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***          REPORT OF SEQUENCED PCR AMPLICONS (NANOPORE)          ***
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Analysis of barcoded sample (BC30):
Date of report: Fri Aug  2 18:10:51 2019
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Total number of reads in the input fasta file: *392*
The reference database *Myl6SDB* contains *55807* sequences
== A) Read counts =====
Total: 392 reads aligned to references,
100.0% (392 reads) were kept after applying
>100 cutoff reads mapping per taxonomic level

== B) Selection of taxonomic groups based on mapped reads =====
-(296,75.5%)  Corynebacterium_tuberculoostearicum

== C) STATISTICS ABOUT CONSENSUS SEQUENCES =====

Len    N    -    Taxonomic levels
-----
448    0    4    Corynebacterium_tuberculoostearicum
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[Len]: length (bp) of the consensus sequences; [N] number of unknown bases,
i.e. not unique A/T/G/C; [-]: number of bases present in the reference sequence
but absent in the consensus sequence (deletions).
NOTE: if too many Ns are present (e.g. >3-5),
the respective consensus sequence is not of good quality.

== D) CONSENSUS SEQUENCES =====

== Reference group: Corynebacterium_tuberculoostearicum
GCTGGCGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGCCCTGCTTGCAGGGTACTCG
AGTGGCGAACGGGTGAGTAACACGTGGGTGATCTGCCCTGCACTTCGGGATAAGCCTGGG
AAACTGGGTCTAATACCGGATAGGAGCCATTTTAGTGTGATGGTTGGAAAGTTTTTCGGT
GTAGGATGAGCTCGCGCCTATCAGCTTGTGTTGGTGGGTAATGGCCTACCAAGGCGGCGA
CGGGTAGCGGCGCTGAGAGGGTGGACGGCCACATTGGGACTGAGATACGGCCCAGACTCC
TACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCG
CGTGGGGATGACGGCCTTCGGGTTGTAACTCCTTTTCGCTAGGGACGAAGCTTTTGTGAC
GGTACCTAGATAAGAAGCACCGGCTAAC

== E) Checking the taxonomic classification of the obtained consensus sequences
(using Blastn on Myl6SDB database)
# Query: BC30_using_Corynebacterium_tuberculoostearicum_consensus_448bp_N0_D4_Aug_02_2019
# Fields:
% id/Nber identical/alignment length/Nber mismatches/Nber gaps  subject_id
99.115/448/452/0/4 Corynebacterium_tuberculoostearicum~v~TT~URS000000BD4B...
98.894/447/452/1/4 Corynebacterium_tuberculoostearicum~v~N~URS00009EE730...
98.894/447/452/1/4 Corynebacterium_tuberculoostearicum~v~N~URS00005E4DF7...
98.451/445/452/3/4 Corynebacterium_tuberculoostearicum~v~N~URS0000055677...
98.230/444/452/4/4 Corynebacterium_accolens~v~N~URS000031F940...
98.013/444/453/4/5 Corynebacterium_segmentosum~v~N~URS00000886D72...
98.009/443/452/5/4 Corynebacterium_accolens~v~N~URS000000ABEEE...
98.009/443/452/5/4 Corynebacterium_accolens~v~N~URS00002AB58B...
98.004/442/451/6/3 Corynebacterium_macginleyi~v~N~URS000048F30F...
97.792/443/453/5/5 Corynebacterium_fastidiosum~v~N~URS000020110B...
=====
Query= BC30_using_Corynebacterium_tuberculoostearicum_consensus_448bp_N0_D4_
Aug_02_2019

Length=448

Sequences producing significant alignments:

Corynebacterium_tuberculoostearicum~v~TT~URS000000BD4B      809      0.0
Corynebacterium_tuberculoostearicum~v~N~URS00009EE730      806      0.0

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Corynebacterium_tuberculoostearicum~v~N~URS00005E4DF7	804	0.0
Corynebacterium_tuberculoostearicum~v~N~URS0000055677	793	0.0
Corynebacterium_accolens~v~N~URS000031F940	787	0.0
Corynebacterium_segmentosum~v~N~URS0000886D72	782	0.0
Corynebacterium_accolens~v~N~URS00000ABEEE	782	0.0
Corynebacterium_accolens~v~N~URS00002AB58B	782	0.0
Corynebacterium_macginleyi~v~N~URS000048F30F	780	0.0
Corynebacterium_fastidiosum~v~N~URS000020110B	776	0.0

Query_1	1	GCTGGCGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGCCCTGCTTGCAGGGTACTCG	60
2458	1	60
38252	1	60
26347	1	60
35057	1	60
43180	1	60
39634	1	60
32858	1	60
4024	1	60
30589	1G.....	60
3404	1	60

Query_1	61	AGTGGCGAACGGGTGAGTAACACGTGGGTGATCTGCCCTGCACTTCGGGATAAGCCTGGG	120
2458	61	120
38252	61	120
26347	61	120
35057	61TC.T.....	120
43180	61T.....	120
39634	61T.....	120
32858	61T.....	120
4024	61T.....	120
30589	61T.....	120
3404	61T.....	120

Query_1	121	AAACTGGGTCTAATACCGGATAGGAGCCA-T-TTtagtGTGATGGTTGGAAAG-TTTTTTC	177
2458	121T-.....T.....	179
38252	121T-.....T.....	179
26347	121T-.....T.....	179
35057	121T-.....T.....	179
43180	121A-.....C.....T.....	179
39634	121-.....C.....G.....T.....	179
32858	121A-.....C.....G.....T.....	179
4024	121A-.....C.....G.....T.....	179
30589	121-.....C.....G.....T.....	179
3404	121A-.....C.....G.....T.....	179

Query_1	178	GGTGTAGGATGAGCTCGCGGCCTATCAGCTTGTGGTGGGGTAATGGCCTACCAAGGCGG	237
2458	180	239
38252	180	239
26347	180	239
35057	180	239
43180	180	239
39634	180	239
32858	180	239
4024	180	239
30589	180T.....	239
3404	180	239

Query_1	238	CGACGGGTAGCCGGCCTGAGAGGGTGGACGGCCACATTGGGACTGAGATACGGCCCAGAC	297
2458	240	299
38252	240	299
26347	240C.....	299
35057	240	299
43180	240T.....	299
39634	240T.....	299
32858	240T.....	299


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+**Corynebacterium_fastidiosum~v~N~URS000020110B
|
|                                     +**BC30_using_Corynebacterium_tuberculo
|                                     | (96)
|                                     +**Corynebacterium_tuberculo
|                                     |
|                                     +**Corynebacterium_tuberculo
|                                     |
|                                     +-----Corynebacterium_tuberculo
|                                     |
|                                     +-----Corynebacterium_tuberculo
+***** (55)
+**Corynebacterium_accolens~v~N~URS000031F940
|
|                                     +-----Corynebacterium_segmen
+***** (47)
|                                     +-----Corynebacterium_macginleyi~v~N~URS000048F30F
+**Corynebacterium_accolens~v~N~URS000000ABEEE
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