Figure S1. Alignment of *map-1.1* partial sequences amplified from 122 *Meloidogyne incognita* individuals belonging to 16 isolates. Nomenclature of isolates is as in Table S3. Stars below alignment indicate conserved positions. Orange and blue sequences above alignment encode the 58 and 13-aa repeat regions, respectively. Sequences encoding the tandemly arranged 13-aa repeats are separated by arrows. Mutated positions are highlighted in yellow.

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                                CCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAAG-CCTCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
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Minc_18_11      TACAACAGG-AGCTCAACCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAAG-CCTCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
Minc_18_13      TACAACAGG-AGCTCAACCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAAG-CCTCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
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Minc_18_4       TACAACAGG-AGCTCAACCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAAG-CCTCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
Minc_18_5       TACAACAGG-AGCTCAACCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAAG-CCTCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
Minc_18_7       TACAACAGG-AGCTCAACCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAAG-CCTCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
Minc_18_8       TACAACAGG-AGCTCAACCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAAG-CCTCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
Minc_18_9       TACAACAGG-AGCTCAACCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAAG-CCTCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
Minc_22_14      TACAACAGG-AGCTCAACCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAA---CTCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
Minc_22_15      TACAACAGG-AGCTCAACCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAAC---TCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
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Minc_51_10      TACAACAGG-AGCTCAACCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAAG-CCTCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
Minc_51_11      TACAACAGG-AGCTCAACCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAAG-CCTCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
Minc_51_4       TACAACAGG-AGCTCAACCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAAG-CCTCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
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Minc_76_13   TACAACAGG-AGCTCAACCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAAG-CCTCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
Minc_76_14   TACAACAGG-AGCTCAACCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAAG-CCTCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
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Minc_78_11   TACAACAGG-AGCTCAACCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAAG-CCTCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
Minc_78_13   TACAACAGG-AGCTCAACCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAAG-CCTCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
Minc_78_15   TACAACAGG-AGCTCAACCAACTTCACGAAACGTTTACCCATCTGGGCCAGAATCATCTACACCAGGAGGACAAGTAGCATCGCATAA--C-TCCGGCAGCACCTTCTACTCCACAGCCTGGATGTCA
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