

Supplementary material. Alignments between *penA* amplicon sequences and the closest *penA* allelic variant.

01

Score	Expect	Identities	Gaps	Strand
331 bits(179)	5e-95	184/186(99%)	2/186(1%)	Plus/Plus
Query 14	GTC-AT-CGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGGCGC			71
Sbjct 835	GTCAATACGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGGCGC			894
Query 72	AACCGTGCCGTTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			131
Sbjct 895	AACCGTGCCGTTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			954
Query 132	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAA			191
Sbjct 955	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAA			1014
Query 192	ATCGGT	197		
Sbjct 1015	ATCGGT	1020		

02

Score	Expect	Identities	Gaps	Strand
331 bits(179)	5e-95	179/179(100%)	0/179(0%)	Plus/Plus
Query 17	CGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGGCGCAACCGTG			76
Sbjct 842	CGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGGCGCAACCGTG			901
Query 77	CCGTTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAGCAT			136
Sbjct 902	CCGTTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAGCAT			961
Query 137	TGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATCGGT			195
Sbjct 962	TGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATCGGT			1020

03

Score	Expect	Identities	Gaps	Strand
324 bits(175)	8e-93	178/179(99%)	1/179(0%)	Plus/Plus
Query 17	CGCCTGCCTATGAG-CCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGGCGCAACCGTG			75
Sbjct 842	CGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGGCGCAACCGTG			901
Query 76	CCGTTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAGCAT			135
Sbjct 902	CCGTTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAGCAT			961
Query 136	TGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATCGGT			194
Sbjct 962	TGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATCGGT			1020

04

Score	Expect	Identities	Gaps	Strand
313 bits(169)	2e-89	174/176(99%)	2/176(1%)	Plus/Plus
Query 26	CTG-CTATGAG-CCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGGCGCAACCGTGCCG			83
Sbjct 845	CTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGGCGCAACCGTGCCG			904
Query 84	TTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAGCATTGG			143
Sbjct 905	TTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAGCATTGG			964
Query 144	ATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATCGGT			199
Sbjct 965	ATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATCGGT			1020

05

Score	Expect	Identities	Gaps	Strand
324 bits(175)	8e-93	178/179(99%)	1/179(0%)	Plus/Plus
Query 17	CGCCTGCCTATGAG-CCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGGCGCAACCGTG			75
Sbjct 842	CGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGGCGCAACCGTG			901
Query 76	CCGTTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAGCAT			135
Sbjct 902	CCGTTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAGCAT			961
Query 136	TGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATCGGT			194
Sbjct 962	TGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATCGGT			1020

06

Score	Expect	Identities	Gaps	Strand
331 bits(179)	5e-95	184/186(99%)	2/186(1%)	Plus/Plus
Query 12	GTC-ATACGCCTGCCTATGAG-CCAACAAACCCGGTCAGGCAGACAGCGAACAGAGGCGT			69
Sbjct 835	GTCAATACGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGAGGCGT			894
Query 70	AACCGCGCCGTAACCGACATGATCGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			129
Sbjct 895	AACCGCGCCGTAACCGACATGATCGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			954
Query 130	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACATTCAATACCCTGCCTTACAAA			189
Sbjct 955	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACATTCAATACCCTGCCTTACAAA			1014
Query 190	ATCGGT 195			
Sbjct 1015	ATCGGT 1020			

07

Score	Expect	Identities	Gaps	Strand
324 bits(175)	8e-93	183/186(98%)	3/186(1%)	Plus/Plus
Query 14	GTC-AT-CGCCTGCCTATGAG-CCAACAAACCCGGTCAGGCAGACAGCGAACAGAGGCCT			70
Sbjct 835	GTCAATACGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGAGGCCT			894
Query 71	AACCGCGCCGTAACCGACATGATCGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			130
Sbjct 895	AACCGCGCCGTAACCGACATGATCGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			954
Query 131	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACATTCAATACCCTGCCTTACAAA			190
Sbjct 955	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACATTCAATACCCTGCCTTACAAA			1014
Query 191	ATCGGT 196			
Sbjct 1015	ATCGGT 1020			

08

Score	Expect	Identities	Gaps	Strand
329 bits(178)	2e-94	181/182(99%)	1/182(0%)	Plus/Plus
Query 17	ATACG-CTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGAGGCCTAACC			75
Sbjct 839	ATACGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGAGGCCTAACC			898
Query 76	GCGCCGTAACCGACATGATCGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAG			135
Sbjct 899	GCGCCGTAACCGACATGATCGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAG			958
Query 136	CATTGGATTCCGGCAAAGTGGATGCAACCGATACATTCAATACCCTGCCTTACAAAATCG			195
Sbjct 959	CATTGGATTCCGGCAAAGTGGATGCAACCGATACATTCAATACCCTGCCTTACAAAATCG			1018
Query 196	GT 197			
Sbjct 1019	GT 1020			

09

Score	Expect	Identities	Gaps	Strand
324 bits(175)	8e-93	183/186(98%)	3/186(1%)	Plus/Plus
Query 14	GTC-AT-CGCCTGCCTATGAG-CCAACAAACCCGGTCAGGCAGACAGCGAACAGAGGCCT			70
Sbjct 835	GTCAATACGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGAGGCCT			894
Query 71	AACCGCGCCGTAACCGACATGATCGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			130
Sbjct 895	AACCGCGCCGTAACCGACATGATCGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			954
Query 131	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACATTCAATACCCTGCCTTACAAA			190
Sbjct 955	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACATTCAATACCCTGCCTTACAAA			1014
Query 191	ATCGGT 196			
Sbjct 1015	ATCGGT 1020			

10

Score	Expect	Identities	Gaps	Strand
335 bits(181)	4e-96	188/191(98%)	2/191(1%)	Plus/Minus
Query 6	ATCGGATGCAT - CACTTTGCCGG - ATCCAATGCTTTGGCAATGGTAAACGGCTTCATGGC	63		
Sbjct 990	ATCGGTTGCATCCACTTTGCCGGAATCCAATGCTTTGGCAATGGTAAACGGCTTCATGGC	931		
Query 64	AGAGCCGGGTTCAATCATATCGGTTACGGCACGGTTACGCCTCTGTTTCGCTGTCTGCCTG	123		
Sbjct 930	AGAGCCGGGTTCAATCATATCGGTTACGGCACGGTTACGCCTCTGTTTCGCTGTCTGCCTG	871		
Query 124	ACCGGGTTTGTGGGCTCGTAGGCAGGCGTATTGACCAAGGCGAGGATTTCCCCAGTACG	183		
Sbjct 870	ACCGGGTTTGTGGGCTCGTAGGCAGGCGTATTGACCAAGGCGAGGATTTCCCCAGTACG	811		
Query 184	GGCATCCAACA 194			
Sbjct 810	GGCATCCAACA 800			

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Score	Expect	Identities	Gaps	Strand
335 bits(181)	4e-96	188/191(98%)	2/191(1%)	Plus/Minus
Query 6	ATCGGCTGCATC - ACTTTGCCGG - ATCCAATGCTTTGGCAATGGTAAACGGCTTCATGGC	63		
Sbjct 990	ATCGGTTGCATCCACTTTGCCGGAATCCAATGCTTTGGCAATGGTAAACGGCTTCATGGC	931		
Query 64	AGAACC GG GTTCGATCATGTCGGTTACGGCGCGGTTACGCCTCTGTTTCGCTGTCTGCCTG	123		
Sbjct 930	AGAACC GG GTTCGATCATGTCGGTTACGGCGCGGTTACGCCTCTGTTTCGCTGTCTGCCTG	871		
Query 124	ACCGGGTTTGTGGGCTCATAGGCAGGCGTATTGACCAATGCGAGGATTTCCCCAGTACG	183		
Sbjct 870	ACCGGGTTTGTGGGCTCATAGGCAGGCGTATTGACCAATGCGAGGATTTCCCCAGTACG	811		
Query 184	GGCATCCAACA 194			
Sbjct 810	GGCATCCAACA 800			

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Score	Expect	Identities	Gaps	Strand
320 bits(173)	1e-91	185/190(97%)	3/190(1%)	Plus/Minus
Query 5	ATCGGATGC - T - CACTTTGCCGG - ATCCAATGCTTTGGCAATGGTAAACGGCTTCATGGC	61		
Sbjct 990	ATCGGTTGCATCCACTTTGCCGGAATCCAATGCTTTGGCAATGGTAAACGGCTTCATGGC	931		
Query 62	AGAACC GG GTTC AATCATATCGGTAACGGCACGGTTGCGCCGCTGTTTCGCTGTCTGCCTG	121		
Sbjct 930	AGAACC GG GTTC AATCATATCGGTAACGGCACGGTTGCGCCGCTGTTTCGCTGTCTGCCTG	871		
Query 122	ACCGGGTTTGTGGGCTCATAGGCAGGCGTATTGACCAATGCGAGGATTTCCCCAGTACG	181		
Sbjct 870	ACCGGGTTTGTGGGCTCATAGGCAGGCGTATTGACCAAGGCGAGGATTTCCCCAGTACG	811		
Query 182	GGCATCCAAC 191			
Sbjct 810	GGCATCCAAC 801			

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Score	Expect	Identities	Gaps	Strand
318 bits(172)	4e-91	177/179(99%)	1/179(0%)	Plus/Minus
Query 16	CACTTTGCCGG-ATCCAATGCTTTGGCAATGGTAAACGGCTTCATGGCAGAACC	GGGTTTC	74	
Sbjct 978	CACTTTGCCGGAATCCAATGCTTTGGCAATGGTAAACGGCTTCATGGCAGAACC	GGGTTTC	919	
Query 75	AATCATATCGGTAACGGCACGGTTGCGCCGCTGTTTCGCTGTCTGCCTGACC	GGGTTTGT	134	
Sbjct 918	AATCATATCGGTAACGGCACGGTTGCGCCGCTGTTTCGCTGTCTGCCTGACC	GGGTTTGT	859	
Query 135	GGGCTCATAGGCAGGCGTATTGACCAATGCGAGGATTTCCCAGTACGGGCAT	CCAACA	193	
Sbjct 858	GGGCTCATAGGCAGGCGTATTGACCAAGGCGAGGATTTCCCAGTACGGGCAT	CCAACA	800	

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Score	Expect	Identities	Gaps	Strand
329 bits(178)	2e-94	187/191(98%)	2/191(1%)	Plus/Minus
Query 5	ATCGGATGCATCCACTTTGC-GG-ATCCAATGCTTTGGCAATGGTAAACGGCTTCATGGC		62	
Sbjct 990	ATCGGTTGCATCCACTTTGCCGGAATCCAATGCTTTGGCAATGGTAAACGGCTTCATGGC		931	
Query 63	AGAACC	GGGTTCAATCATATCGGTAACGGCACGGTTGCGCCGCTGTTTCGCTGTCTGCCTG	122	
Sbjct 930	AGAACC	GGGTTCAATCATATCGGTAACGGCACGGTTGCGCCGCTGTTTCGCTGTCTGCCTG	871	
Query 123	ACCGGGTTTGTGGGCTCATAGGCAGGCGTATTGACCAATGCGAGGATTTCCCAGTACG		182	
Sbjct 870	ACCGGGTTTGTGGGCTCATAGGCAGGCGTATTGACCAAGGCGAGGATTTCCCAGTACG		811	
Query 183	GGCATCCAACA		193	
Sbjct 810	GGCATCCAACA		800	

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Score	Expect	Identities	Gaps	Strand
318 bits(172)	4e-91	177/179(99%)	1/179(0%)	Plus/Plus
Query 17	CGCCTGCCTATGAG-CCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGC	GCAACCGTG	75	
Sbjct 842	CGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGC	GCAACCGTG	901	
Query 76	CCGTTACCGATATGATTGAACCCGGTTCTGCCATGAGGCCGTTTACCATTGCC	AAAGCAT	135	
Sbjct 902	CCGTTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC	AAAGCAT	961	
Query 136	TGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAA	ATCGGT	194	
Sbjct 962	TGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAA	ATCGGT	1020	

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Score	Expect	Identities	Gaps	Strand
307 bits(166)	8e-88	173/176(98%)	2/176(1%)	Plus/Plus
Query 26	CTG-CTATGAG-CCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGGCGCAACCGTGCCG			83
Sbjct 845	CTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGGCGCAACCGTGCCG			904
Query 84	TTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAGCGTTGG			143
Sbjct 905	TTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAGCATTGG			964
Query 144	ATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATCGGT			199
Sbjct 965	ATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATCGGT			1020

17

Score	Expect	Identities	Gaps	Strand
326 bits(176)	2e-93	183/186(98%)	2/186(1%)	Plus/Plus
Query 12	GTC-ATACGCCTGCCTATGAG-CCAACAAACCCGGTCAGGCAGACAGCGAACAGAGGGCGT			69
Sbjct 835	GTCAATACGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGAGGGCGT			894
Query 70	AACCGCGCCGTAACCGACATGATCGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			129
Sbjct 895	AACCGCGCCGTAACCGACATGATCGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			954
Query 130	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACAGTCAATACCCTGCCTTACAAA			189
Sbjct 955	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACATTCAATACCCTGCCTTACAAA			1014
Query 190	ATCGGT 195			
Sbjct 1015	ATCGGT 1020			

18

Score	Expect	Identities	Gaps	Strand
331 bits(179)	5e-95	184/186(99%)	2/186(1%)	Plus/Plus
Query 14	GTC-AT-CGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGCGC			71
Sbjct 835	GTCAATACGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGCGC			894
Query 72	AACCGTGCCGTTACCGATATGATTGAACCCGGTCTGCCATGAAGCCGTTTACCATTGCC			131
Sbjct 895	AACCGTGCCGTTACCGATATGATTGAACCCGGTCTGCCATGAAGCCGTTTACCATTGCC			954
Query 132	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAA			191
Sbjct 955	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAA			1014
Query 192	ATCGGT 197			
Sbjct 1015	ATCGGT 1020			

19

Score	Expect	Identities	Gaps	Strand
324 bits(175)	8e-93	182/185(98%)	2/185(1%)	Plus/Minus
Query 12	TGCATC-ACTTTGCCGG-ATCCAATGCTTTGGCAATGGTAAACGGCTTCATGGCAGAACC			69
Sbjct 984	TGCATCCACTTTGCCGGAATCCAATGCTTTGGCAATGGTAAACGGCTTCATGGCAGAACC			925
Query 70	GGGTTTCGATCATGTTCGGTTACGGCGCGGTTACGCCTCTGTTTCGCTGTCTGCCTGACCGGG			129
Sbjct 924	GGGTTTCGATCATGTTCGGTTACGGCGCGGTTACGCCTCTGTTTCGCTGTCTGCCTGACCGGG			865
Query 130	TTTGTTGGGCTCATAGGCAGGCGTATTGACCAATGCGAGGATTTCCCCAGTACGGGCATC			189
Sbjct 864	TTTGTTGGGCTCATAGGCAGGCGTATTGACCAATGCGAGGATTTCCCCAGTACGGGCATC			805
Query 190	CTACA 194			
Sbjct 804	CAACA 800			

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Score	Expect	Identities	Gaps	Strand
320 bits(173)	1e-91	176/177(99%)	1/177(0%)	Plus/Plus
Query 17	CGCCTGCCTATGAG-CCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGCGCAACCGTG			75
Sbjct 842	CGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGCGCAACCGTG			901
Query 76	CCGTTACCGATATGATTGAACCCGGTCTGCCATGAAGCCGTTTACCATTGCCAAAGCAT			135
Sbjct 902	CCGTTACCGATATGATTGAACCCGGTCTGCCATGAAGCCGTTTACCATTGCCAAAGCAT			961
Query 136	TGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATCG			192
Sbjct 962	TGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATCG			1018

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22

5
01

Score	Expect	Identities	Gaps	Strand
331 bits(179)	5e-95	184/186(99%)	2/186(1%)	Plus/Plus
Query 14	GTC-AT-CGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGCGC			71
Sbjct 835	GTCAATACGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGCGC			894
Query 72	AACCGTGCCGTTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			131
Sbjct 895	AACCGTGCCGTTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			954
Query 132	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAA			191
Sbjct 955	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAA			1014
Query 192	ATCGGT 197			
Sbjct 1015	ATCGGT 1020			

23

Score	Expect	Identities	Gaps	Strand
320 bits(173)	1e-91	180/183(98%)	2/183(1%)	Plus/Plus
Query 12	GTC-ATACGTCTGCCTATGAG-CCAACAAACCCGGTCAGGCAGACAGCGAACAGAGGCGT			69
Sbjct 835	GTCAATACGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGAGGCGT			894
Query 70	AACCGCGCCGTAACCGACATGATCGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			129
Sbjct 895	AACCGCGCCGTAACCGACATGATCGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			954
Query 130	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACATTCAATACCCTGCCTTACAAA			189
Sbjct 955	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACATTCAATACCCTGCCTTACAAA			1014
Query 190	ATC 192			
Sbjct 1015	ATC 1017			

24

Score	Expect	Identities	Gaps	Strand
322 bits(174)	3e-92	176/177(99%)	0/177(0%)	Plus/Plus
Query 17	CGCCTGCCTATGAGTCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGCGCAACCGTG			76
Sbjct 842	CGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGCGCAACCGTG			901
Query 77	CCGTTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAGCAT			136
Sbjct 902	CCGTTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAGCAT			961
Query 137	TGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATCG			193
Sbjct 962	TGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATCG			1018

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Score	Expect	Identities	Gaps	Strand
331 bits(179)	5e-95	184/186(99%)	2/186(1%)	Plus/Plus
Query 14	GTC-AT-CGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGCGC			71
Sbjct 835	GTCAATACGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGCGC			894
Query 72	AACCGTGCCGTTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			131
Sbjct 895	AACCGTGCCGTTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			954
Query 132	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAA			191
Sbjct 955	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAA			1014
Query 192	ATCGGT 197			
Sbjct 1015	ATCGGT 1020			

26

Score	Expect	Identities	Gaps	Strand
302 bits(163)	4e-86	170/173(98%)	2/173(1%)	Plus/Plus
Query 26	CTG-CTATGAG-CCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGCGCAACCGTGCCG			83
Sbjct 845	CTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGCGCAACCGTGCCG			904
Query 84	TTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAGCATTGG			143
Sbjct 905	TTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAGCATTGG			964
Query 144	ATTCCGGTAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATC 196			
Sbjct 965	ATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATC 1017			

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Score	Expect	Identities	Gaps	Strand
329 bits(178)	2e-94	187/191(98%)	2/191(1%)	Plus/Minus
Query 6	ATCGGATGCAT-CACTTTGCCGG-ATCCAATGCTTTGGCAATGGTAAACGGCTTCATGGC			63
Sbjct 990	ATCGGTTGCATCCACTTTGCCGGAATCCAATGCTTTGGCAATGGTAAACGGCTTCATGGC			931
Query 64	AGAGCCGGGTTCAATCATATCGGTTACGGCACGGTTACGCCTCTGTTTCGCTGTCTGCCTG			123
Sbjct 930	AGAGCCGGGTTCAATCATATCGGTTACGGCACGGTTACGCCTCTGTTTCGCTGTCTGCCTG			871
Query 124	ACCGGGTTTGTGGGCTCGTAGGCAGGCGTATTGACCAAGGCGAGGATTTCCCCAGTACG			183
Sbjct 870	ACCGGGTTTGTGGGCTCGTAGGCAGGCGTATTGACCAAGGCGAGGATTTCCCCAGTACG			811
Query 184	GGCATCCACCA 194			
Sbjct 810	GGCATCCAACA 800			

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Score	Expect	Identities	Gaps	Strand
331 bits(179)	5e-95	184/186(99%)	2/186(1%)	Plus/Plus
Query 12	GTC-ATACGCCTGCCTATGAG-CCAACAAACCCGGTCAGGCAGACAGCGAACAGAGGCGT	69		
Sbjct 835	GTCAATACGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGAGGCGT	894		
Query 70	AACCGCGCCGTAACCGACATGATCGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC	129		
Sbjct 895	AACCGCGCCGTAACCGACATGATCGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC	954		
Query 130	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACATTCAATACCCTGCCTTACAAA	189		
Sbjct 955	AAAGCATTGGATTCCGGCAAAGTGGATGCAACCGATACATTCAATACCCTGCCTTACAAA	1014		
Query 190	ATCGGT 195			
Sbjct 1015	ATCGGT 1020			

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Score	Expect	Identities	Gaps	Strand
331 bits(179)	5e-95	179/179(100%)	0/179(0%)	Plus/Plus
Query 17	CGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGGCGCAACCGTG	76		
Sbjct 842	CGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGCGGGCGCAACCGTG	901		
Query 77	CCGTTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAGCAT	136		
Sbjct 902	CCGTTACCGATATGATTGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCCAAAGCAT	961		
Query 137	TGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATCGGT	195		
Sbjct 962	TGGATTCCGGCAAAGTGGATGCAACCGATACGTTCAATACCCTGCCTTACAAAATCGGT	1020		

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Score	Expect	Identities	Gaps	Strand
329 bits(178)	2e-94	187/191(98%)	2/191(1%)	Plus/Minus
Query 6	ATCGGCTGCATC-AC	TTTGCCCG-ATCCAATGCTTTGGCAATGGTAAACGGCTTCATGGC		63
Sbjct 990	ATCGGTTGCATCCACTTTGCCGGAATCCAATGCTTTGGCAATGGTAAACGGCTTCATGGC			931
Query 64	AGAACCGGGTTCGATCATGTTCGGTTACGGCGCGGTTACGCCTCTGTTTCGCTGTCTGCCTG			123
Sbjct 930	AGAACCGGGTTCGATCATGTTCGGTTACGGCGCGGTTACGCCTCTGTTTCGCTGTCTGCCTG			871
Query 124	ACCGGGTTTGTGGGGCTCATAGGCAGGCGTATTGACCAATGCGAGGATTTCCCCAGTACG			183
Sbjct 870	ACCGGGTTTGTGGGGCTCATAGGCAGGCGTATTGACCAATGCGAGGATTTCCCCAGTACG			811
Query 184	GGCATCCAACA	194		
Sbjct 810	GGCATCCAACA	800		

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Score	Expect	Identities	Gaps	Strand
320 bits(173)	1e-91	181/184(98%)	3/184(1%)	Plus/Plus
Query 14	GTC-AT-CGCCTGCCTATGAG-CCAACAAACCCGGTCAGGCAGACAGCGAACAGAGGCGT			70
Sbjct 835	GTCAATACGCCTGCCTATGAGCCCAACAAACCCGGTCAGGCAGACAGCGAACAGAGGCGT			894
Query 71	AACCGCGCCGTAACCGACATGATCGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			130
Sbjct 895	AACCGCGCCGTAACCGACATGATCGAACCCGGTTCTGCCATGAAGCCGTTTACCATTGCC			954
Query 131	AAAGCATTTGGATTCCGGCAAAGTGGATGCAACCGATAACATTCAATACCCTGCCTTACAAA			190
Sbjct 955	AAAGCATTTGGATTCCGGCAAAGTGGATGCAACCGATAACATTCAATACCCTGCCTTACAAA			1014
Query 191	ATCG	194		
Sbjct 1015	ATCG	1018		