

Supplementary material 2

2.1. Sequence alignment results with BCR1 primer, using the BLASTN tool

Download	GenBank	Graphics	Sort by: E value	Next	Previous	Descriptions
Pseudomonas sp. CMR5c chromosome, complete genome						
Sequence ID: CP027705.1 Length: 6796817 Number of Matches: 2						
Range 1: 3914375 to 3914798			GenBank	Graphics	Next Match	Previous Match
Score	Expect	Identities	Gaps	Strand		
719 bits(797)	0.0	416/425(98%)	2/425(0%)	Plus/Plus		
Query 5	GGACA -GGTCGCGCCCTGGGCCAACGAAAGCGCCGACTACACGACACCCGCAACATGC	63				
Sbjct 3914375	GGACAAGGTCGCGCCCTGG -CCAACGAAAGCGCCGTACTACACGACACCCGCAACATGC	3914433				
Query 64	TGCAGGGCGAACGGACCCACAATGCCGAATCTGGCCAGGCCCTCAAGGACTACGACCTGC	123				
Sbjct 3914434	TGCAGGGCGAACGGACCCACAATGCCGAATCTGGCCAGGCCCTCAAGGACTACGACCTGC	3914493				
Query 124	GCCTGGCCGACAAGGAACAGCAGATCCGCTCCCTGGAAGAAAAGCACCTGCATGCCCGCG	183				
Sbjct 3914494	GCCTGGCCGACAAGGAACAGCAGATCCGCTCCCTGGAAGAAAAGCACCTGCATGCCCGCG	3914553				
Query 184	ACGCCCTGGAGATTACCGCGCAGCCAGCAAGGAGCAGCGGACAGGAATCGCTCGCC	243				
Sbjct 3914554	ACGCCCTGGAGATTACCGCGCAGCCAGCAAGGAGCAGCGGACAGGAATCGCTCGCC	3914613				
Query 244	ACGAGGGCCAAATGCAGCAAGTCCAGATGGAGTTGCGCCAGGCCAGCAGAGCTCTCTGG	303				
Sbjct 3914614	ACGAGGGCCAAATGCAGCAAGTCCAGATGGAGTTGCGCCAGGCCAGCAGAGCTCTCTGG	3914673				
Query 304	TACGCGAGGATGAGATCACCCAGCTGACCGCGACAACGAACGCTGCTCAGCGAGCAAC	363				
Sbjct 3914674	TACGCGAGGATGAGATCACCCAGCTGACCGCGACAACGAACGCTGCTCAGCGAGCAAC	3914733				
Query 364	GCACCACTCTCAAGGAACTCAAACAGACCCAGGAAGCGCTGAGCCAGAGCAGCACTCTGC	423				
Sbjct 3914734	GCACCACTCTCAAGGAACTCAAAGAGCTCAAGCAGACCCAGGAAGCGCTGAGCCAGGGCAGCACTCTGC	3914793				
Query 424	AAACG 428					
Sbjct 3914794	AGACG 3914798					

2.2. Sequence alignment results with BCR2 primer, using the BLASTN tool

Download	GenBank	Graphics	Next	Previous	Descriptions
Pseudomonas sp. CMR5c chromosome, complete genome					
Sequence ID: CP027705.1 Length: 6796817 Number of Matches: 1					
Range 1: 3915726 to 3916081			GenBank	Graphics	Next Match Previous Match
Score	Expect	Identities	Gaps	Strand	
618 bits(685)	2e-172	352/357(99%)	1/357(0%)	Plus/Minus	
Query 5	ACTTGCTGGTCAACAGCGGGCGTGACCTGCACGAAGGGCATGCCAAGTTGATCGATCCG	64			
Sbjct 3916081	ACTTGCTGGTCAACAGCGG -CGTGACCTGCACGAAGGGCATGCCAAGTTGATCGATCCG	3916023			
Query 65	CATCAGGTGGAGGTCAATGGCCAGCGCTATACCGCCAGGCCATCCTGATCGCCACTGGC	124			
Sbjct 3916022	CATCAGGTGGAGGTCAATGGCCAGCGCTATACCGCCAGGCCATCCTGATCGCCACTGGC	3915963			
Query 125	GGCTGGCCGAGATCCCGGACATCCCGGGCGCGAACATGCCATCAGCTCCAATGAAGCC	184			
Sbjct 3915962	GGCTGGCCGAGATCCCGGACATCCCGGGCGCGAACATGCCATCAGCTCCAATGAAGCC	3915903			
Query 185	TTCTATCTAAAGGAATGCCCAAGCGCATCTGGTGGTGGGCGGCGGTACATCGCGGTG	244			
Sbjct 3915902	TTCTATCTAAAGGAATGCCCAAGCGCATCTGGTGGTGGGCGGCGGTACATCGCGGTG	3915843			
Query 245	GAGTTCGCCGGAATCTTCCACGGCTGGGGCGGACACCAAGTTGTTGATCGCGGTGAC	304			
Sbjct 3915842	GAGTTCGCCGGAATCTTCCACGGCTGGGGCGGACACCAAGTTGTTGATCGCGGTGAC	3915783			
Query 305	TTGTTCTGCGCGGCTTCAATGGCGGCGTGCAGCACCTGCAGGAATAGGTGACC	361			
Sbjct 3915782	TTGTTCTGCGCGGCTTCAATGGCGGCGTGCAGCACCTGCAGGAATAGGTGACC	3915726			