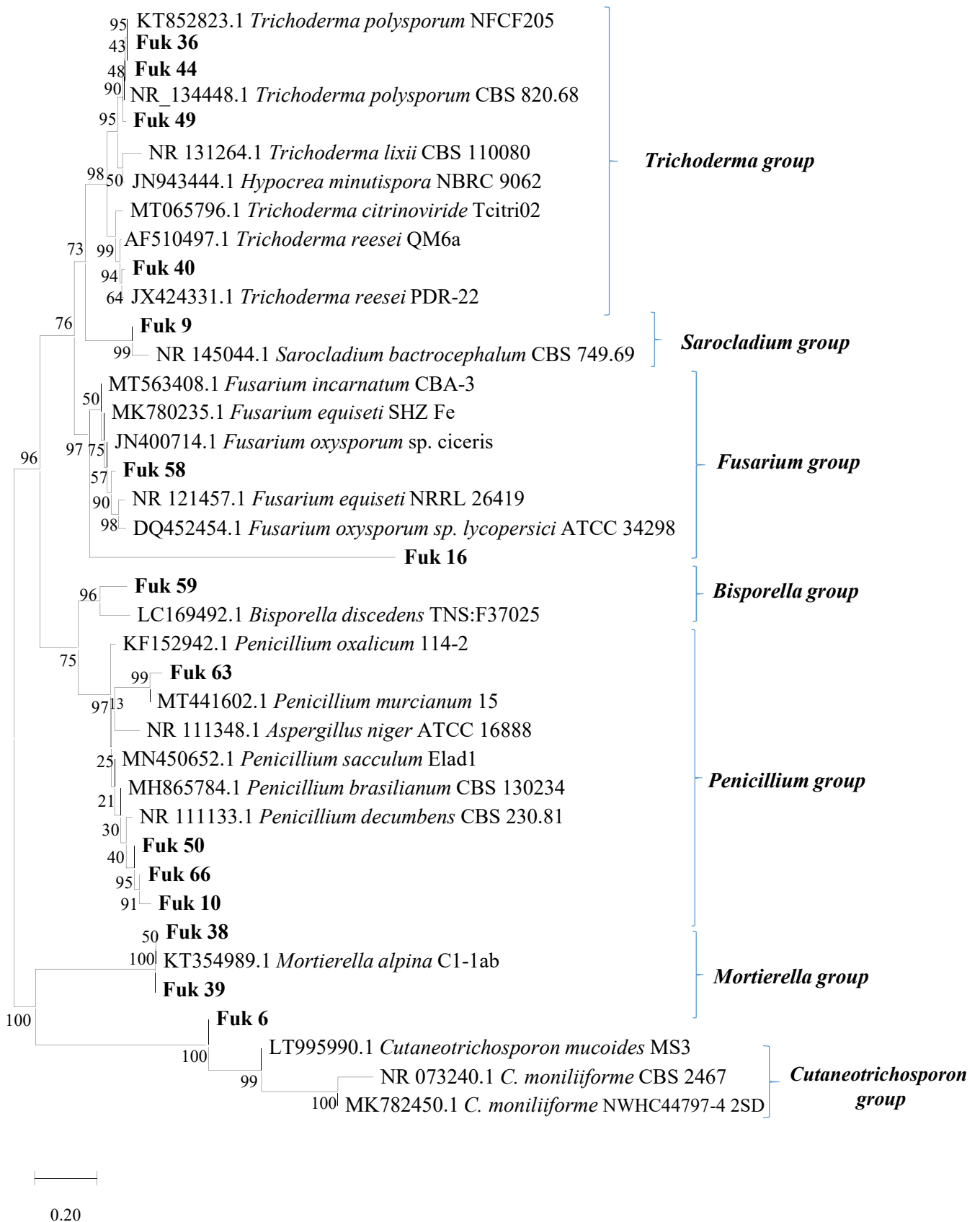
95 | KT852823.1 *Trichoderma polysporum* NFCF205
43 | **Fuk 36**
48 | **Fuk 44**
90 | NR_134448.1 *Trichoderma polysporum* CBS 820.68
95 | **Fuk 49**

NR 131264.1 *Trichoderma lixii* CBS 110080
98 50 | JN943444.1 *Hypocrea minutispora* NBRC 9062
MT065796.1 *Trichoderma citrinoviride* Tcitri02
73 99 | AF510497.1 *Trichoderma reesei* QM6a
94 | **Fuk 40**
64 | JX424331.1 *Trichoderma reesei* PDR-22

Trichoderma group

76
Fuk 9
99 | NR 145044.1 *Sarocladium bactrocephalum* CBS 749.69

Sarocladium group

50 | MT563408.1 *Fusarium incarnatum* CBA-3
MK780235.1 *Fusarium equiseti* SHZ Fe
97 75 | JN400714.1 *Fusarium oxysporum* sp. ciceris
57 | **Fuk 58**
90 | NR 121457.1 *Fusarium equiseti* NRRL 26419
98 | DQ452454.1 *Fusarium oxysporum sp. lycopersici* ATCC 34298

Fuk 16

Fusarium group

96

96 | **Fuk 59**
LC169492.1 *Bisporella discedens* TNS:F37025

Bisporella group

KF152942.1 *Penicillium oxalicum* 114-2
75
99 | **Fuk 63**
97 13 | MT441602.1 *Penicillium murcianum* 15
NR 111348.1 *Aspergillus niger* ATCC 16888
25 | MN450652.1 *Penicillium sacculum* Elad1
MH865784.1 *Penicillium brasilianum* CBS 130234
21 | NR 111133.1 *Penicillium decumbens* CBS 230.81
30 | **Fuk 50**
40 | **Fuk 66**
95 | **Fuk 10**
91

Penicillium group

75

50 | **Fuk 38**
100 | KT354989.1 *Mortierella alpina* C1-1ab
Fuk 39

Mortierella group

Fuk 6
100

100 | LT995990.1 *Cutaneotrichosporon mucoides* MS3
99 | NR 073240.1 *C. moniliiforme* CBS 2467
100 | MK782450.1 *C. moniliiforme* NWHC44797-4 2SD

Cutaneotrichosporon group

0.20

Figure S3. Phylogenetic tree based on ITS sequences of Fukushima isolates, constructed with a 150 bp DNA fragment from sequences. The numbers at the branch nodes indicate bootstrap values (%) based on a neighbor-joining analysis of 1000 re-sampled datasets. The scale bar indicates changes per site.
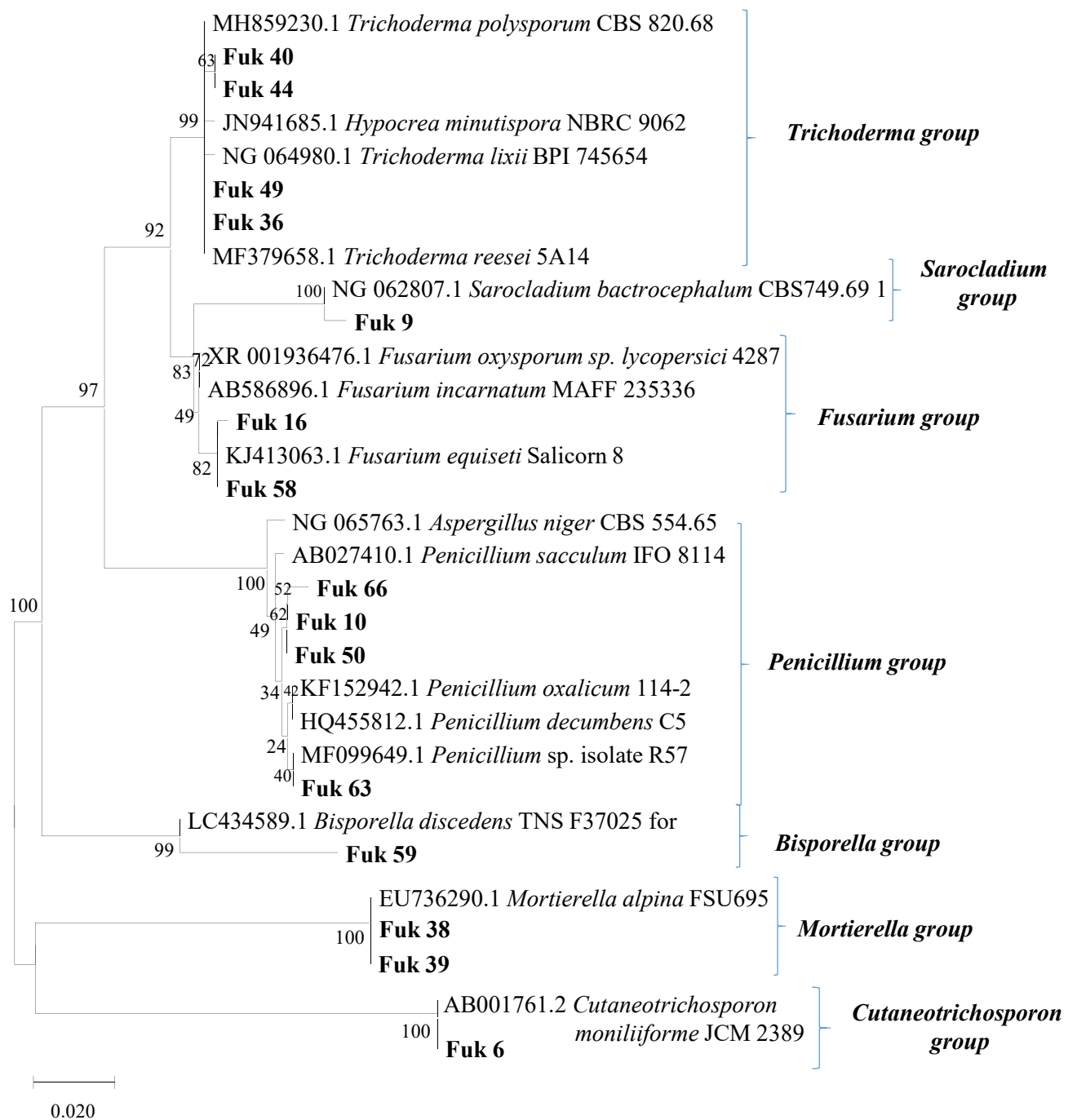
Figure S4. Phylogenetic tree based on 18S rRNA sequences of Fukushima isolates, constructed with 1000 bp DNA fragment gene sequences. The numbers at the branch nodes indicate bootstrap values (%) based on a neighbor-joining analysis of 1000 re-sampled datasets. The scale bar indicates changes per site.