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Bsu_reference      AAGGTACGTCTTGGACTTATCCAAGGCAACTAGCATGATATTTCGTCATTCATATAAAGA 60
L1-1               AGCACGAGGACACTGACATGGACTGAAGGAGTAGAAA----------------------- 37
L1-2               AGCACGAGGACACTGACATGGACTGAAGGAGTAGAAA----------------------- 37
L1-3               AGCACGAGGACACTGACATGGACTGAAGGAGTAGAAA----------------------- 37
L1-4               AGCACGAGGACACTGACATGGACTGAGGGAGTAGAAAATATTTCGTCATTCATATAAAGA 60
L1-5               AGCACGAGGACACTGACATGGACTGAAGGAGTAGAAA----------------------- 37
L11-1              AGCACGAGGACACTGACATGGACTGAAGGAGTAGAAAATATTTCGTCATTCATATAAAGA 60
L11-2              AGCACGAGGACACTGACATGGACTGAAGGAGTAGAAA----------------------- 37
L11-3              AGCACGAGGACACTGACATGGACTGAAGGAGTAGAAA----------------------- 37
L11-4              AGCACGAGGACACTGACATGGACTGAAGGAGTAGAAA----------------------- 37
L11-5              AGCACGAGGACACTGACATGGACTGAAGGAGTAGAAA----------------------- 37
L11-6              AGCAGGAGGACAATGACATGGAATGAAGGAGTAGAAA----------------------- 37
L11-7              AGCACGAGGACACTGACATGGACTGAAGGAGTAGAAA----------------------- 37
L11-8              AGCACGAGGACACTGACATGGACTGAAGGAGTAGAAA----------------------- 37
L11-9              AGCACGAGGACAGTGACATGGATCGACGGAGTAGAAAG---------------------- 38
L11-10             AGCAC-AGGACACTGACATGGACTGAAGGAGTAGAAA----------------------- 36
L11-11             AGCACGAGGTCACTGACATGGACTGAAGGAGTAGAAA----------------------- 37

Bsu_reference      ATGAAACCTTGAGTGGGAGGGTTTACCCTATTACCACATCACGGACTTAAGGAGGTGTGT 120
L1-1               -------------------------------------------GACTTAAGGAGGTGTGT 54
L1-2               -------------------------------------------GACTTAAGGAGGTGTGT 54
L1-3               --------------------------------------------ACTTAAGGAGGTGTGT 53
L1-4               ATGAAACCTTGAGTGGGAGGGTTTACCCTATTACCACATCACGGACTTAAGGAGGTGTGT 120
L1-5               -------------------------------------------GACTTAAGGAGGTGTGT 54
L11-1              ATGAAACCTTGAGTGGGAGGGTTTACCCTATTACCACATCACGGACTTAAGGAGGTGTGT 120
L11-2              -------------------------------------------GACTTAAGGAGGTGTGT 54
L11-3              ------------------------------------------GGACTTAAGGAGGTGTGT 55
L11-4              --------TTGAGTGGGAGGGTTTACCCTATTACCACATCACGGACTTAAGGAGGTGTGT 89
L11-5              -------------------------------------------GACTTAAGGAGGTGTGT 54
L11-6              ---------------------------------------------CTTAAGGAGGTGTGT 52
L11-7              -------------------------------------------GACTTAAGGAGGTGTGT 54
L11-8              -------------------------------------------GACTTAAGGAGGTGTGT 54
L11-9              ---------CGAGTGGGAGGGTTTACCCTATTACCACATAACAGACTTAAGGAGGTGTGT 89
L11-10             --------TTGAGTGGGAGGG-TTACCCTATTACCACATCACGGACTTAAGGAGGTGTGT 87
L11-11             ------------------------------------------GGACTTAAGGAGGTGTGT 55

Bsu_reference      CTCGTGGCTAAAAAAGTAGTTAAAGTTGTAAAATTGCAAATTCCTGCTGGAAAAGCTAAC 180
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L1-2               CTCGTGGCTAAAAAAGTAGTTAAAGTTGTAAAATTGCAAATTCCTGCTGGAAAAGCTAAC 114
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L1-4               CTCGTGGCTAAAAAAGTAGTTAAAGTTGTAAAATTGCAAATTCCTGCTGGAAAAGCTAAC 180
L1-5               CTCGTGGCTAAAAAAGTAGTTAAAGTTGTAAAATTGCAAATTCCTGCTGGAAAGGCTAAC 114
L11-1              CTCGTGGCTAAAAAAGTAGTTAAAGTTGTAAAATTGCAAATTCCTGCTGGAAAGGCTAAC 180
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L11-6              CTCGTGGCTAAAAAAGTAGTTAAAGTTGTAAAATTGCAAATTCCTGCTGGAAAAGCTAAC 112
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L11-9              CTCGTGGCTAAAAAAGTAGTTAAAGTTGTAAAATTGCAAATTCCTGCTGGAAAAGCTAAC 149
L11-10             CTCGTGGCTAAAAAAGTAGTTAAAGTTGTAAAATTGCAAATTCCTGCTGGAAAAGCTAAC 147
L11-11             CTCGTGGCTAAAAAAGTAGTTAAAGTTGTAAAATTGCAAATTCCTGCTGGAAAAGCTAAC 115
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L1-3                CCAGCACCACCAGTTGGACCTGCACTTGGTCAAGCCGGTGTTAACATCATGGGATTCTGT 173
L1-4                CCAGCACCGCCAGTTGGACCTGCACTTGGTCAAGCCGGTGTTAACATCATGGGATTCTGT 240
L1-5                CCAGCACCACCAGTTGGACCTGCACTTGGTCAAGCCGGTGTTAACATCATGGGATTCTGT 174
L11-1               CCAGCACCACCAGTTGG------------------------------------------- 203
L11-2               CCAGCACCACCAGTTGG------------------------------------------- 131
L11-3               CCAGCACCACCAGTTGG------------------------------------------- 132
L11-4               CCAGCACCACCAGTTGG------------------------------------------- 165
L11-5               CCAGCACCACCAGTTGG------------------------------------------- 131
L11-6               CCAGCACCACCAGTTGG------------------------------------------- 129
L11-7               CCAGCACCACCAGTTGG------------------------------------------- 131
L11-8               CCAGCACCACCAGTTGG------------------------------------------- 131
L11-9               CCAGCACCACCAGTTGG------------------------------------------- 166
L11-10              CCAGCACCACCAGTTGG------------------------------------------- 164
L11-11              CCAGCACCACCAGTTGG------------------------------------------- 132

Bsu_reference       AAGGAGTTTAACGCTCGTACAGCTGACCAAGCTGGTTTAATCATTCCTGTTGAAATTTCG 300
L1-1                AAGGAGTTTAACGCTCGTACAGCTGACCAAGCTGGTTTAATCATTCCTGTTGAAATTTCG 234
L1-2                AAGGAGTTTAACGCTCGTACAGCTGACCAAGCTGGTTTAATCATTCCTGTTGAAATTTCG 234
L1-3                AAGGAGTTTAACGCTCGTACAGCTGACCAAGCTGGTTTAATCATTCCTGTTGAAATTTCG 233
L1-4                AAGGAGTTTAACGCTCGTACAGCTGACCAAGCTGGTTTAATCATTCCTGTTG-AATTTCG 299
L1-5                AAGGAGTTTAACGCTCGTACAGCTGACCAAGCTGGTTTAATCATTCCTGTTGAAATTTCG 234

Bsu_reference       GTTTACGAAGACCGTTCATTTACATTTATTACAAAAACTCCACCTGCTGCAGTATTGCTT 360
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L1-2                GTTTACGAAGACCGTTCATTTACATTTATTACAAAAACTCCACCTGCTGCAGTATTGCTT 294
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L1-4                GTTTACGAAGACCGTTCATTTACATTTATTACAAAAACTCCACCTGCTGCAGTATTGCTT 359
L1-5                GTTTACGAAGACCGTTCGTTTACATTTATTACAAAAACTCCACCTGCTGCAGTATTGCTT 294

Bsu_reference       AAAAAAGCAGCTGGAATTGAGTCTGGTTCTGGTGAACCAAACCGTAATAAAGTGGCAACC 420
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L1-3                AAAAAAGCAGCTGGAATTGAGTCTGGTTCTGGTGAACCAAACCGTAATAAAGTGGCAACC 353
L1-4                AAAAAAGCAGCTGGAATTGAGTCTGGTTCTGGTGAACCAAACCGTAATAAAGTGGCAACC 419
L1-5                AAAAAAGCAGCTGGAATTGAGTCTGGTTCTGGTGAACCAAACCGTAATAAAGTGGCAACC 354

Bsu_reference       GTTAAGCGCGATAAAGTACGCGAAATCGCTGAAACGAAAATGCCTGACTTAAACGCAGCA 480
L1-1                GTTAAGCGCGATAAAGTACGCGAAATCGCTGAAACGAAAATGCCTGACTTAAACGCAGCA 414
L1-2                GTTAAGCGCGATAAAGTACGCGAAATCGCTGAAACGAAAATGCCTGACTTAAACGCAGCA 414
L1-3                GTTAAGCGCGATAAAGTACGCGAAATCGCTGAAACGAAAATGCCTGACTTAAACGCAGCA 413
L1-4                GTTAAGCGCGATAAAGTACGCGAAATCGCTGAAACGAAAATGCCTGACTTAAACGCAGCA 479
L1-5                GTTAAGCGCGATAAAGTACGCGAAATCGCTGAAACGAAAATGCCTGACTTAAACGCAGCA 414

Bsu_reference       GACGTTGAAGCGGCAATGCGCATGGTTGAAGGTACTGCCCGCAGTATGGGTATTGTAATC 540
L1-1                GACGTTGAAGCGGCAATGCGCATGGTTGAAGGTACTGCCCGCAGTATGGGTATTGTAATC 474
L1-2                GACGTTGAAGCGGCAATGCGCATGGTTGAAGGTACTGCCCGCAGTATGGGTATTGTAATC 474
L1-3                GACGTTGAAGCGGCAATGCGCATGGTTGAAGGTACTGCCCGCAGTATGGGTATTGTAATC 473
L1-4                GACGTTGAAGCGGCAATGCGCATGGTTGAAGGTACTGCCCGCAGTATGGGTATTGTAATC 539
L1-5                GACGTTGAAGCGGCAATGCGCATGGTTGAAGGTACTGCCCGCAGTATGGGTATTGTAATC 474

Bsu_reference       GAGGATTAATTTGTTTCTTGTCGGGTTGCGAGTTTTAACAAGTTCGCAACCCTTATTCGT 600
L1-1                GAGGATTAATTTGTTTCTTGTCGGGTTGCGAGTTTTAACANNTTCGCAACCCTTATTCNT 534
L1-2                GAGGATTAATTTGTTTCTTGTCGGGTTGCGAGTTTTAACAAGTTCGCAACCCTTATTCGT 534
L1-3                GAGGATTAATTTGTTTCTTGTCGGGTTGCGAGTTTTAACAAGTTCGCAACCCTTATTCGT 533
L1-4                GAGGATTAATTTGTTTCTTGTCGGGTTGCGAGTTTTAACAAGTTCGCAACCCTTATTCGT 599
L1-5                GAGGATTAATTTGTTTCTTGTCGGGTTGCGAGTTTTAACAAGTTCGCAACCCTTATTCGT 534
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Bsu_reference      GGGAGGTTATTCCGCTATAACCACATAAGGAGGAAATTTTAAAATGGCTAAAAAAGGTAA 660
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L1-2               GGGAGGTTATTCCGCTATAACCACATAAGGAGGAAATTTTAAAATGGCTAAAAAAGGTAA 594
L1-3               GGGACGTTATTCCGCTATAACCACATAAGGAGGAAATTTTAAAATGGCTAAAAAAGGTAA 593
L1-4               GGGAGGTTATTCCGCTATAACCACATAAGGAGGAAATTTTAAAATGGCTAAAAAAGGTAA 659
L1-5               GGGAGGTTATTCCG---------------------------------------------- 548

Bsu_reference      AAAGTACGTTGAAGCTGCTAAGCTTGTAGACCG 693
L1-1               ---------------------------------
L1-2               AAAGTACGTTGAAGCTGCTAAGCTTGTAGACCG 627
L1-3               AAAGTACGTTGAAGCTGCTAAGCTTGTAGACCG 626
L1-4               AAAGTACGTTGAAGCTGCTAAGCTTGTAGACCG 692
L1-5               ---------------------------------
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Supplementary Figure 1: Summary of 5’-RACE results from gene specific primers within *rplA* (L1) and *rplK* (L11). Regions corresponding to primer sequences are underlined on the *Bacillus subtilis* genome reference sequence (gene specific primers), the sequence of the 5’-linker is indicated by italics on the sequences obtained. Bolded regions correspond to translation initiation codons (GTG and ATG) and to the putative structured RNA portions of the sequence. Sequences for L1 that do not extend to the 3’ gene specific primer (L1-1, and L1-5) are the result of short sequencing reads. All L11 reads are trimmed to the 3’ primer within *rplK*.