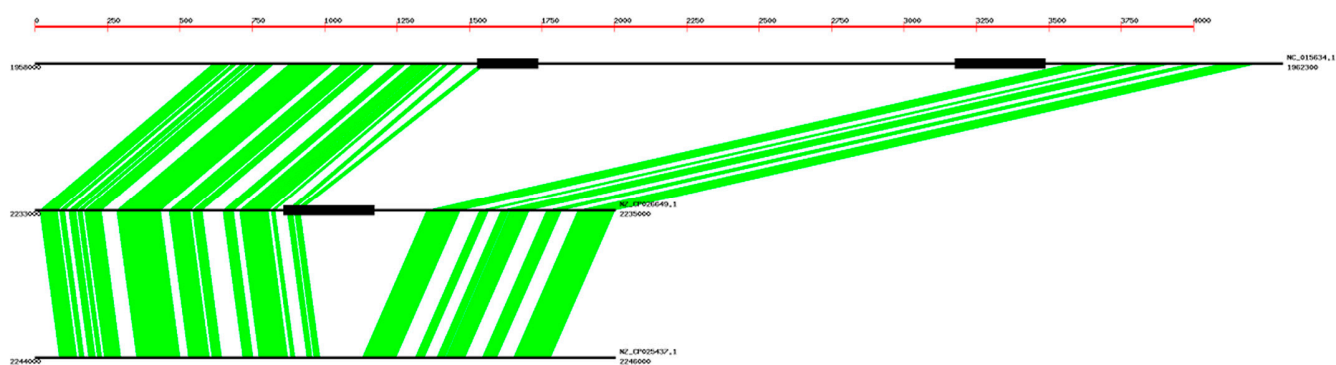
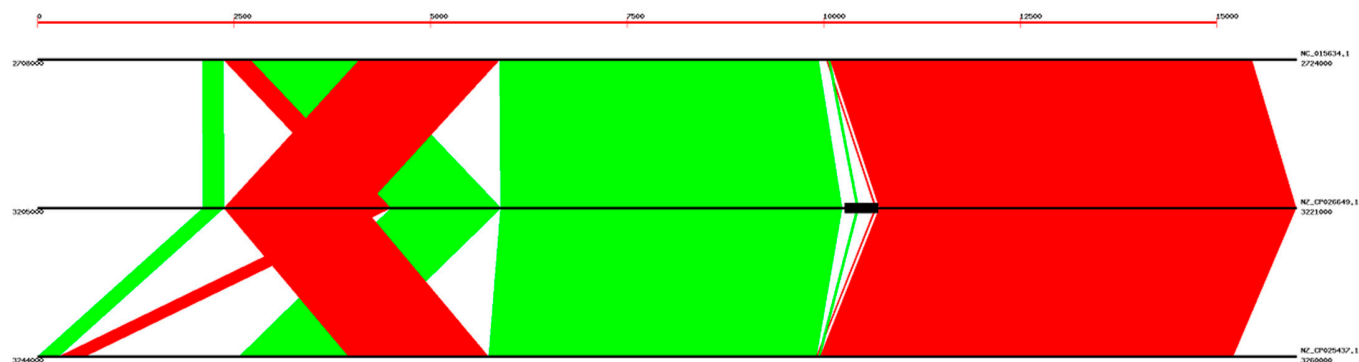


A



B



C

Figure S2. Comparison of selected genome regions of 3 strains of *B. coagulans*. (A), A small tandem repeat is found at the center of the upper NC_015634 genome, not visible in the drawing. Corresponding tandem repeats are found in the other two genomes, but they differ in length. A comparison of sequences is shown in the next page. (B), The tandem repeat in NC_015634 is broken in two by a non-repetitive region. A corresponding tandem repeat is only found in one of the other two genomes. (C), A tandem repeat is only found in one genome. A few bases at right a gene is found for a stress protein, which appears as a 60 nt repeat tandem repeat at the corresponding region of NC_015634.

Here the sequences of the central tandem repeat in the A frame are shown. The characteristic signals in the sequence are underlined. In NC_025437 two tandem repeats

are present, separated by an unrelated sequence. Only a small portion of the sequence (shown in red) is identical with the corresponding tandem repeat in **NZ_CP026649**.

NC_015634 (Tandem repeat not shown in the figure)

```
> ACCGGAGCAA Con:1 reps=6 [1108127,1108450] l-int=324 l-seq = 52
ACCGGAGCAAATTGTTCTTTTAGAGCATTCAAAGAGACAAAAGGAGCCATGA
ACCGGAGCAAATTGTTCTTTTGGAGCATTCAAAAAGACAAAAGGAGCCCGTG
GACCGGAGCAATCGTCCTTTTGGAGCATTCAAAAGGACAAAAAGAACTCGTGA
ACCGGAGCAAATTGTTCTTTTGGAGCATTCAAAAGGACAAAAAGGAGCCATGA
ACCGGAGCAAAATGTCTTTTGGAGTATTCAAAAGGACAAAAAGAACTCGTGG
ACCGGAGCAAATTGTCCTTTTAGAGCATTCAAAAAGACAAAAGGAGCCCGTA
```

NZ_CP026649

```
> CAAAAGGACA Con:1 reps=10 [1310475,1311005] l-int=531 l-seq = 52
CAAAAGGACAAAACACGCTGCATCCGGGCCCCGAAATGTCTTTTTGAAGCTGC
CAAAAGGACAAAACACGTTGCATCTGGTCTCGGAATTGTCCTTTTGAAGCTGC
CAAAAGGACAAAACCGGTTGCATCTGGGATCGGAATTGTCCTTTTGAAGCAGT
CAAAAGGACAAAAAGGAGCCGTGAACTGAAACAAAATTGTCCTTTTGAAGCTGT
CAAAAGGACAAAAAGGAGCCGTGGACCGGAGCAAAAAGTCCTTTTGGAGTATT
CAAAAGGACAAAAAGGAGCCGTGGACCGGAGCAAAAAGTCCTTTTGGAGTATT
CAAAAGGACAAAAAGGAGCCGTGAACCAGAGCAAAAAGTCCTTTTGGAGTATT
CAAAAGGACAAAAAGGAGCCGTGAACTGAAACAAAATTGTCCTTTTGAAGCTGT
CAAAAGGACAAAAAGGAGCCGTGGACCGGAGCAAATTGTTCTTTTGGAGCATC
CAAAAGGACAAAAAGGAGCCATTGACCGGAACAAAATGTCTTTTGGAGTGTT
```

NZ_CPO25437

```
> AAAAGGACAA Con:1 reps=6 [1334805,1335122] l-int=318 l-seq = 52
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--AAGACAAAAAGGAGCCGCACCTAGGCCTGAAATGTTTTTTTCAAGCTGTC
AAAAGGACAAAACACCCTGCATCCGGGCTCGGAATGTCTTTTTGAAGCTGCC
AAAAGGACAAAACACGTTGCATCTGGGCTCGGAATTGTCCTTTTGAAAGTC
AAAAGGACAAAACAAGCTGTATCTGGGCCCGAAATGTCTTTTTGAAGCTGTC
AAAAGGACAAAACAAGCTGTATCTGGTCTCGGAATTGTCCTTTTGAAGCTGCC
> CAAAAGGACA Con:1 reps=7 [1336628,1337002] l-int=375 l-seq = 52
CAAAAGGACAAAACAAGCTGTATCTGGGCTCGGAATTGTCCTTTTGAAGCTGC
CAAAAGGACAAAACACGTTGCATCCGGTCCCGAAAATTGTCCTTTTGAAGCAGT
CAAAAGGACAAAACGCGTTGCATCGGGGTCCAAAATGTCTTTTGAAGCTGT
CAAAAGGACAAAACAAGCTGTATCTGGGCTCGGAATTGTCCTTTTGAAGCTGC
CAAAAGGACAAAAAGGAGCCGTGAACTGAAACAAAATTGTCCTTTTGAAGCTGT
CAAAAGGACAAAAAGGAGCCGTGGACCGGAGCAAATTGTTCTTTTGGAGCATC
CAAAAGGACAAAAAGGAGCCATTGACCGGAACAAAATGTCTTTTGGAGTGTT
```