

**Determination of vector:insert junctions in  $\lambda$ gt10 cDNAs that do not recut with *EcoRI*.  
Nucleotide sequence of the  $\lambda$ imm434 *HindIII-EcoRI* DNA fragment encoding part of the *ci* protein**

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Bacteriophage  $\lambda$ gt10 is often used as a vector for the construction of cDNA libraries.  $\lambda$ gt10 contains the phage 434 immunity region (*imm*<sup>434</sup>) with a unique *EcoRI* restriction site in the repressor protein (*ci*) gene into which double-stranded cDNAs bearing *EcoRI* sticky ends can be inserted (1). This provides a convenient method for selection of recombinant phage (*ci*<sup>-</sup>) and for insert retrieval and subsequent sequencing. However, one or both *EcoRI* sites often are not reconstituted, perhaps because of damage during phage arm dephosphorylation or resection during ligation. In these cases it is necessary to know the *imm*<sup>434</sup> nucleotide sequence in both directions from the *EcoRI* site to determine the boundaries between phage DNA and cDNA insert. The *imm*<sup>434</sup> nucleotide sequence rightwards from the *EcoRI* site was reported previously (2,3). The sequence leftwards up to the *HindIII* site (252 bp) is reported here. This *HindIII-EcoRI* DNA fragment encodes part of the *imm*<sup>434</sup> *ci* protein. There is a low degree of DNA and protein sequence homology between  $\lambda$  and 434 *ci*, consistent with the fact that phage 434 is insensitive to the  $\lambda$  repressor and  $\lambda$  is insensitive to the 434 repressor.

***HindIII***

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.. JAAGCTTCACACCACGAACCAAGCTCTAACCATGCTAATCAATGGATATTTCCCTTTGGGCTCAACGTGCC
.. TTCCGAAGTGTGGTCTTGGTCGAGATTGGTACGATTAGTTACCTATAAAGGGAAACCCGAGTTGCACGGG
   A1aG1uCysTrpSerGlyA1aArgValMetSerIleLeuProTyrLysGlyLysProGluValHisGly
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AACAAATCTAACATTCGAATCAGAGGTGCCATTGAGCAGCCAGTCAACACTTACGCCAAGAGCTGACGCAAG
TTGTTTAGATTGTAAGCTTAGTCTCCACGGTAACTCGTCGGTCAGTTGTGAATGCGGTTCTCGACTGCGTTC
ValPheArgValAsnSerAspSerThrGlyAsnLeuLeuTrpAspValSerValGlyLeuA1aSerA1aLeu
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TTCTGGTAAAAAGCGTGGTCGCTTAGTTTTACCGTTTTCGAGCTGCTCTATAGACTGCTGGGTAGTCCCCAC
AAGACCATTTTTTCGACACGCAATCAAATGGCAAAGCTCGACGAGATATCTGACGACCATCAGGGGTG
GluProLeuPheArgProArgLysThrLysGlyAsnGluLeuGlnGluIleSerGlnGlnThrThrGlyVal
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***EcoRI***

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CTTTTGAGCAAGTTCAGCCTGGTTAAGTCCAAGCTGAATTCCTTTTGTCTTTTACCCTGGAAGAAATACTCAT...
GAAAACCTGTTCAAGTCGGACCAATTCAGGTTCTGACTTAAAGAAAACGAAAATGGGACCTCTTTATGAGTA...
LysGlnA1aLeuGluA1aGlnAsnLeuGlyLeuGlnIleArgLysSerLysValArgSerSerIleSerMet
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← ***ci***

**References:**

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