

[BLAST®](#) » [blastn suite-2sequences](#) » RID-9MHRDDX3114

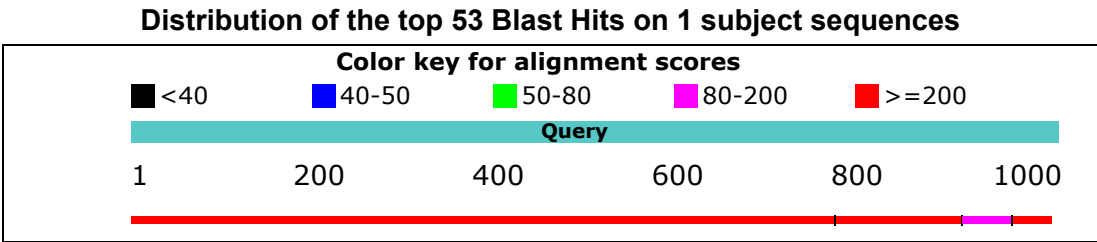
BLAST Results

Blast 2 sequences

Job title: AF137608.1 Sorghum bicolor centromere-associated

<b>RID</b>	<a href="#">9MHRDDX3114</a> (Expires on 02-09 05:15 am)	<b>Subject ID</b>	lcl Query_130561
<b>Query ID</b>	lcl Query_130559	<b>Description</b>	1
<b>Description</b>	AF137608.1 Sorghum bicolor centromere-associated repetitive DNA element CEN38		<a href="#">See details</a>
<b>Molecule type</b>	nucleic acid	<b>Molecule type</b>	nucleic acid
<b>Query Length</b>	1004	<b>Subject Length</b>	73840631
		<b>Program</b>	BLASTN 2.6.1+

Graphic Summary



Dot Matrix View



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
1	816	6302	100%	0.0	81%	Query_130561

Alignments

1  
Sequence ID: Query\_130561 Length: 73840631 Number of Matches: 53  
Range 1: 73443076 to 73443987

Score	Expect	Identities	Gaps	Strand	Frame
816 bits(904)	0.0()	742/917(81%)	16/917(1%)	Plus/Plus	
Features:					
Query 6		AAGCTTCGTTTCGTCCTGTTTGGACATAGTGCTAATCTTTATGCAAGATAGATGCACGGTT			65
Sbjct 73443076		AAGCTTCGTTTCGTCCTGTTTGGAGATAGTGCTAATCTTGATGCAAGATAGGTGTACGGTT			73443135
Query 66		TACGTGGAACATATGATATGCTCAGAAG-CAATTTAGGACGCACCTAATATAACTCCTTG			124
Sbjct 73443136		TGCATGGAACATACCACATTCTCGGAAATCAATTT-GGATGCACCGA-TAGAACTCCTAG			73443193
Query 125		ATGATGTGTGTCACATGGAATCTTGCTTCGGTTTCTTTAGAGACAGTGTTAGTTTGGTA			184
Sbjct 73443194		ATCATGTGTGTCATACGGAATCTTGCTTCAATCTGTTTGGAGATAGTGTAGTTTGGTG			73443253
Query 185		GAAGATATGTGCACAGTGACGCCTAATGCACCATAGGCTAAAGAAACCATTTTAGACGC			244
Sbjct 73443254		CAAGATTGGTGCATGTTTGCGCATAATGCACCATAGGCTCG-GAAACCATTATGGAAGC			73443312
Query 245		ACCCGATGGTACTCGTAGTTGAAGAGGCTCAACTGGAGGCTCGATTTGGTCTGT-TCGGA			303
Sbjct 73443313		ACCCGATAATACTCCTAGGTGAAGAGGCTCAAGTGAAGGTCAATTTCGATCTATGTTGGA			73443372
Query 304		TATAGTGCTAATCTTGATGCAAGATAGTTGCACAATTTGCAGGCAACGTACCATATGTTA			363
Sbjct 73443373		GATAGTGCTAATCTTGATGCAAGATAGGTGCATGGTTTGTATGGAACATACCAAGTGCTA			73443432
Query 364		AGAAATCAATTTGGACGCACCC-AATGGAACCTCTAGATGACGTGTGTCATATGGAA-CT			421
Sbjct 73443433		AGAAATCCATTTGGACGCACCCCAATAGAACTCCTAGATAACATGTGTCATATGGAATCT			73443492
Query 422		CGCTTCGGTCTGTTTGGTGACCATATTAGTTTCACTGCAGGAAAGGTGCATAGTTTGTGC			481
Sbjct 73443493		CACTTTGGTCTGTTTGGAGACAGAGTTAGTTTGGTGCAAGATAGGTACACAGTTTGC GC			73443552
Query 482		CTAATGCACCATAGTCTAAGAAAACCATTTTTGATGCACCTGTTTGTACTTCTATG--AA			539
Sbjct 73443553		CTAATGCATCATAGGCTAAGAAA-CCATTTTGGATGCACCTGATGATACTCTGGGTAA			73443611
Query 540		GAGGCTCAAGTGAAGCTCGGTTTCGGTCT-GTTTGGAGATAGTGCTAATCTTGATGCAAG			598
Sbjct 73443612		GGGGCTCAAGTGAAGCTTAGTTTGCCTTTGTTTGGAGATAGTGGTAATCTTGGTGCAAG			73443671
Query 599		ATAGGTGTACGGTTTGTATGGAACATACCATATGCTTGGAATCAATTTGGATGCACCCG			658
Sbjct 73443672		ATAGGTGCACGAATTGCATGGAACGTGCCATATGCTTCGAAATATATTTGGAAGCACCCA			73443731
Query 659		TTGGAACCTCCTTGA-GAAGTGTGTCTTATGTACCCTCGCTTTGGTCTGTTAGAAATAGT			717
Sbjct 73443732		ATAGAACTCCTAGATGACGTGTGTCATATAGAAATCTCACTTCGGTCTCTCTAGAGATAGT			73443791

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Query 718      GTTAGTTTCAGTGCAAGATATGAGCATGGTTTGC GCCTAACGCACCATAGTCTAAGAAAC 777
Sbjct 73443792 GTTAGTTTGGTGCAAGATAGGTACACAGTTTGTCCCTAATGCACCATAGGCTAAGAAAC 73443851
Query 778      CATTTTGGGAAGCACCTGTTGGTACTTCG--GTGAAGAAGCTCAAGTGAAGCTCGGTTTG 835
Sbjct 73443852 TATTTTGGACGCACACGATGGTACTCTACGTGAAGTGGCTCAAGTGAAGCTCATTTTG 73443911
Query 836      ACCTGTTTGGAGATAGTGCTAATCTTGATGCAAGATA-GTGCATGATTGCAAGGAACAT 894
Sbjct 73443912 CTTTGTTTGGAGATAGTGCTAATCTTGATGCAA-ATAGGTGCACGAATTGCATCGAACGT 73443970
Query 895      ACCATATGCTTAGAAAT 911
Sbjct 73443971 ACCATATGCTTAGAAAT 73443987

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Range 2: 73443070 to 73443808

Score	Expect	Identities	Gaps	Strand	Frame
636 bits(704)	0.0()	594/741(80%)	13/741(1%)	Plus/Plus	

Features:

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Query 275      AACTGGAGGCTCGATTTGGTCTGTTTCGGATATAGTGCTAATCTTGATGCAAGATAGTTGC 334
Sbjct 73443070 AAGTGAAAGCTCGGTTTCGGTCTGTTTGGAGATAGTGCTAATCTTGATGCAAGATAGGTGT 73443129
Query 335      ACAATTTGCAGGCAACGTACCATATGTTAAGAAATCAATTTGGACGCACCCAATGGAAC 394
Sbjct 73443130 ACGGTTTGCATGGAACATACCACATCTCTCGGAAATCAATTTGGATGCACCGA-TAGAACT 73443188
Query 395      CCTAGATGACGTGTGTCTATATGGAA-CTCGCTTCGGTCTGTTTGGTGACCATATTAGTTT 453
Sbjct 73443189 CCTAGATCATGTGTGTCTATACGGAATCTTGCTTCAATCTGTTTGGAGATAGTGTAGTTT 73443248
Query 454      CACTGCAGGAAAGGTGCATAGTTTGTGCCTAATGCACCATAGTCTAAGAAAACCATTTTT 513
Sbjct 73443249 AGGTGCAAGATTGGTGCATGGTTTGGCATAATGCACCATAGGCTCGGAAA-CCATTATG 73443307
Query 514      GATGCACCTGTTTGTACTTCTA--TGAAGAGGCTCAAGTGAAGCTCGGTTTCGGTCTGT- 570
Sbjct 73443308 GAAGCACCCGATAATACTCCTAGGTGAAGAGGCTCAAGTGAAGGTCAATTCGATCTATG 73443367
Query 571      TTGGAGATAGTGCTAATCTTGATGCAAGATAGGTGTACGGTTTGTATGGAACATACCATA 630
Sbjct 73443368 TTGGAGATAGTGCTAATCTTGATGCAAGATAGGTGCATGGTTTGTATGGAACATACCAAG 73443427
Query 631      TGCTTGGAAATCAATTTGGATGCACCCGT-TGGAACCTCCTTGAGAAG-TGTGTCTTATGT 688
Sbjct 73443428 TGCTAAGAAATCCATTTGGACGCACCCCAATAGAACTCCTAGATAACATGTGTCTATGG 73443487
Query 689      ACCCTCGCTTTGGTCTGTTTAGAAATAGTGTTAGTTTCAGTGCAGATATGAGCATGGTT 748
Sbjct 73443488 AATCTCACTTTGGTCTGTTTGGAGACAGAGTTAGTTTGGTGCAAGATAGGTACACAGTT 73443547
Query 749      TGCGCCTAACGCACCATAGTCTAAGAAACCATTTTGGGAAGCACCTGTTGGTACT--TCGG 806
Sbjct 73443548 TGCGCCTAATGCATCATAGGCTAAGAAACCATTTTGGATGCACCTGATGATACTCCTGGG 73443607
Query 807      TGAAGAAGCTCAAGTGAAGCTCGGTTTG-ACCTGTTTGGAGATAGTGCTAATCTTGATG 865
Sbjct 73443608 TAAAGGGGCTCAAGTGAAGCTTAGTTTGTCTTTGTTTGGAGATAGTGGTAATCTTGGTG 73443667
Query 866      CAAGATA-GTGCATGATTTGCAAGGAACATACCATATGCTTAGAAATCAACTTGGACGCA 924
Sbjct 73443668 CAAGATAGGTGCACGAATTGCATGGAACGTGCCATATGCTTCGAAATATATTTGGAAGCA 73443727
Query 925      CGCCCCGCAACTCCTACATCACGTGTGCATATGGAATCTTACTTCGGTC-CATTTGTAA 983
Sbjct 73443728 CCCAATAGAACTCCTAGATGACGTGTGTCTATAGAACTCTCACTTCGGTCTCTCTAGAGA 73443787
Query 984      CATTGTAAGTTTTAGTGCAAG 1004
Sbjct 73443788 TAGTGTTAGTTTTGGTGCAAG 73443808

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Range 3: 73443368 to 73443987

Score	Expect	Identities	Gaps	Strand	Frame
562 bits(622)	4e-159()	506/624(81%)	10/624(1%)	Plus/Plus	

Features:

Query	24	TTGGACATAGTGCTAATCTTTATGCAAGATAGATGCACGGTTTACGTGGAACATATGATA	83
Sbjct	73443368	TTGGAGATAGTGCTAATCTTGATGCAAGATAGGTGCATGGTTTGTATGGAACATACCAAG	73443427
Query	84	TGCTCAGAAG-CAATTTAGGACGCACCT-AATATAACTCCTTGATGATGTGTGTCACATG	141
Sbjct	73443428	TGCTAAGAAATCCATTT-GGACGCACCCCAATAGAACTCCTAGATAACATGTGTCATATG	73443486
Query	142	GAATCTTGCTTCGGTTTCTTTAGAGACAGTGTAGTTTTGGTAGAAGATATGTGCACAGT	201
Sbjct	73443487	GAATCTCACTTTGGTCTGTTTGGAGACAGAGTTAGTTTTGGTGCAAGATAGGTACACAGT	73443546
Query	202	GTACGCCTAATGCACCATAGGCTAAAGAAACCATTTTAGACGCACCCGATGGTACTCGTA	261
Sbjct	73443547	TTGCGCCTAATGCATCATAGGCTAA-GAAACCATTTTGATGCACCTGATGATACTCCTG	73443605
Query	262	GTTGAAGAGGCTCAACTGGAGGCTCGATTTGGTCT-GTTCGGATATAGTGCTAATCTTGA	320
Sbjct	73443606	GGTAAAGGGGCTCAAGTGGAAGCTTAGTTTGCCTTTGTTTGGAGATAGTGGAATCTTGG	73443665
Query	321	TGCAAGATAGTTGCACAATTTGCAGGCAACGTACCATATGTTAAGAAATCAATTTGGACG	380
Sbjct	73443666	TGCAAGATAGGTGCACGAATTGCATGGAACGTGCCATATGCTTCGAAATATATTTGGAAG	73443725
Query	381	CACCCAATGGAACCTCTAGATGACGTGTGTCATATGGAA-CTCGCTTCGGTCTGTTTGGT	439
Sbjct	73443726	CACCCAATAGAACTCCTAGATGACGTGTGTCATATAGAATCTCACTTCGGTCTCTCTAGA	73443785
Query	440	GACCATATTAGTTTCACTGCAGGAAAGGTGCATAGTTTGTGCCTAATGCACCATAGTCTA	499
Sbjct	73443786	GATAGTGTTAGTTTTGTGCAAGATAGGTACACAGTTTGTCCCTAATGCACCATAGGCTA	73443845
Query	500	AGAAAACCATTTTTGATGCACCTGTTTGTACTTCTA--TGAAGAGGCTCAAGTGGAAGCT	557
Sbjct	73443846	AG-AAACTATTTTGGACGCACACGATGGTACTCCTACGTGAAGTGGCTCAAGTGGAAGCT	73443904
Query	558	CGGTTTCGGTCTGTTTGGAGATAGTGCTAATCTTGATGCAAGATAGGTGTACGGTTTGTAT	617
Sbjct	73443905	CATTTTGCCTTTGTTTGGAGATAGTGCTAATCTTGATGCAA-ATAGGTGCACGAATTGCAT	73443963
Query	618	GGAACATACCATATGCTTGGAAT	641
Sbjct	73443964	CGAACGTACCATATGCTTAGAAAT	73443987

Range 4: 73443070 to 73443533

Score	Expect	Identities	Gaps	Strand	Frame
468 bits(518)	7e-131()	388/465(83%)	8/465(1%)	Plus/Plus	
Features:					
Query	547	AAGTGGAAGCTCGGTTTCGGTCTGTTTGGAGATAGTGCTAATCTTGATGCAAGATAGGTGT			606
Sbjct	73443070	AAGTGAAAGCTCGGTTTCGGTCTGTTTGGAGATAGTGCTAATCTTGATGCAAGATAGGTGT			73443129
Query	607	ACGGTTTGTATGGAACATACCATATGCTTGGAAATCAATTTGGATGCACCCGTTGGAAC			666
Sbjct	73443130	ACGGTTTGCATGGAACATACCACATTCGCGAAATCAATTTGGATGCA-CCGATAGAACT			73443188
Query	667	CCTTGA-GAAGTGTGTCTTATGTACCCTCGCTTTGGTCTGTTTAGAAATAGTGTTAGTTT			725
Sbjct	73443189	CCTAGATCATGTGTGTCATACGGAATCTTGCTTCAATCTGTTTGGAGATAGTGTTAGTTT			73443248
Query	726	CAGTGCAAGATATGAGCATGGTTTGCGCCTAACGCACCATAGTCTAAGAAACCATTTTGG			785
Sbjct	73443249	AGGTGCAAGATTGGTGCATGGTTTGCGCATAATGCACCATAGGCTCGGAAACCATTATGG			73443308
Query	786	AAGCACCTGTTGGTACT--TCGGTGAAGAAGCTCAAGTGGAAGCTCGGTTTGACCTGT-T			842
Sbjct	73443309	AAGCACCCGATAATACTCCTAGGTGAAGAGGCTCAAGTGGAAGGTCAATTCGATCTATGT			73443368
Query	843	TGGAGATAGTGCTAATCTTGATGCAAGATA-GTGCATGATTTGCAAGGAACATACCATAT			901
Sbjct	73443369	TGGAGATAGTGCTAATCTTGATGCAAGATAGGTGCATGGTTTGTATGGAACATACCAAGT			73443428
Query	902	GCTTAGAAATCAACTTGGACGCACGCC-CCGCAACTCCTACATCACGTGTGTCATATGGA			960
Sbjct	73443429	GCTAAGAAATCCATTTGGACGCACCCCAATAGAACTCCTAGATAACATGTGTCATATGGA			73443488
Query	961	ATCTTACTTTCGGTCCATTTGTA-ACATTGTAAGTTTTAGTGCAAG		1004	
Sbjct	73443489	ATCTCACTTTGGTCTGTTTGGAGACAGAGTTAGTTTGGTGCAAG		73443533	

Range 5: 73443625 to 73443987

Score	Expect	Identities	Gaps	Strand	Frame
336 bits(372)	3e-91()	296/365(81%)	3/365(0%)	Plus/Plus	
Features:					
Query 6	AAGCTTCGTTT-CGTCTGTTTGGACATAGTGCTAATCTTTATGCAAGATAGATGCACGGT	64			
Sbjct 73443625	AAGCTTAGTTTGGCTTTTGTGGAGATAGTGGTAATCTTGGTGCAAGATAGGTGCACGAA	73443684			
Query 65	TTACGTGGAACATATGATATGCTCAGAAGCAATTTAGGACGCACCTAATATAACTCCTTG	124			
Sbjct 73443685	TTGCATGGAACGTGCCATATGCTTCGAAATATATTTGGAAGCACCAATAGAACTCCTAG	73443744			
Query 125	ATGATGTGTGTCACATGGAATCTTGCTTCGGTTTCTTTAGAGACAGTGTAGTTTGGTA	184			
Sbjct 73443745	ATGACGTGTGTCATATAGAATCTCACTTCGGTCTCTCTAGAGATAGTGTAGTTTGGTG	73443804			
Query 185	GAAGATATGTGCACAGTGTACGCCTAATGCACCATAGGCTAAAGAAACCATTTTAGACGC	244			
Sbjct 73443805	CAAGATAGGTACACAGTTTGTCCCTAATGCACCATAGGCT-AAGAACTATTTTGGACGC	73443863			
Query 245	ACCCGATGGTACTCGTAGTTGAAGAGGCTCAACTGGAGGCTCGATTGGTCTGTTTCGGAT	304			
Sbjct 73443864	ACACGATGGTACTCCTACGTGAAGTGGCTCAAGTGAAGCTCATTTGCTTTGTTGGAG	73443923			
Query 305	ATAGTGCTAATCTTGATGCAAGATAGTTGCACAATTTGCAGGCAACGTACCATATGTTAA	364			
Sbjct 73443924	ATAGTGCTAATCTTGATGCAA-ATAGGTGCACGAATTGCATCGAACGTACCATATGCTTA	73443982			
Query 365	GAAAT 369				
Sbjct 73443983	GAAAT 73443987				

Range 6: 73443207 to 73443986

Score	Expect	Identities	Gaps	Strand	Frame
206 bits(228)	4e-52()	524/785(67%)	14/785(1%)	Plus/Plus	
Features:					
Query 1	TACGTAAGCTTCGTTTCGTCTGTTTGGACATAGTGCTAATCTTTATGCAAGATAGATGCA	60			
Sbjct 73443207	TACGGAATCTTGCTTCAATCTGTTTGGAGATAGTGTTAGTTTAGGTGCAAGATTGGTGCA	73443266			
Query 61	CGGTTTACGTGGAACATATGATATGCTCAGAAGCAATTTAGGACGCACCTAATATAACTC	120			
Sbjct 73443267	TGGTTTGGCATAATGCACCATAGGCTCGGAAACCATTATGGAAGCACCCGATAATACTC	73443326			
Query 121	CTTGATGATGTGTGTCACATGGAATCTTGCTTCGGTTTCT-TTAGAGACAGTGTAGTTT	179			
Sbjct 73443327	CTAGGTGAAGAGGCTCAAGTGAAGTCAATTCGATCTATGTTGGAGATAGTGCTAATCT	73443386			
Query 180	TGGTAGAAGATATGTGCACAGT--GTACGCCTAATGCACCATAGGCTAAAGAAACCATTT	237			
Sbjct 73443387	TGATGCAAGATAGGTGCATGGTTTGTATGGAACAT--ACCAAGTGCTAAGAAATCCATTT	73443444			
Query 238	TAGACGCACCCGA-TGGTACTCGTAGTTGAAGAGGCTCAACTGGAGGCTCGATTGGTCT	296			
Sbjct 73443445	G-GACGCACCCCAATAGAACTCCTAGATAACATGTGTCATATGGAATCTCACTTTGGTCT	73443503			
Query 297	GTTTCGGATATAGTGCTAATCTTGATGCAAGATAGTTGCACAATTTGCAGGCAACGTACCA	356			
Sbjct 73443504	GTTTGGAGACAGAGTTAGTTTTGGTGCAAGATAGGTACACAGTTTGCGCCTAATGCATCA	73443563			
Query 357	TATGTTAAGAAATCAATTTGGACGCACCCAATGGAACCTCTAGATGACGTGTGTCATATG	416			
Sbjct 73443564	TAGGCTAAGAAACCATTTTGGATGCACCTGATGATACTCCTGGGTAAAGGGGCTCAAGTG	73443623			
Query 417	GAA--CTCGCTTCGGTCTGTTTGGTGACCATATTAGTTTCACTGCAGGAAAGGTGCATAG	474			
Sbjct 73443624	GAAGCTTAGTTTGTCTTTGTTTGGAGATAGTGGTAATCTTGGTGCAAGATAGGTGCACGA	73443683			
Query 475	TTTGTGCCAATGCACCATAGTCTAAGAAAACCATTTTGTATGCACCTGTTGTACTTCT	534			
Sbjct 73443684	ATTGCATGGAACGTGCCATATGCTTCGAAATATA-TTGGAAGCACCAATAGAACTCCT	73443742			
Query 535	--ATGAAGAGGCTCAAGTGAAGCTCGGTTTCGGTCTGTTTGGAGATAGTGCTAATCTTGA	592			
Sbjct 73443743	AGATGACGTGTGTCATATAGAATCTCACTTCGGTCTCTCTAGAGATAGTGTAGTTTGG	73443802			
Query 593	TGCAAGATAGGTGTACGGTTTGTATGGAACATACCATATGCTTGGAAATCAATTTGGATG	652			
Sbjct 73443803	TGCAAGATAGGTACACAGTTTGTCCCTAATGCACCATAGGCTAAGAACTATTTTGGACC	73443862			

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Query 653      CACCCGTTGGAACCTCT-TGAGAAAGTGTGTCTTATGTACCCTCGCTTTGGTCTGTTTAGA 711
Sbjct 73443863 CACACGATGGTACTCCTACGTGAAGTGGCTCAAGTGGAAGCTCATTTTGCCTTTGTTTGGA 73443922
Query 712      AATAGTGTAGTTTTCAGTGCAAGATATGAGCATGGTTTGCGCCCTAACGCACCATAGTCTA 771
Sbjct 73443923 GATAGTGTCTAATCTTGATGCAA-ATAGGTGCACGAATTGCATCGAACGTACCATATGCTT 73443981
Query 772      AGAAA 776
Sbjct 73443982 AGAAA 73443986

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Range 7: 65386100 to 65386280

Score	Expect	Identities	Gaps	Strand	Frame
188 bits(208)	1e-46()	154/184(84%)	5/184(2%)	Plus/Minus	

Features:

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Query 467      GTGCATAGTTTGTGCCTAATGCACCATAGTCTAAGAAAACCATTTTGGATGCACCTGTTT 526
Sbjct 65386280 GTGCACGGTTTGGCGATAATGCACCATAGGCTTAGAAA-CCATTGTTGAAGCATCCGATG 65386222
Query 527      GTACTTCTA--TGAAGAGGCTCAAGTGGAAGCTCGGTTCCGGTCTGTTTGGAGATAGTGCT 584
Sbjct 65386221 ATACTCCTAGGTGAAGAGACTCAAGTGGAAGCTCGGTTCCGGTGTGTTTGGAGATAGTGCT 65386162
Query 585      AATCTTGTATGCAAGATAGGTGTACGGTTTGTATGGAACATACCATATGCTTGGAAATCAA 644
Sbjct 65386161 AATCTTGA--CCCTATAGGTGCACGGTTTGCACGGAACGTACCATATGCTCGAAAATCAA 65386104
Query 645      TTTG 648
Sbjct 65386103 TTTG 65386100

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Range 8: 73443073 to 73443904

Score	Expect	Identities	Gaps	Strand	Frame
187 bits(206)	4e-46()	554/836(66%)	15/836(1%)	Plus/Plus	

Features:

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Query 140      TGGAATCTTGCTTCGGTTTCTTTAGAGACAGTGTAGTTTTGGTAGAAGATATGTGCACA 199
Sbjct 73443073 TGAAAGCTCGGTTTCGGTCTGTTTGGAGATAGTGCTAATCTTGATGCAAGATAGGTGTACG 73443132
Query 200      GTGTACGCCAATGCACCATAGGCTAAAGAAACCATTTTAGACGCACCCGATGGTACTCG 259
Sbjct 73443133 GTTTGCATGGAACATACCACATTCCTCG-GAAATCAATTTGGATGCACC-GATAGAATCC 73443190
Query 260      TAGTTGAAGAGGCTCAACTGGAGGCTCGATTTGGTCTGTTTCGGATATAGTGCTAATCTTG 319
Sbjct 73443191 TAGATCATGTGTGTCATACGGAATCTTGCTTCAATCTGTTTGGAGATAGTGTTAGTTTAC 73443250
Query 320      ATGCAAGATAGTTGCACAATTTGCAGGCAACGTACCATATGTTAAGAAATCAATTTGGAC 379
Sbjct 73443251 GTGCAAGATTGGTGCATGGTTTGGCGATAATGCACCATAGGCTCGGAAACCATATGGAA 73443310
Query 380      GCACCCAATGGAACCTCTAGATGACGTGTGTCATATGGAAC-TCGCTTCGGTCTGT-TTG 437
Sbjct 73443311 GCACCCGATAATACTCCTAGGTGAAGAGGCTCAAGTGGAAGGTCAATTCGATCTATGTTG 73443370
Query 438      GTGACCATATTAGTTTCACTGCAGGAAAGGTGCATAGTTTGTGCCTAATGCACCATAGT- 496
Sbjct 73443371 GAGATAGTGCTAATCTTGATGCAAGATAGGTGCATGGTTTGTATGGAACATACCA-AGTG 73443429
Query 497      CTAAGAAAACCATTTTGTATGCACCTGTTT-GTACTTCTATG-AAGAGGC-TCAAGTGA 553
Sbjct 73443430 CTAAGAAATCCATTTG-GACGCACCCCAATAGAACTCCTAGATAACATGTGTCTATGGA 73443488
Query 554      AGCTCGGTTTCGGTCTGTTTGGAGATAGTGCTAATCTTGATGCAAGATAGGTGTACGGTTT 613
Sbjct 73443489 ATCTCACTTTGGTCTGTTTGGAGACAGAGTTAGTTTGGTGCAGATAGGTACACAGTTT 73443548
Query 614      GTATGGAACATACCATATGCTTGGAAATCAATTTGGATGCACCCGTTGGAACCTCT-TGA 672
Sbjct 73443549 GCGCCTAATGCATCATAGGCTAAGAAACCATTTTGGATGCACCTGATGATACTCCTGGGT 73443608
Query 673      GAAGTGTGTCTTATGTACCCTCGCTTTG-GTCTGTTTAGAAATAGTGTAGTTTTCAGTGC 731
Sbjct 73443609 AAAGGGGCTCAAGTGGAAGCTTAGTTTGCTTTTGTGTTGGAGATAGTGGTAATCTTGGTGC 73443668

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Query 732      AAGATATGAGCATGGTTTGC GCCTAACGCACCATAGTCTAAGAAACCATTTTGAAGCAC 791
Sbjct 73443669 AAGATAGTGCACGAATTGCATGGAACGTGCCATATGCTTCGAAATATATTTGAAGCAC 73443728
Query 792      CTGTTGGTACT--TCGGTGAAGAAGCTCAAGTGAAGCTCGGTTTGACCTGTTTGAGAT 849
Sbjct 73443729  CCAATAGAACTCCTAGATGACGTGTGTCATATAGAATCTCACTTCGGTCTCTCTAGAGAT 73443788
Query 850      AGTGCTAATCTTGATGCAAGATA-GTGCATGATTTGCAAGGAACATACCATATGCTTAGA 908
Sbjct 73443789  AGTGTTAGTTTTTGGTGCAGATAGGTACACAGTTTGTCCCTAATGCACCATAGGCTAAGA 73443848
Query 909      AATCAACTTGGACGCACGCCCCGCAACTCCTACATCACGTGTGTCATATGGAATCT 964
Sbjct 73443849  AACTATTTTGGACGCACACGATGGTACTCTACGTGAAGTGGCTCAAGTGAAGCT 73443904

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Range 9: 65386096 to 65386289

Score	Expect	Identities	Gaps	Strand	Frame
174 bits(192)	2e-42()	157/195(81%)	3/195(1%)	Plus/Minus	

Features:

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Query 730      GCAAGATATGAGCATGGTTTGC GCCTAACGCACCATAGTCTAAGAAACCATTTTGAAGC 789
Sbjct 65386289  GCAAGATTAGTGCACGGTTTGC GCATAATGCACCATAGGCTTAGAAACCATTTGTTGAAGC 65386230
Query 790      ACCTGTTGGTACTTC--GGTGAAGAAGCTCAAGTGAAGCTCGGTTTGACCTGTTTGAG 847
Sbjct 65386229  ATCCGATGATACTCCTAGGTGAAGAGACTCAAGTGAAGCTCGGTTTCGGTGTGTTTGAG 65386170
Query 848      ATAGTGCTAATCTTGATGCAAGATAGTGCATGATTTGCAAGGAACATACCATATGCTTAG 907
Sbjct 65386169  ATAGTGCTAATCTTGACCTATA-GGTGCACGGTTTGCACGGAACGTACCATATGCTCGA 65386111
Query 908      AAATCAACTTGGACG 922
Sbjct 65386110  AAATCAATTTGCACG 65386096

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Range 10: 65386096 to 65386287

Score	Expect	Identities	Gaps	Strand	Frame
174 bits(192)	2e-42()	157/195(81%)	3/195(1%)	Plus/Minus	

Features:

```

Query 186      AAGATATGTGCACAGTGTACGCCTAATGCACCATAGGCTAAAGAAACCATTTTAGACGCA 245
Sbjct 65386287  AAGATTAGTGCACGGTTTGC GCATAATGCACCATAGGCTTA-GAAACCATTTGTTGAAGCA 65386229
Query 246      CCCGATGGTACTCGTAGTTGAAGAGGCTCAACTGGAGGCTCGATTTGGTCTGTTCCGATA 305
Sbjct 65386228  TCCGATGATACTCCTAGGTGAAGAGACTCAAGTGAAGCTCGGTTTCGGTGTGTTTGAGAG 65386169
Query 306      TAGTGCTAATCTTGATGCAAGATAGTTGCACAAATTTGCAGGCAACGTACCATATGTTAAG 365
Sbjct 65386168  TAGTGCTAATCTTGA--CCCTATAGGTGCACGGTTTGCACGGAACGTACCATATGCTCGA 65386111
Query 366      AAATCAATTTGGACG 380
Sbjct 65386110  AAATCAATTTGCACG 65386096

```

Range 11: 73443070 to 73443257

Score	Expect	Identities	Gaps	Strand	Frame
168 bits(186)	1e-40()	153/189(81%)	3/189(1%)	Plus/Plus	

Features:

```

Query 818      AAGTGGAAGCTCGGTTTGACCTGTTTGGAGATAGTGCTAATCTTGATGCAAGATA-GTGC 876
Sbjct 73443070  AAGTGAAAGCTCGGTTTCGGTCTGTTTGGAGATAGTGCTAATCTTGATGCAAGATAGGTGT 73443129
Query 877      ATGATTTGCAAGGAACATACCATATGCTTAGAAATCAACTTGGACGCACGCCCCGCAACT 936
Sbjct 73443130  ACGGTTTGCATGGAACATACCACATCTCGGAAATCAATTTGGATGCAC-CGATAGAACT 73443188

```

```

Query 937      CCTACATCACGTGTGTCATATGGAATCTTACTTCGGTCCATTTGTA-ACATTGTAAGTTT 995
Sbjct 73443189 CCTAGATCATGTGTGTCATACGGAATCTTGCTTCAATCTGTTTGGAGATAGTGTAGTTT 73443248
Query 996      TAGTGCAAG 1004
Sbjct 73443249 AGGTGCAAG 73443257

```

Range 12: 73443496 to 73443924

Score	Expect	Identities	Gaps	Strand	Frame
163 bits(180)	4e-39()	299/432(69%)	7/432(1%)	Plus/Plus	
Features:					
Query 14	TTTCGTCTGTTTGGACATAGTGCTAATCTTTATGCAAGATAGATGCACGGTTTACGTGGA	73			
Sbjct 73443496	TTTGGTCTGTTTGGAGACAGAGTTAGTTTGGTGCAAGATAGGTACACAGTTTGCGCCTA	73443555			
Query 74	ACATATGATATGCTCAGAAGCAATTTAGGACGCACCTAATATAACTCCTTGATGATGTGT	133			
Sbjct 73443556	ATGCATCATAGGCTAAGAAACCATTTTGGATGCACCTGATGATACTCCTGGGTAAAGGGG	73443615			
Query 134	GTCACATGGAATCTTGCTTCGGTTTC-TTTAGAGACAGTGTAGTTTGGTAGAAGATAT	192			
Sbjct 73443616	CTCAAGTGAAGCTTAGTTTGCTTTTGGTGGAGATAGTGGTAATCTTGGTGCAAGATAG	73443675			
Query 193	GTGCAC--AGTGACGCCAATGCACCATAGGCTAAAGAAACCATTTTAGACGCACCCGA	250			
Sbjct 73443676	GTGCACGAATTGCATGG--AACGTGCCATATGCTTC-GAAATATATTTGGAAGCACCCAA	73443732			
Query 251	TGGTACTCGTAGTTGAAGAGGCTCAACTGGAGGCTCGATTGGTCTGTTTCGGATATAGTG	310			
Sbjct 73443733	TAGAACTCTAGATGACGTGTGTCATATAGAATCTCACTTCGGTCTCTCTAGAGATAGTG	73443792			
Query 311	CTAATCTTGATGCAAGATAGTTGCACAATTTGCAGGCAACGTACCATATGTTAAGAAATC	370			
Sbjct 73443793	TTAGTTTTGGTGCAAGATAGGTACACAGTTTGCCCTAATGCACCATAGGCTAAGAACT	73443852			
Query 371	AATTTGGACGCACCCCAATGGAACCTCTAGATGACGTGTGTCATATGGAA-CTCGCTTCGG	429			
Sbjct 73443853	ATTTTGGACGCACACGATGGTACTCCTACGTGAAGTGGCTCAAGTGAAGCTCATTTTGC	73443912			
Query 430	TCTGTTTGGTGA 441				
Sbjct 73443913	TTTGTTTGGAGA 73443924				

Range 13: 73443079 to 73443590

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	7e-30()	347/515(67%)	12/515(2%)	Plus/Plus	
Features:					
Query 420	CTCGCTTCGGTCTGTTTGGTGACCATATTAGTTTCACTGCAGGAAAGGTGCATAGTTTGT	479			
Sbjct 73443079	CTCGGTTTCGGTCTGTTTGGAGATAGTGCTAATCTTGATGCAAGATAGGTGTACGGTTTGC	73443138			
Query 480	GCCTAATGCACCATAGTCTAAGAAAACCATTTTTGATGCACCTGTTTGTACTTCTA--TG	537			
Sbjct 73443139	ATGGAACATACCACATCTCGGAAATCAATTTG-GATGCACC-GATAGAACTCCTAGATC	73443196			
Query 538	AAGAGGCTCAAGTGAAGCTCGGTTTCGGTCTGTTTGGAGATAGTGCTAATCTTGATGCAA	597			
Sbjct 73443197	ATGTGTGTCATACGGAATCTTGCTTCAATCTGTTTGGAGATAGTGTAGTTTAGGTGCAA	73443256			
Query 598	GATAGGTGTACGGTTTGTATGGAACATACCATATGCTTGGAAATCAATTTGGATGCACCC	657			
Sbjct 73443257	GATTGGTGCATGGTTTGCGCATAATGCACCATAGGCTCGGAAACCATTATGGAAGCACCC	73443316			
Query 658	GTTGGAATCCTTGA-GAAGTGTGCTTATGTACCCTCGCTTTGGTCTGT-TTAGAAATA	715			
Sbjct 73443317	GATAATACCTTAGGTGAAGAGGCTCAAGTGAAGGTCAATTCGATCTATGTTGGAGATA	73443376			
Query 716	GTGTTAGTTTCAGTGCAAGATATGAGCATGGTTTGCGCCTAACGCACCATAGT-CTAAGA	774			
Sbjct 73443377	GTGCTAATCTTGATGCAAGATAGGTGCATGGTTTGTATGGAACATACCA-AGTGCTAAGA	73443435			
Query 775	AACCATTTTGAAGCACCTGT-TGGTACTTCG-GTGAAGAAGC-TCAAGTGAAGCTCGG	831			
Sbjct 73443436	AATCATTTTGGACGCACCCCAATAGAACTCCTAGATAACATGTGTCATATGGAATCTCAC	73443495			



```

Query   832      TTTGACCTGTTTGGAGATAGTGCTAATCTTGATGCAAGATA-GTGCATGATTGCAAGGA 890
Sbjct   73443496 TTTGGTCTGTTTGGAGACAGAGTTAGTTTGGTGCAAGATAGGTACACAGTTTGC GCCTA 73443555
Query   891      ACATACCATATGCTTAGAAATCAACTTGGACGCAC 925
Sbjct   73443556 ATGCATCATAGGCTAAGAAACCATTTTGGATGCAC 73443590

```

Range 14: 71676829 to 71677010

Score	Expect	Identities	Gaps	Strand	Frame
114 bits(126)	2e-24()	138/185(75%)	6/185(3%)	Plus/Minus	

Features:

```

Query   714      TAGTGTTAGTTTCAGTGCAAGATATGAGCATGGTTTGC GCCTAACGCACCATAGTCTAAG 773
Sbjct   71677010 TAGTGTTAATCTCGATGCAAGATAGGTGCATGGTTTGTGCCAAACATACCATAGGCTCAG 71676951
Query   774      AAACCATTTTGGAAGCACCTGTTGGTACTTC--GGTGAAGAAGCTCAAGTGGAAGCTCGG 831
Sbjct   71676950 AAATCATTTTGGGTGCACTCGATGGTAATCCTAGGTGACGTGGGTCAAGTGGAAGCTCGT 71676891
Query   832      TTTGACCTGTTTGGAGATAGTGCTAATCTTGATGCAAGATA-GTGCATGATTGCAAGGA 890
Sbjct   71676890 GTTGCTCCATTTGGACACTG---TTATCTCGGTGCAAGATAGGTGCACGGTTTGCATCGA 71676834
Query   891      ACATA 895
Sbjct   71676833 ACGTA 71676829

```

Range 15: 71676831 to 71677010

Score	Expect	Identities	Gaps	Strand	Frame
109 bits(120)	8e-23()	136/183(74%)	4/183(2%)	Plus/Minus	

Features:

```

Query   578      TAGTGCTAATCTTGATGCAAGATAGGTGTACGGTTTGTATGGAACATACCATATGCTTGG 637
Sbjct   71677010 TAGTGTTAATCTCGATGCAAGATAGGTGCATGGTTTGTGCCAAACATACCATAGGCTCAG 71676951
Query   638      AAATCAATTTGGATGCACCCGTTGGAACCTCT-TGAGAAGTGTGTCTTATGTACCCTCGC 696
Sbjct   71676950 AAATCATTTTGGGTGCACTCGATGGTAATCCTAGGTGACGTGGGTCAAGTGGAAGCTCGT 71676891
Query   697      TTTGGTCTGTTTAGAAATAGTGTTAGTTTTCAGTGCAAGATATGAGCATGGTTTGC GCCTA 756
Sbjct   71676890 GTTGCTCCATTTGG--ACACTGTTA-TCTCGGTGCAAGATAGGTGCACGGTTTGCATCGA 71676834
Query   757      ACG 759
Sbjct   71676833 ACG 71676831

```

Range 16: 71676829 to 71676995

Score	Expect	Identities	Gaps	Strand	Frame
107 bits(118)	3e-22()	128/171(75%)	6/171(3%)	Plus/Minus	

Features:

```

Query   457      TGCAGGAAAGGTGCATAGTTTGTGCCTAATGCACCATAGTCTAAGAAAACCATTTTGTAT 516
Sbjct   71676995 TGCAAGATAGGTGCATGGTTTGTGCCAAACATACCATAGGCTCAGAAATC-ATTTTGGGT 71676937
Query   517      GCACCTGTTTGTACTTCTA--TGAAGAGGCTCAAGTGGAAGCTCGGTTTCGTCTGTTTGG 574
Sbjct   71676936 GCACTCGATGGTAATCCTAGGTGACGTGGGTCAAGTGGAAGCTCGTGTGCTCCATTTGG 71676877
Query   575      AGATAGTGCTAATCTTGATGCAAGATAGGTGTACGGTTTGTATGGAACATA 625
Sbjct   71676876 ACACGTGT---ATCTCGGTGCAAGATAGGTGCACGGTTTGCATCGAACGTA 71676829

```

Range 17: 71676840 to 71677010

Score	Expect	Identities	Gaps	Strand	Frame
96.9 bits(106)	5e-19()	128/174(74%)	4/174(2%)	Plus/Minus	
Features:					
Query 306		TAGTGTCTAATCTTGATGCAAGATAGTTGCACAATTTGCAGGCAACGTACCATATGTTAAG			365
Sbjct 71677010		TAGTGTCTAATCTCGATGCAAGATAGGTGCATGGTTTGTGCCAAACATACCATAGGCTCAG			71676951
Query 366		AAATCAATTTGGACGCACCCAATGGAACCTCTAGATGACGTGTGTTCATATGGAA-CTCGC			424
Sbjct 71676950		AAATCATTTTGGGTGCACTCGATGGTAATCCTAGGTGACGTGGGTCAAGTGGAAGCTCGT			71676891
Query 425		TTCGGTCTGTTTGGTGACCATATTAGTTTCTACTGCAGGAAAGGTGCATAGTTTG			478
Sbjct 71676890		GTTGCTCCATTG--GACACTGTTA-TCTCGGTGCAAGATAGGTGCACGGTTTG			71676840

Range 18: 57571359 to 57571509

Score	Expect	Identities	Gaps	Strand	Frame
89.7 bits(98)	7e-17()	114/153(75%)	3/153(1%)	Plus/Minus	
Features:					
Query 233		CATTTTGTAGACGCACCCGATGGTACTCGTAGTTGAAGAGGCTCAACTGGAGGCTCGATTTG			292
Sbjct 57571509		CATTTTGGACACATCTGATGATACTCTTAGGTGATGAGGCTCAAGTGTAAGCTTCGTTTA			57571450
Query 293		GTCTGTTTCGGATATAGTGCTAATCTTGATGCAAGATAGTTGCACAATTTGCAGGC-AACG			351
Sbjct 57571449		GTCCGGTTAAAGATATTGCTAATCTTGACACAAGATACATACAC-GTTTG-AGCCAAACG			57571392
Query 352		TACCATATGTTAAGAAATCAATTTGGACGCACC		384	
Sbjct 57571391		TACCATAGACTTAGAAATTATTTAGGACGCACC		57571359	

Range 19: 73443079 to 73443314

Score	Expect	Identities	Gaps	Strand	Frame
89.7 bits(98)	7e-17()	164/237(69%)	4/237(1%)	Plus/Plus	
Features:					
Query 692		CTCGCTTTGGTCTGTTTAGAAATAGTGTTAGTTTCAGTGCAAGATATGAGCATGGTTTGC			751
Sbjct 73443079		CTCGGTTTCGGTCTGTTTGGAGATAGTGCTAATCTTGATGCAAGATAGGTGTACGGTTTGC			73443138
Query 752		GCCTAACGCACCATAGTCTAAGAAACCATTTTGGAAAGCACCTGTTGGTACTTC--GGTGA			809
Sbjct 73443139		ATGGAACATACCACATTCTCGGAAATCAATTTGGATGCACC-GATAGAATCCTTAGATCA			73443197
Query 810		AGAAGCTCAAGTGAAGCTCGGTTTGACCTGTTTGGAGATAGTGCTAATCTTGATGCAAG			869
Sbjct 73443198		TGTGTGTCATACGGAATCTTGCTTCAATCTGTTTGGAGATAGTGTTAGTTTAGGTGCAAG			73443257
Query 870		A-TAGTGCATGATTGCAAGGAACATACCATATGCTTAGAAATCAACTGGACGCAC			925
Sbjct 73443258		ATTGGTGCATGGTTTGCGCATAATGCACCATAGGCTCGGAAACCATATGGAAGCAC			73443314

Range 20: 57571360 to 57571509

Score	Expect	Identities	Gaps	Strand	Frame
82.4 bits(90)	1e-14()	111/151(74%)	4/151(2%)	Plus/Minus	
Features:					
Query 778		CATTTTGGGAAGCACCTGTTGGTACT--TCGGTGAAGAAGCTCAAGTGAAGCTCGGTTTG			835
Sbjct 57571509		CATTTTGGACACATCTGATGATACTCTTAGGTGATGAGGCTCAAGTGTAAGCTTCGTTTA			57571450
Query 836		ACCTGTTTGGAGATAGTGCTAATCTTGATGCAAGATA-GTGCATGATTGCAAGGAACAT			894
Sbjct 57571449		GTCCGGTTAAAGATATTGCTAATCTTGACACAAGATACATACACG-TTTGAGCCAAACGT			57571391

Query 895 ACCATATGCTTAGAAATCAACTTGGACGCAC 925  
 Sbjct 57571390 ACCATAGACTTAGAAATTATTTAGGACGCAC 57571360

Range 21: 57571359 to 57571509

Score	Expect	Identities	Gaps	Strand	Frame
78.8 bits(86)	1e-13()	110/152(72%)	3/152(1%)	Plus/Minus	

Features:

Query 507 CATTTTTGATGCACCTGTTTGTACTTCTA--TGAAGAGGCTCAAGTGGAAGCTCGGTTTCG 564  
 Sbjct 57571509 CATTTTGGACACATCTGATGATACTCTTAGGTGATGAGGCTCAAGTGTAAGCTTCGTTTA 57571450  
 Query 565 GTCTGTTTGGAGATAGTGCTAATCTTGATGCAAGATAGGTGTACGGTTTGTATGGAACAT 624  
 Sbjct 57571449 GTCCGGTTAAAGATATTGCTAATCTTGACACAAGATACATACAC-GTTTGAGCCAAACGT 57571391  
 Query 625 ACCATATGCTTGGAAATCAATTTGGATGCACC 656  
 Sbjct 57571390 ACCATAGACTTAGAAATTATTTAGGACGCACC 57571359

Range 22: 71676878 to 71677010

Score	Expect	Identities	Gaps	Strand	Frame
78.8 bits(86)	1e-13()	98/133(74%)	1/133(0%)	Plus/Minus	

Features:

Query 849 TAGTGCTAATCTTGATGCAAGATAG-TGCATGATTTGCAAGGAACATACCATATGCTTAG 907  
 Sbjct 71677010 TAGTGTTAATCTCGATGCAAGATAGGTGCATGGTTTGTGCCAAACATACCATAGGCTCAG 71676951  
 Query 908 AAATCAACTTGGACGCACGCCCCGCAACTCCTACATCACGTGTGTCATATGGAATCTTAC 967  
 Sbjct 71676950 AAATCATTTTGGGTGCACTCGATGGTAATCCTAGGTGACGTGGGTCAAGTGGAAGCTCGT 71676891  
 Query 968 TTCGGTCCATTTG 980  
 Sbjct 71676890 GTTGCTCCATTTG 71676878

Range 23: 71676843 to 71677010

Score	Expect	Identities	Gaps	Strand	Frame
68.0 bits(74)	2e-10()	119/171(70%)	3/171(1%)	Plus/Minus	

Features:

Query 31 TAGTGCTAATCTTTATGCAAGATAGATGCACGGTTTACGTGGAACATATGATATGCTCAG 90  
 Sbjct 71677010 TAGTGTTAATCTCGATGCAAGATAGGTGCATGGTTTGTGCCAAACATACCATAGGCTCAG 71676951  
 Query 91 AAGCAATTTAGGACGCACCTAATATAACTCCTTGATGATGTGTGTCACATGGAATCTTGC 150  
 Sbjct 71676950 AAATCATTTTGGGTGCACTCGATGGTAATCCTAGGTGACGTGGGTCAAGTGGAAGCTCGT 71676891  
 Query 151 TTCGGTTTCTTTAGAGACAGTGTTAGTTTGGTAGAAGATATGTGCACAGT 201  
 Sbjct 71676890 GTTGCTCCATTT--GGACACTGTTA-TCTCGGTGCAAGATAGGTGCACGGT 71676843

Range 24: 73443915 to 73443985

Score	Expect	Identities	Gaps	Strand	Frame
68.0 bits(74)	2e-10()	59/72(82%)	1/72(1%)	Plus/Plus	

Features:

Query 21 TGTTTGGACATAGTGCTAATCTTTATGCAAGATAGATGCACGGTTTACGTGGAACATATG 80  
 Sbjct 73443915 TGTTTGGAGATAGTGCTAATCTTGATGCAA-ATAGGTGCACGAATTGCATCGAACGTACC 73443973

Query 81 ATATGCTCAGAA 92  
 Sbjct 73443974 ATATGCTTAGAA 73443985

Range 25: 57571359 to 57571463

Score	Expect	Identities	Gaps	Strand	Frame
66.2 bits(72)	8e-10()	79/106(75%)	1/106(0%)	Plus/Minus	

Features:

Query 4 GTAAGCTTCGTTTCGTTCTGTTTGGACATAGTGCTAATCTTTATGCAAGATAGATGCACGG 63  
 Sbjct 57571463 GTAAGCTTCGTTTAGTCCGGTTAAAGATATTGCTAATCTTGACACAAGATACATACAC-G 57571405  
 Query 64 TTTACGTGGAACATATGATATGCTCAGAAGCAATTTAGGACGCACC 109  
 Sbjct 57571404 TTTGAGCCAAACGTACCATAGACTTAGAAATTATTTAGGACGCACC 57571359

Range 26: 65386101 to 65386193

Score	Expect	Identities	Gaps	Strand	Frame
66.2 bits(72)	8e-10()	73/95(77%)	3/95(3%)	Plus/Minus	

Features:

Query 6 AAGCTTCGTTTCGTTCTGTTTGGACATAGTGCTAATCTTTATGCAAGATAGATGCACGGTT 65  
 Sbjct 65386193 AAGCTTCGTTTCGTTGTTTGGAGATAGTGCTAATCTTGA--CCCTATAGGTGCACGGTT 65386136  
 Query 66 TACGTGGAACATATGATATGCTC-AGAAGCAATTT 99  
 Sbjct 65386135 TGCACGGAACGTACCATATGCTCGAAAATCAATTT 65386101

Range 27: 65386058 to 65386096

Score	Expect	Identities	Gaps	Strand	Frame
53.6 bits(58)	5e-06()	35/39(90%)	0/39(0%)	Plus/Minus	

Features:

Query 618 GGAACATACCATATGCTTGGAATCAATTTGGATGCACC 656  
 Sbjct 65386096 GGAACGTACCATATGCTTGAAAATCAATTTGGACGTACC 65386058

Range 28: 65386059 to 65386096

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	8e-04()	33/38(87%)	0/38(0%)	Plus/Minus	

Features:

Query 888 GGAACATACCATATGCTTAGAAATCAACTTGGACGCAC 925  
 Sbjct 65386096 GGAACGTACCATATGCTTGAAAATCAATTTGGACGTAC 65386059

Range 29: 65386058 to 65386094

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	0.003()	32/37(86%)	0/37(0%)	Plus/Minus	

Features:

Query 348 AACGTACCATATGTTAAGAAATCAATTTGGACGCACC 384  
 Sbjct 65386094 AACGTACCATATGCTTGAAAATCAATTTGGACGTACC 65386058

Range 30: 25355018 to 25355037

Score	Expect	Identities	Gaps	Strand	Frame
37.4 bits(40)	0.41()	20/20(100%)	0/20(0%)	Plus/Minus	

Features:

Query 541 AGGCTCAAGTGAAGCTCGG 560  
 Sbjct 25355037 AGGCTCAAGTGAAGCTCGG 25355018

Range 31: 70572832 to 70572961

Score	Expect	Identities	Gaps	Strand	Frame
37.4 bits(40)	0.41()	87/130(67%)	10/130(7%)	Plus/Minus	

Features:

Query 618 GGAACATACCATATGCTTGGAAATCAATTTGGATGCACCCG-TTGGAACTCCT---TGAG 673  
 Sbjct 70572961 GGAACATACCATTTGCCCTCAGAAATTATTTTGGATATACCCGATAAAAACCTTATATGAC 70572902  
 Query 674 AAGTGT-----GTCTTATGTACCCTCGCTTTGGTCTGTTTAGAAATAGTGTAGTTTCA 727  
 Sbjct 70572901 ATGGGTCATTAGGTCACGTGGAATCTCATTTTCGATTCGTTTGAAATTAGTGTAGTGTCTG 70572842  
 Query 728 GTGCAAGATA 737  
 Sbjct 70572841 GTGCAAGATA 70572832

Range 32: 23363484 to 23363511

Score	Expect	Identities	Gaps	Strand	Frame
35.6 bits(38)	1.4()	26/29(90%)	1/29(3%)	Plus/Plus	

Features:

Query 801 CTTTCGGTGAAGAAGCTCAAGTGAAGCTC 829  
 Sbjct 23363484 CTACGGTGAA-AAGCTCAAGTGGAGGCTC 23363511

Range 33: 23368839 to 23368866

Score	Expect	Identities	Gaps	Strand	Frame
35.6 bits(38)	1.4()	26/29(90%)	1/29(3%)	Plus/Plus	

Features:

Query 801 CTTTCGGTGAAGAAGCTCAAGTGAAGCTC 829  
 Sbjct 23368839 CTACGGTGAA-AAGCTCAAGTGGAGGCTC 23368866

Range 34: 43991314 to 43991332

Score	Expect	Identities	Gaps	Strand	Frame
35.6 bits(38)	1.4()	19/19(100%)	0/19(0%)	Plus/Minus	

Features:

Query 351 GTACCATATGTTAAGAAAT 369  
 Sbjct 43991332 GTACCATATGTTAAGAAAT 43991314

Range 35: 62079580 to 62079598

Score	Expect	Identities	Gaps	Strand	Frame
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35.6 bits(38) 1.4() 19/19(100%) 0/19(0%) Plus/Plus

Features:

```

Query   949      GTGTCATATGGAATCTTAC  967
Sbjct   62079580  GTGTCATATGGAATCTTAC  62079598

```

Range 36: 4646505 to 4646522

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	18/18(100%)	0/18(0%)	Plus/Minus	

Features:

```

Query   806      GTGAAGAAGCTCAAGTGG  823
Sbjct   4646522  GTGAAGAAGCTCAAGTGG  4646505

```

Range 37: 22573145 to 22573162

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	18/18(100%)	0/18(0%)	Plus/Plus	

Features:

```

Query   806      GTGAAGAAGCTCAAGTGG  823
Sbjct   22573145  GTGAAGAAGCTCAAGTGG  22573162

```

Range 38: 23753021 to 23753038

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	18/18(100%)	0/18(0%)	Plus/Plus	

Features:

```

Query   806      GTGAAGAAGCTCAAGTGG  823
Sbjct   23753021  GTGAAGAAGCTCAAGTGG  23753038

```

Range 39: 24152927 to 24152947

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	20/21(95%)	0/21(0%)	Plus/Minus	

Features:

```

Query   878      TGATTTGCAAGGAACATACCA  898
Sbjct   24152947  TGATTTACAAGGAACATACCA  24152927

```

Range 40: 25355018 to 25355035

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	18/18(100%)	0/18(0%)	Plus/Minus	

Features:

```

Query   814      GCTCAAGTGAAGCTCGG  831
Sbjct   25355035  GCTCAAGTGAAGCTCGG  25355018

```

Range 41: 28652706 to 28652736

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	26/31(84%)	0/31(0%)	Plus/Minus	

Features:

Query 702 TCTGTTTAGAAATAGTGTTAGTTTCAGTGCA 732  
 Sbjct 28652736 TCGGTTTAGATATATTATTAGTTTCAGTTCA 28652706

Range 42: 41415655 to 41415672

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	18/18(100%)	0/18(0%)	Plus/Minus	

Features:

Query 806 GTGAAGAAGCTCAAGTGG 823  
 Sbjct 41415672 GTGAAGAAGCTCAAGTGG 41415655

Range 43: 42273339 to 42273359

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	20/21(95%)	0/21(0%)	Plus/Plus	

Features:

Query 878 TGATTTGCAAGGAACATACCA 898  
 Sbjct 42273339 TGATTTACAAGGAACATACCA 42273359

Range 44: 43198439 to 43198469

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	26/31(84%)	0/31(0%)	Plus/Minus	

Features:

Query 852 TGCTAATCTTGATGCAAGATAGTGCATGATT 882  
 Sbjct 43198469 TGCCAATCAAGATGCAATAGAGTGCATGATT 43198439

Range 45: 44215902 to 44215926

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	23/25(92%)	1/25(4%)	Plus/Minus	

Features:

Query 260 TAGTTGAAGAGGCTCAACT-GGAGG 283  
 Sbjct 44215926 TAGTTGAAGAGGCTAAACTAGGAGG 44215902

Range 46: 44334150 to 44334175

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	23/26(88%)	0/26(0%)	Plus/Plus	

Features:

Query 261 AGTTGAAGAGGCTCAACTGGAGGCTC 286  
 Sbjct 44334150 AGATGAAGAAGCTCAACTGGAGGGTC 44334175

Range 47: 44464365 to 44464382

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	18/18(100%)	0/18(0%)	Plus/Plus	

Features:

```

Query   807      TGAAGAAGCTCAAGTGG      824
Sbjct   44464365 TGAAGAAGCTCAAGTGG      44464382

```

Range 48: 46610918 to 46610938

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	20/21(95%)	0/21(0%)	Plus/Plus	

Features:

```

Query   878      TGATTTGCAAGGAACATACCA 898
Sbjct   46610918 TGATTTACAAGGAACATACCA 46610938

```

Range 49: 47603373 to 47603403

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	26/31(84%)	0/31(0%)	Plus/Plus	

Features:

```

Query   544      CTCAAGTGAAGCTCGGTTCGGTCTGTTTGG 574
Sbjct   47603373 CTCAAGTGAAGCTCTTCCGTTCTCTTTGG 47603403

```

Range 50: 49804276 to 49804300

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	23/25(92%)	1/25(4%)	Plus/Plus	

Features:

```

Query   704      TGTTTA-GAAATAGTGTAGTTTCA 727
Sbjct   49804276 TGTTTATGAAATATTGTAGTTTCA 49804300

```

Range 51: 50647241 to 50647268

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	24/28(86%)	0/28(0%)	Plus/Plus	

Features:

```

Query   360      GTTAAGAAATCAATTTGGACGCACCCAA 387
Sbjct   50647241 GTTAACACATCAATTTGGATGCACCTAA 50647268

```

Range 52: 58059644 to 58059672

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	26/30(87%)	1/30(3%)	Plus/Minus	

Features:

```

Query   47      GCAAGATAGATGCACGGTTTACGTGGAACA 76
Sbjct   58059672 GCTAGATAGATGCATGGTTTA-GTGGAGCA 58059644

```



Range 53: 71467301 to 71467332

Score	Expect	Identities	Gaps	Strand	Frame
33.7 bits(36)	5.0()	28/33(85%)	1/33(3%)	Plus/Minus	
Features:					
Query	28	ACATAGTGCTAATCTTTATGCAAGATAGATGCA		60	
Sbjct	71467332	ACATAGTGCTAATTTTTA-GCAAGTTGGATCCA		71467301	

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