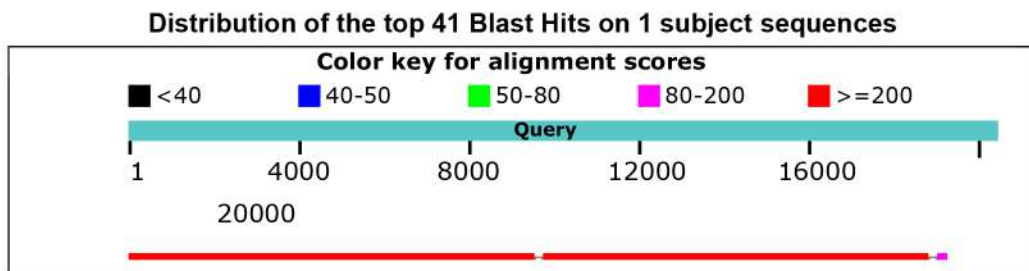


BLAST 2 sequences results

Query ID lcl|Query_175919
Description BP1_new_chr15:82478935-82498934
Molecule type nucleic acid
Query Length 20000

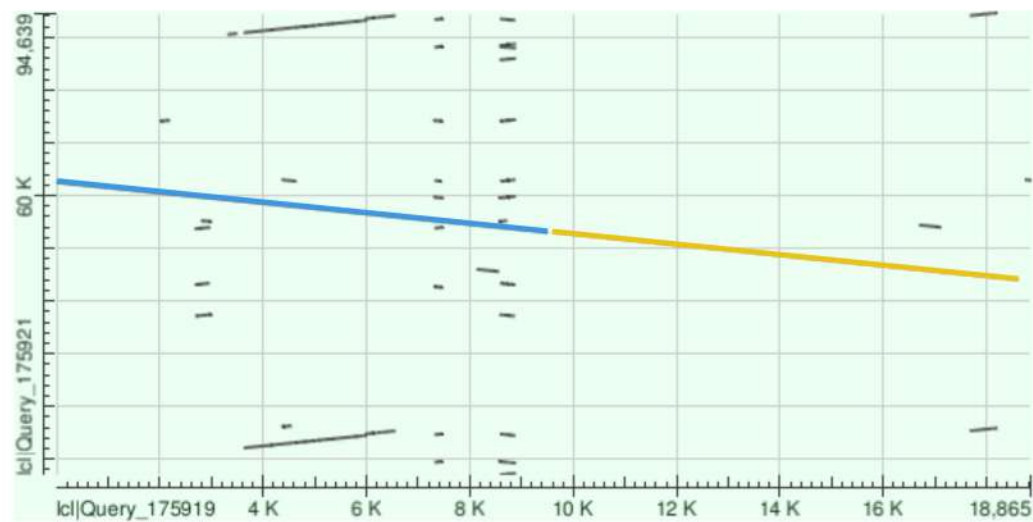
Subject ID lcl|Query_175921
Description BP2_new_chr15:84404774-84506312
Molecule type nucleic acid
Subject Length 101539
Program BLASTN 2.8.1+

Graphic Summary



Dot Matrix View

Plot of lcl|Query_175919 vs lcl|Query_175921



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
BP2_new_chr15:84404774-84506312 5'pad=0 3'pad=0 strand=+ repeatMasking=none	16755	48777	93%	0.0	99%	Query_175921

Alignments

1) BLAST2SeqA

BP2_new_chr15:84404774-84506312 5'pad=0 3'pad=0 strand=+ repeatMasking=none
Sequence ID: Query_175921 Length: 101539 Number of Matches: 41
Range 1: 53057 to 62500

Score	Expect	Identities	Gaps	Strand	Frame
16755 bits(9073)	0.0()	9374/9504(99%)	81/9504(0%)	Plus/Minus	
Features:					
Query 1		CAGTTC	CCAGGTTT	TAGGCATATGTGACTAGATAGAGTGCTAGGAGATGGATACGTGAAAA	60
Sbjct 62500		CAGTTC	CCAGGTTT	TAGGCATATGTGACTAGATAGAGTGCTAGGAGATGGATACGTGAAAA	62441
Query 61		TTTAAATATCATCATTTT	GAAACCCCATGTCACTCCAAGTGAGATTCCCTAAATATATGA	120	
Sbjct 62440		TTTAAATATCATCATTTT	GAAACCCCATGTCACTCCAAGTGAGATTCCCTAAATATATGA	62381	
Query 121		TATACAGACAGATATATGGGTTT	GAAACTCTGGAGATGAATACAAATTTAGGAGTCCCTG	180	
Sbjct 62380		TATACAGACAGATATATGGGTTT	GAAACTCTGGAGATGAATACAAATTTAGGAGTCCCTG	62321	
Query 181		GAACACAGGTCATGACTTAAAGTAATGGGAGTCAAAGATTACTC	agagaaaagcacagaaatg	240	
Sbjct 62320		GAACACAGGTCATGACTTAAAGTAATGGGAGTCAAAGATTACTC	CAGAGAAAGCACAGAAATG	62261	
Query 241		agaagagagaagaagtaggacaaaggaagaagagatcggaggagacc	aaagaaaggGTGATAAG	300	
Sbjct 62260		AGAAGAGAGAAGAAGTAGGACAAGGAAGAAGAGATCGGAGGAGAC	CAAGAAAGGGTGATAAG	62201	
Query 301		ATCAAAACAGGAGAGAAAAGAATCCGACAGAAAGTCTCATTGATTATCATGTCCCTTCCCAG	360		
Sbjct 62200		ATCAAAACAGGAGAGAAAAGAATCCGACAGAAAGTCTCATTGATTATCATGTCCCTTCCCAG	62141		
Query 361		AGGACAGGGACATGTCTTTTTTGTCTTTTATACCCAATTATCACAGGTCCTGGTGCAGCA	420		
Sbjct 62140		AGGACAGGGACATGTCTTTTTTGTCTTTTATACCCAATTATCACAGGTCCTGGTGCAGCA	62081		
Query 421		GACACACAG	tttttttttttttttAATTGTGTGTACTATTACAGTTTCCTGTATTACACC	480	
Sbjct 62080		GACACACAG	TTTTTTTTTTTTTT-AATTGTGTGTACTATTACAGTTTCCTGTATTACACC	62022	

[illegible]

Query	2154	GTGTGTGCCACAGACACCCAGCTAATTGTCATCTACCCGCCTCAGCTTCCCAAACGTGTTT	2213
Sbjct	60353	GTGTGTGCCACAGACACCCAGCTAATTGTCATCTACCCGCCTCAGCTTCCCAAACGTGTTT	60294
Query	2214	GGATTACAGGTATGAGCCACTGTGCCCAGCAGAAATTACATTTACAAATTAATATGAAGA	2273
Sbjct	60293	GGATTACAGGTATGAGCCACTGTGCCCAGCAGAAATTACATTTACAAATTAATATGAAGA	60234
Query	2274	CATGGTGATAACTAACATATTTATAACATGAAATCTGCTCATCCAGGAACATAGAATGCA	2333
Sbjct	60233	CATGGTGATAACTAACATATTTATAACATGAAATCTGCTCATCCAGGAACATAGAATGCA	60174
Query	2334	AATCTTTTCATTCCACTCAGCAAAATTTTGTCTGTCTTGATAAAAAGTCCTGCACATCTA	2393
Sbjct	60173	AATCTTTTCATTCCACTCAGCAAAATTTTGTCTGTCTTGATAAAAAGTCCTGCACATCTA	60114
Query	2394	AGTTTATTCCTAGGTATTTAATTTTTGTCTGAAATACCTGAAAAAATACTTCATCACTATA	2453
Sbjct	60113	AGTTTATTCCTAGGTATTTAATTTTTGTCTGAAATACCTGAAAAAATACTTCATCACTATA	60054
Query	2454	TCTTCTATGTGATTATAGCTAACATTGGGGAAGGCTATTGATTTTTATATAAAAGAAGCTT	2513
Sbjct	60053	TCTTCTACGTGATTATAGCTAACACTGGGGAAGGCTATTGATTTTTATATAAAAGAAGCTT	59994
Query	2514	TTAACCAGTAATCTTAAAAATTGTTTTTCTCAGTTGGTTCCTTTGGATATTTTTAGGTA	2573
Sbjct	59993	TTAACCAGTAATCTTAAAAATTGTTTTT-CTCAGTTGGTTCCTTTGGATATTTTTAGGTA	59935
Query	2574	AACAATCATGTCAACTGAAAATAATGATTATTTTCTATAAAGACTATGACATCACAGGA	2633
Sbjct	59934	AACAATCATGTCAACTGAAAATAATGATAAATTTTCTATAAAGACTATGACATCACAGGA	59875
Query	2634	AAATACAGTAAATACTTTTTTAAAAAGAAATATAAAAGGGCCAGGCACAGTGGCTCACGCCTG	2693
Sbjct	59874	AAATACAGTAAATACTTTTTTAAAAAGAAATATAAAAGGGCCAGGCACAGTGGCTCACGCCTG	59815
Query	2694	TAATCCCAGCACTTTGGGAGGCCAAGGTGGGCAGACCATGAGGTCAGGAGATCGAGACCA	2753
Sbjct	59814	TAATCCCAGCACTTTGGGAGGCCAAGGTGGGCAGACCATGAGGTCAGGAGATCGAGACCA	59755
Query	2754	TCCTGGCTAACACGGTGAACCCCATCTCTACTaaaaaaatacaaaaaaTTAGCCGGGAAT	2813
Sbjct	59754	TCCTGGCTAACACGGTGAACCCCATCTCTACTAAAAAATACAAAAAATTAGCCGGGAAT	59695
Query	2814	GGTGGCGGGCGCCTGTAGTCCCAGCTACTGGGGAGGCTGAGGCAGGAGAATGGTGGGAAC	2873
Sbjct	59694	GGTGGCGGGCGCCTGTAGTCCCAGCTACTGGGGAGGCTGAGGCAGGAGAATGGTGGGAAC	59635
Query	2874	CCAGGAGGTGGAGCTTGCAGTGAGCCGAGACCACGGCACTGCACTCCAGCCTGGGTGACA	2933
Sbjct	59634	CCAGGAGGTGGAGCTTGCAGTGAGCCGAGATCACGGCACTGCACTCCAGCCTGGGTGACA	59575
Query	2934	GAGCAAGACTCTGTCTCaaaaaaaaaaaaaaaaaaaaaaaaaaaaatatatatatata	2993
Sbjct	59574	GAGCAAGACTCTGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA-----GA	59527
Query	2994	tatatataaaaaaCTATAGAGAATATGACCTCAACTATTAAGCATATGTGTAAGGGTTATGT	3053
Sbjct	59526	-ATAT--AAACTATAGAGAATATGACCTCAACTATTAAGCATATGTGTAAGGGTTATGT	59470
Query	3054	ATTTTAATAGCAAAGAAAAAATATATACTGGTAGAAAAATGACCATCATGTCAACAGTCAA	3113
Sbjct	59469	ATTTTAATAGCAAAGAAAAAATATATACTGGTAGAAAAATGACCATCATGTCAACAGTCAA	59410
Query	3114	TAGTGGTTATATTAGATAGAGAAATTATGGGAGACTTTAAAttttttCTTTTATCTTTTC	3173
Sbjct	59409	TAGTGGTTATATTAGATAGAGAAATTATGGGAGACTTTAAATTTTTTCTTTTATCTTTTC	59350
Query	3174	TGTACTTTACCAATTTTCTCAACAATGGTTGCTTATGAGTTTTAAAAATaaaaaaGGTT	3233
Sbjct	59349	TGTACTTTACCAATTTTCTCAACAATGGTTGCTTATGAGTTTTAAAAATAAAAAAGGTT	59290
Query	3234	TTAAAAATTTTCCAAACATGGAAGTTATATTTCTTTATATACTAAAAcaaaaacaaaac	3293
Sbjct	59289	TTAAAAATTTTCCAAACATGGAAGTTATATTTCTTTATATACTAAAACAAAAACAAAAC	59230
Query	3294	tttctatttgaatacctatggcaaaacccctatctctacaaaaaatacaaaaaaTTAGCAA	3353
Sbjct	59229	TTTCTATTGAATACCTATGGCAAAACCCATCTCTACAAAAAATACAAAAAATTAGCAA	59170
Query	3354	GGTGGGGTAGTACACACCTGTAGTCCCAGCTACTCTAGAGGCTGAGGTGGGAGGATCACC	3413
Sbjct	59169	GGTGGGGTAGTACACACCTGTAGTCCCAGCTACTCTGGAGGCTGAGGTGGGAGGATCACC	59110
Query	3414	TGAGTCCCCAGAGAATGAGGCTCCAGTGAGCCGTGATCATAGCACTGCATTCCAGCCTGG	3473
Sbjct	59109	TGAGTCCCCAGAGAATGAGGCTCCAGTGAGCCGTGATCATAGCACTGCATTCCAGCCTGG	59050
Query	3474	GAGACAGAGAAAGACCCCATCTCaaaaaaaaaaaaaaaaaagaaagaaagaaaaaagaaTA	3533
Sbjct	59049	GAGACAGAGAAAGACCCCATCTCAAAAAAAAAAAAAA--GAAAGAAAGCAAAAGAAATA	58992
Query	3534	TCCACAATGATCTGAAATGCCTATCTGTATGAGACTGTCTTTGTTCACATTTTTTCAAG	3593
Sbjct	58991	TCCATAATGATCTGAAATGCCTATCTGTATGAGACTGTCTTTGTTCACATTTTTTCAAG	58932
Query	3594	CAAATATCACACAATAAATTGAATGCAGGTACAAATGACATATCAAACATCAAAGAAATT	3653
Sbjct	58931	CAAATATCACACAATAAATTGAATGCAGGTACAAATGACATATCAAACATCAAAGAAATT	58872
Query	3654	TGCAAAAGATGTAAGACTGTACTACCTTGGGTTTAGAAATTTTCTTATCATAAAAGCATT	3713
Sbjct	58871	TGCAAAAGACGTAAGACTGTACTACCTTGGGTTTAGAAATTTTCTTATCATAAAAGCATT	58812
Query	3714	TATAACAATATTTTGTGAGCTTTTAAGGAATATTTTAAGTATTCTGATTTAATTTCTAG	3773
Sbjct	58811	TATAACAATATTTTGTGAGCTTTTAAGGAATATTTTAAGTATTCTGATTTAATTTCTAG	58752
Query	3774	TGATAAATACCAATAGATATAACCCACATACACAAAAGCTCCTTGGGCCCTCAATATACT	3833
Sbjct	58751	TGATAAATACCAATAGATATAACCTACATACACAAAAGCTCCTTGGGCCCTCAATATACT	58692

Query	3834	TTTAAGAGTGTTAAAGGAATCCTGACCCCAAACCTTTGAGAACTGCTGCCTTCCCTCTAC	3893
Sbjct	58691	TTTAAGAGTGTTAAAGGAATCCTGACCCCAAACCTTTGAGAACTGCTGCCTTCCCTCCAC	58632
Query	3894	TTTATTCCTTCCCTAGAAATTTCTTCCTTGAAGAAACATTTCCTTTGCCATTCTATGTTAA	3953
Sbjct	58631	TTTATTCCTTCCCTAGAAATTTCTTCCTTGAAGAAACATTTCCTTTGCCATTCTATGTTAA	58572
Query	3954	CTTACATAGTTCATTGAGGCCAGTTTTTGCTACCTCTCTCCCATCTTTCCACATCCCTCT	4013
Sbjct	58571	CTTACATAGTTCATTGAGGCCAGTTTTTGCTACCTCTCTCCCATCTTTCCACATCCCTCT	58512
Query	4014	CTTGACACAAAACCTGACCAAAGGACTCTACGGCCCCGCCCATTTCCAGTGATTAGCTG	4073
Sbjct	58511	CTTGACACAAAACCTGACCAAAGGACTCTACGGCCCCACCCATTTCCAGTGATTAGCTG	58452
Query	4074	TCAGGTGGGCTAAGCCAAGAAAACTGGGTTTTCCCTGAGACTAGACCTCTCTTTCTGGG	4133
Sbjct	58451	TCAGGTGGGCTAAGCCAAGAAAACTGGGTTTTCCCTGAGACTAGACCTCTCTTTCTGGG	5839
Query	4134	AGATACGGAATCACAGGGACAAGGCTGGCCCTGTCTAGAATTCATCTTGTCTAAATGGGAA	4193
Sbjct	58391	AGATACGGAATCACAGGGACAAGGCTGGCCCTGTCTAGAATTCATCTTGTCTAAATGGGAA	58332
Query	4194	GAGGTTAGGCAAGTTTCTAGAATGCCAGACTGCTTTCTAGAAAGTCAAAGATAATTATAC	4253
Sbjct	58331	GAGGTTAGGCAAGTTTCTAGAATGCCAGACTGCTTTCTAGAAAGTCAAAGATAATTATAC	58272
Query	4254	TTTCTGCCACGACTGTGAAAATGCCATTTCATTGCACGCTTTCTAACATTTATACCAAT	4313
Sbjct	58271	TTTCTGCCACGACTGTGAAAATGCCATTTCATTGCACGCTTTCTAACATTTATACCAAT	58212
Query	4314	CTGATAAATAAAAGCTGGTACCTAGAAGaaaaaaaaGGCTGGGTATGGTGGCTCATGCCTG	4373
Sbjct	58211	CTGATAAATAAAAGCTGGTACCTAGAAGAAAAAAAAAGGCTGGGTATGGTGGCTCATGCCTG	58152
Query	4374	TAATCCCAGTACTTTGGGAGACCAAGGTGAGTGGATCACCTGAGGTCAGGAGTTCGAGAC	4433
Sbjct	58151	TAATCCCAGTACTTTGGGAGACCAAGGTGAGTGGATCACCTGAGGTCAGGAGTTCGAGAC	58092
Query	4434	AAGCCTGGCCAACATGATGAAACCCCATCTCTAGTAAAAACACAAACATTAGCCGGGCAT	4493
Sbjct	58091	AAGCCTGGCCAACATGATGAAACCCCATCTCTAGTAAAAACACAAACATTAGCCGGGCAT	58032
Query	4494	GGTGGCAGGCCCTGTAAATCCCAACTACTCGGGAGGCTGAGGCAAGAGGATCACTTGAAC	4553
Sbjct	58031	GGTGGCAGGCCCTGTAAATCCCAACTACTCGGGAGGCTGAGGCAAGAGAATCACTTGAAC	57972
Query	4554	CTGGGAGGTGGAGGTTTTAGTGAGCCAAGATCATGCCATTGCCCTCCAGCCTGGGTGACA	4613
Sbjct	57971	CTGGGAGGTGGAGGTTTTAGTGAGCCAAGATCATGCCATTGCCCTCCAGCCTGGGTGACA	57912
Query	4614	AGCTGAGACTTTGTCTCaaaaaaaaaaaaaaaaaaaaaGTTTCATACAATATAAATTGT	4673
Sbjct	57911	AGGTGAGACTTTGTCTCAAAAAAAAAAAAAAAAA-----GTTTCATACAATATAAATTGT	57858
Query	4674	TCCATCTCTAAAAACCAATTCTAGCAATAACTGAAAGCCACCCTTGGAAGGTTTCAAGGA	4733
Sbjct	57857	TCCATCTCTAAAAACCAATTCTAGCAATAACTGAAAGCCACCCTTGGAAGGTTTCAAGGA	57798
Query	4734	TTTAGCTCTACCTGTTGATGATGTCCAAAGCATTAGTTAAGGTAGaaaaaaaaTcacacac	4793
Sbjct	57797	TTTAGCTCTACCTGTTGATGATGTCCAAAGCATTAGTTAAGGTAGAAAAAAAAATA-----	57743
Query	4794	acacacacacacacacacacacacacacacacacacTCACCCCTATGTAGTCAGTACCAGGAAA	4853
Sbjct	57742	---TACACACACACACACACACACACACACACTCACCCCTATGTAGTCAGTACCAGGAAA	57686
Query	4854	CACGAAAGACTAGATGGTACAGTCATCCAACACAAAGCACACAATAACTGAAGGCACTGT	4913
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Query	4914	AGAGGAGTAACCTTATGACACAGATCTACAATATTGAGTGAAAATGCAGATTACaaaaaaa	4973
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Query	5034	ATGACTGAAAGATACAAAATTCTGATAGTGGTACATTCTGAGTGGTAGAATTATCAGTAT	5093
Sbjct	57506	ATGACTGAAAGATACAAAATTCTGATAGTGGTACATTCTGAGTGGTAGAATTATCAGTAT	57447
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Sbjct	57446	TATTTTCTAGTTTTTGCCTAAAAATTTTCTAAATTTCTTAAGAACTTTTTGTATCCATAT	57387
Query	5154	TATCAAATATCCATACCCCAGGAAACTTAACCTTGAGCACAACTCTACAACAAGTTCA	5213
Sbjct	57386	TATCAAATATCCATACCCCAGGAAACTTAACCTTGAGCACAACTCTACAACAAGTTCA	57327
Query	5214	ATGTTTGTTCAGTTTAATATTTAAGAGACAACCTATTTTGAAAGACATCTAAAATGATGA	5273
Sbjct	57326	ATGTTTGTTCAGTTTAATATTTAAGAGACAACCTATTTTGAAAGACATCTAAAATGATGA	57267
Query	5274	CCAATATTTAAACCTATGCATTAATATTTTCAATCATATCCTTCACATTTTGTAATTTT	5333
Sbjct	57266	CCAATATTTAAACCTATGCATTAATATTTTCAATCATATCCTTCACATTTTGTAATTTT	57207
Query	5334	GATAAGGTAAAGCTTTAGATCCATCTTGAAAAGATAAGCTTTCTGTTTGTCTTTAAAAATA	5393
Sbjct	57206	GATAAGGTAAAGCTTTAGATCCATCTTGAAAAGATAAGTTTTCTGTTTGTCTTTAAAAATA	57147
Query	5394	TGACCCACAATATGCCTGTTTTTAAACAGTGAATGATGCTCTAAAATCACAAATATAAATT	5453
Sbjct	57146	TGACCCACAATATGCCTGTTTTTAAACAGTGAATGATGCTCTAAAATCACAAATATAAATT	57087
Query	5454	CAGGCAGTGCTCCTTACATGGAAAGTTTAAGTACTTCTAACACTGCTCTTTTCACTTGT	5513
Sbjct	57086	CAGGCAGTGCTCCTTACATGGAAAGTTTAAGTACTTCTAACACTGCTCTTTTCACTTGT	5702

Query	5514	TATGAAAACACAGAACAATTATCTAAGCATCTAATTATTCAGGTCCTTTGTTTCTCCTCC	5573
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Query	5574	AATCTATTAGTTTTATAGTAATTTTAGGGCCTGTGAGGATGAAGCTGTCTGTGACAGCTA	5633
Sbjct	56966	AATCTATTAGTTTTATAGTAATTTTAGGGCCTGTGAGGATGAAGCTGTCTGTGACAGCTA	56907
Query	5634	CCACAAAGGTTACTATAGGTGGACAAATTTCAAACAAGTTTATCACCCTACCATCCCCA	5693
Sbjct	56906	CCACAAAGGTTACTATAGGTGGACAAATTTCAAACAAGTTTATCACCCTACCATCCCCA	56847
Query	5694	CCATAAACTGTCTCAATCAAGGGCAACACAATTCAATATTAGCCAAGACAACCTCTTTA	5753
Sbjct	56846	CCATAAACTGTCTCAATCAAGGGCAACACAATTCAATATTAGCCAAGACAACCTCTTTA	56787
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Sbjct	56786	CCTGTCACTGCTTAAGAAAAGGATTTTGGTCTTATTTAGAAATAACTTTCTGTACCTAT	56727
Query	5814	TTTCTCCATAAATCCACTGAGACCAATGTGTGGCTCTATCGCAAGCACCAGCAAGCAA	5873
Sbjct	56726	TTTCTCCATAAATCCACTGAGACCAATGTGTGGCTCTATCTCAAGCACCAGCAAGCAA	56667
Query	5874	ACTGCCTGCTAGAAGGTTCAAGTTTGTATCTTTCCAAATGTAGAACACAGCTATCTTCA	5933
Sbjct	56666	ACTGCCTGCTAGAAGGTTCAAGTTTGTATCTTTCCAAATGTAGAACACAGCTATCTTCA	56607
Query	5934	AGGATTTTCATAATTTTGGAAATTTGATGCACAACTTCTTGAAAGTTTCAGAGACACAGC	5993
Sbjct	56606	AGGATTTTCATAATTTTGGAAATTTGATGCACAACTTCTTGAAAGTTTCAGAGACACAGC	56547
Query	5994	AGCTGTAATTATCTGAAGGCTGGTTACGGGACACATTACCTTCATACTTTGCTGTTTAA	6053
Sbjct	56546	AGCTGTAATTCTCTGAAGGCTGGTTATGGGACACATTACCTTCATACTTTGCTGTTTAA	56487
Query	6054	GAAATGTGGGGTGGAGAATCAAGTAACTGATAGAATTTCCATATAAAATTTCTAAGTGCT	6113
Sbjct	56486	GAAATGTGGGGTGGAGAATCAAGTAACTGATAGAATTTCCATATAAAATTTCTAAGTGCT	56427
Query	6114	CTGAGAACAAAAGAACTTAAATACACACACACACACACACACACACACACACACAC	6173
Sbjct	56426	CTGAGAACAAAAGAACTTAAATACACACACACACACACACACACACACACACACAC	56367
Query	6174	-----GGTTTCCCTACTAATCATTTTACAACATAACAACCAAGTTGCTAAAC	6221
Sbjct	56366	ACACACACACACGGTTTCCCTACTAATCATTTTACAACATAACAACCAAGTTGCTAAAC	56307
Query	6222	CAGAGCCCAAAAAGCAGAGTCAAAGTTCTAACACTTGGTAAAAGAAAAATGCACACATA	6281
Sbjct	56306	CAGAGCCCAAAAAGCAGAGTCAAAGTTCTAACACTTGGTAAAAGAAAAATGCACACATA	56247
Query	6282	CCCCTGTGAGCTAAAAAAAAAATGCTTAAGTATTCAAAGACAGCAATTACAGCTACTGA	6341
Sbjct	56246	CCCCTGTGAGCTAAAAAAAAAATGCTTAAGTATTCAAAGACAGCAATTACAGCTACTGA	56189
Query	6342	GAACATCACTGTAAGCAAACCTGAGGCAGAGAAAACAAACGTGCTGATGAGGATTTGAACC	6401
Sbjct	56188	GAACATCACTGTAAGCAAACCTGAGGCAGAGAAAACAAACGTGCTGATGAGGATTTGAACC	56129
Query	6402	ACCTAAGCTGCAGAAACCCACTGGATGGTTTCCCTAGGTTCCGAGTTGGCATTATCTTTCA	6461
Sbjct	56128	ACCTAAGCTGCAGAAACCCACTGGATGGTTTCCCTAGGTTCCGAGTTGGCATTATCTTTCA	56069
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Sbjct	56068	GAACAATCTTCTAGAAGAGATCACATAACACTGTTACAAAGGATCTGGAGAAAGGGACCC	56009
Query	6522	TGGCTTCATCACTGTGGCTCTCCAGTCATGCTTTACATTTGGCAGTGACTATCTCCATTC	6581
Sbjct	56008	TGGCTTCATCACTGTGGCTCTCCAGTCATGCTTTACATTTGGCAGTGACTATCTCCATTC	55949
Query	6582	AACTCAATTCCCTAACCTTAACTAGCTGACATTTATCAAATACTGCCCTTTACCAGGTC	6641
Sbjct	55948	AACTCAATTCCCTAACCTTAACTAGCTGACATTTATCAAATACTGCCCTTTACCAGGTC	55889
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Sbjct	55888	TAAGTAAGTTTAACTCCCCCACCACCACCAAAAAAATCAAGATACTAAGGGATATAC	55829
Query	6702	TATTCACAAAAGGGAAACCTGTCTCCTCTTCATATACCTGTTCCCTTCAAGGAAGGGTAT	6761
Sbjct	55828	TATTCACAAAAGGGAAACCTGTCTCCTCTTCATATACCTGTTCCCTTCAAGGAAGGGTAT	55769
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Sbjct	55768	AAAAATGGGGATGAGGGAGGATAACCACTAGGAATTTGACCTTATATTATAAATTTGGTCA	55709
Query	6822	GATAAATGAAAAATAATTCCTCTGGACTCAAAGTGATATGGCTCTGAAAATGGGAGAAACA	6881
Sbjct	55708	GATAAATGAAAAATAATTCCTCTGGACTCAAAGTGATATGGCTCTGAAAACGGGAGAAACA	55649
Query	6882	TCGGGGTCCTTTGTCTCAGCCAGTTAAACGACATGGACACACAGGAGTGGTTTTAAGGA	6941
Sbjct	55648	TCGGGGTCCTTTGTCTCAGCCAGTTAAACGACATGGACACACAGGAGTGGTTTTAAGGA	55589
Query	6942	ACAGAAAGTTTAAATAGGCAAGAAAGAAAGGCTCCCTGCGGTACAGAAAAAGGGGGT	7001
Sbjct	55588	GCAGAAAGTTTAAATAGACAAGAAAGAAAGGCTCCCTGCGGTACAGAAAAAGGGGG-T	55530
Query	7002	CTGAACAGAGAAAAAGCCCCGTGTGTGGCAGAACAGTACTCGGTTATATTGGGAGGCTGG	7061
Sbjct	55529	CTGAACAGAGAAAAAGCCCCGTGTGTGGCAGAACAGTACTCGGTTATATTGGGAGGCTGG	55470
Query	7062	AGGAGGTGGTGTCTGATTTGCACAGGGCCAGGGCATTGGTTTGACCAGGCAGGTCATTC	7121
Sbjct	55469	AGGAGGTGGTGTCTGATTTGCACAGGGCCAGGGCATTGGTTTGACCAGGCAGGTCATTC	55410
Query	7122	ATGTAGCCCGAGAAAAACGTGGCCCTCCACCTAGCCTTTTAAATATGCAAAATGTAGGTC	7181
Sbjct	55409	ATGTAGCCCGAGAAAAACGTGGCCCTCCACCTAGCCTTTTAAATATGCAAAATGTAGGTC	55350

[illegible]

Query	8862	GGATTACAGGGGCGAGCCACTGTGCCAGCCTGATCATTTGTTTCTAACAACTCTGGGGGC	8921
Sbjct	53677	GGATTACAGGGGCGAGCCACTGCGCCAGCCTGATCATTTGTTTCTAACAACTCTGGGGGC	53618
Query	8922	TCGTCTGGAATTCCCAATTCTCCTCTGAGAAAAGGGTCTCCAGTCACCAATAGTGAGGAGA	8981
Sbjct	53617	TCGTCCGGAATTCCCAATTCTCCTCTGAGAAAAGGGTCTCCAGTCACCAATAGTGAGGAGA	53558
Query	8982	AGCATCCCACTGCCTCACTGAGGTGGCCTCATGGTGAGGGATCAGGACCCACCCAGTGTG	9041
Sbjct	53557	AGCATCCCACTGCCTCATTGAGGTGGCCTCATGGTGAGGGATCAGGACCCACCCAGTGTG	53498
Query	9042	ATGAATAAACCCGGACTCTCAGCAGTCTGGAAAGGAACAGACCAACAACCTTAAGAGAAAA	9101
Sbjct	53497	ATGAATAAACCCGGACTCTCAGCAGTCTGGAAAGGAACAGACCAACAACCTTAAGAGAAAA	53438
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Sbjct	53437	GGATCCTCACATACCATGGTGACCAGGTAAGTATGTGCACAGACCAACGTAAGAAACATC	53378
Query	9162	ACAAGAGCGACAAAGTATTTTCTTGGTGTTGGGATATCTTGAGGATTGAAAGTGTGTGT	9221
Sbjct	53377	ACAAGAGCGACAAAGTATTTTCTTGGTGTTGGGATATCTTGAGGATTGAAAGTGTGTGT	53318
Query	9222	TGAGACTCACAATTGAGTGCAAAGCAAGTGTTCAGTCCAGATCTGCAGTTCTGTGGTCAC	9281
Sbjct	53317	TGAGACTCACAATTGAGTGCAAAGCAAGTGTTCAGTCCAGATCTGCAGTTCTGTGGTCAC	53258
Query	9282	CTTATACAGCTTAAGGTAGCCCTTCTGTAAAGGAGTCTGGGTCAGGGGTTTCTACTGAAA	9341
Sbjct	53257	CTTATACAGCTTAAGGTAGCCCTTCTGTAAAGGAGTCTGGGTCAGGGGTTTCTACTGAAA	53198
Query	9342	CAGCCATTGCTAAGAGGAAACCAACGTTCCCATGAGGGAAGCAGCCAGAGAAGGATGAAG	9401
Sbjct	53197	CAGCCATTGCTAAGAGGAAACCAACGTTCCCGTGAGGGAAGCAGCCAGAGAAGGATGAAG	53138
Query	9402	CGAAAGGAGAAAAGTGCAAGAAACCTCCAGCAGGGGGGTTGAGCCTC--ggaaagggaag	9459
Sbjct	53137	CGAAAGGAGAAAAGTGCAAGAAACCTCCAGCAGGGGGGTTGAGCCTCTAGGAAAGGAAAG	53078
Query	9460	ggaaagggaagggaagggaagg	9483
Sbjct	53077	G-AAAGGAAAGG-AAAGG-AAAGG	53057

Range 2: 44083 to 53089

Features:

Query	10444	TCCATCCTAGGCATCCTTTTCTCAGGGGAAGAAAGAAGCATCATCTGTAGAGCTGCTATG	10503
Sbjct	52249	TCCATCCTAGGCATCCTTTTCTCAGGGGAAGAAAGAAGCATCATCTGTAGAGCTGCTATG	52190
Query	10504	GTACCCTGGGAACATGAACACCCTCCTGGCCAAAACATTTCATGCAGCGGATCAAAAATTC	10563
Sbjct	52189	GTAGCCTGGGAACATGAACACCCTCCTGGCCAAAACATTTCATGCAGCGGATCAAAAATTC	52130
Query	10564	CCCAACCAAGACCCCTGCTGGGACAATAATAACGCAGCCCACTGAAGAGGATACGCAAGA	10623
Sbjct	52129	CCCAACCAAGACCCCTGCTGGGACAATAATAACGCAGCCCACTGAAGAGGATACGCAAGA	52070
Query	10624	ACTTAGGGAAATGATAATAAAAGGGATTTCGGGAGTCAGTACTCCGAACCCAAAATCTTAC	10683
Sbjct	52069	ACTTAGGGAAATGATAATAAAAGGGATTTCGGGAGTCAGTACTCCGAACCCAAAATCTTAC	52010
Query	10684	TCGAGCATTTCGACATACAACAAAGGAAAGATGAAGGGCCTATCGAACTTTTAGACAGGTT	10743
Sbjct	52009	TCGAGCATTTCGACATACAACAAAGGAAAGATGAAGGGCCTATCGAACTTTTAGACAGGTT	51950
Query	10744	GAAAGAACAAATGAGAAAATATGCTGGCCTAGATTTAGAAGATCCTCTTAGGCAGTGAAT	10803
Sbjct	51949	GAAAGAACAAATGAGAAAATATGCTGGCCTAGATTTAGAAGATCCTCTTAGGCAGTGAAT	51890
Query	10804	GTTAAAGCTTCATTTTGTTACTAACAGCCAGATATCACAAGGAAATTACAAAAGATAGGA	10863
Sbjct	51889	GTTAAAGCTTCATTTTGTTACTAACAGCCAGATATCACAAGGAAATTACAAAAGATAGGA	51830
Query	10864	AATTGGAAGGACCATCCACGAAACGAGCTTCTTAGAGAAGCTCAGAAAGTGTGTGTAAGG	10923
Sbjct	51829	AATTGGAAGGACCATCCACGAAACGAGCTTCTTAGAGAAGCTCAGAAAGTGTGTGTAAGG	51770
Query	10924	AGGGATGAGGAGAAGCaaaaagaaaaaatgaaaaTTATGTTATCCACCTTCCAACAGGGG	10983
Sbjct	51769	AGGGATGAGGAGAAGCAAAAAGAAAAAATGAAAATTATGTTATCCACCTTCCAACAGGGG	51710
Query	10984	GCCCCAAAGGATAAAACACACCAGTATTACTCTCTGTTACCCAGAGACCCACACACTCCC	11043
Sbjct	51709	GCCCCAAAGGATAAAACACACCAGTATTACTCTCTGTTACCCAGAGACCCACACACTCCC	51650
Query	11044	AAACAAAGCCTCCCGAGAGCCAAAACCTATAAAGATCCTTAGGCCCCACTTCCTAAGCCA	11103
Sbjct	51649	AAACAAAGCCTCCCGAGAGCCAAAACCTATAAAGATCCTTAGGCCCCACTTCCTAAGCCA	51590
Query	11104	TATAAAGAACATAAGGAGACAAAGCCGAGAAACCCAAAAATAGAGAGAAGAGACAGAATC	11163
Sbjct	51589	TATAAAGAACATAAGGAGGCAAGCCGAGAAACCCAAAAATAGAGAGAAGAGACAGAATC	51530
Query	11164	AATGCTTCAATTGTGAGAAAGTAGGCCACTTCAAGAGGTATTGTCCCAAATTAAATCAG	11223
Sbjct	51529	AATGCTTCAATTGTGAGAAAGTAGGCCACTTCAAGAGGTATTGTCCCAAATTAAATCAG	51470
Query	11224	AAAGAGAAGTCGTCCCACTTACGACCTTTGAGGAGGAATAGGGGGGTAGGGGCTCTGTC	11283
Sbjct	51469	AAAGAGAAGTCGTCCCACTTACGACCTTTGAGGAGGAATAGGGGGGTAGGGGCTCTGTC	51410
Query	11284	TCTTTTACCTTGAATCCACCAAGAGCCCTTGATAAATTTAGAAGTGAACCCAAATCCG	11343
Sbjct	51409	TCTTTTACCTTGAATCCACCAAGAGCCCTTGATAAATTTAGAAGTGAACCCAAATCTG	51350
Query	11344	AGCTTATGACCTTTTTTAGTAGACTCAGGAGCAGCCTGCTCCTCTGTTTGTACCTTCCCC	11403
Sbjct	51349	AGCTTATGACCTTTTTTAGTAGACTCAGGAGCAGCCTGCTCCTCTGTTTGTACCTTCCCC	51290
Query	11404	CACAATATAACCTGGTCCTCAGAGGAGCTTGTAGTCTCAGGGGTAAAAGGAGAGGGAATC	11463
Sbjct	51289	CACAATATAACCTGGTCCTCAGAGGAGCTTGTAGTCTCAGGGGTAAAAGGAGAGGGAATC	51230
Query	11464	AAACTAAAAATTTTAAAGAAACAGAAATTAGATGTAAAACTGCTCAGCTAATGTTGAA	11523
Sbjct	51229	AAACTAAAAATTTTAAAGAAACAGAAATTAGATGTAAAACTGCTCAGCTAATGTTGAA	51170
Query	11524	TTTTTGTTAATTTTCAGAGGCAGGAACTAATCTATTAGGAAGAACTTAATGTTAAAATTA	11583
Sbjct	51169	TTTTTGTTAATTTTCAGAGGCAGGAACTAATCTATTAGGAAGAACTTAATGTTAAAATTA	51110
Query	11584	GGTATAGGTTTACGTATTGGCTCAGAAGGATTCTACACTTCATTAAACCTGCTCACCCT	11643
Sbjct	51109	GGTATAGGTTTACGTATTGGCTCAGAAGGATTCTACACTTCATTAAACCTGCTCACCCT	51050
Query	11644	GCAGAAGAAACATACATTCATCTGATGTTTGGGCAAGGGAAGGAAATGGGGAAAACCTC	11703
Sbjct	51049	GCAGAAGAAACATACATTCATCTGATGTTTGGGCAAGGGAAGGAAATGGGGAAAACCTC	50990
Query	11704	CAAATTCCCCCATACATATAAAGTTAAAAACCCCTGGAGAAATAGTAAGAAGAAAGCAA	11763
Sbjct	50989	CAAATTCCCCCATACATATAAAGTTAAAAACCCCTGGAGAAATAGTAAGAAGAAAGCAA	50930
Query	11764	TATCCTATTCCCTTTAGAAGGCAGAATAGGCCTGAAACCTGTAATTGAAAGCCTCATCAAG	11823
Sbjct	50929	TATCCTATTCCCTTTAGAAGGCAGAATAGGCCTGAAACCTGTAATTGAAAGCCTCATCAAG	50870
Query	11824	GATGGGCTCCTTGAACCCTGTATGTCCCCCTTATAACACCCCAATACTGCCTGTGAAGAAA	11883
Sbjct	50869	GATGGGCTCCTTGAACCCTGTATGTCCCCCTTATAACACCCCAATACTGCCTGTGAAGAAA	50810
Query	11884	CCAGATAGGTCATGTGCTAGCTAGCATAAGACCTCTGGGCCATCAACCAGACAGTCTAGACT	11943
Sbjct	50809	CCAGATAGGTCATGTGCTAGCTAGCATAAGACCTCTGGGCCATCAACCAGACAGTCTAGACT	50750
Query	11944	ACCCATCCTGTTGTCCCTAATCCTTAAACCATTCTCAGTAAAAATCCATATGAACATCAA	12003
Sbjct	50749	ACCCATCCTGTTGTCCCTAATCCTTAAACCATTCTCAGTAAAAATCCATATGAACATCAA	50690
Query	12004	TGGTTTACAGTAATAGGTTTAAAGATGCCTTTTGAGCATGCTCCTTGGATGAGGACAGC	12063
Sbjct	50689	TGGTTTACAGTAATAGGTTTAAAGATGCCTTTTGAGCATGCTCCTTGGATGAGGACAGC	50630
Query	12064	TGAGACATTTTGTCTTCGAATGGGAAGATCCCCATTCTGGATGACAGCAACAGTATCGA	12123
Sbjct	50629	TGAGACATTTTGTCTTCGAATGGGAAGATCCCCATTCTGGATGACAGCAACAGTATCGA	50570

Query	12124	TAGACAGTTCTACCCCAGGGCTTCACAGATTCCCTAATCTCTTTGGTCAAATTCTAGAA	12183
Sbjct	50569	TAGACAGCTCTACCCCCGGGCTTCACAGATTCCCTAATCTCTTTGGTCAAATTCTAGAA	50510
Query	12184	CAAGTGTTAGAACAAGTTTATACCCCAAAATGTATATGTCTGCTCCAGTACGTAGATGAC	12243
Sbjct	50509	CAAGTGTTAGAACAAGTTTATACCCCAAAATGTATATGTCTGCTCCAGTACGTAGATGAC	50450
Query	12244	TTATTAATATCCGGTTAGGCTATAGAAAAGGTATCTGCTTTCTCCGTCCATATCCTTAAC	12303
Sbjct	50449	TTATTAATATCCGGTTAGGCTATAGAAAAGGTATCTGCTTTCTCCATCCATATCCTTAAC	50390
Query	12304	CATTTGTAAGGAGAGGGGCTATGGGTTTCAAAGAGAAAGCTTCAATTCATAGAGCCTGAA	12363
Sbjct	50389	CATTTGTAAGGAGAGGGGCTATGGGTTTCAAAGAGAAAGCTTCAATTCATAGAGCCTGAA	50330
Query	12364	GTTAAATACCTAGGACACTTAATAAGTAACGGCAAACGAAGGATAGGGCCTGAGAGGGTT	12423
Sbjct	50329	GTTAAATACCTAGGACACTTAATAAGTAACGGCAAACGAAGGATAGGGCCTGAGAGGGTT	50270
Query	12424	GAAAGGATTGTATCCATACCTTTTGCTTAAGACTAAACAAGAACTCAGAAAATTCCTAGGG	12483
Sbjct	50269	GAAAGGATTGTATCCATACCTTTTGCTTAAGACTAAACAAGAACTCAGAAAATTCCTAGGG	50210
Query	12484	ATAGCTGGATATTGCCGCTTATGGATTGACTCATATGCCCTTGTCATAAAGCCTCTCTAC	12543
Sbjct	50209	ATAGCCGGATATTGCCGCTTATGGATTGACTCATATGCCCTTGTCATAAAGCCTCTCTAC	50150
Query	12544	CTAAAAATCACCCAAGAAAAGCCTGACCTCTCCTCTGGACTTCTGAAGAACTCCACCAG	12603
Sbjct	50149	CTAAAAATCACCCAAGAAAAGCCTGACCTCTCCTCTGGACTTCTGAAGAACTCCACCAG	50090
Query	12604	GTTGAGGAGCTAAAACATCTGCTTATAACTGCCTCTGTTTTAGCTTTGCCTTCCCTAGAA	12663
Sbjct	50089	GTTGAGGAGCTAAAACATCTGCTTATAACTGCCTCTGTTTTAGCTTTGCCTTCCCTAGAA	50030
Query	12664	AAGCCATTTACCTTTCTGTTAACATAAATAAGGGGGTAGCTTTAGGGGTCTTACCCAA	12723
Sbjct	50029	AAGCCATTTACCTTTCTGTTAACATAAATAAGGGGGTAGCTTTAGGGGTCTTACCCAA	49970
Query	12724	GAACACGGAGGTCAACGCAACCCATGGATCTCCTATCAAAAGTTTTAGATCCAGTAACC	12783
Sbjct	49969	GAACACGGAGGTCAACGCAACCCATGGATCTCCTATCAAAAGTTTTAGATCCAGTAACC	49910
Query	12784	TGTGGATGGCCTGAATGTTTCAATCCATTGCAGCTACCGCCTTGTTAACTAAAGAAAGCA	12843
Sbjct	49909	TGTGGATGGCCTGAATGTTTCAATCCATTGCAGCTACCGCCTTGTTAACTAAAGAAAGCA	49850
Query	12844	GAAAACTAACCTTTGGGGGAAAGTTAGTTGTAAACATGCCCCATCAGGTTAGAGCCATCT	12903
Sbjct	49849	GAAAACTAACCTTTGGGGGAAAGTTAGTTGTAAACATGCCCCATCAGGTTAGAGCCATCT	49790
Query	12904	TAAATTAAGAGCAGGAAGGTGGCTTACTGACTTGAGAATTTTAAAGTATGAAGCTATCC	12963
Sbjct	49789	TAAATTAAGAGCAGGAAGGTGGCTTACTGACTTGAGAATTTTAAAGTATGAAGCTATCC	49730
Query	12964	TGTTAGAAAGAGATGATTTAACACTAACCCTGATAATTCACTTAACCCAGAGGTTTCCT	13023
Sbjct	49729	TGTTAGAAAGAGATGATTTAACACTAACCCTGATAATTCACTTAACCCAGAGGTTTCCT	49670
Query	13024	GACTGGAGATCCAAATCTAAAGAGACCTGAGCATGAGTGTTTAGATTTAATGATCATACA	13083
Sbjct	49669	GACTGGAGATTCAAATCTAAAGAGACCTGAGCATGAGTGTTTAGATTTAATGATCATACA	49610
Query	13084	AAAGTTAGGCCTGATTTAAGAGAGACCCCTTACAAAACGGGGCAGGGCTTCTTTATAGAT	13143
Sbjct	49609	AAAGTTAGGCCTGATTTAAGAGAGACCCCTTACAAAACGGGGCAGGGCTTCTTTATAGAT	49550
Query	13144	GGCTCTTCCCAAGTAATTGAAGGAAAAAGGCATAATAGGTACTCAGTAGTAGATGGGGAG	13203
Sbjct	49549	GGCTCTTCCCAAGTAATTGAAGGAAAAAGGCATAATAGGTACTCAGTAGTAGATGGGGAG	49490
Query	13204	GCACCTGAAGAAGTAGAGTCAGGAAGCCTGCCAAATAATTGGTCTGCCCAAACATGTGAA	13263
Sbjct	49489	GCACCTGAAGAAGTAGAGTCAGGAAGCCTGCCAAATAATTGGTCTGCCCAAACATGTGAA	49430
Query	13264	TGAATTGTTTGCATTAAATCAAGCCTTAAAGCACTTGCAAAACCAAGAACGGACTATTTA	13323
Sbjct	49429	TGAATTGTTTGCATTAAATCAAGCCTTAAAGCACTTGCAAAACCAAGAACGGACTATTTA	49370
Query	13324	TACTGATTCCAAGTATGCCTTTTGGGGTAGCTCACACCTTTGGAAAAATTTGGACTGAACG	13383
Sbjct	49369	TACTGATTCCAAGTATGCCTTTTGGGGCAGCTCACACCTTTGGAAAAATTTGGACTGAACG	49310
Query	13384	AGATCTTATTAATAGCAAAGGCCAAGACCTGGGCCACAAAGAATTAATCACCCAAGTATT	13443
Sbjct	49309	AGATCTTATTAATAGCAAAGGCCAAGACCTGGGCCACAAAGAATTAATCACCCAAGTATT	49250
Query	13444	AGATAACCTGCAGCTGCCAGAATAGCTATTGTCCATGTTCCAGGACATCAGAAAAGTCTT	13503
Sbjct	49249	AGATAACCTGCAGCTGCCAGAATAGCTATTGTCCATGTTCCAGGACATCAGAAAAGTCTT	49190
Query	13504	TCTTTTCAAAGCGGAAGGAATAACCTAGCAGATCAAATAGCCAAACACACTGCCGTTTCC	13563
Sbjct	49189	TCTTTTCAAAGCGGAAGGAATAACCTAGCAGATCAAATAGCCAAACACACTGCCGTTTCC	49130
Query	13564	TCTGAAAATGTCTGTTTTTCACTTAGCCCTTGCCCTTCCTCCCTCGACTGCAGTCCCCAT	13623
Sbjct	49129	TCTGAAAATGCCTGTTTTTCACTTAGCCCTTGCCCTTCCTCCCTCGACTGCAGTCCCCAT	49070
Query	13624	CTTTTCTCCCGCTgaaaaggaaaaattaataaaaaataggagccaaagaaaattcagaagg	13683
Sbjct	49069	CTTTTCTCCCGCTGAAAAGGAAAAATTAATAAAAAATAGGAGCCAAAGAAAATTCAGAAGG	49010
Query	13684	gaaatGGGTGTCACCAGACCAAAGAGAAATGTTATCCAAACCCCTCATGAGGGAAATCTT	13743
Sbjct	49009	GAAATGGGTGTCACCAGACCAAAGAGAAATGTTATCCAAACCCCTCATGAGGGAAATCTT	48950
Query	13744	CTCCCATCTGCATCAAGGGACTCATTAGGGACCTCAAGCTAAGTGTGATGCAGTCCTCGG	13803
Sbjct	48949	CTTTCATCTGCATCAAGGGACTCATTAGGGACCTCAAGCTAAGTGTGATGCAGTCCTCGG	48890

Query	13804	GGTCTACAGATGTATAGGAATTTATATTTTGGCAAGACAAGTTACAGATAGTTGCCTAGT	13863
Sbjct	48889	GGTCTACAGATGTATAGGAATTTACATTTTGGCAAGACAAGTTACAGATAGTTGCCTAGT	48830
Query	13864	ATGTAAGAAGACTAATAAGCAGATCCTCAGAAAACCACTGTTGGAGGGAGAAATCCAGG	13923
Sbjct	48829	ATGTAAGAAGACTAATAAGCAGATCCTCAGAAAACCACTGTTGGAGGGAGAAATCCAGG	48770
Query	13924	ATTAAGGCTGTTCCAAAGTGTCCAAATTGATTATGCCGAAATGCCCCCAATTGGTCACTT	13983
Sbjct	48769	ATTAAGGCTGTTCCAAATTGTCCAAATTGATTATGCCGAAATGCCCCCAATTGGTCACTT	48710
Query	13984	AAAATATTTATTAGTGATAGATCACCTTACTCATTGGGTAGAAGCTATTCCCTTTTCAAG	14043
Sbjct	48709	AAAATATTTATTAGTGATAGATCACCTTACTCATTGGGTAGAAGCTATTCCCTTTTCAAG	48650
Query	14044	TGCAACTGCTAGTAATGTACTCAAGGCATTAGTTGAAAATATTATACCCAGGTTTGGATT	14103
Sbjct	48649	TGCAACTGCTAGTAATGTACTCAAGGCATTAGTTGAAAATATTATACCCAGGTTTGGATT	48590
Query	14104	AATAGAAAATGCTGATTGATCAGACAATAGGACTCATTTCACTGCACATGTTCTTAAGAACT	14163
Sbjct	48589	AATAGAAAATGCTGATTGATCAGACAACAGGACTCATTTCACTGCACATGTTCTTAAGAACT	48530
Query	14164	AGCCCAAGTACTAGATATAACATGGGACTACCATAACCCCTGGCACCCACCTTCATCAGG	14223
Sbjct	48529	AGCCCAAGTACTAGATATAACATGGGACTACCATAACCCCTGGCACCCACCTTCATCAGG	48470
Query	14224	AAGAGTAGAAAAGATGAATCAGACTCTGAAAAACCACTAACCAAATTAGTCCTAGAGAC	14283
Sbjct	48469	AAGAGTAGAAAAGATGAATCAGACTCTGAAAAACCACTAACCAAATTAGTCCTAGAGAC	48410
Query	14284	TCGGTTGCCATGGACTAAATGCCTCCCATGGTCTTGTGAAGATTCCAAACTGCCCCTAG	14343
Sbjct	48409	TCGGTTGCCATGGACTAAATGCCTCCCATGGTCTTGTGAAGATTCCAAACTGCCCCTAG	48350
Query	14344	GAAAGATGTCGGCTCACCTCCTTATGAAATGCTGTATGAGTTGCCTTATCTACACTCCAC	14403
Sbjct	48349	GAAAGATGTCGGCTCACCTCCTTATGAAATGCTGTATGAGTTGCCTTATCTACACTCCAC	48290
Query	14404	TGCTGACATTCTCGTTCGAAACAAAAGATCTGTTTCTCAAGAACTATATACTTGGTCTA	14463
Sbjct	48289	TGCTGACATTCTCGTTCGAAACAAAAGATCTGTTTCTCAAGAACTATATACTTGGTCTA	48230
Query	14464	TCCTCCACTTTCTCTTTCCCTTAGGACTAAAGGCCTCTTGGCACATACACCACCCCTTGAA	14523
Sbjct	48229	TCCTCCACTTTCTCTTTCCCTTAGGACTAAAGGCCTCTTGGCACATACACCACCCCTTGAA	48170
Query	14524	TTTCCAGTTCACCACCACCAGCCCGACAGTGACCACATTCTCATCAAAGGTCAGAAAGA	14583
Sbjct	48169	TTTCCAGTTCACCACCACCAGCCCGACAGTGACCACATTCTCATCAAAGGTCAGAAAGA	48110
Query	14584	AAGGAAGCTCAAGCCCACCTGGGAGGGACATTATCTAGTGTTCCTAATGACTGAGACAGC	14643
Sbjct	48109	AAGGAAGCTCAAGCCCACCTGGGAGGGACATTATCTAGTGTTCCTAATGACTGAGACAGC	48050
Query	14644	CGTCCACACCACTGAAAAAGAATGGACTCACCATACCTGAGTCAAAAGAGCACCACCAC	14703
Sbjct	48049	CGTCCACACCACTGAAAAAGAATGGACTCACCATACCTGAGTCAAAAGAGCACCACCAC	47990
Query	14704	TCCAGAATCATGGACAGCTATTTTCAGGGCCAATTCCAACCAAGTTAAAGCTAAAACGGGT	14763
Sbjct	47989	TCCAGAATCATGGACAGCTATTTTCAGGGCCAATTCCAACCAAGTTAAAGCTAAAACGGGT	47930
Query	14764	TTGATCCTCTTATGCTATATTTCTTTTCCCTTCTATTGCTAGTCCTCTCGTTATTAATG	14823
Sbjct	47929	TTGATCCTCTTATGCTATATTTCTTTTCCCTTCTATTGCTAGTCCTCTCGTTATTAATG	47870
Query	14824	TAACTAGGTCGAGCTCACCCCAAATATTACCTTTGATGCTTGCTTGTATATCCTGTG	14883
Sbjct	47869	TAACTAGGTCGAGCTCACCCCAAATATTACCTTTGATGCTTGCTTGTATATCCTGTG	47810
Query	14884	GAGATCTCCAAAGTCAAAAGCAACTCTCAGCCTCAGAGAAGTATCTCCGTCCTTTTCA	14943
Sbjct	47809	GAGCTCTCCAAAGTCAAAAGCAACTCTCAGCCTCAGAGAAGTATCTCCGTCCTTTTCA	47750
Query	14944	CAAAAGCCTCCCCATTACGACTCTTGTTCCCTTAAGAAATGTAGGGAAACAGGCCTGCCA	15003
Sbjct	47749	CAAAAGCCTCCCCATTACGACTCTTGTTCCCTTAAGAAATGTAGGGAAACAGGCCTGCCA	47690
Query	15004	CAGCTGGAATGATATTATGTGGACAACCTGAACATCAGGGCTTTGTCAACAGGCAGTTGTA	15063
Sbjct	47689	CAGCTGGAATGATATTATGTGGACAACCTGAACATCAGGGCTTTGTCAACAGGCAGTTGTA	47630
Query	15064	AGTCTCTAAAACCATGTTTGTCTTGTAAAGGAAACATTCCCCACCCCTGACTGCCAGT	15123
Sbjct	47629	AGTCTCTAAAACCATGTTTGTCTTGTAAAGGAAACATTCCCCACCCCTGACTGCCAGT	47570
Query	15124	ATAACCAATGTAATCCAGTGCAAAATTTCTATTCTTATCCCCACTTCTGCCAACCTAAAC	15183
Sbjct	47569	ATAACCAATGTAATCCAGTGCAAAATTTCTATTCTTATCCCCACTTCTGCCAACCTAAAC	47510
Query	15184	CTACTTTAAGTCGCTTATACGGCATAGGAGCCAAAATAGCAGGGACACATCTTATAGAAT	15243
Sbjct	47509	CTACTTTAAGTCGCTTATACGGCATAGGAGCCAAAATAGCAGGGACACATCTTATAGAAT	47450
Query	15244	CCTTTGAAATGCATTTTCATTACTTTCTCACCTCCTCCACCTCCTTCTACACTCTCTCTCA	15303
Sbjct	47449	CCTTTGAAATGCATTTTCATTACTTTCTCACCTCCTCCACCTCCTTCTACACTCTCTCTCA	47390
Query	15304	ACGAAACCGCTGTTCTTCCTTCAACCAAGGATAAAATCAAGGTAAGCCATTGTAGAAGTT	15363
Sbjct	47389	ACGAAACCGCTGTTCTTCCTTCAACCAAGGATAAAATCAAGGTAAGCCATTGTAGAAGTT	47330
Query	15364	AAAAATTTGAAACAAACCATAGCAACTGAGACAGGGTACCAAGATGCAAAATGCTTGGTTA	15423
Sbjct	47329	AAAAATTTGAAACAAACCATAGCAACTGAGACAGGGTACCAAGATGCAAAATGCTTGGTTA	47270
Query	15424	GAATGGATTAAATATTCTGTCCGCACTCTAAACAAAAGCAACTGTTACACTTGTGCGCAC	15483
Sbjct	47269	GAATGGATTAAATATTCTGTCCGCACTCTAAACAAAAGCAACTGTTACACTTGTGCGCAC	47210

Query	15484	AGTAGGCCAGAGGCCAGGTTGTCCCTTTCCACTCGGATGGTCTTCAGCCAACTGGGC	15543
Sbjct	47209	AGTAGGCCAGAGGCCAGGTTGTCCCTTTCCACTCGGATGGTCTTCAGCCAACTGGGC	47150
Query	15544	ATGAGCTGTATGGTAGCTCTTCTCCAAGACCCACAGCCTGGGGTAATGAATCTTGCCAA	15603
Sbjct	47149	ATGAGCTGTATGGTAGCTCTTCTCCAAGACCCACAGCCTGGGGTAATGAATCTTGCCAA	47090
Query	15604	GCTCTCTCTCTGCTATTCCCTAAAGTCCAACACCCTGCAGGTCAGTCCCTGAGGGCCATC	15663
Sbjct	47089	GCTCTCTCTCTGCTATTCCCTAAAGTCCAACACCCTGCAGGTCAGTCCCTGAGGGCCATC	47030
Query	15664	CAGCCTCCATCTATTGACACCAATTTTTACCTCGGGTCTCTCACAACAAGGGGAAAACCTT	15723
Sbjct	47029	CAGCCTCCATCTATTGACACCAATTTTTACCTCGGGTCTCTCACAACAAGGGGAAAACCTT	46970
Query	15724	GGCATTTCATGAAGACCTAAAGGGATGCGGTGAACCTAAACTCTCCCAAGAGCTTACCAG	15783
Sbjct	46969	GGCATTTCATGAAGACCTAAAGGGATGCGGTGAACCTAAACTCTCCCAAGAGCTTACCAG	46910
Query	15784	TCAGTCTGCCCTTGTTTCATCTCGAGCATACTGATGGTGGTATTGTGGTGGACCCTTACT	15843
Sbjct	46909	TCAGTCTGCCCTTGTTTCATCTCGAGCATACTGATGGTGGTATTGTGGTGGACCCTTACT	46850
Query	15844	GGACACTCTGCCAAGCAACTGGAGTGGTACTTGTGCTCTAGTCCAACCTGGCCATCCCTTT	15903
Sbjct	46849	GGACACTCTGCCAAGTAACCTGGAGTGGTACTTGTGCTCTAGTCCAACCTGGCCATCCCTTT	46790
Query	15904	CACCCCTAGCATTCATTAAACATAATAGAAGAGAAAAATCAGAAGAGAAGAAGTGACCTTCA	15963
Sbjct	46789	CACCCCTAGCATTCATTAAACATAATAGAAGAGAAAAATCAGAAGAGAAGAAGTGACCTTCA	46730
Query	15964	TGGGTCCCTTTGACTCCACGTTTATAAAGATGCTACTGGAGTTCACGAGGGGTACCAGA	16023
Sbjct	46729	TGGGTCCCTTTGACTCCACGTTTATAAAGATGCTACTGGAGTTCACGAGGGGTACCAGA	46670
Query	16024	TAAATTTAAGGCCCGAAATCAACAGCTTCAGGATTTGAATCTGTGCTGTTTTGGTGGTC	16083
Sbjct	46669	TAAATTTAAGGCCCGAAATCAACAGCTTCAGGATTTGAATCTGTGCTGTTTTGGTGGTC	46610
Query	16084	AACTGTAAATAAAAAATGTAGATCGGATAAACTACATTTATTACAACCAACAAAGGTTTGT	16143
Sbjct	46609	AACTGTAAATAAAAAATGTAGATCGGATAAACTACATTTATTACAACCAACAAAGGTTTGT	46550
Query	16144	TAACTACACAAGACATGCCATTAAGGGAACAGCCTCCCAATTAGGTCCCATTAACTAAAT	16203
Sbjct	46549	TAACTACACAAGACATGCCATTAAGGGAACAGCCTCCCAATTAGGTCCCATTAACTAAAT	46490
Query	16204	AGTCTGGGAAAAACAGGATAGCCCTAGATACGATGCTAGCAGAAAAAGGTGGTGTCTGTGT	16263
Sbjct	46489	AGTCTGGGAAAAACAGGATAGCCCTAGATACGATGCTAGCAGAAAAAGGTGGTGTCTGTGT	46430
Query	16264	CATGATTGGAGTCCAATGATGTACTTTTATTCTTAATAACACAGCCCCTGACGGAACAGT	16323
Sbjct	46429	CATGATTGGAGTCCAATGATGTACTTTTATTCTTAATAACACAGCCCCTGACGGAACAGT	46370
Query	16324	AACAAAAGCTTTGCAGGACCTAACCTCCTTATCCAATGAGTTAGCAAGCAATTCTGGAAT	16383
Sbjct	46369	AACAAAAGCTTTGCAGGACCTAACCTCCTTATCCAATGAGTTAGCAAGCAATTCTGGAAT	46310
Query	16384	AAATGATCCCTTTTACAAGTTTAAATGGAGAAATGGTCTGGAAAAATGGAAAGGCTTAATGTC	16443
Sbjct	46309	AAATGATCCCTTTTACAAGTTTAAATGGAGAAATGGTCTGGAAAAATGGAAAGGCTTAATGTC	46250
Query	16444	CTCAATATTTACTTCTCTTGCAATCGTTATAGGTGTGCTTATTCTTGTGGATGCTGTAT	16503
Sbjct	46249	CTCAATATTTACTTCTCTTGCAATCGTTATAGGTGTGCTTATTCTTGTGGATGCTGTAT	46190
Query	16504	CATACCATACATTTTGTGGACTACTGCAAAGACTCATAGACACAGAACCTACCAAAACCTC	16563
Sbjct	46189	CATACCATACATTTTGTGGACTACTGCAAAGACTCATAGACACAGAACCTACCAAAACCTC	46130
Query	16564	TCTTAGCTCTCCTCCACCTTATTCAGATAAGCTTTTCTTCTAGAAAACCAAGCAGAACA	16623
Sbjct	46129	TCTTAGCTCTCCTCCACCTTATTCAGATAAGCTTTTCTTCTAGAAAACCAAGCAGAACA	46070
Query	16624	GCAAAGCAAAGACATGCTAAAAAGTTTGAAGAGGAAGAATTACAAAATTAAGAGGGGG	16683
Sbjct	46069	GCAAAGCAAAGACATGCTAAAAAGTTTGAAGAGGAAGAATTACAAAATTAAGAGGGGG	46010
Query	16684	GAATTGTTAGGTACAGTAAGTTCTCTTCAAAGGTTAACTTGTTCACCTTCCTTGTCT	16743
Sbjct	46009	GAATTGTTAGGTACAGTAAGTTCTCTTCAAAGGTTAACTTGTTCACCTTCCTTGTCT	45950
Query	16744	CTGTTCTTAAGAACAATTTCCCTGTACCTTCTCGACCCCTACTTACCAGCTTAGTTACCTG	16803
Sbjct	45949	CTGTTCTTAAGAACAATTTCCCTGTACCTTCTCGACCCCTACTTACCAGCTTAGTTACCTG	45890
Query	16804	CTTAGTAACCTGCCTTGTAACAACCTCTTCTACCAGCCCCAATCTGTAACCTCACATTCC	16863
Sbjct	45889	CTTAGTAACCTGCCTTGTAACAACCTCTTCTACCAGCCCCAATCTGTAACCTCACATTCC	45830
Query	16864	CCCTCCCTTTCTTATTAGAGAAAAATTCACAATATCCAGCTGAGTCAGCTAAGATTGTG	16923
Sbjct	45829	CCCTCCCTTTCTTATTAGAGAAAAATTCACAATATCCAGCTGAGTCAGCTAAGATTGTG	45770
Query	16924	CAGTCCTACCCAGCCCATGTTGGAATGACACAGAGGTAGGGAGTGCATTAGGGATAAGA	16983
Sbjct	45769	CAGTCCTACCCAGCCCATGTTGGAATGACACAGAGGTAGGGAGTGCATTAGGGATAAGA	45710
Query	16984	ACCCCTGCTCCACCCGTTTGGTGTGCTCTTGCAATCATGACTAATGCAAGCAGCATACT	17043
Sbjct	45709	ACCCCTGCTCCACCCGTTTGGTGTGCTCTTGCAATCATGACTAATGCAAGCAGCATACT	45650
Query	17044	TGCAGAAGCAAATTGTCTTGCTGAGAAAACCTTTTTTGCCTGAGTGCTGCTTCTTCTCAC	17103
Sbjct	45649	TGCAGAAGCAAATTGTCTTGCTGAGAAAACCTTTTTTGCCTGAGTGCTGCTTCTTCTCAC	45590
Query	17104	AGCACCGATCATTTGTTTCTAACAATCTCGCTAAAAGCAGCCTAGAAAGCAGCCACTTAT	17163
Sbjct	45589	AGCACCAATCATTTGTTTCTAACAATCTCGCTAAAAGCAGCCTAGAAAGCAGCCACTTAT	45530

Query	17164	GCAGAAAGAGTAATAATTTATGCTCTACAAGTCATATAAAAAATGAAGTTTCATTTGTTT	17223
Sbjct	45529	GCAGAAAGAGTAATAATTTATGCTCTACAAGTCATATAAAAAATGAAGTTTCATTTGTTT	45470
Query	17224	ACCGGCTAATTTACTTCCTGGGAGACATTTTTCATTCTAAAACAGTGATTCCCTACCAAG	17283
Sbjct	45469	ACCGGCTAATTTACTTCCTGGGAGACATTTTTCATTCTAAAACAGTGATTCCCTACCAAG	45410
Query	17284	AGTTCATAGATGCCAAGAAGTCCATAAAAGGCGTAATGGAATTGCCAAATTATGTAAAT	17343
Sbjct	45409	AGTTCATAGATGCCAAGAAGTCCATAAAAGGCGTAATGGAATTGCCAAATTATGTAAAT	45350
Query	17344	ACTTCAAAAGGACTCAAAGCCATATACTAGTTCCCAATAGGCCTGCACAAGTTATTAGAA	17403
Sbjct	45349	ACTTCAAAAGGACTCAAAGCCATATACTAGTTCCCAATAGGCCTGCACAAGTTATTAGAA	45290
Query	17404	CAAGCTGCTTTGCATTCTTGTGTGATCAGAACAGTAACTAGATGGCAATCAGGTCGT	17463
Sbjct	45289	CAAGCTGCTTTGCATTCTTGTGTGATCAGAACAGTAACTAGATGGCAATCAGGTCGT	45230
Query	17464	ACTGAAGATGGAAAACTATACTTAAGTTTGTATAACAATCTTTCATAACATGGCTTCAC	17523
Sbjct	45229	ACTGAAGATGGAAAACTATACTTAAGTTTGTATAACAATCTTTCATAACATGGCTTCAC	45170
Query	17524	AGAAAAGAAGTATAAAAAAGGATTCCCTTGTTGAAAAAGAGTGCTCTTTTCCCTTCATTAT	17583
Sbjct	45169	AGAAAAGAAGTATAAAAAAGGATTCCCTTGTTGAAAAAGAGTGCTCTTTTCCCTTCATTAT	45110
Query	17584	TTAAGATTAGGACAAATTTATAAAACAGGaaaaaaTAGCACAAATCCCTTGGAACACAG	17643
Sbjct	45109	TTAAGATTAGGACAAATTTATAAAACAGGAAAAAATAGCACAAATCCCTTGGAACACAG	45050
Query	17644	AGTAAACATCTACTCTGTTTTGCTttttttCACTTCTTACACTCTCTTTCATAGGAAGT	17703
Sbjct	45049	AGTAAACATCTACTCTGTTTTGCTTTTTTCACTTCTTACACTCTCTTTCATAGGAAGT	44990
Query	17704	CAATTTACAGACTTCCATCAAGCCCTTAGAGACCTTTTGTACTATCCATGACAAGCTCT	17763
Sbjct	44989	CAATTTACAGACTTCCATCAAGCCCTTAGAGACCTTTTGTACTATCCATGACAAGCTCT	44930
Query	17764	TGATGTTATCTCTGCACTTTTGACAAATCTTAGCAGTTAACTTACAAGGCAGTTAAGAT	17823
Sbjct	44929	TGATGTTATCTCTGCACTTTTGACAAATCTTAGCAGTTAACTTACAAGGCAGTTAAGAT	44870
Query	17824	TTTGTTCAGCACAAATATAGCTAGAATAGGCTCATACATTCAATAAAACAAATATTTAC	17883
Sbjct	44869	TTTGTTCAGCACAAATATAGCTAGAATAGGCTCATACATTCAATAAAACAAATATTTAC	44810
Query	17884	CAAGCATTTATTGAGTGGAAGATAAAAGCACAAAGCATAATTATAAAATATTTTCCCT	17943
Sbjct	44809	CAAGCATTTATTGAGTGGAAGATAAAAGCACAAAGCATAATTATAAAATATTTTCCCT	44750
Query	17944	GCCACCATAaaaaaaTTAAACAGGCTTACAGAATACAGTGTAAGAAAACATGACCAAAGC	18003
Sbjct	44749	GCCACCATAAAAAATTTAAACAGGCTTACAGAATACAGTGTAAGAAAACATGACCAAAGC	44690
Query	18004	AAAAATAGTAAGGACTAAAGAAGGGAGGAAGGGGAAATATCAACATGGACTGAATATGAC	18063
Sbjct	44689	AAAAATAGTAAGGACTAAAGAAGGGAGGAAGGGGAAATATCAACATGGACTGAATATGAC	44630
Query	18064	CCAAAAGAGCCTTGATGGATGGTCAGACATGTAAAGGCAAATTTGGTTAGGGTTAAGGGGT	18123
Sbjct	44629	CCAAAAGAGCCTTGATGGATGGTCAGACATGTAAAGGCAAATTTGGTTAGGGTTAAGGGGT	44570
Query	18124	GGAGGTCAGGGCACGTTCTATAGGGAAACGGCAGCTGATACAGAAGCCTGAAAGGAAAAG	18183
Sbjct	44569	GGAGGTCAGGGCACGTTCTATAGGGAAACGGCAGCTGATACAGAAGCCTGAAAGGAAAAG	44510
Query	18184	CGGGCAGAGCACCTGGACAGGCCTCTTCAGGAACGAGCACGCACGTGCGTGAAAAACAAC	18243
Sbjct	44509	CGGGCAGAGCACCTGGACAGGACTCTTCAGGAACGAGCACGCACGTGCGTGAAAAACAAC	44450
Query	18244	TTAGTGAGGTACCGTTCACCCAAACATTAGAGAAACCGCGTAAAAATGCTTCTTGTTAAG	18303
Sbjct	44449	TTAGTGAGGTACCGTTCACCCAAACATTAGAGAAACCGCGTAAAAATGCTTCTTGTTAAG	44390
Query	18304	CATGAAGAAGGCAGGGCTCGCCCTGTAGAAGAACTCAATAAACATTTGAACTGTCTAAAG	18363
Sbjct	44389	CATGAAGAAGGCAGGGCTCGCCCTGTAGAAGAACTCAATAAACATTTGAACTGTCTAAAG	44330
Query	18364	AGTAAAAGTTAATGAATAGGCCAACTCACTCCTTTCTTTGTTTAAAGAGCTACAACTTT	18423
Sbjct	44329	AGTAAAAGTTAATGAATAGGCCAACTCACTCCTTTCTTTGTTTAAAGAGCTACAACTTT	44270
Query	18424	AGAGAATAACAAATCACAACCCAGTAGACAGGTCCTGGCATTTCAAATCCAACCCATT	18483
Sbjct	44269	AGAGAATAACAAATCACAACCCAGTAGACAGGTCCTGGCATTTCAAATCCAACCCATT	44210
Query	18484	TTTCCCTTAATCTTTCCCTCTGAGCAAAATGGTATCGACATGAACAAGCCATGTTGATTT	18543
Sbjct	44209	TTTCCCTTAATCTTTCCCTCTGAGCAAAATGGTATCGACATGAACAAGCCATGTTGATTT	44150
Query	18544	GATCAAGACACTCATCCATGGTTAAAAGAGTCTTTTACCTTCAAGAGATACAAACAGAAAT	18603
Sbjct	44149	GATCAAGACACTCATCCATGGTTAAAAGAGTCTTTTACTTTCAGAGATACAAACAGAAAT	44090
Query	18604	ATTGACA	18610
Sbjct	44089	ATTTACA	44083