

Supplementary Data S1.Complete sequence of the bacterium SCA13. Result of the analysis of sequence similaritie s with the species Enterococcus faecalis in the BLAST database (Basic Local Alignment Search Tool - NCBI)

Query: None Query ID: lcl|Query_63917 Length: 962

>Enterococcus faecalis strain BE11 chromosome, complete genome
Sequence ID: CP110069.1 Length: 2913763
Range 1: 2865041 to 2865991

Score:1674 bits(906), Expect:0.0,
Identities:937/952(98%), Gaps:10/952(1%), Strand: Plus/Minus

Query 18 ATACATGCAAGTCGAACGCTTCTTTYCTCCCGAGTGCTTGCACTCAATTGGAAAGAGGAG
77

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Sbjct 2865991 ATACATGCAAGTCGAACGCTTCTTTCCTCCCGAGTGCTTGCACTCAATTGGAAAGAGGA
G 2865932

Query 78 TGGCGGACGGGTGAGTAACACGTGGGTAACTACCCATCAGAGGGGGGATAAACTTGGAA
A 137

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Sbjct 2865931 TGGCGGACGGGTGAGTAACACGTGGGTAACTACCCATCAGAGGGGGGATAAACTTGG
AA 2865872

Query 138 ACAGGTGCTAATACCGCATAACAGTTTATGCCGCATGGCATAAGAGTGAAAGGCGCTTT
C 197

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Sbjct 2865871 ACAGGTGCTAATACCGCATAACAGTTTATGCCGCATGGCATAAGAGTGAAAGGCGCTT
TC 2865812

Query 198 GGGTGTCGCTGATGGATGGACCCGCGGTGCATTAGCTAGTTGGTGAGGTAACGGCTCAC
C 257

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Sbjct 2865811 GGGTGTCGCTGATGGATGGACCCGCGGTGCATTAGCTAGTTGGTGAGGTAACGGCTCA
CC 2865752

Query 258 AAGGCCRCGATGCATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACAC
GG 317

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Sbjct 2865751 AAGGCCACGATGCATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACAC
GG 2865692

Query 318 CCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGACGAAAGTCTGACC
G 377

|||||

Sbjct 2865691 CCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGACGAAAGTCTGAC
CG 2865632

Query 378 AGCAACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAACTCTGTTGTTAGAGAAGA
A 437

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Sbjct 2865631 AGCAACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAACTCTGTTGTTAGAGAAG
AA 2865572

Query 438 CAAGGACGTTAGTAACTGAACGTCCCCTGACGGTATCTAACCAGAAAGCCACGGCTAAC

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Sbjct 2865571 CAAGGACGTTAGTAAGTGAACGTCCCCTGACGGTATCTAACCAGAAAGCCACGGCTAA
CT 2865512

Sbjct 2865511 ACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGATTATTGGGCG
TA 2865452

Sbjct 2865451 AAGCGAGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCGGCTCAACCGGGGAG
GG 2865392

Sbjct 2865391 TCATTGGAACTGGGAGACTTGAGTGCAGAAGAGGAGAGTGGAATTCATGTGTAGCG
GT 2865332

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Sbjct 2865331 GAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGTAAC
TG 2865272

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Sbjct 2865271 ACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGC
CG 2865212

Sbjct 2865211 TAAACGATGAGTGCTAAGTGTTGGAGGGTTTCCGCCCTTCAGTGCTGCAGCAAACGCAT
T 2865152

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Sbjct 2865151 AAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGC
GC 2865092

Sbjct 2865091 ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGC-GAAGAACCTTACC 2865041

Score:1664 bits(901), Expect:0.0,
Identities:938/955(98%), Gaps:13/955(1%), Strand: Plus/Plus

Query 18 ATACATGCAAGTCGAACGCTTCTTTYCTCCCGAGTGCTTGCACTCAATTGGAAAGAGGAG
77

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Sbjct 222951 ATACATGCAAGTCGAACGCTTCTTTCCTCCCGAGTGCTTGCACTCAATTGGAAAGAGGA
G 223010

Query 78 TGGCGGACGGGTGAGTAACACGTGGGTAACTACCCATCAGAGGGGGATAACACTTGGA
A 137

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Sbjct 223011 TGGCGGACGGGTGAGTAACACGTGGGTAACTACCCATCAGAGGGGGATAACACTTG
AA 223070

Query 138 ACAGGTGCTAATACCGCATAACAGTTTATGCCGCATGGCATAAGAGTGAAAGGCGCTTTC
197

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Sbjct 223071 ACAGGTGCTAATACCGCATAACAGTTTATGCCGCATGGCATAAGAGTGAAAGGCGCTT
C 223130

Query 198 GGGTGTCGCTGATGGATGGACCCGCGGTGCATTAGCTAGTTGGTGAGGTAACGGCTCACC
257

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Sbjct 223131 GGGTGTCGCTGATGGATGGACCCGCGGTGCATTAGCTAGTTGGTGAGGTAACGGCTCAC
C 223190

Query 258 AAGGCCRCGATGCATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACG
G 317

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Sbjct 223191 AAGGCCACGATGCATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACAC
GG 223250

Query 318 CCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGACGAAAGTCTGACC
G 377

|||||

Sbjct 223251 CCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGACGAAAGTCTGACC
G 223310

Query 378 AGCAACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAACTCTGTTGTTAGAGAAGA
A 437

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Sbjct 223311 AGCAACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAACTCTGTTGTTAGAGAAGA
A 223370

Query 438 CAAGGACGTTAGTAACTGAACGTCCCCTGACGGTATCTAACCAGAAAGCCACGGCTAAC
T 497

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Sbjct 223371 CAAGGACGTTAGTAACTGAACGTCCCCTGACGGTATCTAACCAGAAAGCCACGGCTAAC
T 223430

Query 498 ACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTA
557

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Subject 961048 ATACATGCAAGTCGAACGCTTCTTTCCTCCCGAGTGCTTGCCTCAATTGGAAAGAGGA

G 961107

Query 78 TGGCGGACGGGTGAGTAACACGTGGGTAACCTACCCATCAGAGGGGGATAAACACTTGGA
A 137

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Sbjct 961108 TGGCGGACGGGTGAGTAACACGTGGGTAACCTACCCATCAGAGGGGGATAAACACTTG
AA 961167

Query 138 ACAGGTGCTAATACCGCATAACAGTTTATGCCGCATGGCATAAGAGTGAAAGGCGCTTTC
197

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Sbjct 961168 ACAGGTGCTAATACCGCATAACAGTTTATGCCGCATGGCATAAGAGTGAAAGGCGCTTT
C 961227

Query 198 GGGTGTCGCTGATGGATGGACCCGCGGTGCATTAGCTAGTTGGTGAGGTAACGGCTCACC
257

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Sbjct 961228 GGGTGTCGCTGATGGATGGACCCGCGGTGCATTAGCTAGTTGGTGAGGTAACGGCTCAC
C 961287

Query 258 AAGGCCRCGATGCATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACG
G 317

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Sbjct 961288 AAGGCCACGATGCATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACAC
GG 961347

Query 318 CCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGACGAAAGTCTGACC
G 377

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Sbjct 961348 CCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGACGAAAGTCTGACC
G 961407

Query 378 AGCAACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAACTCTGTTGTTAGAGAAGA
A 437

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Sbjct 961408 AGCAACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAACTCTGTTGTTAGAGAAGA
A 961467

Query 438 CAAGGACGTTAGTAACTGAACGTCCCCTGACGGTATCTAACCAGAAAGCCACGGCTAAC
T 497

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Sbjct 961468 CAAGGACGTTAGTAACTGAACGTCCCCTGACGGTATCTAACCAGAAAGCCACGGCTAAC
T 961527

Query 498 ACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTA
557

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Sbjct 961528 ACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGT
A 961587

Query 558 AAGCGAGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGG
G 617

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Sbjct 961588 AAGCGAGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGG
G 961647

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8 ATACATGCAAGTCGA

8 TGGCGGACGGGTGAC

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Query 138 ACAGGTGCTAATACCGCATAACAGTTTATGCCGCATGGCATAAGAGTGAAAGGCGCTTT
C 197

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Sbjct 2418366 ACAGGTGCTAATACCGCATAACAGTTTATGCCGCATGGCATAAGAGTGAAAGGCGCTT
TC 2418307

Query 198 GGGTGTCGCTGATGGATGGACCCGCGGTGCATTAGCTAGTTGGTGAGGTAACGGCTCAC
C 257

|||||

Sbjct 2418306 GGGTGTCGCTGATGGATGGACCCGCGGTGCATTAGCTAGTTGGTGAGGTAACGGCTCA
CC 2418247

Query 258 AAGGCCRCGATGCATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACAC
GG 317

|||||

Sbjct 2418246 AAGGCCACGATGCATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACAC
GG 2418187

Query 318 CCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGACGAAAGTCTGACC
G 377

|||||

Sbjct 2418186 CCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGACGAAAGTCTGAC
CG 2418127

Query 378 AGCAACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAACTCTGTTGTTAGAGAAGA
A 437

|||||

Sbjct 2418126 AGCAACGCCGCGTGAGTGAAGAAGGTTTTTCGGATCGTAAAACTCTGTTGTTAGAGAAG
AA 2418067

Query 438 CAAGGACGTTAGTAACTGAACGTCCCCTGACGGTATCTAACCAGAAAGCCACGGCTAAC
T 497

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Sbjct 2418066 CAAGGACGTTAGTAACTGAACGTCCCCTGACGGTATCTAACCAGAAAGCCACGGCTAA
CT 2418007

Query 498 ACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGT
A 557

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Sbjct 2418006 ACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCG
TA 2417947

Query 558 AAGCGAGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGG
G 617

|||||

Sbjct 2417946 AAGCGAGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAG
GG 2417887

Query 618 TCATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGG
T 677

|||||

Sbjct 2417886 TCATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCG
GT 2417827

Query 678 GAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGTAAC

G 737

Sbjct 2417826 GAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGTAAC
TG 2417767

Query 738 ACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC
G 797

|||||
Sbjct 2417766 ACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGC
CG 2417707

Query 798 TAAACGATGAGTGCTAAGTGTTGGAGGGTTTCCGCCCTTCAGTGCTGCAGCAAACGCATT
857

Sbjct 2417706 TAAACGATGAGTGCTAAGTGTTGGAGGGTTTCCGCCCTTCAGTGCTGCAGCAAACGCAT
T 2417647

Query 858 AAGCACTCCGCCTGGGGAGTACGAC-GCA-GGTTGAA-CTCAA-G-AAT-GACGGG--CC 909

|||||
Sbjct 2417646 AAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGG
CC 2417587

Query 910 -GCAC-AGCGGTGGAGCATGKG-TTT-ATTCGAAGCAACGCSGAARAACCTTACC 960

Sbjct 2417586 CGCACAAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGC-GAAGAACCTTACC 2417
533