

Figure 1S. Alignment of *T. pallidum* Nichols and Sea 81-4 strain *tprJ-tprI* (A) and *tprG-tprF* (B) loci. Identical residues are indicated by black shading and non-synonymous changes are indicated in a gray or no shading, respectively. Predicted start codons (according to Fraser et al, 1998) are indicated by asterisks for each *tpr* gene along with stop codons in the Nichols strain sequences. The Sea 81-4 *tprJ* locus contains a *tprG*-like ORF whose central nonconserved region shows sequence identity with the corresponding Nichols and Sea 81-4 strain *tprG* sequence. Frameshift and premature stop codon positions in Sea 81-4 *tprG*, are indicated by asterisks. -35 and -10 predicted Sigma 70 consensus sequences are underlined. Due to its premature termination, the Sea 81-4 *tprG* intergenic spacer is 422 bp long instead of 58 bp as in Nichols.

Figure 2S. Alignment of TprI homologs in *T. pallidum* Nichols and Sea 81-4 Strain.

Figure 3S. Alignment of TprG homologs in *T. pallidum* Nichols and Sea 81-4 Strain showing a shorter TprG ORF in Sea 81-4. Frameshift position is indicated by an asterisk.

Figure 4S. Alignment of TprF homologs in *T. pallidum* Nichols and Sea 81-4 Strain.

Sea 81-4	<i>tprJ/I</i> loci	780	CCACACGCGCCGTGGGCAGCACCCGGCACTGTATGCGGAGCTGAAGGTGGCGGACCTGCA
Nichols	<i>tprJ/I</i> loci	781	CCACACGCGCCGTGGGCAGCACCCGGCACTGTATGCGGAGCTGAAGGTGGCGGACCTGCA
Sea 81-4	<i>tprJ/I</i> loci	840	GGCGGACCTGAGTCAGGGGAAGGCAGGTTTTGCCATTAAGCGCAAGGGGAAGGTAGAGGC
Nichols	<i>tprJ/I</i> loci	841	GGCGGACCTGAGTCAGGGGAAGGCAGGTTTTGCCATTAAGCGCAAGGGGAAGGTAGAGGC
Sea 81-4	<i>tprJ/I</i> loci	900	GACACTACACTGTTATGGGGCTACCTGACGATTGGGAAGAACCCACGTTTCTGACGAA
Nichols	<i>tprJ/I</i> loci	901	GACACTACACTGTTATGGGGCTACCTGACGATTGGGAAGAACCCACGTTTCTGACGAA
Sea 81-4	<i>tprJ/I</i> loci	960	CTTTGCCCGGCTGTGGAAGCCGTGGGTGACAGCGCAGTACCAGGAGGATGCGGTACAGTA
Nichols	<i>tprJ/I</i> loci	961	CTTTGCCCGGCTGTGGAAGCCGTGGGTGACAGCGCAGTACCAGGAGGATGCGGTACAGTA
Sea 81-4	<i>tprJ/I</i> loci	1020	TGCGCCGGGTTTGGGGTTTAGGCGGCAAGGTTGGGTATCGGGCACAGGACATTGGGGG
Nichols	<i>tprJ/I</i> loci	1021	TGCGCCGGGTTTGGGGTTTAGGCGGCAAGGTTGGGTATCGGGCACAGGACATTGGGGG
Sea 81-4	<i>tprJ/I</i> loci	1080	CAGTGGGGTCAGCCTTGATGTGGGGTTTTCTCCTTTGCCTCTAACGGTGCCTGGGATAG
Nichols	<i>tprJ/I</i> loci	1081	CAGTGGGGTCAGCCTTGATGTGGGGTTTTCTCCTTTGCCTCTAACGGTGCCTGGGATAG
Sea 81-4	<i>tprJ/I</i> loci	1140	TACTGACCCACGCACAGTAAGTATGGCTTTGGGGCAGACTTGAAGCTAATGTATGCGCG
Nichols	<i>tprJ/I</i> loci	1141	TACTGACCCACGCACAGTAAGTATGGCTTTGGGGCAGACTTGAAGCTAATGTATGCGCG
Sea 81-4	<i>tprJ/I</i> loci	1200	TGCAGGACACCCTCTGTGCACGGTAGAGCTTGCCAGCAATGTTACGCTAGAAGACGGATA
Nichols	<i>tprJ/I</i> loci	1201	TGCAGGACACCCTCTGTGCACGGTAGAGCTTGCCAGCAATGTTACGCTAGAAGACGGATA
Sea 81-4	<i>tprJ/I</i> loci	1260	CCTCATCGGTGCACAGAAGGACGCAAAACAATCAGAACAAGGATAAACTGCTGTGGAATGT
Nichols	<i>tprJ/I</i> loci	1261	CCTCATCGGTGCACAGAAGGACGCAAAACAATCAGAACAAGGATAAACTGCTGTGGAATGT
Sea 81-4	<i>tprJ/I</i> loci	1320	AGGGGGCCGACTCACCTCGAACCAGGCGCGGCTTCCGCTTCTCCTTCGCCCTCGACGC
Nichols	<i>tprJ/I</i> loci	1321	AGGGGGCCGACTCACCTCGAACCAGGCGCGGCTTCCGCTTCTCCTTCGCCCTCGACGC
Sea 81-4	<i>tprJ/I</i> loci	1380	CGGTAACCAACACCAGAGTGCACAGGACTTTCAAAATCGCACACAGAGGGCGCAGAGTGA
Nichols	<i>tprJ/I</i> loci	1381	CGGTAACCAACACCAGAGTGCACAGGACTTTCAAAATCGCACACAGAGGGCGCAGAGTGA
Sea 81-4	<i>tprJ/I</i> loci	1440	ACTCACCGCCTCTCAAATAACCTCTTCCAGGGAGAAAGTCAAAAACAGGAAGCCTGGCT
Nichols	<i>tprJ/I</i> loci	1441	ACTCACCGCCTCTCAAATAACCTCTTCCAGGGAGAAAGTCAAAAACAGGAAGCCTGGCT
Sea 81-4	<i>tprJ/I</i> loci	1500	GGAC--GAATAATGCAA-AGAAAGGTGCTTGATGCCGTAACGGCAGCCAC-CGAAACCGCC
Nichols	<i>tprJ/I</i> loci	1501	AACCCAGGTAGTGCAACAGCCGACGC---AGACAGTAACGGCTGGAGTTCGAAGC-GCGC
Sea 81-4	<i>tprJ/I</i> loci	1556	TTCAGTCGAGGGGAAACCGGTACATAA-CG-----GCAGTGTCAAACGTAAAAGTC-
Nichols	<i>tprJ/I</i> loci	1557	TGGAAATCTCGGGGACTACGTACATAAACCGGTAGAGGCAGT-TCAACCTAATCCTGCT
Sea 81-4	<i>tprJ/I</i> loci	1606	-ACCCCTCCGGTA--GCTGC-CACGCTTTTGACGAACCTGAAGGTGTTTCATTACCGACCC
Nichols	<i>tprJ/I</i> loci	1616	AAACCTACCGGTAAGGTTGTGCAAAATCTTACACCCCGCAGGGAAGTC--CGCCGAACC
Sea 81-4	<i>tprJ/I</i> loci	1662	TCCCTACACCGTCAACCGCTTCCCGCGCTTCTGCATTTTCCCTGATGGGGCAGGTTTTGCT
Nichols	<i>tprJ/I</i> loci	1674	TGC-----CGCCGCTTCCCTGCACTTCTGCATTTTCCCTGATGGGGCAGGTTTTGCT

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Sea 81-4 tprJ/I loci 1722 GCAGTACGATGCGGAGCAGGTGGTGAAGGGGTTGAGCAGGTACAGACGCAAATCGTTGC
Nichols tprJ/I loci 1726 GCAGTACGATGCGGAGCAGGTGGTGAAGGGGTTGAGCAGGTACAGACGCAAATCGTCA
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----- tprJ central unique region -----
Sea 81-4 tprJ/I loci 1782 TGAAATTAACAGAAAGTGAAGCGGCTGTGGCTCAGAGCAAGGCTGCAGCACAGGCATT
Nichols tprJ/I loci 1786 TGAAATTAATCAGAAAGTGAAGCGGCTGTGGCAAAAAATAATGCAA----ACATGCAAG
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Sea 81-4 tprJ/I loci 1842 CA--TCAACGGTCTTACCAAGGCAATA----GAAGACG--TGGCTGATGCGTTGCTT--GC
Nichols tprJ/I loci 1842 CGGTGCGGGGTAGT--CTAGCGGATACTGCGAGAATGGTAGGC-GAAGCGCTCATTAGC
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Sea 81-4 tprJ/I loci 1893 A-CCGCATAAGCGGAAATCCGATGAGCCTCTTCA-ACCTTCCGGATCAA-CAAAAATTACT
Nichols tprJ/I loci 1899 AGCAACTATCACGTAAGCAGAACAGCA--TTCTGACCAATGGTGAGCGTGCAAGATGACGT
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Sea 81-4 tprJ/I loci 1950 GAAGGACGATCTCGCTGATCTTATTCCAAAGCTTACGG-CTGAGGCTACAAAGTTTTTCA
Nichols tprJ/I loci 1957 GAAACAGGATCTGGCAGATTTAGTGCCGATG-ATGCGAACGGAAATAACGGCGTTTTTTC
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Sea 81-4 tprJ/I loci 2009 CTGAGGGTCAGACGTTT-CTAACCGAAGAAGTGAAGAAGAAGACGGATGCGTTGAATGCG
Nichols tprJ/I loci 2016 C-GAGTGTCCAGCAACACAATAACCGAAGAAGTGAAGAAGAAGACGGATGCGTTGAATGCG
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Sea 81-4 tprJ/I loci 2068 GGGCAGCAGATACGTCAGGCTATACAGAACCTGCGTGCGTCTGCATGGCGTGCCTTTCTA
Nichols tprJ/I loci 2075 GGGCAGCAGATACGTCAGGCTATACAGAACCTGCGTGCGTCTGCATGGCGTGCCTTTCTA
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Sea 81-4 tprJ/I loci 2128 ATGGGAGTCAGCGCCGTGTGCTGTATCTTGACACCTACAATGTCGCCCTTCGATGCACTG
Nichols tprJ/I loci 2135 ATGGGAGTCAGCGCCGTGTGCTGTATCTTGACACCTACAATGTCGCCCTTCGATGCGCTG
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Sea 81-4 tprJ/I loci 2188 CTTACAGCGCAGTGGAAAGTGGCTGTCTTCTGGCATATACGTTGCCACAGCACCGGCAAAAC
Nichols tprJ/I loci 2195 TTTACGGCGCAGTGGAAAGTGGCTGTCTTCTGGCATATACTTTGCCACAGCACCGGCAAAAC
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Sea 81-4 tprJ/I loci 2248 GTTTTTGGCACCAGGGTGTAGATAACACCATCGCAAGCTGTGGCGACTTTGCCGGATTG
Nichols tprJ/I loci 2255 GTTTTTGGCACCAGGGTGTAGATAACACCATCGCAAGCTGTGGCGACTTTGCCGGATTG
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Sea 81-4 tprJ/I loci 2308 CTCAAACCTCGAAACTAAGAGCGGTGACCCCTACACCCACCTGCTCACCGGCTGGACGCC
Nichols tprJ/I loci 2315 CTTAAGCTCGAAACTAAGAGCGGTGACCCCTACACCCACCTGCTCACCGGCTGGACGCC
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Sea 81-4 tprJ/I loci 2368 GCGTGTGAAACACGCGTGTACATCCCCCTCACCCATGACCTGTACAAAAATAATAACGGG
Nichols tprJ/I loci 2375 GCGTGTGAAACACGCGTGTACATCCCCCTCACCCATGACCTGTACAAAAATAATAACGGG
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Sea 81-4 tprJ/I loci 2428 AACCCCTCTCCCTTCCGGCGGTTCCCTCAGGGCACATTGGCTGCCGGTGGTGGGAAAGGCG
Nichols tprJ/I loci 2435 AACCCCTCTCCCTTCCGGCGGTTCCCTCAGGGCACATTGGCTGCCGGTGGTGGGAAAGGCG
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Sea 81-4 tprJ/I loci 2488 TGGTGTAGCTATCGCATCCCGGTGCAGGATTATGGCTGGGTGAAGCCAAGCGTTACGGTC
Nichols tprJ/I loci 2495 TGGTGTAGCTATCGCATCCCGGTGCAGGATTACGGCTGGGTGAAGCCAAGCGTTACGGTC
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Sea 81-4 tprJ/I loci 2548 CATGCCTCTACCAACCGTGACACCTGAATGCCCTGCTGCAGGTGGAGCAGTAGGAGCT
Nichols tprJ/I loci 2555 CATGCCTCTACCAACCGTGACACCTGAATGCCCTGCTGCAGGTGGAGCAGTAGGAGCT

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Sea 81-4 *tprJ/I* loci 2608 ACCTATCTAACCAAGGAGTACTGTGCACAGCTGCGTGTGGTATTTTCAGCCAGTCTCATA
Nichols *tprJ/I* loci 2615 ACCTATCTAACCAAGGAGTACTGTGCACAGCTGCGTGTGGTATTTTCAGCCAGTCTCATA

Sea 81-4 *tprJ/I* loci 2668 GAGAAGACGGTATTCTCCCTTGATTGGGAACAGGGTATGCTCTCTGATGTCCCGTACCTG
Nichols *tprJ/I* loci 2675 GAGAAGACGGTATTCTCCCTTGATTGGGAACAGGGTATGCTCTCTGATGTCCCGTACCTG

Sea 81-4 *tprJ/I* loci 2728 CTGGTGTCCGAGTGCCTCACCCAGGGAATCGGCCGCATCGTGTGCGGGCCTACCCTCTCC
Nichols *tprJ/I* loci 2735 CTGGTGTCCGAGTGCCTCACCCAGGGAATCGGCCGCATCGTGTGCGGGCCTACCCTCTCC

tprJ stop (genome sequence)

Sea 81-4 *tprJ/I* loci 2788 TGGTAGTCACACGCGGCTAGACGGGTGGGGGGGGTGGAGGTAGAAGTGAGAGGAGGGGA
Nichols *tprJ/I* loci 2795 TGGTAGTCACACGCGGCTAGACGGGTGGGGGGGG-TGAGGTAGAAGTGAGAGGAGGGGA

tprI start (genome sequence)

Sea 81-4 *tprJ/I* loci 2848 GTGAGTGGGCAGGCAGGTGATGCAAGCGGGGTACTTGCGGGCATGGTATGTGCTGCTTC
Nichols *tprJ/I* loci 2854 GTGAGTGGGCAGGCAGGTGATGCAAGCGGGGTACTTGCGGGCATGGTATGTGCTGCTTC

Sea 81-4 *tprJ/I* loci 2908 TGGTTATGCAGGCGTACTCACTCCGCAGGTCAGTGGCACAGCCAGCTCCAGTGGGGCAT
Nichols *tprJ/I* loci 2914 TGGTTATGCAGGCGTACTCACTCCGCAGGTCAGTGGCACAGCCAGCTCCAGTGGGGCAT

Sea 81-4 *tprJ/I* loci 2968 TCGGTTCCAGAAGAATCCACGCACTGGCCCGGGCAAGCACACCCATGGGTTTCGCACCTAC
Nichols *tprJ/I* loci 2974 TCGGTTCCAGAAGAATCCACGCACTGGCCCGGGCAAGCACACCCATGGGTTTCGCACCTAC

Sea 81-4 *tprJ/I* loci 3028 CAATGGTCTGACTATTTCCCTGCCGTTGGTGTCAAAGCACACCCACACCCGCCGAGGGGA
Nichols *tprJ/I* loci 3034 CAATAGTCTGACTATTTCCCTGCCGTTGGTGTCAAAGCACACCCACACCCGCCGAGGGGA

Sea 81-4 *tprJ/I* loci 3088 GGCACGCTCAGGGGTGTGGGCACAGCTGCAGCTGAAGGACCTGGCAGTAGAGCTTGCCTC
Nichols *tprJ/I* loci 3094 GGCACGCTCAGGGGTGTGGGCACAGCTGCAGCTGAAGGACCTGGCAGTAGAGCTTGCCTC

Sea 81-4 *tprJ/I* loci 3148 TTCTAAAAGCTCAACGGCCCTGTCCTTTACCAAACCTTACCCTTCCTTCCAGGCAACCCT
Nichols *tprJ/I* loci 3154 TTCTAAAAGCTCAACGGCCCTGTCCTTTACCAAACYTACCCTTCCTTCCAGGCAACCCT

Sea 81-4 *tprJ/I* loci 3208 GCACTGTTATGGGGCCTACCTGACAGTGGGTACCAGTCCCTTCCCTGTGTGGTTAACTTTGC
Nichols *tprJ/I* loci 3214 GCACTGTTATGGGGCCTACCTGACAGTGGGTACCAGTCCCTTCCCTGTGTGGTTAACTTTGC

Sea 81-4 *tprJ/I* loci 3268 CCAGCTGTGAAACCCTTTGTCACCCGTGCTATTTCAGAAAAGGACACTCGCTATGCCCC
Nichols *tprJ/I* loci 3274 CCAGCTGTGAAACCCTTTGTCACCCGTGCTATTTCAGAAAAGGACACTCGCTATGCCCC

Sea 81-4 *tprJ/I* loci 3328 TGGTTTCTCCGGCTCCGGGGCAAAACTCGGCTACCAGGCCACAATGTGGGAAACAGCGG
Nichols *tprJ/I* loci 3334 TGGTTTCTCCGGYTCCGGGGCAAAACTCGGCTACCAGGCCACAATGTGGGAAACAGCGG

Sea 81-4 *tprJ/I* loci 3388 AGTAGATGTGGACATCGGTTTCCCTCTCCTTCCCTTTCCAATGGTGCCTGGGATAGTACTGA
Nichols *tprJ/I* loci 3394 AGTAGATGTGGACATCGGTTTCCCTCTCCTTCCCTTTCCAATGGTGCCTGGGATAGTACTGA

Sea 81-4 *tprJ/I* loci 3448 CACCACGCACAGCAAGTATGGCTTCGGGGACCGATGCAACGCTTTCCTATGGCGTCGACCG
Nichols *tprJ/I* loci 3454 CACCACGCACAGCAAGTATGGCTTCGGGGCCCGATGCAACGCTTTCCTATGGCGTCGACCG

Sea 81-4	<i>tprJ/I</i>	loci	3508	TCAGCGGCTGCTTACGTTGGAGCTGGCAGGGAATGCCACACTGGACCAGAACTACGTAA
Nichols	<i>tprJ/I</i>	loci	3514	TCAGCGGCTGCTTACGTTGGAGCTGGCAGGGAATGCCACACTGGAGCAGCACTACCGTAA
Sea 81-4	<i>tprJ/I</i>	loci	3568	GGGTACCGAAGACTCCAAAGAACGAAAACAAAACAGCACTCCTGTGGGGAGTAGGAGGCCG
Nichols	<i>tprJ/I</i>	loci	3574	GGGTACCGAAGACTCCACGAACGAAAACAAAACAGCACTCCTGTGGGGAGTAGGAGGCCG
Sea 81-4	<i>tprJ/I</i>	loci	3628	ACTCACCTCGAACCAGGCGCCGGCTTCCGCTTCTCCTTCGCCCTCGACGCCGGTAACCA
Nichols	<i>tprJ/I</i>	loci	3634	ACTCACCTCGAACCAGGCGCCGGCTTCCGCTTCTCCTTCGCCCTCGACGCCGGTAACCA
Sea 81-4	<i>tprJ/I</i>	loci	3688	ACGCCAGGACCCTGCCGATGCAGGTAATCGCCTTCTGGCAACGGGGAGCTCACGGGAGAA
Nichols	<i>tprJ/I</i>	loci	3694	ACACCAGGACCCTGCCGATGCAGGTAATCGCCTTCTGGCAACGGGGAGCTCACGGGAGAA
Sea 81-4	<i>tprJ/I</i>	loci	3748	GTTTCACAGCGGTTTCGATGCCCTCAGGGTGGAGCAATACCGTGTAAGGATAAGTATCT
Nichols	<i>tprJ/I</i>	loci	3754	GTTTGACAGCGGTTTCGATGCCCTCAGGGTGGAGCAATACCGTGTAAGGATAAGTATCT
Sea 81-4	<i>tprJ/I</i>	loci	3808	TGAATTTTTGCTGGGACAGATGGCGGAGTCTCGATTCTCGAGCGGGTGGGGCTTGCCCT
Nichols	<i>tprJ/I</i>	loci	3814	TGAATTTTTGCTGGGACAGATGGCGGAGTCTCGATTCTCGAGCGGGTGGGGCTTGCCCT
Sea 81-4	<i>tprJ/I</i>	loci	3868	CACGCTGCAGGACGGTACGCTCGTCTCTACGCTGACGAAGGTTGCCACTGATAGTGGAGA
Nichols	<i>tprJ/I</i>	loci	3874	CACGCTGCAGGACGGTACGCTCGTCTCTACGCTGACGAAGGTTGCCACTGATAGTGGAGA
Sea 81-4	<i>tprJ/I</i>	loci	3928	TCGGTTTTATCAAATGGCGTTGGTAAAACCTTGCCCCAGAGGGCGCAGGCGGAGCAGAG
Nichols	<i>tprJ/I</i>	loci	3934	TCGGTTTTATCAAATGGCGTTGGTAAAACCTTGCCCCAGAGGGCGCAGGCGGAGCAGAG
Sea 81-4	<i>tprJ/I</i>	loci	3988	ACTACAGGAGATTGTGGCGCCGAGTCAGTCGGACATCGTGCTTATCATGCTGCTAACCTG
Nichols	<i>tprJ/I</i>	loci	3994	ACTACAGGAGATTGTGGCGCCGAGTCAGTCGGACATCGTGCTTATCATGCTGCTAACCTG
Sea 81-4	<i>tprJ/I</i>	loci	4048	GCTTGAGCGTGCACGGCTGGACCGGTTCAATGCTGATGCGCTGCTTACGGCGCAGTGGAC
Nichols	<i>tprJ/I</i>	loci	4054	GCTTGAGCGTGCACGGCTGGACCGGTTCAATGCTGATGCGCTGCTTACGGCGCAGTGGAC
Sea 81-4	<i>tprJ/I</i>	loci	4108	CTATGTGTCGGCTGGACTGTATGGGGCGACGGCGGGTACCAATGTATTTGGTAAGCGCGT
Nichols	<i>tprJ/I</i>	loci	4114	CTATGTGTCGGCTGGACTGTATGGGGCGACGGCGGGTACCAATGTATTTGGTAAGCGCGT
Sea 81-4	<i>tprJ/I</i>	loci	4168	GCTGCCTGCGCTGCGGTCTGGCATTGATTTTGCCGGATTCTCAAACCTCGAAACCAA
Nichols	<i>tprJ/I</i>	loci	4174	GCTGCCTGCGCTGCGGTCTGGCATTGATTTTGCCGGATTCTCAAACCTCGAAACCAA
Sea 81-4	<i>tprJ/I</i>	loci	4228	AAGCGGTGACCCCTACACCCACCTGCTCACCGGCCTGAACGCCGGCGTGAAGCACGCGT
Nichols	<i>tprJ/I</i>	loci	4234	AAGCGGTGACCCCTACACCCACCTGCTCACCGGCCTGAACGCCGGCGTGAAGCACGCGT
Sea 81-4	<i>tprJ/I</i>	loci	4288	GTACATCCCCCTCACCTACATCCGTTACAGAAATAACGGAGGGTACGAACTGAATGGAGC
Nichols	<i>tprJ/I</i>	loci	4294	GTACATCCCCCTCACCTACATCCGTTACAGAAATAACGGAGGGTACGAACTGAATGGAGC
Sea 81-4	<i>tprJ/I</i>	loci	4348	TGTGCCCCCTGGGACTATCAATATGCCAATTTTGGGGAAGGCGTGGTGCAGCTATCGCAT
Nichols	<i>tprJ/I</i>	loci	4354	TGTGCCCCCTGGGACTATCAATATGCCAATTTTGGGGAAGGCGTGGTGCAGCTATCGCAT
Sea 81-4	<i>tprJ/I</i>	loci	4408	CCCCCTCGGTTCCACGCCTGGCTTACACCGCATAACATCCGTGCTCGGCACAACCAATCG
Nichols	<i>tprJ/I</i>	loci	4414	CCCCCTCGGTTCCACGCCTGGCTTACACCGCATAACATCCGTGCTCGGCACAACCAATCG

Sea 81-4 *tprJ/I* loci 4468 CTTTAACGTTATTAACCCCGGTACACCCTGTTGAATGAACGAGCGCTCCAGTACCAGGT
Nichols *tprJ/I* loci 4474 CTTTAACGTTATTAACCCCGGTACACCCTGTTGAATGAACGAGCGCTCCAGTACCAGGT

Sea 81-4 *tprJ/I* loci 4528 GGGACTGACGTTTCAGTCCCTTCGAGAAGGTGGAGCTCAGCGCCAGTGGGAACAGGGGGT
Nichols *tprJ/I* loci 4534 GGGACTGACGTTTCAGTCCCTTCGAGAAGGTGGAGCTCAGCGCCAGTGGGAACAGGGGGT

Sea 81-4 *tprJ/I* loci 4588 GCTTGCTGACGCTCCTTACATGGGTATTGCCGAGAGTATGTGGTCTGAGCGTACTTTGG
Nichols *tprJ/I* loci 4594 GCTTGCTGACGCTCCTTACATGGGTATTGCCGAGAGTATGTGGTCTGAGCGTACTTTGG

tprI stop (genome sequence)

Sea 81-4 *tprJ/I* loci 4648 CACGTTTATCTGTGGGGTGAAGGTGGTTTGGTGAGGGGTGTCGTGTGGGCCAGAGAACG
Nichols *tprJ/I* loci 4654 CACGTTTATCTGTGGGGTGAAGGTGGTTTGGTGAGGGGTGTCGTGTGGGCCAGAGAACG

Sea 81-4 *tprJ/I* loci 4708 GGTACGGTGGGGTGC CGCTTTTCCCGTGGGGCTGTGCGCGCTCAGTTTACAGGCGAG
Nichols *tprJ/I* loci 4714 GGTACGGTGGGGTGC CGCTTTTCCCGTGGGGCTGTGCGCGCTCAGTTTACAGGCGAG

Sea 81-4 *tprJ/I* loci 4768 GGATTGCAGGGGTATGTGCGGGAAGCGTCTGGGTAAAGTGATGGTGCTCGGGTGTATGTT
Nichols *tprJ/I* loci 4773 GGATTGCAGGGGTATGTGCGGGAAGCGTCTGGGTAAAGTGATGGTGCTCGGGTGTATGTT

Sea 81-4 *tprJ/I* loci 4828 GCCGGGTGTGGCGGCGCTGTTTCTCTCTCCCCAAGCTCGGGGTGTACGGGGACGCACG
Nichols *tprJ/I* loci 4833 GCCGGGTGTGGCGGCGCTGTTTCTCTCTCCCCAAGCTCGGGGTGTACGGGGACGCACG

Sea 81-4 *tprJ/I* loci 4888 CGGCGGTTCTGACCTGTGGGCATCTGCATACAAGCTCCACAATGCCAGATACAGAGAA
Nichols *tprJ/I* loci 4893 CGGCGGTTCTGACCTGTGGGCATCTGCATACAAGCTCCACAATGCCAGATACAGAGAA

Sea 81-4 *tprJ/I* loci 4948 CCAGGCGCCTCCGCGCTATGCGCCGAGACACCGTTGGTGGGGCTGGACGTGGCGTTCCG
Nichols *tprJ/I* loci 4953 CCAGGCGCCTCCGCGCTATGCGCCGAGACACCGTTGGTGGGGCTGGACGTGGCGTTCCG

Sea 81-4 *tprJ/I* loci 5008 TCGGAAAAATGGCTTCCCTGCTCCAAGTACGGTGGACGCGGCACTCACGCGTTAATGTT
Nichols *tprJ/I* loci 5013 TCGGAAAAATGGCTTCCCTGCTCCAAGTACGGTGGACGCGGCACTCACGCGTTAATGTT

Sea 81-4 *tprJ/I* loci 5068 CTGCGGCCGGTGTGGCCGGTTATTCGTTTCAGACCGGGGAAGGTAGTACGCATCTGTC
Nichols *tprJ/I* loci 5073 CTGCGGCCGGTGTGGCCGGTTATTCGTTTCAGACCGGGGAAGGTAGTACGCATCTGTC

Sea 81-4 *tprJ/I* loci 5128 GGTAGCGGCGGGTTTTGAGTGCACCGCGCTCATCTACGATAGCCAGCACTTTCTTTCCGGT
Nichols *tprJ/I* loci 5133 GGTAGCGGCGGGTTTTGAGTGCACCGCGCTCATCTACGATAGCCAGCACTTTCTTTCCGGT

Sea 81-4 *tprJ/I* loci 5188 TCTTGGGCAGGGCTTACT
Nichols *tprJ/I* loci 5193 TCTTGGGCAGGGCTTACT

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Sea 81-4 <i>tprG/F</i> loci	1	CCCTGCGTTTCCCATCTGCGGCTGTGCTCTTAGAGCAGCCGATGAGCAGCATGGCGCA
Nichols <i>tprG/F</i> loci	1	CCCTGCGTTTCCCATCTGCGGCTGTGCTCTTAGAGCAGCCGATGAGCAGCATGGCGCA
Sea 81-4 <i>tprG/F</i> loci	61	AAAAACGCCCGCAAACCCCTTCGCGTACCCACTTCTCTCTCACAGAATCCTCCCCCTTT
Nichols <i>tprG/F</i> loci	61	AAAAACGCCCGCAAACGC---GCGTACCCACTTCTCTCTCACAGAATCCTCCCCCTTT
Sea 81-4 <i>tprG/F</i> loci	121	ATCGACAAACATGCGCAAATAAGGGGTACAGTGTAAACCAAGGGGACAAGGAGGTGCA
Nichols <i>tprG/F</i> loci	118	ATCGACAAACATGCGCAAATAAGGGGTACAGTGTAAACCAAGGGGACAAGGAGGTGCA
Sea 81-4 <i>tprG/F</i> loci	181	AGGAGTGGTGAGTTTTTTCGCTGTGTGCAGGTGGCAGGGTGAGGGGGCTACTAGACAGGGC
Nichols <i>tprG/F</i> loci	178	AGGAGTGGTGAGTTTTTTCGCTGTGTGCAGGTGGCAGGGTGAGGGGGCTACTAGACAGGGC

		-10
		<i>tprG</i> start
		(genome sequence)

Sea 81-4 <i>tprG/F</i> loci	241	CGGGGGGGGGGTGAGGTAGCATGGGGTGCATGCGGTGGGGGAGTGTGCTGTGTGTGGTG
Nichols <i>tprG/F</i> loci	238	CGGGGGGGGGGTGAGGTAGCATGGGGTGCATGCGGTGGGGGAGTGTGCTGTGTGTGGTG

		-35
		Predicted Sigma 70 consensus sequences
Sea81-4 <i>tprG/F</i> loci	301	GTGGGGGTAGGAGCGAGCGGGGAGTGCTCGGACAGGAGTTTCCCCGAAGCTAACTGGC
Nichols <i>tprG/F</i> loci	298	GTGGGGGTAGGAGCGAGCGGGGAGTGCTCGGACAGGAGTTTCCCCGAAGCTAACTGGC
Sea 81-4 <i>tprG/F</i> loci	361	TCTGCCACACTTGAGTGGGCATCAGCTATGGCAAGGGGTAGGCAGTCATGGCCAGGCC
Nichols <i>tprG/F</i> loci	358	TCTGCCACACTTGAGTGGGCATCAGCTATGGCAAGGGGTAGGCAGTCATGGCCAGGCC
Sea 81-4 <i>tprG/F</i> loci	421	CCTGGTGCAGTTATGGGCACCGGTCCCTACAATCTGAAGCACGGGTTTCGTA CTACCAAC
Nichols <i>tprG/F</i> loci	418	CCTGGTGCAGTTATGGGCACCGGTCCCTACAATCTGAAGCACGGGTTTCGTA CTACCAAC
Sea 81-4 <i>tprG/F</i> loci	481	ACGGTGGGAGTATCCTTTCCCTGGTTATGCGCACCACCCACACGCGCCGTGGGCAGCAC
Nichols <i>tprG/F</i> loci	478	ACGGTGGGAGTATCCTTTCCCTGGTTATGCGCACCACCCACACGCGCCGTGGGCAGCAC
Sea 81-4 <i>tprG/F</i> loci	541	CCGGCACTGTATGCGGAGCTGAAGGTGGCGGACCTGCAGGCGGACCTGAGTCAGGGGAAG
Nichols <i>tprG/F</i> loci	538	CCGGCACTGTATGCGGAGCTGAAGGTGGCGGACCTGCAGGCGGACCTGAGTCAGGGGAAG
Sea 81-4 <i>tprG/F</i> loci	601	GCAGGTTTTGCCGTTAAGCGCAAGGGGAAGGTAGAGGCGACACTACACTGTTATGGGGCC
Nichols <i>tprG/F</i> loci	598	GCAGGTTTTGCCGTTAAGCGCAAGGGGAAGGTAGAGGCGACACTACACTGTTATGGGGCC
Sea 81-4 <i>tprG/F</i> loci	661	TACCTGACGATTGGGAAGAACCCACGTTTCTGACGAACTTTGCCCGGCTGTGGAAGCCG
Nichols <i>tprG/F</i> loci	658	TACCTGACGATTGGGAAGAACCCACGTTTCTGACGAACTTTGCCCGGCTGTGGAAGCCG
Sea 81-4 <i>tprG/F</i> loci	721	TGGGTGACAGCGCAGTACCAGGAGGATGCGGTACAGTATGCGCCGGGTTTGGGGGTTTA
Nichols <i>tprG/F</i> loci	718	TGGGTGACAGCGCAGTACCAGGAGGATGCGGTACAGTATGCGCCGGGTTTGGGGGTTTA

Sea 81-4	<i>tprG/F</i> loci	781	GCGCGCAAGGTTGGGTATCGGGCACAGGACATTGGGGGCAGTGGGGTCAGCCTTGATGTG
Nichols	<i>tprG/F</i> loci	778	GCGCGCAAGGTTGGGTATCGGGCACAGGACATTGGGGGCAGTGGGGTCAGCCTTGATGTG
Sea81-4	<i>tprG/F</i> loci	841	GGGTTTCTCTCCTTTGCCTCTAACGGTGCCTGGGATAGTACTGACCCACGCACAGTAAG
Nichols	<i>tprG/F</i> loci	838	GGGTTTCTCTCCTTTGCCTCTAACGGTGCCTGGGATAGTACTGACCCACGCACAGTAAG
Sea 81-4	<i>tprG/F</i> loci	901	TATGGCTTTGGGGCAGACTTGAAGCTAATGTATGCGCGTGCAGGACACCCTCTGTGCAGC
Nichols	<i>tprG/F</i> loci	898	TATGGCTTTGGGGCAGACTTGAAGCTAATGTATGCGCGTGCAGGACACCCTCTGTGCAGC
Sea 81-4	<i>tprG/F</i> loci	961	GTAGAGCTTGCCAGCAATGTACGCTAGAAGACGGATACCTCATCGGTGCACAGAAGGAC
Nichols	<i>tprG/F</i> loci	958	GTAGAGCTTGCCAGCAATGTACGCTAGAAGACGGATACCTCATCGGTGCACAGAAGGAC
Sea 81-4	<i>tprG/F</i> loci	1021	GCAAACAATCAGAACAAGGATAAACTGCTGTGGAATGTAGGGGGCCGACTCACCCCTCGAA
Nichols	<i>tprG/F</i> loci	1018	GCAAACAATCAGAACAAGGATAAACTGCTGTGGAATGTAGGGGGCCGACTCACCCCTCGAA
Sea 81-4	<i>tprG/F</i> loci	1081	CCAGGCGCCGGCTTCCGCTTCTCCTTCGCCCTCGACGCCGTAACCAACACCAGAGTGCA
Nichols	<i>tprG/F</i> loci	1078	CCAGGCGCCGGCTTCCGCTTCTCCTTCGCCCTCGACGCCGTAACCAACACCAGAGTGCA
Sea 81-4	<i>tprG/F</i> loci	1141	CAGGACTTTCAAATCGCACACAGAGGGCGCAGAGTGAATCACCGCCCTCTCAAATAAC
Nichols	<i>tprG/F</i> loci	1138	CAGGACTTTCAAATCGCACACAGAGGGCGCAGAGTGAATCACCGCCCTCTCAAATAAC
Sea 81-4	<i>tprG/F</i> loci	1201	CTCTTCCAGGGAGAAAGTCAAAAACAGGAAGCCTGGCTGGACGAATATGCAAAGAAGGTG
Nichols	<i>tprG/F</i> loci	1198	CTCTTCCAGGGAGAAAGTCAAAAACAGGAAGCCTGGCTGGACGAATATGCAAAGAAGGTG
Sea 81-4	<i>tprG/F</i> loci	1261	CTTGATGCCGTAACGGCAGCACCCGAAACCGCCCTTCAGTCGAGGGGAAACGCGTACATA
Nichols	<i>tprG/F</i> loci	1258	CTTGATGCCGTAACGGCAGCACCCGAAACCGCCCTTCAGTCGAGGGGAAACGCGTACATA
Sea 81-4	<i>tprG/F</i> loci	1321	ACGGCAGTGTCAAACGTAAAAGTCACCCCTCCGGTAGCTGCCACGCTTTTGACGAACCTG
Nichols	<i>tprG/F</i> loci	1318	ACGGCAGTGTCAAACGTAAAAGTCACCCCTCCGGTAGCTGCCACGCTTTTGACGAACCTG
Sea 81-4	<i>tprG/F</i> loci	1381	AAGGTGTTCAATTACCGACCTCCTACACCGTCACCGCTTCCCGCGCTTCTGCATTTTCC
Nichols	<i>tprG/F</i> loci	1378	AAGGTGTTCAATTACCGACCTCCTACACCGTCACCGCTTCCCGCGCTTCTGCATTTTCC
Sea 81-4	<i>tprG/F</i> loci	1441	CTGATGGGGCAGGTTTTTGCTGCAGTACGATGCGGAGCAGGTGGTGAAGGGGTTTGAGCAG
Nichols	<i>tprG/F</i> loci	1438	CTGATGGGGCAGGTTTTTGCTGCAGTACGATGCGGAGCAGGTGGTGAAGGGGTTTGAGCAG
Sea 81-4	<i>tprG/F</i> loci	1501	GTACAGACGCAAAATCGTTGCTGAAATTAACCAGAAAGTCAAGCGGCTGTGGCTCAGAGC
Nichols	<i>tprG/F</i> loci	1498	GTACAGACGCAAAATCGTTGCTGAAATTAACCAGAAAGTCAAGCGGCTGTGGCTCAGAGC
Sea 81-4	<i>tprG/F</i> loci	1561	AAGGCTGCAGCACAGGCATTATCAACGGTCTTACCAAGGCAATAGAAGACGTGGCTGAT
Nichols	<i>tprG/F</i> loci	1558	AAGGCTGCAGCACAGGCATTATCAACGGTCTTACCAAGGCAATAGAAGACGTGGCTGAT
Sea 81-4	<i>tprG/F</i> loci	1621	GCGTTGCTTGACCCGCATAAGGGAAATCCGATGAGCCTTTCAACCTTCCGGATCAACAA
Nichols	<i>tprG/F</i> loci	1618	GCGTTGCTTGACCCGCATAAGGGAAATCCGATGAGCCTTTCAACCTTCCGGATCAACAA
Sea 81-4	<i>tprG/F</i> loci	1681	AAATTAAGGACGATTCGCCGATCTTATTCCAAGCTTACGGCTGAGGCTACAAAG
Nichols	<i>tprG/F</i> loci	1678	AAATTAAGGACGATTCGCCGATCTTATTCCAAGCTTACGGCTGAGGCTACAAAG

Sea 81-4 *tprG/F* loci 3481 GGGGAGCTCACGGGAGAAGTTTGACAGCGCGTTCGATGCCCTCAGGGTGGAGCAATACCG
Nichols *tprG/F* loci 3466 GGGGAGCTCACGGGAGAAGTTTGACAGCGCGTTCGATGCCCTCAGGGTGGAGCAATACCG

Sea 81-4 *tprG/F* loci 3541 TGTAAAGGATAAGTATCTTGAATTTTTGCTGGGACAGATGGCGGAGTCCTCGATTCTCGA
Nichols *tprG/F* loci 3526 TGTAAAGGATAAGTATCTTGAATTTTTGCTGGGACAGATGGCGGAGTCCTCGATTCTCGA

Sea 81-4 *tprG/F* loci 3601 CCGGGTGGGGCTTGCCCTCACGCTGCAGGACGGTACGCTCGTCTCTACGCTGACGAAGGT
Nichols *tprG/F* loci 3586 CCGGGTGGGGCTTGCCCTCACGCTGCAGGACGGTACGCTCGTCTCTACGCTGACGAAGGT

tprF stop

Sea 81-4 *tprG/F* loci 3661 TGCCACTGATAGTGGAGCTCAGCGCCCAGTGGGAACAGGGGTGCTTGTGACGCTCCTT
Nichols *tprG/F* loci 3646 TGCCACTGATAGTGGAGCTCAGCGCCCAGTGGGAACAGGGGTGCTTGTGACGCTCCTT

Sea 81-4 *tprG/F* loci 3721 ACATGGGTATTGCCGAGAGTATGTGGTCTGAGCGTTACTTTGGCACGTTTATCTGTGGGG
Nichols *tprG/F* loci 3706 ACATGGGTATTGCCGAGAGTATGTGGTCTGAGCGTTACTTTGGCACGTTTATCTGTGGGG

Sea 81-4 *tprG/F* loci 3781 TGAAGGTGGTTTGGTGAGGGGTGTGCGTGTGGGCCAGAGAACGGGTACGGTGGGGGTGCG
Nichols *tprG/F* loci 3766 TGAAGGTGGTTTGGTGAGGGGTGTGCGTGTGGGCCAGAGAACGGGTACGGTGGGGGTGCG

Sea 81-4 *tprG/F* loci 3841 CGTTTTCCCGTGGGGCTGTGCGCGCTCAGTTTACAGGCAGGGATTGCAGGGGTATGTG
Nichols *tprG/F* loci 3826 CGTTTTCCCGTGGGGCTGTGCGCGCTCAGTTTACAGGCAGGGATTGCAGGGGTATGTG

Sea 81-4 *tprG/F* loci 3901 CGGGAAGCGTCTGGGTAAAGTGATGGTGCTCGGGTGTATGTTGCCGGGTGTGGCGGCGCG
Nichols *tprG/F* loci 3886 CGGGAAGCGTCTGGGTAAAGTGATGGTGCTCGGGTGTATGTTGCCGGGTGTGGCGGCGCG

Sea 81-4 *tprG/F* loci 3961 TGTTTCTCTCTCCCCAAGCTCGGGGTGTACGGGGACGCACGGCGGTTCTGACCTGTG
Nichols *tprG/F* loci 3946 TGTTTCTCTCTCCCCAAGCTCGGGGTGTACGGGGACGCACGGCGGTTCTGACCTGTG

Sea 81-4 *tprG/F* loci 4021 GGGCATCTGCATAACAAGCTCCCACAATGCCAGATACAGAGAACCAGGCGCTCCGCGCTA
Nichols *tprG/F* loci 4006 GGGCATCTGCATAACAAGCTCCCACAATGCCAGATACAGAGAACCAGGCGCTCCGCGCTA

Sea 81-4 *tprG/F* loci 4081 TGCGCCGGAGACACCGTTGGTGGGGCTGGACGTGGCGTTCCGTGCGGAAAATGGCTTCCT
Nichols *tprG/F* loci 4066 TGCGCCGGAGACACCGTTGGTGGGGCTGGACGTGGCGTTCCGTGCGGAAAATGGCTTCCT

Sea 81-4 *tprG/F* loci 4141 GCTCCAAGTACGGTGGACGCGGCACTCACGCGTTTAAATGTTCTGCGGCGGTTGTTGGC
Nichols *tprG/F* loci 4126 GCTCCAAGTACGGTGGACGCGGCACTCACGCGTTTAAATGTTCTGCGGCGGTTGTTGGC

Sea 81-4 *tprG/F* loci 4201 CGGTTATTCGTTTCAGACCGGGGAAGGTAGTAC
Nichols *tprG/F* loci 4186 CGGTTATTCGTTTCAGACCGGGGAAGGTAGTAC

===== : Sea81-4 strain *tprG/F* intergenic spacer
>>>>>>> : Nichols strain *tprG/F* intergenic spacer

FIGURE 2S

Sea 81-4 TprI	1	MGRQVMQAGVLAGMVCAASGYAGVLT	1	MGRQVMQAGVLAGMVCAASGYAGVLT
Nichols TprI	1	MGRQVMQAGVLAGMVCAASGYAGVLT	1	MGRQVMQAGVLAGMVCAASGYAGVLT
Sea 81-4 TprI	61	GLTISLPLVSKHHTTRRGEARSGVWAQLQLKDLAVELASSKSSTALSFTKPTASFOATLH	61	GLTISLPLVSKHHTTRRGEARSGVWAQLQLKDLAVELASSKSSTALSFTKPTASFOATLH
Nichols TprI	61	GLTISLPLVSKHHTTRRGEARSGVWAQLQLKDLAVELASSKSSTALSFTKPTASFOATLH	61	GLTISLPLVSKHHTTRRGEARSGVWAQLQLKDLAVELASSKSSTALSFTKPTASFOATLH
Sea 81-4 TprI	121	CYGAYLTVGTSPSCVVFNAQLWKPFVTRAYSEKDTRYAPGFSGSGAKLGYQAHNVGNSGV	121	CYGAYLTVGTSPSCVVFNAQLWKPFVTRAYSEKDTRYAPGFSGSGAKLGYQAHNVGNSGV
Nichols TprI	121	CYGAYLTVGTSPSCVVFNAQLWKPFVTRAYSEKDTRYAPGFSGSGAKLGYQAHNVGNSGV	121	CYGAYLTVGTSPSCVVFNAQLWKPFVTRAYSEKDTRYAPGFSGSGAKLGYQAHNVGNSGV
Sea 81-4 TprI	181	DVDIGFLSFLSNGAWDSTDTTHSKYGFGD	181	DATLSYGVDQRLLTLELAGNATLD
Nichols TprI	181	DVDIGFLSFLSNGAWDSTDTTHSKYGFGD	181	DATLSYGVDQRLLTLELAGNATLE
Sea 81-4 TprI	241	TEDSK	241	NENKTALLWGVGGRLTLEPGAGFRFSFALDAGNQ
Nichols TprI	241	TEDST	241	NENKTALLWGVGGRLTLEPGAGFRFSFALDAGNQ
Sea 81-4 TprI	301	HSAFDALRVEQYRVKDKYLEFLLGQMAESSILERVGLALTLQDGTLVSTLT	301	HSAFDALRVEQYRVKDKYLEFLLGQMAESSILERVGLALTLQDGTLVSTLT
Nichols TprI	301	HSAFDALRVEQYRVKDKYLEFLLGQMAESSILERVGLALTLQDGTLVSTLT	301	HSAFDALRVEQYRVKDKYLEFLLGQMAESSILERVGLALTLQDGTLVSTLT
Sea 81-4 TprI	361	FIQMALVKLLPQRAQAEQRLQEIIVAPSQSDIVLIMLLTWLERARLDRFNADALLTAQWTY	361	FIQMALVKLLPQRAQAEQRLQEIIVAPSQSDIVLIMLLTWLERARLDRFNADALLTAQWTY
Nichols TprI	361	FIQMALVKLLPQRAQAEQRLQEIIVAPSQSDIVLIMLLTWLERARLDRFNADALLTAQWTY	361	FIQMALVKLLPQRAQAEQRLQEIIVAPSQSDIVLIMLLTWLERARLDRFNADALLTAQWTY
Sea 81-4 TprI	421	VSAGLYGATAGTNVFGKRVLPALRSWHFDFAGFLKLET	421	VSAGLYGATAGTNVFGKRVLPALRSWHFDFAGFLKLET
Nichols TprI	421	VSAGLYGATAGTNVFGKRVLPALRSWHFDFAGFLKLET	421	VSAGLYGATAGTNVFGKRVLPALRSWHFDFAGFLKLET
Sea 81-4 TprI	481	IPLTYIRYRNNGGYELNGAVPPGTINM	481	IPLTYIRYRNNGGYELNGAVPPGTINM
Nichols TprI	481	IPLTYIRYRNNGGYELNGAVPPGTINM	481	IPLTYIRYRNNGGYELNGAVPPGTINM
Sea 81-4 TprI	541	NVINPAYTLLNERALQYQVGLTFS	541	NVINPAYTLLNERALQYQVGLTFS
Nichols TprI	541	NVINPAYTLLNERALQYQVGLTFS	541	NVINPAYTLLNERALQYQVGLTFS
Sea 81-4 TprI	601	FICGVKVVW	601	FICGVKVVW
Nichols TprI	601	FICGVKVVW	601	FICGVKVVW

FIGURE 3S

Sea 81-4 TprG	1	MGCMRWGSVLCVVVGVGASGGVLGQEEF	PKLTGSATLEWGISYGKGVGSHGQAPGAVMGT
Nichols TprG	1	MGCMRWGSVLCVVVGVGASGGVLGQEEF	PKLTGSATLEWGISYGKGVGSHGQAPGAVMGT
Sea 81-4 TprG	61	GPYNLKHGFRTTNTVGVSFPLVMRTHTRRGQHPALYAELKVADLQADLSQGKAGFAVKR	
Nichols TprG	61	GPYNLKHGFRTTNTVGVSFPLVMRTHTRRGQHPALYAELKVADLQADLSQGKAGFAVKR	
Sea 81-4 TprG	121	KGKVEATLHCYGAYLTI GKNPTFLTNFARLWKPWVTAQYQEDAVQYAPGFGGLGGKVGYR	
Nichols TprG	121	KGKVEATLHCYGAYLTI GKNPTFLTNFARLWKPWVTAQYQEDAVQYAPGFGGLGGKVGYR	
Sea 81-4 TprG	181	AQDIGSGVSLDVGF LSFASNGAWDSTDP THSKYGF GADLKL MYARAGHP LCTVELASNV	
Nichols TprG	181	AQDIGSGVSLDVGF LSFASNGAWDSTDP THSKYGF GADLKL MYARAGHP LCTVELASNV	
Sea 81-4 TprG	241	TLEDGYLIGAQKDANNQNKDKLLWNVGGRLTLEPGAGFRFSFALDAGNQHQSAQDFQNR	
Nichols TprG	241	TLEDGYLIGAQKDANNQNKDKLLWNVGGRLTLEPGAGFRFSFALDAGNQHQSAQDFQNR	
Sea 81-4 TprG	301	QRAQSELTALSNNLFQGESQKQEAWLDEYAKKVLDAVTAATETALQSRGNAYITAVSNVK	
Nichols TprG	301	QRAQSELTALSNNLFQGESQKQEAWLDEYAKKVLDAVTAATETALQSRGNAYITAVSNVK	
Sea 81-4 TprG	361	VTPPVAATLLTNLKVFI TDPPTPSPLPALPAFSLMGQVLLQYDAEQVVKGF EQVQTQIVA	
Nichols TprG	361	VTPPVAATLLTNLKVFI TDPPTPSPLPALPAFSLMGQVLLQYDAEQVVKGF EQVQTQIVA	
Sea 81-4 TprG	420	EINQKVQAAVAQSKAAAQAFINGLTKAIEDVADALLAPHKGNP	MSLFNLPDQQKLLKDD
Nichols TprG	420	EINQKVQAAVAQSKAAAQAFINGLTKAIEDVADALLAPHKGNP	MSLFNLPDQQKLLKDD
Sea 81-4 TprG	479	LADLIPKLTAEATKFFTEGQTFVTEEVKKKTDALDAGQQIRQAIQNLRASAWRAFLMGVS	
Nichols TprG	479	LADLIPKLTAEATKFFTEGQTFVTEEVKKKTDALDAGQQIRQAIQNLRASAWRAFLMGVS	
Sea 81-4 TprG	539	AVCLYLDTYNVAFDALFTAQWKWLSSGIYV	VATAPANVFGTRVLDNTIASCDFAGFLKLE
Nichols TprG	539	AVCLYLDTYNVAFDALFTAQWKWLSSGIYV	VATAPANVFGTRVLDNTIASCDFAGFLKLE
			frameshift
			*
Sea 81-4 TprG	599	TKSGDPYTHLLTGLDAGVETRVYIPLTHDAIQK	-----
Nichols TprG	599	TKSGDPYTHLLTGLDAGVETRVYIPLTY	ALYKNNGGTAVRGIQEKEYIRPPVVGKAWCS
Sea 81-4 TprG		-----	
Nichols TprG	658	YRIPVQDYGWVKPSVTVHASTNRAHLNAPAAGGAVGATYLTKEYCAQLRAGISASLIEKT	
Sea 81-4 TprG		-----	
Nichols TprG	718	VFSLDWEQGM LSDVPYLLVSECLTQGIGRIVCGVTL SW	

FIGURE 4S

Sea 81-4 TprF	1	VGRQVMQAGVLAGMVCAASGYAGVLT	PQVSGTAQLQWGI	AFQKNPRTGPGKHTHGFR	TN
Nichols TprF	1	VGRQVMQAGVLAGMVCAASGYAGVLT	PQVSGTAQLQWGI	AFQKNPRTGPGKHTHGFR	TN
Sea 81-4 TprF	61	NLTISLPLVSKHHTTRRGEARSGVWAQ	LKDLAVELASSKSSTALSFTKPTAS	FQATLH	
Nichols TprF	61	NLTISLPLVSKHHTTRRGEARSGVWAQ	LKDLAVELASSKSSTALSFTKPTAS	FQATLH	
Sea 81-4 TprF	121	CYGAYLTVGTSPSCVVFNAQLWKPFV	TRAYSEKDTRYAPGFP	GSGAKLGYQAHNVGNSGV	
Nichols TprF	121	CYGAYLTVGTSPSCVVFNAQLWKPFV	TRAYSEKDTRYAPGFS	GSGAKLGYQAHNVGNSGV	
Sea 81-4 TprF	181	DVDIGFLSFLSNGAWDSTDTTHSKYGF	GADATLSYGVDRQRLLTLELAGNATLE	QHRYK	
Nichols TprF	181	DVDIGFLSFLSNGAWDSTDTTHSKYGF	GADATLSYGVDRQRLLTLELAGNATLE	QHRYK	
Sea 81-4 TprF	241	TEDSTNENKTALLWGVGRLTLEPGAGFR	FSFALDAGNQHQDPADAGNRLLATGSS	REKF	
Nichols TprF	241	TEDSTNENKTALLWGVGRLTLEPGAGFR	FSFALDAGNQHQDPADAGNRLLATGSS	REKF	
Sea 81-4 TprF	301	DSAFDALRVEQYRVKDKYLEFLLGQMA	ESSILERVGLALTLQDGT	LVSTLTKVATDSGAQ	
Nichols TprF	301	DSAFDALRVEQYRVKDKYLEFLLGQMA	ESSILERVGLALTLQDGT	LVSTLTKVATDSGAQ	
Sea 81-4 TprF	361	RPVGTGGAC			
Nichols TprF	361	RPVGTGGAC			