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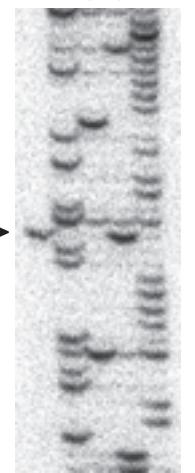
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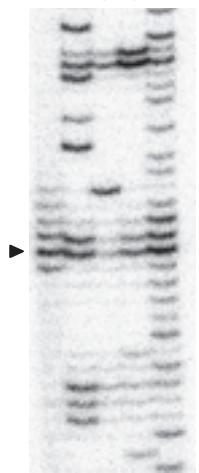
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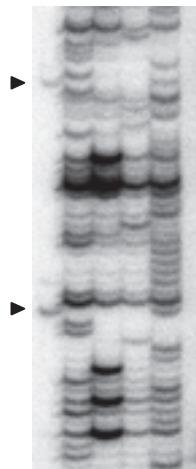
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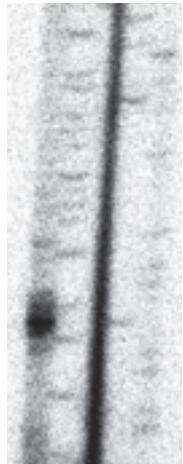
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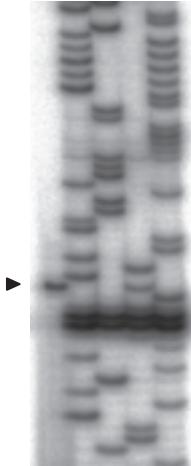
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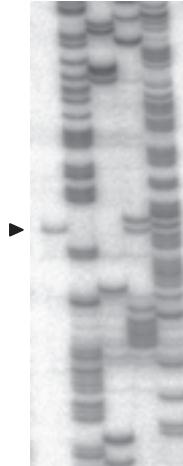
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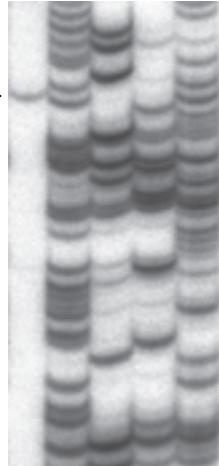
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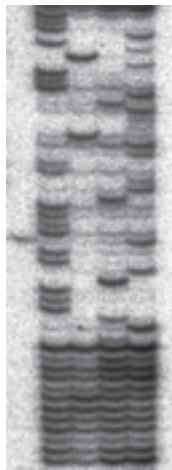
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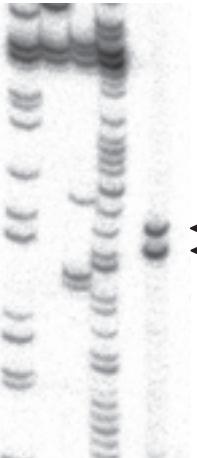
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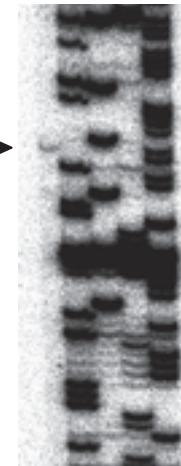
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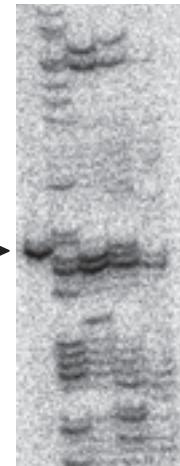
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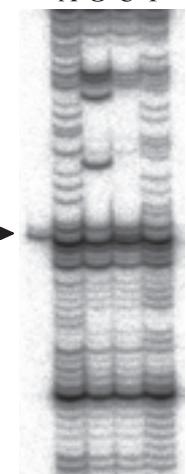
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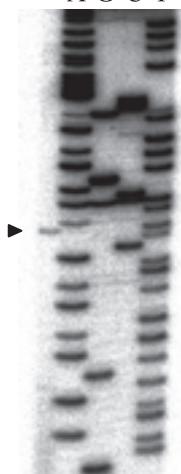
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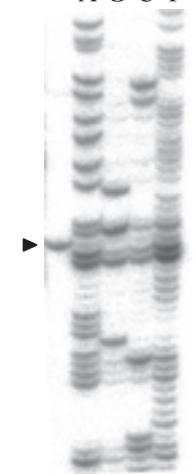
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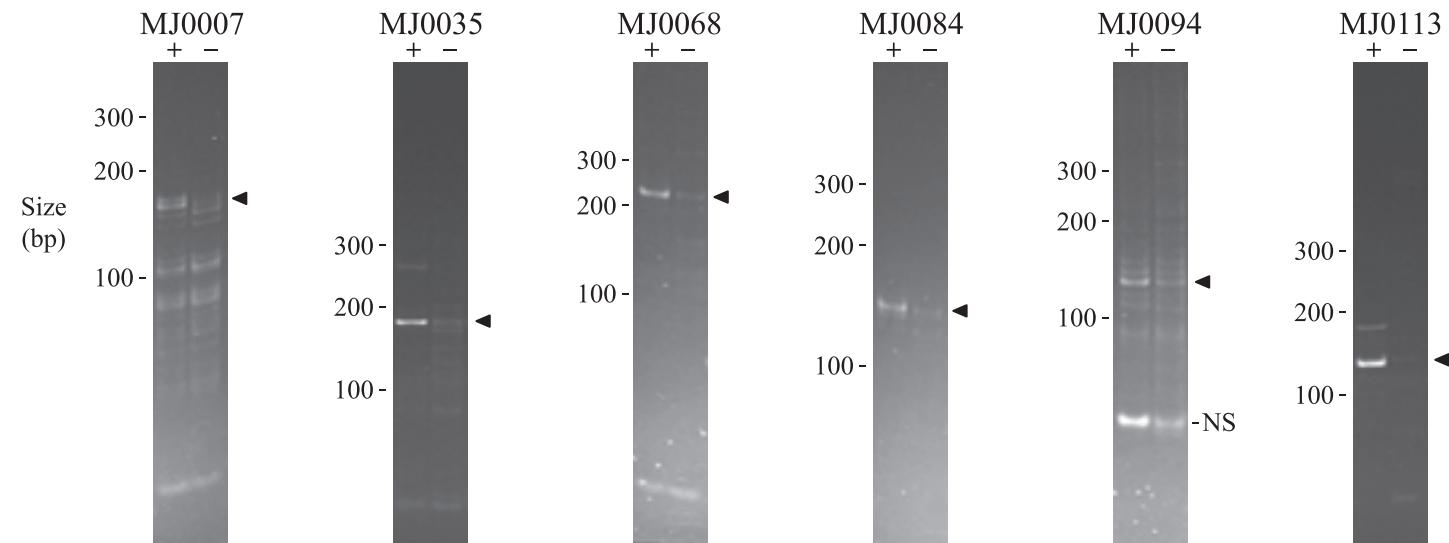


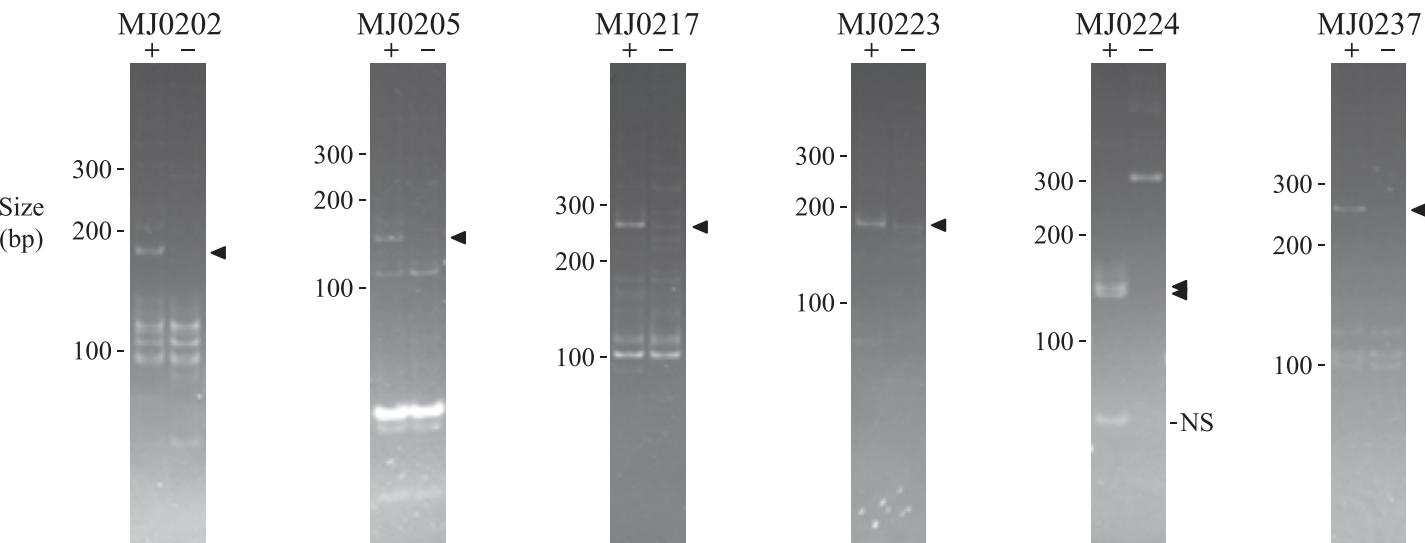
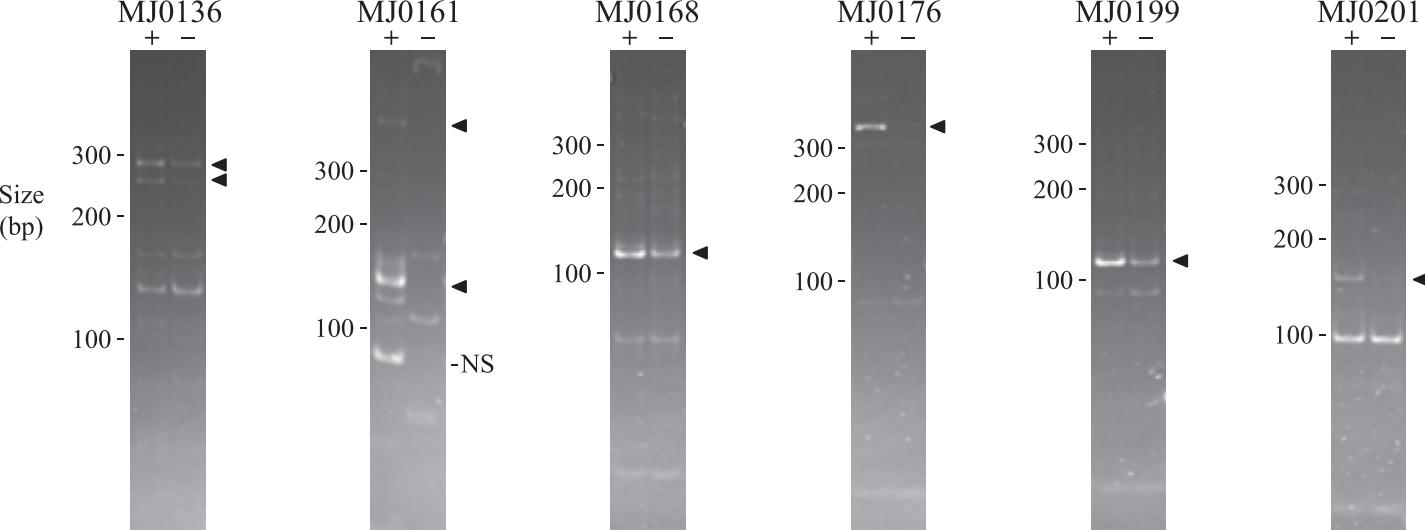
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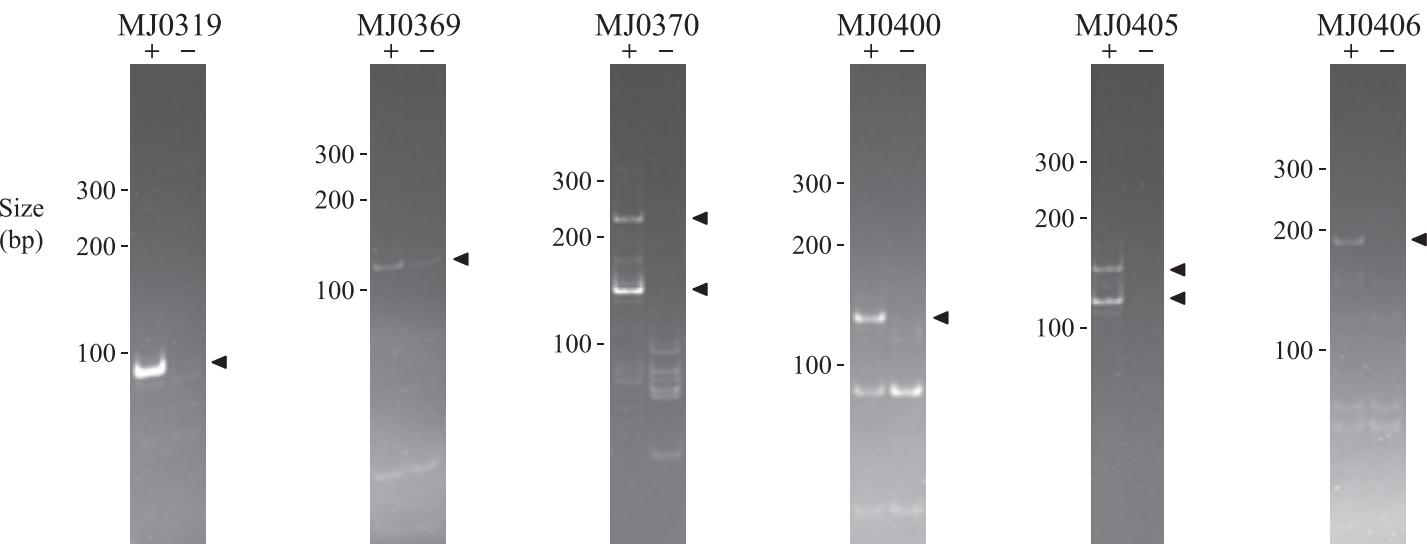
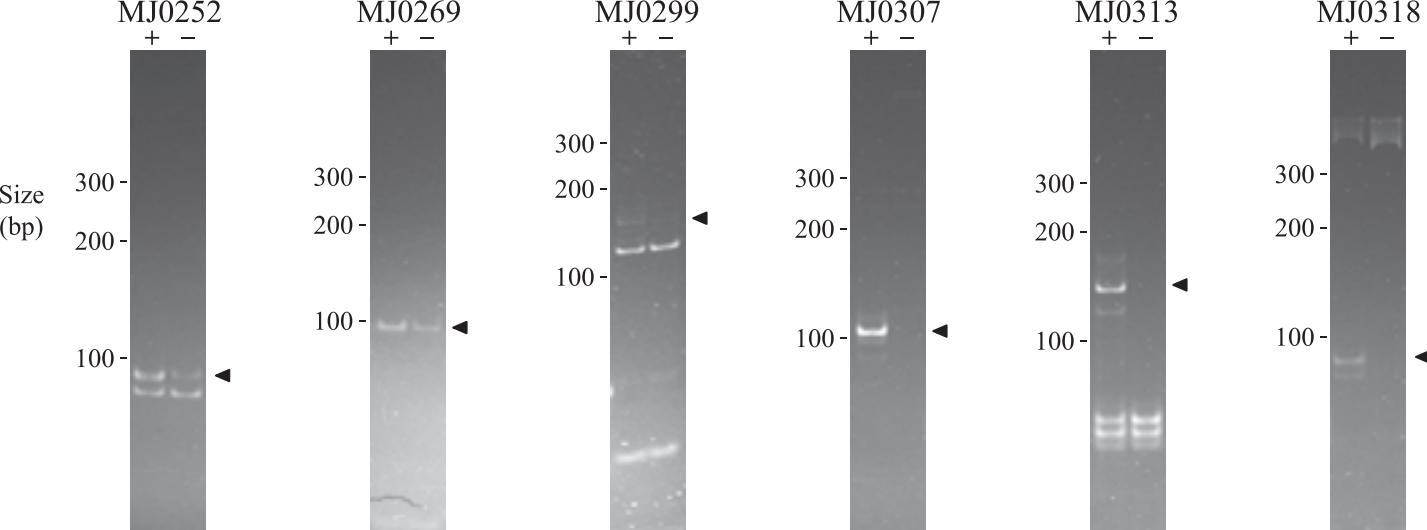


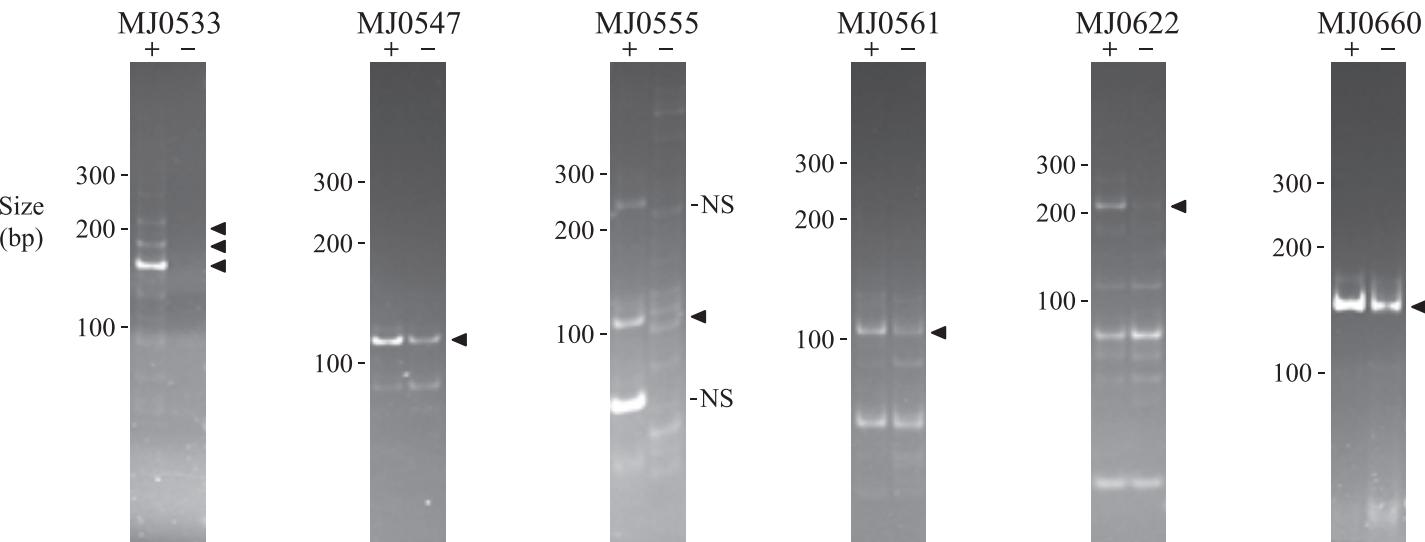
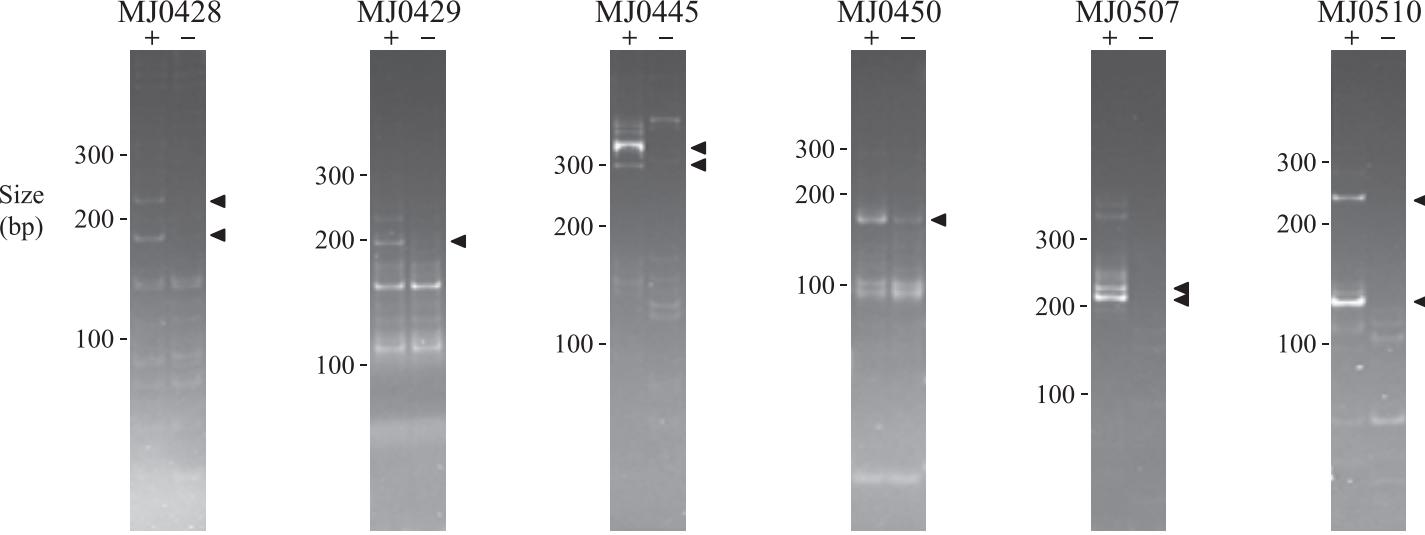


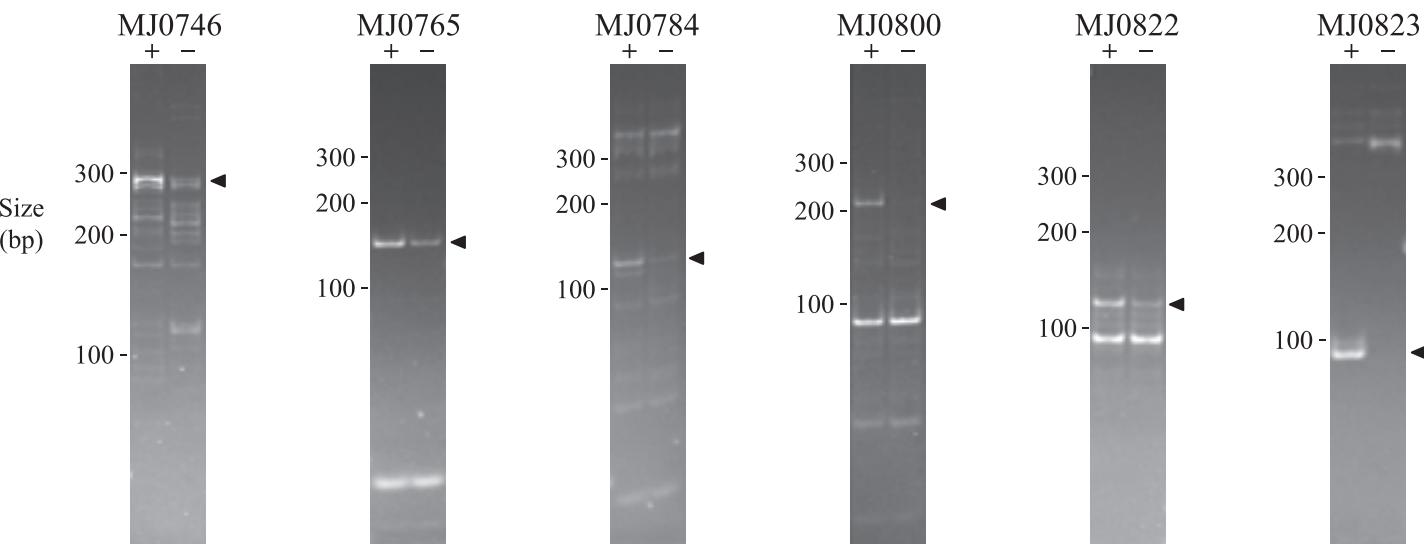
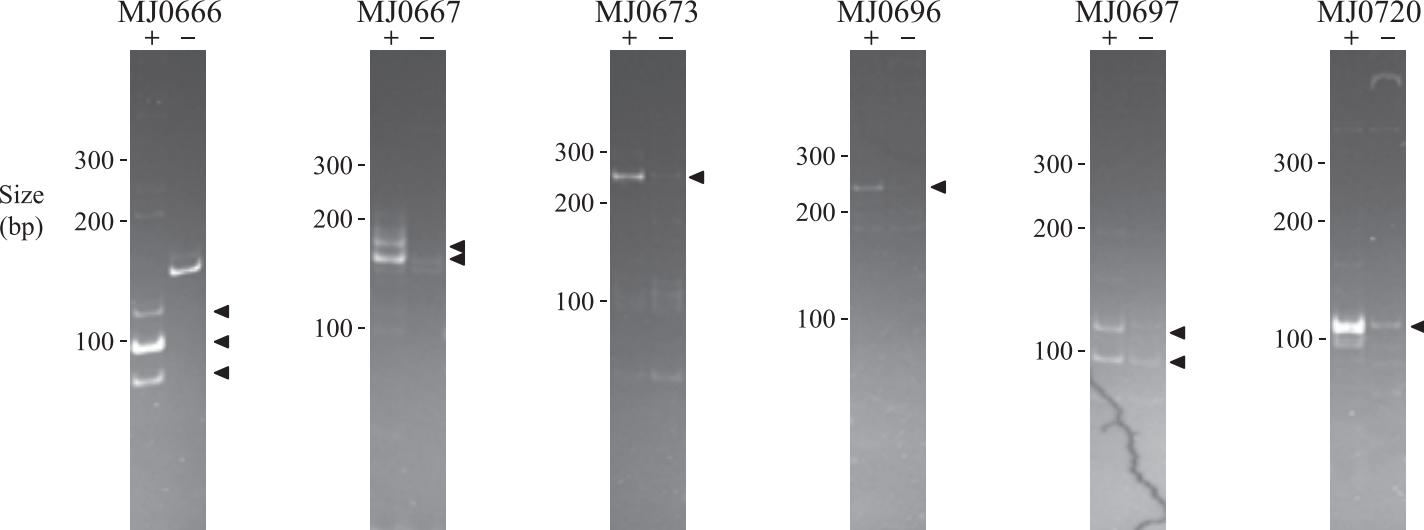
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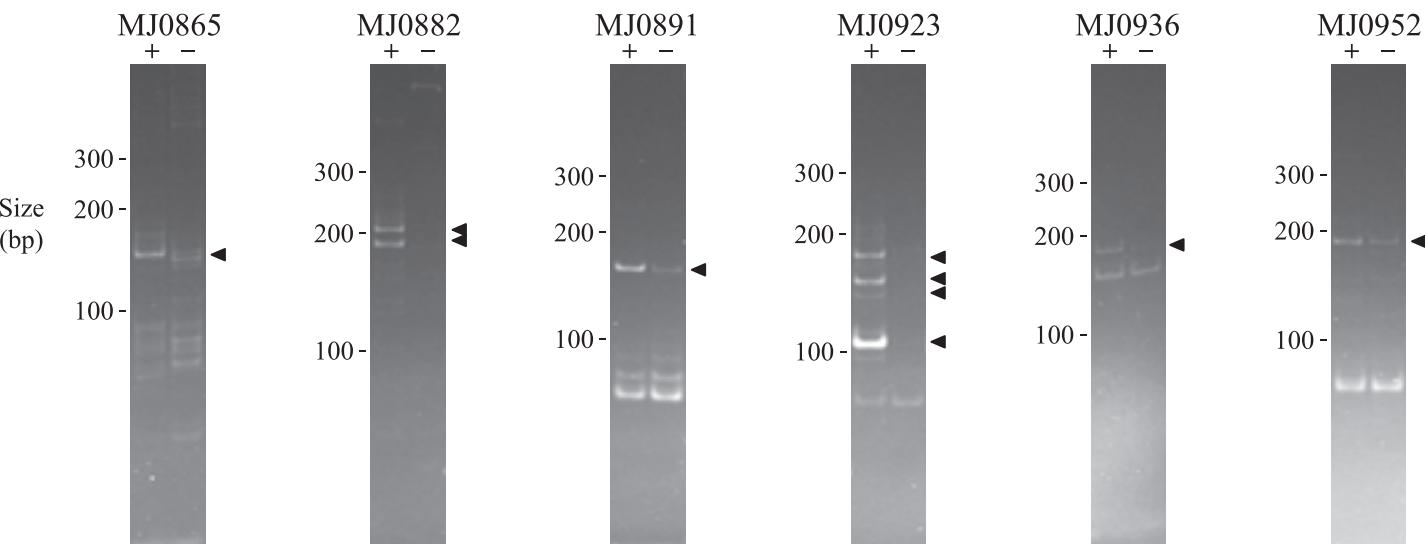
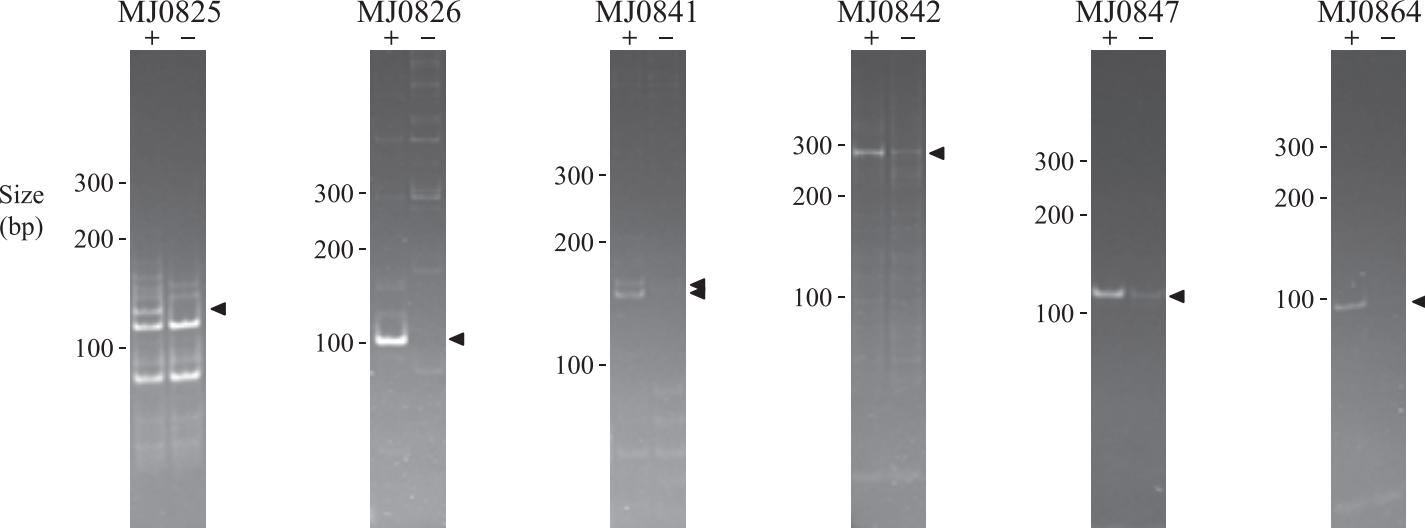


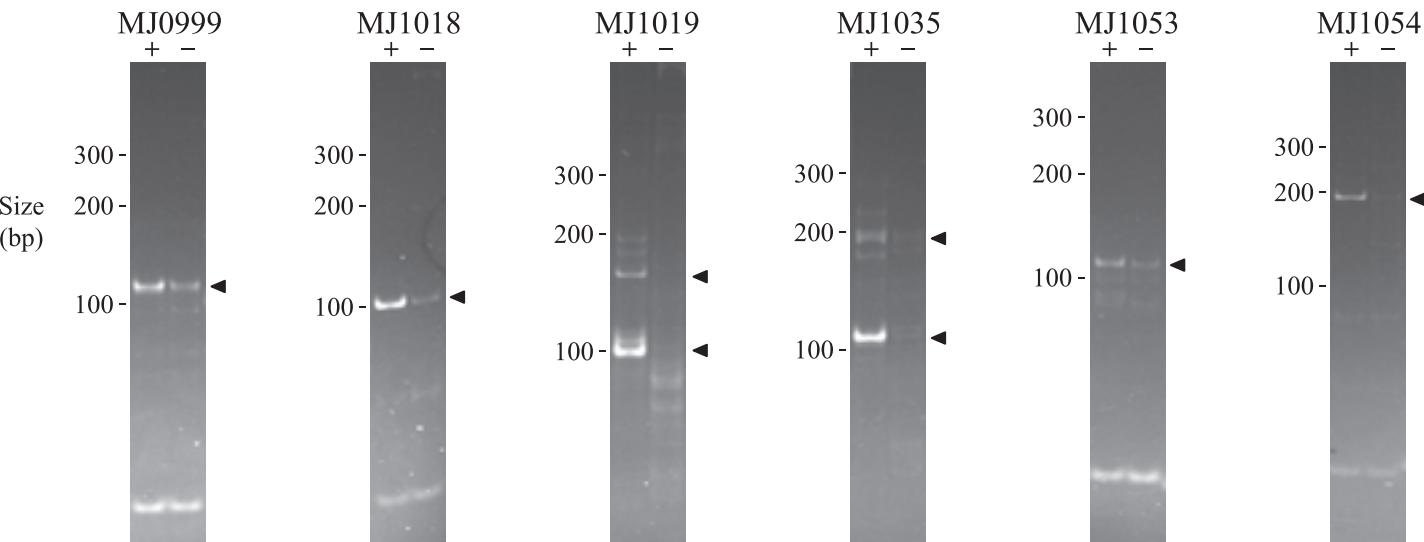
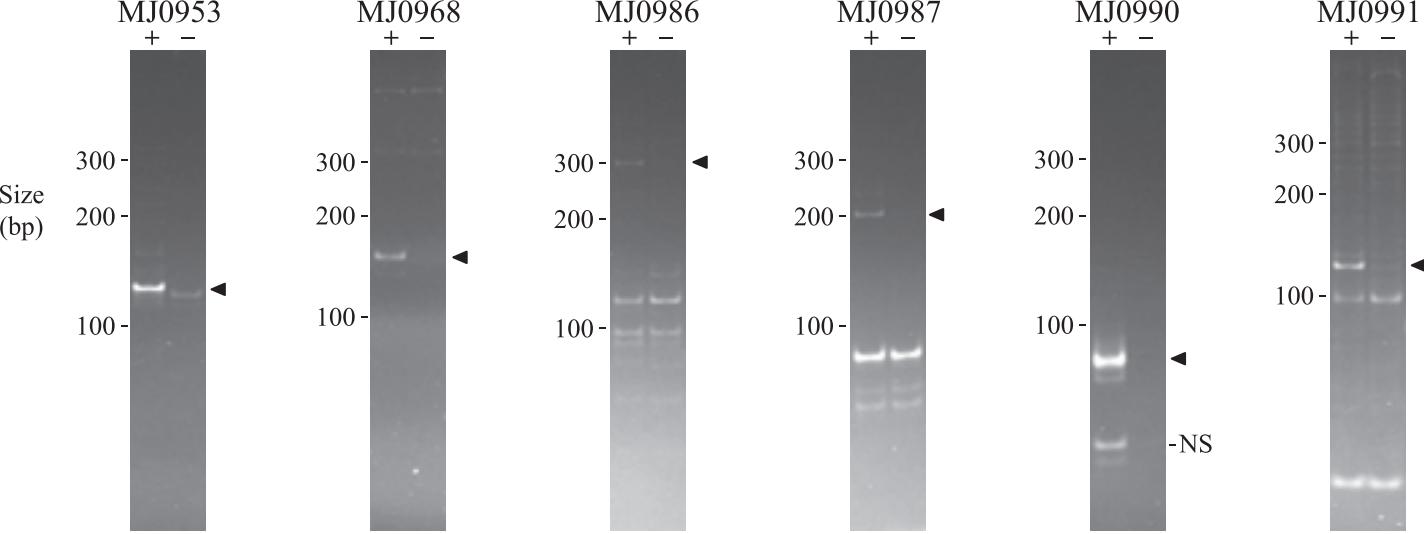


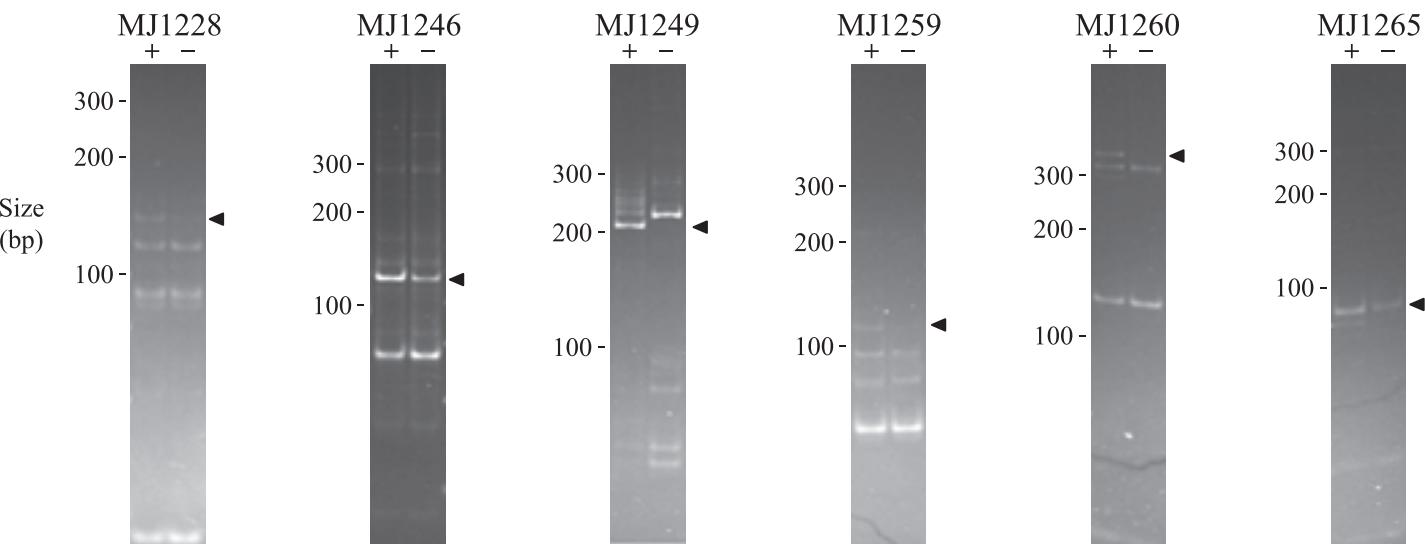
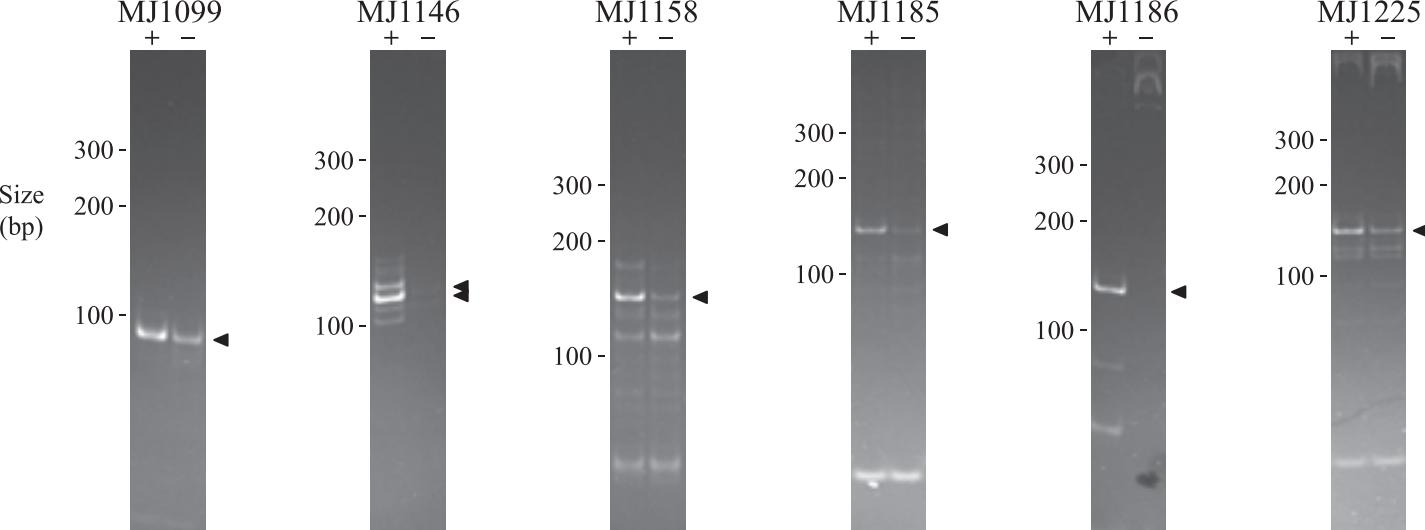


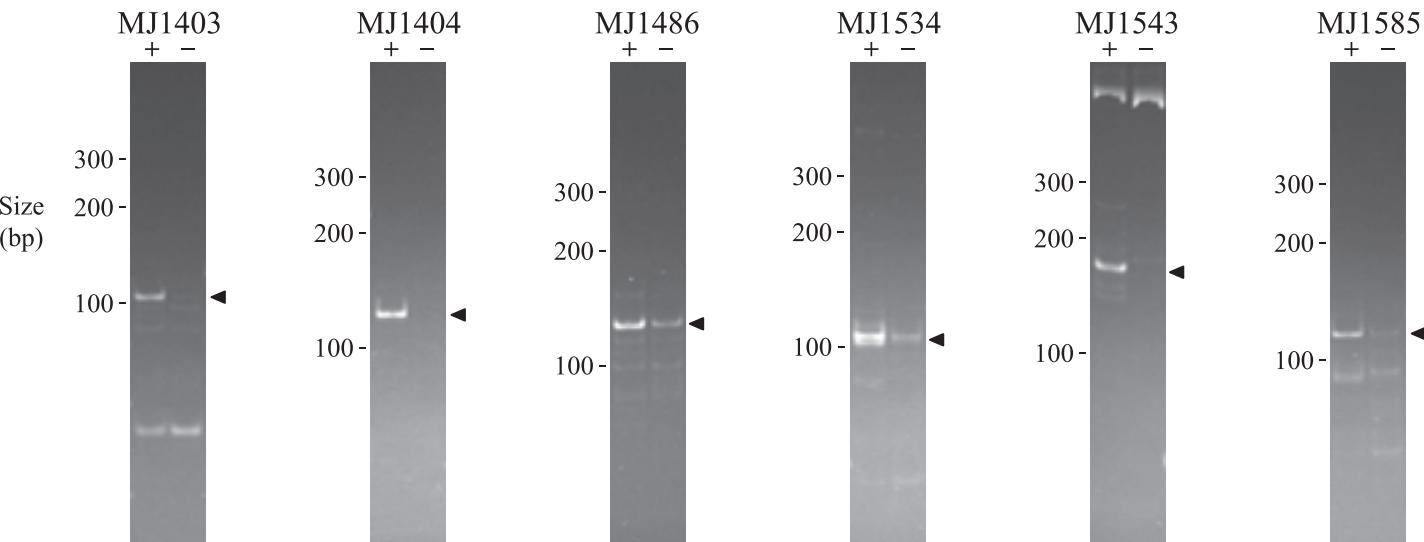
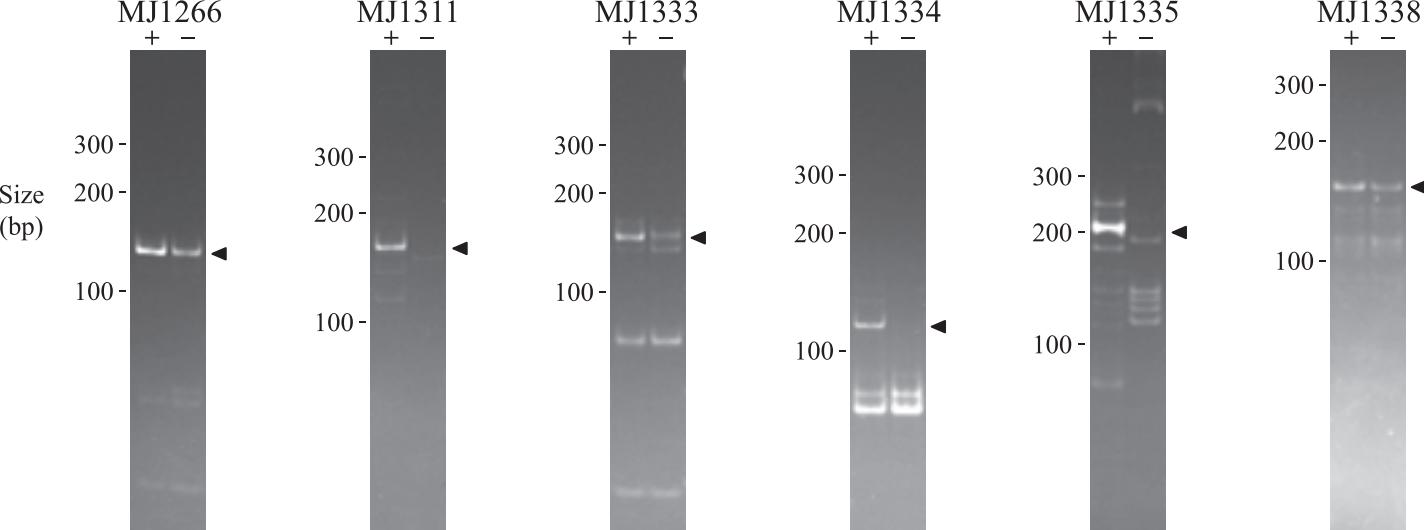












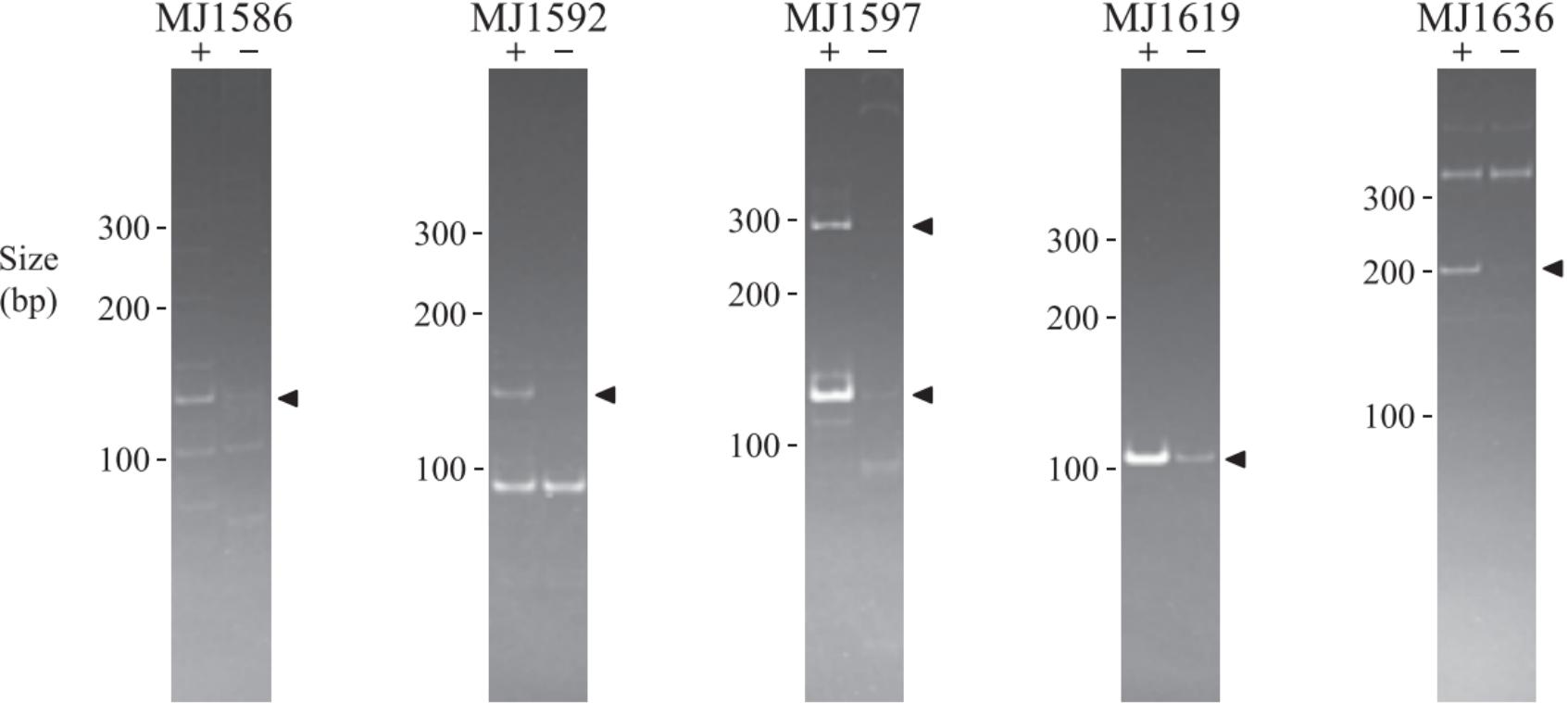


Figure S1. Primer extension and 5'-RACE results. **(A)** Primer extension results. Arrowheads indicate runoff transcripts. **(B)** 5'-RACE results. +, RT-PCR products from TAP-treated RNA; -, RT-PCR products from untreated RNA (control). Arrowheads indicate transcription start sites. NS, non-specific band.