

A. Typical examples of highly conserved introns in domesticated genes of placental mammals

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>gb|AAGU03047692.1| Loxodonta africana cont3.47691, whole genome shotgun sequence
Length=17341
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Score = 527 bits (584), Expect = 6e-147
Identities = 546/717 (76%), Gaps = 55/717 (7%)
Strand=Plus/Plus

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>gb|ABRP01216211.1| Pteropus vampyrus cont1.216210, whole genome shotgun sequence
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Length=5874

Score = 765 bits (848), Expect = 0.0
Identities = 581/685 (84%), Gaps = 19/685 (2%)
Strand=Plus/Minus

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Query 1 ATTTACACATTTCCCTCCTCAGCAATGGGTACACAGACAGCCAAGCTCCTGGACTAAGTC 60
      ||| ||||| ||||| ||||| ||| ||| ||||| ||| ||||| ||||| |||
Sbjct 3056 ATTCACACACTTCCCTCCTCAGCGATGAGTACGCAGACAGCCGATCTCCTGGACTAAGTC 2997

Query 61 TCTGAATGGTAACGTACATTTATAAAGATTATTTTCTTAACTATTTTGAGGTATTTTATA 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Sbjct 2996 TCTGAATGGTAATGTACATTTATAAAGATTATTCTCTTAACTATTTTGAGCCATTTTATA 2937

Query 121 AATAATATGCATGTGTCTTCTGAGGGCcatatatatatatatatatatatatTTAGTCGAC 180
      ||||| || ||||| ||||| ||| | ||| ||| ||||| ||||| |||
Sbjct 2936 AATAAAATACATGTGTCTGCTG-----TGCACATATACACATATATATTTAGTCAAC 2885

Query 181 TTTTGCTTGTTTTCTCCTGAGGCTGGTCTTGTTGTTACTTATGTGGTATGATTTCTGA 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Sbjct 2884 TTTTGCTTGTTTTCTTCTGAGGCTGGTCTTGTTGTTATTTATGTGGTCTGATTTCTGA 2825

Query 241 GGTGTCAGAAAGAGCTCCCTCCTACTTCTACCACCCTAGTCACCCAAAAATATCTCTTG 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Sbjct 2824 GGTGTCAGAAAGAGCTCCCCCTACCTCCT---ACCCAGCCACCCAAAAATATCTTTTA 2768

Query 301 GGCTGGCCCACCGCAGAGCCTAAATTTCCACATTGCTCAAACATTTGATTTAGTCACTG 360
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Sbjct 2767 GACTGGCCCACCCAGAGCCTAAATGCCCCACATTGCTCAAACATTTGAGTTAGTCATTG 2708

Query 361 AAAGCAGCTGTTAAAAATCCAAATGTTACATTGGGATATTAGGCAGATATTCAAGATTAAA 420
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Sbjct 2707 AAAGCAGCTGTTAAAAATCCAAGTGTACATTGAGATATTAGGCAGACA---GAAATTAAA 2651

Query 421 GACTATATAAAACAGAAAATAATATTA AAAAGTTGCTTTTGATATAATGTTAAGTTTCAA 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Sbjct 2650 GACTATGTAAAAACAGAAAAAATATGGAGAAATTGCTTCTAATATAATGTTAAGTTTCAA 2591

Query 481 AGGATAAATGCAAAATGACATGTGCAGTTTGGGACAGATGCTGTTCTTAAATGTCGTGG 540
      | || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Sbjct 2590 AAGAAGAATGCAAAATTACATACACAGTCTGGGTCAGATGATGTTCAAAAATGTCATGG 2531

Query 541 AGTCAGATCCAGCATATATACCCAGCTCATGAACATAAGCCTATGGTAAAAGAAACCCA 600
      ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Sbjct 2530 AGTGAGAGCCAGCATATATGACCCAACTCATGAATATGACCCTATAGTAAGAGAAATCCA 2471

Query 601 GCATTGTTGGGCAGATTTTGT-----TTTATGTTGAATGTGTGCTTTCACAGTTTCTGA 655
      ||| | ||||| || || ||| ||||| ||||| ||||| ||||| ||||| |||
Sbjct 2470 GCACTATTGGGTAGGTTCTGTTCTTATTTATTTTGAATGAGTGCTTCTACTGTTTCTGA 2411

Query 656 TCCTCAGCTCCCACTCTCTTCGCAG 680
      ||||| | ||||| ||||| |||
Sbjct 2410 TCCTCAGATTCCACTCTCTTCACAG 2386
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b) Query was intron 3 (located in the CDS) of the Homo RGAG1 gene

>gb|AAGU03056054.1| *Loxodonta africana* cont3.56053, whole genome shotgun sequence
Length=37961

Score = 529 bits (586), Expect = 2e-147
Identities = 496/621 (79%), Gaps = 20/621 (3%)
Strand=Plus/Minus

Query	111	TAGAATTGGGAAGAGGCAAGGGGAGGCATGGAGCTCCTAGACCATTAACCCCA----G	166
Sbjct	21276	TAGAATAAGGAAGGGGCAATGGGAGGCGTTGAGGTCCCAGACTAT-AAACCCACACTG	21218
Query	167	CAGTTTCATCAAGTGAGCATGGCTCTGCAGTTATTTGGGTATATTAACACTTTGAGGA	226
Sbjct	21217	GAGTTTCATCA-GTGATCACGGCTACACAGTTATTTGGGTGTATTAACCATTTGAGGG	21159
Query	227	GCAATGTCCTGCCCAAGTTACTGAGAACGTGGGATAGTTGAAGTACTAATCTTCTCATT	286
Sbjct	21158	GCAATGCCCTGCCCAAATTACTTTAGGAGTGGGATGGTTAAAGAACTAAATCTG---ATT	21102
Query	287	ATGAGGGAAGTGGATGGGCTCAGTTCCAATTCTCCCTTGTTCCAAGTCCAATTCTAATA	346
Sbjct	21101	ATGAGGGAATTGGCTGGGCTCAGCCCGAGTTCTCCACTTATTCCAAGTTCAGTTCTAAGG	21042
Query	347	AATGGGTCTT----TTGGGAGCTGGGGCCCATCTACAGCA-ACATG-TGTTGTGGAGTCA	400
Sbjct	21041	AAGCAGTATTCATTTTGGGAGGTGGGTCCCACTTATAGCCCATATGGTGTATGGAATCA	20982
Query	401	GGTCACTAGGGAATTAGAATAGCCTACTCCTTGGTCACACTGTATGCAAGTGA-GATAAA	459
Sbjct	20981	GGTCATTAGGGAATTGGTTAGCCCGAGCCTTTGGTCTCCCTTTGTACAAGTTAAGATAAA	20922
Query	460	TTAGCAAAGTGTCTTGATCTGCTAAGTCACAGAAGTTATCCAGGCAGAACACCCGTTGCC	519
Sbjct	20921	TTAGCCAAGTTCCTTGATCTGCTAATTG-CTGAATTTATTCAGGCAGAACACCTCTTGTC	20863
Query	520	ATAGTAAGTGTGGCTCTTACCTCTGTTGTCTTTTCTCACTCCCAGCACCAGCATGTTTC	579
Sbjct	20862	ACAGTAAGTGTGGTTTTTACTGCTGCTGTGTTTTTCTTTCTACTAGCACCAGCATGTTCC	20803
Query	580	CAAACGCTGTTACTACCTGAAAGAGCATGGAGACCCCCAAGAAGGTCTTCATGATCACCT	639
Sbjct	20802	CAAACGCTGTTACTACCTGAAAGAGCATGGAGACCCCCAAGAAGGTCTTCACGATCACCT	20743
Query	640	TGGACAGAGCACAGGCCATCATCAGAAGGCCCATACCAACAAGTAAACTCCATGGAATC	699
Sbjct	20742	TCGACAGAGCACAGGC---CATCCGAAGGCCCCCACTGACAAGTAATGCTCAATGGATTC	20686
Query	700	TTCTCCTGTGATATCTGACTC	720
Sbjct	20685	TTCTCCTGTGGTATCCGACTC	20665

c) Q was intron 1 (26 kb long) of the Homo RGAG1 gene

>gb|AAGU03056056.1| *Loxodonta africana* cont3.56055, whole genome shotgun sequence
Length=18534

sequence by: Sort alignments for this subject

position	E value	Score	Percent identity	Query start position	Subject start
Score = 2078 bits (2304), Expect = 0.0 Identities = 1755/2136 (82%), Gaps = 67/2136 (3%) Strand=Plus/Minus					
Query 685		aaatttaacaaaagaaataaaaaagcataaaaaGCTAAGTTTTTATTGGGTATTTACTATG	744		
Sbjct 13794		AAATCAAACAAAAAGAATAAAACGCCCTAAGAGGTTAACTTTTTACTGAGTGCTTACTATG	13735		
Query 745		TGCCAGGAAGTGTCTAAGTGTTCACACAGATTATCTCATTTAATCCTCATCATAACCC	804		
Sbjct 13734		TGCCAAGAACTGTCTAAGTGTTCACACTGATTATCTCATTTAATTTTCATAATGGCCC	13675		
Query 805		AATGACGTCAACTCTATTATTAGTCCATTTAACAGATGAAGGAATTGAGGCTCTGGGAT	864		
Sbjct 13674		AATGATGTAGATTCTATTTTATAGTCCATTTATAGATGAGGGAATTGAGGCTCTGAGAT	13615		
Query 865		GTTAAGAAAAGTGCCCAAGGTCACACAGCTAGCAAGAGACAGAACCAAAAGTTGAAGTCA	924		
Sbjct 13614		GTGAAGCAAGGGTCCCAAGATCACCCAGCTTGTGGGAGGCAGAACCAAAAGTTGAACCCA	13555		
Query 925		AGGCAGTCTGAGTCCA-AGTCCACAACTAAATCATCTATGCCAC-CTGCAGCCCCACC	982		
Sbjct 13554		AGGCAGTCTGAGTCCCTAGTCCATGCAATACATCACGGATGCCTCTCTGCAG-----ACA	13500		
Query 983		TCATGTTACCTTACACCTCCCACGCCACCCCGAGGCACGATTCTACTACAGCACTGGCCA	1042		
Sbjct 13499		GGATGCTTCCTTGACGCCCT--GGCACACCTTGCCAGAAT-----ACTCATCA	13452		
Query 1043		CATTGCAGAACAGGGGTTTGTCTTACTTG--TCTGTCCTTCTACTAGACGAGGAGCTTCT	1100		
Sbjct 13451		CATTGTAGTACAGGGGTTTGTCTTACTCTCATCTGTCCTTCCCACTAGACTGAGAGCCTCT	13392		
Query 1101		CAAGTGCAGAGACTGGATCTTATTCATTTTGTCTTCCCCTGTGCCTGGAAGAGAGCTTGT	1160		
Sbjct 13391		AAAGTGTAGGGACC--ATCTT---CATTTTGTCTTCCCCTGCG--TAGAGTAGAGCTTGT	13339		
Query 1161		TCTGGAATAGCTAACCAAGGAATATTCTGTTGAATGAGCAAATGAGTGAGGGAGTAAGTGA	1220		
Sbjct 13338		TCCAGAGTA-CGGACCGATCAATATTTGTGACTGAATGAATGAATGAG-----TGA	13288		
Query 1221		ATCCATATTCCTTAATATTTTCAGGCTTCAGGCTTATGGGCTCATGTGTATTTCCCTGGT	1280		
Sbjct 13287		ATCCATGTTCCTTTTCTTTTAGGCTTCAAGCTTATGGGCTCGTGTTCATTTCCCTGGT	13228		
Query 1281		CAA-----GCATAGCACTGGGCACAAGGGTATCTGGTGCAAGAGGTGCCTCTCACCA	1333		
Sbjct 13227		TTATATTAACGTGTAGCACTGGGGACAAGGGTGTGCTGGTGCAAGAGATCCCTTGACCA	13168		
Query 1334		CAGGGTACAAGAAGGACTAGCTCTGGCTGGGTAAACCAAGCAGTGTTCACAGAGCAAG	1393		
Sbjct 13167		TGGGGTAAAAAGAGGACCAGCTCTGACTGGTAAACCAAGCAATGTTCTATAGAGCAAG	13108		
Query 1394		GGGCTTGATCCAGAAGGTTTCATTTTGTTCATCGGTCTAAAAAGTAGCTGGACCTGTTTAG	1453		
Sbjct 13107		GCGCTTGATTCAAAGGGTTTCATTTTGTGCTCGGTTTAGAAAGTAGCTGGACCTGTTTAG	13048		
Query 1454		GACTTAAACAACTTTTCAGTGTTCATCCATCTCAAATCCTTTGCAGAATGAGGCAGG	1513		
Sbjct 13047		GACTTAAACAACTTTCAATGTTCAAATCCATCTCAAATCCTTCTCAGAATGAGGCGGG	12988		
Query 1514		GTGTGGGGAG-GTGG--TGGTGGGGCAGTTATAAATAAACAAATACCCACAAACCGGCTG	1570		
Sbjct 12987		TTGTGGGGGAGAGGCAAGAGGAGGGAGTTATAAATAAACAAATACCCACAAACCGGCTG	12928		
Query 1571		GTTTTTTTAAACAGAATTTGCTTCAGTCAGTGCTGCACCACATTTTCCCACTGGCCTCCG	1630		

Sbjct	12927	GT TTT TTT AAACAGAATTTACCTCAATCAGCGCTGCGCTACATCTTCCCAACTGGCCTCTG	12868
Query	1631	TCGTGAGAACAAAGTGGGAAC TTT CATACTGAATGGCTTTA--TTTTTATTCTGACCAGA	1687
Sbjct	12867	TCATGAGAACAAAGTGGGAACGTT CATACTGAATGGCTTTATTTT TTTT TCCGACCAGA	12808
Query	1688	TGAATGGCAGGAGTTT TGGCTCGGAGGCAGGTTCCGATCCTCAGCACACAGTTTGCTG	1747
Sbjct	12807	TGAATGGCAGGAGTTT TGGCTCGAGAGGCAGGTTCAAATCCTTGACACACAGTTTGCTG	12748
Query	1748	CCCTACTGTGCCCCGTCCATCACACACAGCGCCCTGCACAACATACCCAGTCATTGCATC	1807
Sbjct	12747	CCCTACTGTGCCCCATCCGTCACACACAGTGCATGCACAACATACCCAGTCATCACATC	12688
Query	1808	TACTGCCTCAGCCCTTGAAAAATAATTGGGTCATTGTTTTATTACACCAGCGAGAGAGCTG	1867
Sbjct	12687	TGCTGCTTCAGTCC-TCAAAAAAACTGGGTCATTGTTTTATTACACCAGCGAGAGAGCTG	12629
Query	1868	CAAGCCTGTTAGGATTATGTCATTGATATTTGCGTGAAAAGGCAATCATGATATGCTGGT	1927
Sbjct	12628	CAAGCCTGTCTACGATTATGTCATTGACATTTGCGTGAAAAGGCAATCATGATATGCTGGT	12569
Query	1928	CATTTAACACAGCTGGGAATGCAACTGTGTTGTCATTGTTTAAGGTTCTCATCC-AGCCC	1986
Sbjct	12568	CATTTAACACAGCTGGGAATGCAACTGTGTTGTCATTGTTCAAGGTTCTCATCCAAACTC	12509
Query	1987	CTCTGACTTTTTTGCACAGCCCAGCCCGTGAAAATGGATCACTCTGATGTATGTCACCTT	2046
Sbjct	12508	TTCTGACTTCGTTTTCCAGCCCAACCAGTGTAAGTGGATCGCTCTGATGTATGTAACTT	12449
Query	2047	T-AAAATGCTTTCTAG-CCCTTCAAGGGACCAAGCAGGATTTAACTCTTTTCATGCACTT	2104
Sbjct	12448	TGAAAGTGTTTTTTAGCCCTTCAAAAGACCAAGCAGGATCTACCTCTTTCCATGCACTT	12389
Query	2105	GGACTTTGCTGCTTGTAGGCACAGCAGTCTGAAGGTGAGAGATGCTTGCTTTTCATACTT	2164
Sbjct	12388	GGACTT---TGCTTGTAGGCACAGCCGTCTGAAGGTGAGAGATGCTTGC-TTTCATGCGT	12333
Query	2165	GTGGGAGTTGTACACCCTAGTGGCAGGATGCTGCCATACAGTGTCAATTTGTTCACTAACT	2224
Sbjct	12332	GTGGGAGTTGTACACCCTAGTGGCAGGATGCTGCAATACAGTGTCAATTTGTTCACTAAGT	12273
Query	2225	GCTGATCAGAGCCAAGGACAATTTTGGCTCAAGAACAAATGAGACCTAA---TGTCTGTG	2281
Sbjct	12272	GCTAATCAGAGCCAAGGACAGTTTTGGCTCAAAAACAAATGAGGGCTAATGTTGTCTGTG	12213
Query	2282	AGGGAAGACTATGTAGATAAGTCACGGGTCAGAGTTGTGTTGCGACTTGTATTGTGTGCT	2341
Sbjct	12212	GGGGAAGATTATTTAGACAATTTCATGAATCAGAATCTGTTGCGACTTCTATTGTGTGTT	12153
Query	2342	AGTTTCAGTAGGACTTGTGCTTTTCATTGCAATTGTCAGTATGCTTAAGCAGGGGTCTCTG	2401
Sbjct	12152	AGTTTAAGTAGGACTTGCCTTGGATTGCAGTTGTCAGTGTGCTTATGCAGGGGTCTCTG	12093
Query	2402	CTAATGAAATTCGAGCATATTTGCATTTATCGACAGGTATTACTGATGGTAGAACATCTT	2461
Sbjct	12092	CTAATGAAATTCAGCATATTTGCATTTATCAACAGGTGTTAATGTTGGGAGAAAAGCTT	12033
Query	2462	ATTTCCACACAAGGCAATGAGTAACATTGATTATAGAAGGTAAACAAAGCTCAAATTCA	2521
Sbjct	12032	ATTTTCAAACAAGGAAATGATTAGCGTTGGCTATAGAA-TATAACGGAGCTCAAAGTCA	11974
Query	2522	TGTGCCAATTTGTCTATTTCAACTCATCGATCCTCTTCTTCC-ACTGGCATGCTAGCCTG	2580
Sbjct	11973	TGTGCTAATTTTTCTGTTGCAACTCTTC--TCTTCTCTACCGGCAGGCACGTTAGCTGG	11916
Query	2581	AGTTTTATGGCATAAGGCCATTAAAGTATTCTTCAAAGGAATCTGTTGCAGACACCTGTT	2640
Sbjct	11915	AGTTTTATGGCATGTGACCATTAATTTATTCTTCGAAGGAATCTATTGCAGGCACCTGGC	11856
Query	2641	CATCCCTCTTCTGGTCCCGGTCCTTGCCAAACCAGCTC--TGCCTTTGCCAACCACCTTG	2698
Sbjct	11855	CATCCATTTTCTAGTCCCAGTCCCCTGGCAAACCAGCTCTGTGCCCTTGCCAGCCACCTTG	11796
Query	2699	AGGTGTGACAGGAAAAGCTGACCCAATAAGGGAGTCAACTGAAGGGATGGAGTGGCTTAG	2758
Sbjct	11795	AGGTGTGACAGGGAGAGTTGGCCCAATAAAGGAGTCAGCTGAAGAGATGGTCTGGGGTAG	11736

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Query    2759    ATGCAAATGGCCAAATCCCAATGGCCATGGCTATAA    2794
          ||||  ||      |||  |||||  |||  |||||  |||
Sbjct   11735    ATGCCAACCTCCAAGTCCCAATCGCCCTGGCTATAA    11700

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Query	11174	TACTAACATTTATTGAGCAATGATTATGTGTCAGGTATCATTTCTAAGTGCTTTGTGTGTA Sbjct	4733	TACTAACATTTATTGAACATTTACTATGTGCCAGGTACCATTCTAAGTACTTTGTGTGTA	4674
Query	11234	TTAACTCATTTAATTCTCACTATGATGTGTGAGGTAGGTTACTATTATTATCTTCACAT Sbjct	4673	TTAATTCACTTTAATTCTCAGTATACTTCA-TGAGGTAGGT-ACCATTATTGTCCCAATTT	4616
Query	11294	TACAGAGGAGGCACCAGACTCAGACAGGCTGAATAACTTGGCCAAGGTCACATAGCTAGT Sbjct	4615	TAGAGAGGTGGCACAGGCTCAGACAGGCTAAGTAACTTGGCCAAGGTCACACAGCTAAT	4556
Query	11354	GAATGGCGGAACACAGATATGAACCCAGGCACCTAGAGACACATCTACTTACCACCTTG Sbjct	4555	AAATGGTAGAACTTGGATATGAACCTAGGCAACCTGGAGCCACATTTAACTGCCATCCTG	4496
Query	11414	TATTGGAGAAGAGGTCAACAGTAGTGACAGAAGCAATAGAGTGGAATTTTCAGTACTGC Sbjct	4495	TATTGAAGAAGAGAGCAACAGTAGTGACAGCAGCAATTGAGTGGACAATTTTCAGTATTAC	4436
Query	11474	CAAAA---CTATGAGAGCCATATAGTCCACACCAGGCATGAAAAGGAAGCTGGCATGGTC Sbjct	4435	CGAAGGGGCGACGAGAGCCACACAGGCCACACCAGGCATGGGAAGGGACTTGGCATGATC	4376
Query	11531	TTGTGTTGTCACTTAACCTTGTATATAGGGTTTTTCATTTCCT--AACTAGAGAAGGAGG Sbjct	4375	TTATATTGGTAGTTAACCTTGTATGTAGTTTTTT--TTTCCTCCAAATAGAATAGGAGC	4318
Query	11589	AGTTTGAAAGCACGAACCATGAATTACAGCTCTTTGAAATGCTCAACATAGATTTGCTGA Sbjct	4317	AGTTTGAAAGTAGGAACCATAGATTACAGCTCTTTGAAACGCTCAATATAGATTTGCTGA	4258
Query	11649	GTGAATAAATGACTGTTTTGAAATTAACACAGGAGTGCTTTGAATAAATTACTTTGCAT Sbjct	4257	GTGAATAAATGAGTCTTTTGAATTAACACATGAGTACTTTGAGTAAGTTACTTCACAT	4198
Query	11709	CTTGATGTCAAACCTGAAATTGGTGAGACATCTTT-CACCTTGTGTTAAAACTAAAAAT Sbjct	4197	CTTGTTGTGTCAAATTGAAATTGGTGACAAAGCTTTTCACTTTGTTTTAAACCTGAAGAC	4138
Query	11768	CCCTAGATGTGGTCATAACATGGCTGGTTATAATGACACCTTGCATTTGTA CT TGTGTAT Sbjct	4137	ACCTAGATATGGCCATAACATGTCTGGGTATGATGACACCTTGCCTTTGTACCAGTGTAT	4078
Query	11828	GATACTCAGGACTCCCTGAGAAAAGGAATGAAGAACTTGGATTTTGCCTTCATAGGCC Sbjct	4077	GG-----GAATAGGACAGAAGAAAGTTAGATTCTGCCTTCATAGGCC	4035
Query	11888	TGAGGCTGT CAGGAACCAAGGGCCACTGTGTTTGAATCCATTCTTTGGCTGCTCTCCA Sbjct	4034	TGGGGCTGT CAGGAACCTAAGGTC ACTAGGTTTGAATCCATTCTTTGGCCTTATGTCCA	3975
Query	11948	AATCTAGGAAGACCTGGAGGAAAGGGGGCTTTATTTTCT---ATCTTTGCCAAGATCAG Sbjct	3974	AATCTAGGAGGACCTAGAGAAAAGGAGGACTTCATTGCTCTTATCCTTGCCAAACT-AG	3916
Query	12005	GAAATAATTG----TGAACCTCAGT---AA--ACATTCTGGGGGCCTTCCCTCTAACA Sbjct	3915	GATCGAATTGAGTGTGGACTCTCTGTTGGAATGAAATCCTAGT----TTCTATCTATCT	3860
Query	12056	CTG-----CTTTGG-----TGGAATAATATCTCCAGTTTTACCA-----ATCTTG--GT Sbjct	3859	GTGGATATCATTGAGACACCTCCAAAAACATACCTGAAATTACCTTTAGATCCTGAAGT	3800
Query	12099	TCAATATTTACCTGGGGGTTTGCA GTGATCA-----TGGGGACAGGGCTCCCA CATGA Sbjct	3799	TC AACCTTTACTTGGGGGTTCG CAGTGAGCAACTAGCTTTGGGGCAGGGCTCCAGAAGGA	3740

Query	12152	AGTGAAGGTTTCATGA--GAAGGAAATGAGGGGAAGGCtgtgtgtgtgtgtgtgtgtgtgtg	12209
Sbjct	3739	AGAGGA-----ATGGAGGAATGGAATTG--GGGAGGGCCGT---TGCTCATATGTGTGTG	3690
Query	12210	tgtgtgtgtgtgCTGGCTGAGGGATGAAGGTGGGAGGAATACCAGGATTCTGAAGCAATGAG	12269
Sbjct	3689	TGTATGTGTACTGGGTGAGGAGTG--GGGGGTGGGTGCCAG-ATAATGAAGCAATGAG	3634
Query	12270	AGTGGGATTGGGAGAGAGAGCTCATGTTGAA-GAAGAAATAACTACCAAGTTCACATGGG	12328
Sbjct	3633	AGTGGGATTGGGATGGAGTGGGAGGGTACCATGAAGAAATAACTTCCCGGTTCAATTGGT	3574
Query	12329	CTCCTTTTTCAAGGGTTTTTCTTTATATAAACAAATTTGCCTGGTTCCAAT--TAGAAGCCC	12386
Sbjct	3573	-TCATTTTCAAGGGCTTCTCTTTGCTGAAACAACCTTGCCTGGTTCTAGTCCTAGAAGCCC	3515
Query	12387	ACATTAGGCAGTTAGCTCCAATTTGGCAGTTCA TTC TTAATTTGGCTTTCCTTATGGGTG	12446
Sbjct	3514	AGATTGGGCAGTTAGTCCCTAAG-----GTT CAT----AATTTG-C TTGCTTTATATGTG	3465
Query	12447	GGAGGGAGGGGCTGACAGTTAAAAGGTTGATGGGAAAAACCTTGGTATCCTGGTGTGAAGA	12506
Sbjct	3464	GGGGTGAGGTT----AATTAAGAGGGTGAAGGGAAGGATTTGGGATCCTGGTATGAAGA	3409
Query	12507	CAGACCC TG GGATCAGAAGGTTGCCCTGATGACTTTG-CCAATGTGTTCA TTGCCCTG-	12564
Sbjct	3408	AAG-----GGTT---TGATTTC CAGACCAAT GTTGGCATGTCCCTTGG	3368
Query	12565	-TCCTGCTGGGGCGCATACAGCAGGCC-----CTTCTTTCTCATACGCC-----TTGACA	12614
Sbjct	3367	ATCAAGAATTG CCCTGATAACTGTGCTATTACTTCATTGAGCTCCCCACCGAGTCCATA	3308
Query	12615	GACCAGGACTCACTGCTAGAAAACCCTGGGG-AAGTCATTGCTGAAGACTCTAGTGTGG	12673
Sbjct	3307	GACCAGGACTAACTCTAAGGAAATCTCTGGGGGAAGAGATTGTTGAAGACTTTAATGTGG	3248
Query	12674	GGCACATTAGGTTTGAGGAGCAGGGGAACATT CAGGCAGCTGGCAAGGTCTGGGCTACC	12733
Sbjct	3247	GACACATTGGGTTTGAGGAGCATGGGGACCACTTAGGCAGCTGGGGAGGTCTGGG-TGGA	3189
Query	12734	AGGAGAGATTGGGAGTTAGAAGCATATTAGGTGAGAGTTGACACTGTCCAAAGGGAGTA	12793
Sbjct	3188	AAGAGAGACATGGGAGCCAGGAGCATAT-AGGGGAGAGTTGAAACTGCCTAAAGGAAGTA	3130
Query	12794	TATAGAAAGAAAAGCAGAGGAAAGGGCTCATGGAGTCATTACAGCCTGTGAGGTGGGAAC	12853
Sbjct	3129	TAGAGAAAGAAAAGCAGAGGAAAGGGCTTATGGGGTTATTGTAGTCTGAGAAGTGGAAC	3070
Query	12854	AGGGTTTGGGAGTACTAAGGGTTTGGGGAGGGTTTATGTGTTTATTCACCCATTCAATTA	12913
Sbjct	3069	AGGGCTTGGGAGTAGTAAGGGTTTGTGGAGGGTCCGT-TG TTCATCCATCCA ACTATTCA	3011
Query	12914	TTCAACATTTCTTGAGCTTTATGGCAGATGCTGAGTTGAAGAGGAAGCTGGGGATTTAAG	12973
Sbjct	3010	TTCATCCTTTATTTGAGCTTTAGGCCAGATACAGAGTTGAAGAGGAAGTTAAGGATTTAAG	2951
Query	12974	AGGGAGAAGAGTTAAGAGGGGATCCCTGGGTGGATCCAGATGAAGGAGAAGGGAGGGGCT	13033
Sbjct	2950	AAGGAGAAGGGTTAAGAGGGGATCCCTGGGTGGATCCAGATGAAGGAGAAGGGAGGGGCC	2891
Query	13034	AAGTGCCTAGGCTCGCTCTTGCCAGGAGAGCACATCTGTTAACACAAAGCTGCATCTGTA	13093
Sbjct	2890	GAGTGCCTGGGCTCCCTCTTGCCAGGAGAACACATCTGT TAGCACAAAGCTGCATCTGTA	2831
Query	13094	TCTCAGCCAGCTCTCTTCCATTTTCATCTCCTCCTCTCTACCCACACTTGCAAGACGGGGA	13153
Sbjct	2830	TCCCAGCCAGCTCTCCTTCCCTTCATCCCTCCTCTCTACCCACCCCCACAAGACAGGGA	2771
Query	13154	GCCACATGGCGGCTTCCTACTCCCTTGTACCATAACACCCCTGCCGGGTTCTTTCTAGG	13213
Sbjct	2770	GCCACATGGCGGCTTCCTACTCCCTGTTCC-----CCCCCCCCAATGTCTTTCTAGG	2717
Query	13214	CATTTAGCTGTGGCATCAGCAGCACCCCTTCTGAGAGATCAGGCAATCCCCAAGGGTGAG	13273
Sbjct	2716	CACCTAGCTGTGGCGCGGCACCAACCCCTTCTGAGAGCTCAGGCAATCCCCAGGGGCGGG	2657

Query	13274	TGGTAGTGGTAGTGGTGGGGAGGGTTGATAGCTTCGAGAGAAGAGCTGGAGAAGGCG---	13330
Sbjct	2656	TGAT-----GAGGGGGCGGGGTTGA-CGGTCTGAGAGAAAAGCCGGAGTAGGAGCTG	2605
Query	13331	-CTGTCTGGCTGTAATTAGCCCCAGCTGCTGTTGTGAGGCAGCGTTGGGGGCCGTCAGGA	13389
Sbjct	2604	TCTGTCTGTCTGTAATTAGCTTCAGCTGCTGTTGCCA-GCAGCGTTGGGGGCCATCAGGA	2546
Query	13390	GTGTACATGCATGTGTATGAACCTGTGAGCGTGGCACCTCATTCATCACTCTATTTTT	13449
Sbjct	2545	GTGTGAATGCATGTATATGAACCTGAGTGCCTGGCGTCTCATCACTATCACTCTATTTTT	2486
Query	13450	CACTGTATTGTGTGCTGGCTGCAGCCTCGCTGCTCTGAAACCCCTCCTGTCCCTGAGGAT	13509
Sbjct	2485	CTCGTATTGTGCGCTGGCTGATGCTCGCTGCTGTGCAACCTCTCCTGTCCCTGAGGAT	2426
Query	13510	CCCGAAAGACAGAGTGTTCACAGGCAGCACAGCTTGAATCACTAATGCTATTAAAGCAG	13569
Sbjct	2425	CCCAGAGGACAGAGTGTTCACAAGCAGCACAGCTTGAATCACTAATGCTGCTAAGCAG	2366
Query	13570	GAGGACAACAAATATAGGCCCCCATATGTCTGGATATGCAAGTCCCTGCTCTCTCTTTC	13629
Sbjct	2365	AAAGACAACAAATATCGGCCCCCATACGCCTTGAATA-CCAAGCCCTGTTC-CCCCCTC	2308
Query	13630	CCCAACCCCTGCTTCTCTGAATGTTTCCAAGTGAGTGAAGTCCAGCACTTGAATTAGCAA	13689
Sbjct	2307	CACTCCCCCACTTCTCTGAATATTTCTAGTGAGTGAAGCCCACTCCTTGAATTAGCAA	2248
Query	13690	CACCTC--ACTTCTGCACAGCCTTTTGGCAAAGAGCTTTACAGCTGCCATGTCATGCAT	13747
Sbjct	2247	CACCTCATATCTCTGCACAGACTTTTGGCAAAGAGCTTTACAGAGATGTCATGCCAGGCAT	2188
Query	13748	CCTCAGAC-GCTTCTAGGAGAAGCATTTTATAGGTGAGGACCCTGTGGTTCAGGGAGGTG	13806
Sbjct	2187	CCTCAGACAGCTCTGGGGGCGAGCATTTACAGGTGAGGACCCTGAGGGTCAGAGAAGCA	2128
Query	13807	GAGAGATTTGCACAGGCTAACCCAGACAGTCAGTGGCAGACTTGTGTCCAGGAAGCAAGT	13866
Sbjct	2127	GAGAGATTTGCTCAGGC-----ATCCAGGATGCAGGC	2096
Query	13867	CCTCGACCTCCTGGCCTGGTGGCCCATCCCCAGCAGAGCACTGCCAAGAGGGCTGCTCCC	13926
Sbjct	2095	CCTTGGTCTCCTGAGGTTGTGCCCTGTCCCTAGCAGAGCACTGCCTCAATG-----	2045
Query	13927	GGGTGGCTCCAGCTGCTGCTGTCTGTGAGCTCGTGAGAACCTGTCAGCTGTGGCTCCAAG	13986
Sbjct	2044	-----AGC---GCTCTCTCTGTGCTTGTGAATACCTATGAGCCCTGACTCCAAG	1999
Query	13987	ACCTGCCTCAGTGATTGCTGAAAACGCTGAGAGTGTGAAAACCAGGA-CCCTCAAGCCG	14045
Sbjct	1998	ACTTGCCTCAGCAATCACTGAGAAAGCTGATACTGCTAATAACTAGGACCCCTGAAGTCA	1939
Query	14046	AGCCTGACGTCACATAGTTGATTGAGTACCTGCTATGTGCCACCACCTGTGCTGGTGCTT	14105
Sbjct	1938	AGCCAGCCTAAAAGAGCTTCTTTAG-----CCA-----GTGCTT	1904
Query	14106	ATGGGAGACA-AAACAGGGGTAGTGCATAGCCCGTATCCTCAAAGAAGTGATAACTTGAA	14164
Sbjct	1903	ATGGGGGACACAAAAGGAGTGGAATA-AGCCCCGTCTCTCAAAGAAATGATAACTTGAG	1845
Query	14165	TGGGGAACAACCTCTTAGATACCAAGTCCAAAGGCAATTCCAAGCACTTCTCTCTCTTCC	14224
Sbjct	1844	TGGGAAGACAAACCCTAGACAACAAGTCCAAAGGCAATTCCAAGAGCATCTCTTCTTCTC-	1786
Query	14225	ACTAAGCAGTCTGTTGTGTCAGTGACAATGACACAGGAACCCCTTCTGAATTCA--TCTGTC	14282
Sbjct	1785	-----CAGAGACAATGACTCAGAGACCACTTCTGCATTCACTTCTGTC	1743
Query	14283	TTATCGCAGGCCTGGGGTtaggagaggatgggaggatgactaggaagggtaatgaggaagg	14342
Sbjct	1742	CTATCACAGCCCTGTG--TGGGCAGG--GGTAGG-TAA--AGGGA-AGTAATAGTGAAGA	1691
Query	14343	gcaggagatgggggaaggaaggggaaAACTGGAGCTCCTAATAAACACCAGGCACATTG	14402
Sbjct	1690	G--GGAAGATGAAAGGAAGAAAGGAAGAACTAGAGTTCCTACTACATGCCAGGCACAGTG	1633
Query	14403	TGAAGTTTATATGTTATACATA	14424

Sbjct 1632 || || ||||| ||| |||
TGGAG--TATATGTCATATATA 1613

Score = 1819 bits (2016), Expect = 0.0
Identities = 1989/2621 (75%), Gaps = 170/2621 (6%)
Strand=Plus/Minus

Query 5259 TAGGTGCTTTGAACCCAGCTACCAGTTGTAGAGTTCAAACCCAGGCCTGCATGAGTCCCT 5318
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Sbjct 9260 TAGGTGCTTTATATTAGCTGCTAATTATAATGCTGAAACCAAGACCTATATGAGTCCAG 9201
Query 5319 TG--CACCCATTCTACTTTTCTGCACTGCTTGTAATGT-AACACAGGAGGTATGGGACAT 5375
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Sbjct 9200 TGTGCTCCCATGCCATTTTCTATATCGCTTGTTATTGTTAACACAGGAGTCATGGGATAT 9141
Query 5376 CCATAACTCAGGTAGGTAATTGACTTCAAGCTTAACATTCAC---TCACCAATCATTTAT 5432
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Sbjct 9140 ATACAATTTGGGGAGATTGTTGACTGCTAGCTCAACTACCAACATTCATCAAATGTTTAC 9081
Query 5433 TGAGCACATATTAGATAAGCAACCTATGGCTCCTGCCTGGAGTTGTTTATAAGACCTTC 5492
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Sbjct 9080 TGAGCATATACTAGATGAACAAGCTATAGCTCCTGCCTCCAGCTGCTCATAAGACCTTC 9021
Query 5493 CAGGCAGACAGCTATGGGACGAATACACTTGAA-----TTTATTAATCTACCTCAGGCA 5547
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Sbjct 9020 AAAAGAGACAGATATGGAAAGAATAAATTAATAAAAAAATTTTATTTGCTGATGTA 8961
Query 5548 AAAACCAAGCATGTAATTATAAGTAGTATATCAGAGTATGTGTAATGGGGTTCTGTAA 5607
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Sbjct 8960 AAAA-CTAGGTACG-ACCTATAATCAGTATATCAGAGAATCTGAAAACAGAC-----AA 8909
Query 5608 AATGTTTGAAAGAGGCAGGCCTGGGTTAGTGGTGAGAACAAGGATCAAGAAGGCTCTGCC 5667
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Sbjct 8908 AGGGCTTGAAAGAGGCAGGCCTACTTTAGTAGTGAGAATAAGAAGAAAGA-GGCCCTGCC 8850
Query 5668 ACCAATAACAACATGAGTGTG-----TCCCGTTAATCTCTCTGGGCTTCTGTTTCCAG 5722
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Sbjct 8849 GTTAAATAGCTACGTAAGCATAGGTAAGTCCC-TTAAACTCTCTGGGCTCCTGTTTCCAC 8791
Query 5723 ATCAAGGACCTCAAATAATAGTCATAGTCACCATTTATTGAGTGCTTTACTGTTAACCA 5782
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Sbjct 8790 ACCTGGAACCTCAAAGAATAGTAACAGCCACTGTTTATTGAGCACTT-ACTGTGCACTA 8732
Query 5783 GGCAGTATGCTAGGTGGTTTTCATTTAGTCTTGACAACAGTATTCTCGCTTCCCTTTTC 5842
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Sbjct 8731 GGCACCAAACAT-TGGCTTCCGTTTCAGTCCTGACAACCGCTTTGTCGCTTCCCTTTTC 8673
Query 5843 TACAGCTGAGACTCAGAGACATTAGGTAATGT---CTAGGTCACACAGCTCTTCAGTGAC 5899
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Sbjct 8672 TACAGCGCAGGCTCAGAGAGGATAGGTAAGTGCTCTAGGTCACACAGCTCATCAGCGGC 8613
Query 5900 CAGTTGTTTCTATGTC-AGAATCCTCTTATAATCACTGAGTTGTATCGCTTCCCTTGCT 5958
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Sbjct 8612 CAATTGTTTCTATCTCTAGAATCCTCTCATAACCATTAAGTTGTATTGCCTCTCTTATCT 8553
Query 5959 CCTG-CTC----CCAAGTCAAGTATTCTCTACTATGTCGCCTGAAAATTAAATTTAAAT 6013
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Sbjct 8552 CCTGACTGAACCTCAAGTCCAGTATTCTCTGCTATGTTGCCTTAAAGTTAAATTTAAAT 8493
Query 6014 CAAGGTAAATCTTGTTCAACTGAGCCAAGAGGATAAACATTAGAAATAGCAATTAGTAGG 6073
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Sbjct 8492 CAAGGGTAATCTTGTTCAACTGAGCCAAGAGGATAAACATTAGAAATAGTAATTAGTAGG 8433
Query 6074 TAGAAATGTTGCCAGGAAGAGCTATACAAAAGCATAGAAAGGCAACCAAGGGAGTTAA-- 6131
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Sbjct 8432 TAGAAATTTTGCCAGGAGGAGCTATACAAGAGTGCGGAAAGACACCAAGTCAGTTAACA 8373
Query 6132 -TGATGGGGGTGTGGCAGGGGTGTCATGTTGATGGGTAATTGGATCCTGGCCAGCTCTTA 6190
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Sbjct 8372 ATGATGGGGGTGCAGC-GGGGTGTCATGTTGAAGGTAAATTGGTTCCCTGCCAGCCCGTA 8314
Query 6191 CCTTCTCTCTTCACCTTCCCACTCCGCAATTTCTCAGGCTTCTCTAGAGAGCACACCCA 6250
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Sbjct 8313 CCTTCTCTCTTCACCTTCTGCTACGAA-----GCCTGCTCTAAAGAACAGGCCCA 8262
Query 6251 CCTAGAGACAGCCTGTGTTGCCACAGGAGGGCACCAGGCCAGGAATGGCAGGCCTAGGGC 6310

Sbjct	8261	CCAAGACAGCCGGAGAT-CCACAGAGGGGCTCA-----GGC	8225
Query	6311	AGTGGGGCTCTGGGCTGGGAACCATAAATAAACCACTTTAATGAAAACCAGCTTTGGCCAA 	6370
Sbjct	8224	AGTGGGGCTCTGGGCTGGGAACCATAAATAACGCCTTAATGAAAGCCAGCTTTTGCTTA	8165
Query	6371	A-AGCCTTATCATTTCTTAAGAGGTTCGTGCTTCTTCTAAT---GACCTAGTTACTTGA 	6426
Sbjct	8164	AGAGCCTTGTCAATTCTTAAGAAATTTTTTGC--CTTCTAATATGGACTTAATTACTTGA	8107
Query	6427	GAAAGGCCTAGCCTAACATATACAACAACAATAATA-----GTTGCCCTATAG 	6474
Sbjct	8106	GAAAG-CCTAGCCTACTCTATACAACAACAATAATAATAATATGGCAGTTGATCTTTGG 	8048
Query	6475	TGAGTACTTACTATGGGCCAGGGCCTGTGCTAAACACTCACTAATTCATTTAATCCTCAC 	6534
Sbjct	8047	TGAGCACCTACTATGGGCTAATACTTG-----ACATACACTAACTCATTTAATTCTCCT	7994
Query	6535	ACAGCCCTACAGGAGCAAGTACTATTATTTCCTCCCACGTTACAGAGCAGGCATCAGGCTG 	6594
Sbjct	7993	GCAGCCCTTTGAGGGCACATATTATTATTCTCCCGTTTACACAGGAGGCATCAGGCTC	7934
Query	6595	AGAGAGGCTAAGTCATTTGCTCAAGATCATATAGCTGGTTGGAGCTGGAATTTGAAGCCT 	6654
Sbjct	7933	AGAGAGGCTAAGTAACTTGCTCAAGGTCATACAGCTGGTTGGAGCTGGAATTTGAAGCTT	7874
Query	6655	GAAGCATCTAGTTCAGGGCCTGAGCTCTTTAATTCTATATTTAATGAATGTCTGTCTGA 	6714
Sbjct	7873	GAAGCATCTGGTTCCAGGGCCAGAGTTCTT-AATTCTGTATTTAATAAATGTCTGTTGG	7815
Query	6715	AGGAATAAACAGATGAATGAATAGACAAATGTATT---CATTTCAATTCACTTTAACAA 	6770
Sbjct	7814	AGTAATAAACAGATGAATGAATGGACAAATGTATTAATTCATTACAGTTTACTTCAGCAA	7755
Query	6771	ACATTTATTGAGTGCTCTGT----GTCAGCTCCTGTGCTAGGCATTGAGGATTTATAAGT 	6826
Sbjct	7754	ACATTTATTGAGTGCTCTGTATATGTCAGCTTCTGTGCTAGGCATTGAGGATTTAAGTGT	7695
Query	6827	TTAGTGCGTGCGTGCGCGcacacacacacacacaaacgcacacacacacacacaca 	6886
Sbjct	7694	TTA-----ACACACACACTCACACACACACACACC---	7662
Query	6887	TCCTGCATGGCCCTTGCTCTCCAGGGGTTACAAAAAG--CATTTCTCTAT--TGTGGCTTG 	6942
Sbjct	7661	-CCCACATGGCCCTGTCTTTGAGAAGCTTACAAAAAACATTCTCTCTAATGTAGCATG	7603
Query	6943	ATTTCTTCTGGAGAGAAGTAATTTGAATGTCTTTGAACAGCAGTTTTTAAATGATGCTATTA 	7002
Sbjct	7602	ATTTCTTTGGGGGAAAAGTAATTTGCGTTTCTTGAATAGTAGTCTT-AATGATGCTATTA	7544
Query	7003	AATTTAACCTAAAGCGGGGGTTTTGTCACCGGTGAGCAAAGTGTTCAAATGAGAATGTGT 	7062
Sbjct	7543	AATTTAACTCAAAGTGGGGGTTGTGTCACCGGTGAGCAAAGAGTTCAAACAGAACATGT	7484
Query	7063	CTTTGATTAATCATCGATT CAGCCAGAGAATAGTTACTACCAGAATG-GAGCTGCAACTC 	7121
Sbjct	7483	CTTTGATTAATCATTGATT CAGGCAGAAAATGGTTACTACCAGAAAGAGGGCTGCAACTC	7424
Query	7122	CTATTATATTAGCTAACTCTTCTTCCATCTATCATGTCTCTATCTTGTCGAACCCTCCCA 	7181
Sbjct	7423	CTATAACATTAGCTAACTCTTCTTCCATCTATTATGTCTGTAT---TCTAACCCTCCCA	7368
Query	7182	CGATACAAAAGTTATCTGTACCCTAATGGACAATTATCCCATCCATCATTCCTGCTGGTC 	7241
Sbjct	7367	CGGCACAGTAGTTATCTGTACTCTAATGGACAATTATCCTATCCATCATTTGTGCTGGCC	7308
Query	7242	TTGTTGATTGCTGGTAGTCTGCTTGCCCCGAGGAGACTTACAAATAGTCATGACCAGT 	7301
Sbjct	7307	CTGCTGATTGCTGGCAATCTACTCGCCCCGAGAGGAGACTTACAA-TAGTCACGACCGAT	7249
Query	7302	GACGCACTGGAAAAGTCTCATTTTTAGACATTTTAAATCTATGTAGAATGAATTATTTT 	7361
Sbjct	7248	GATGCAGTGGAAAATTGCTGATTTTTACACATTTTAAATCTGTGCCGAATGAATTCTTTC	7189
Query	7362	TCAGGCTGTACTT-AAGCTGCATTTGCTTTGTTGGTTATGTAAGAAGAGAT-ATGAATTC 	7419

Sbjct 7188 GCAGGCTGCCCTTTAAGCTGCATTTGTTTTCTGGTTATATAAGAGCAGGTTATGAATTT 7129

Query 7420 CTTACCTATGCGTGAGACATGGCGTCTG--AATATTTTAAAGTT-----CCTGTGGG 7469
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Sbjct 7128 TTTACCTGCATGTGAAATGTGGACTCTGTGAATATTTCAAAGGGAAAAAACCTCTAGG 7069

Query 7470 CAGCAGCCCTATACATATTTGTTAAATGATGAAAGAATAAAGTAAACATACCTAGAGTA 7529
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Sbjct 7068 CAGCAGCCTCATAAATATTTGTTAAATGCGGGCTGATCGAAATAAACACA--TGGGGTA 7011

Query 7530 ATTCCAGAGGAGCAGGCTTCATACCTGGAGCTCGGGTGGGTGGCCATCATGTCAGGTTAG 7589
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Sbjct 7010 ATAAAGAGGAGCAGGTCCCAAGATTAGGGTTTCAAGGGGCTGGTCATCACATCAGAGTGA 6951

Query 7590 TCACC-GTCTTCCTTTTCTTTCTAAGTACTTTGAGGAGAATCCCAAGTTGATTAGGGTC 7648
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Sbjct 6950 CCACAGTCTTCCTTTTCTTTCCAGGTATTTGAAGAGAAACCAAGTTGATGAGGATC 6891

Query 7649 AAGGTGAGGACTCATGGTGCTGAAATAGGGATTGAGTGGACAATGAGAGATGCCTGTTG 7708
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Sbjct 6890 CAGGTGAGGACTCTGGGTACTGAAAGTAGTGGTTGAGTGGGGAGTGAGAGATGCCTGTTG 6831

Query 7709 AATTCCCTGGGACTATTGCTATGAGATTTGAGGCAGAAATGC-CCCCCTC---TC--- 7760
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Sbjct 6830 AATTCCCTGGGAGTATTGCTATGAGATTTGAGGACAGAAATGCTCTCCCTCCATGTCCCA 6771

Query 7761 --CCATGTCCTACCCTAAGCCTGGTAACACATTTAACTTTT 7799
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Sbjct 6770 CTCCATGTCCCATCCAGGCATGGTAACACACTTAACTTTT 6730

Score = 1121 bits (1242), Expect = 0.0
 Identities = 924/1116 (82%), Gaps = 15/1116 (1%)
 Strand=Plus/Minus

Query 2802 AGGTTCTGAAGTTTCTTGGCAACTAGCTCTAACTGCTTTGCCTTCTGAGTG-CTTTGG 2860
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Sbjct 11541 AGGTTCTTAAATTTTCTTGGCAACTGATTCCTCAACTGTCTGTCTTTTGGGGAACCTTTGG 11482

Query 2861 TATTTGTTTAT-TCTAAGTTCAGTTTGTATCTATTTTGCCTTATGGCTGCAGATTC 2919
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Sbjct 11481 TATTTGTTTATTCTCTCTGTTCTGGTTTTGATCTGTCTTTTCTTCTGGCTGTGGTTTT 11422

Query 2920 CCTTCTGGAATAAGGGCTCTGGCTGGGATCAAATCAGAGAACACACCCAGA---CTTG 2976
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Sbjct 11421 CCTTCTGTAAATAAGGGCTTTTGTGGAATCAAAT---AGAACGTACCCAGAAGACCCG 11365

Query 2977 GCATAGTGCTGGCACAGAGTAAGTGCTCAACAAATGGTAGCTGTTGTCTCTTTTCCCT 3036
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Sbjct 11364 GCACAGTGCTGACACAGAGTAAGTGCTCCACAAATGGTAGTTGTTGTCTCTTTTCCCT 11305

Query 3037 GTCCAGGTTTCTTCTGGTTCTGTTCTCTGTACCTCCAGTATTGGCCAGAACAGGAACT 3096
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Sbjct 11304 GTACAGGTTTCTTCTGGGTCAGTTCTCTGCACCTCCAATATTGGCCCTGGACTGGGGCCA 11245

Query 3097 GTTCCCTCCCTGACTGGCAAGTCAGATTACCTGGCCCTCAGACAAGCTGGGCTCCCTTT 3156
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Sbjct 11244 GTTCCCTCCC-TGGCTGGGAAGCCAGGTCACTTGGCCCTCAAACAAGCTGAGCTCCCTT 11186

Query 3157 TCTGGCAGCCTTTTGTGTCTTACCTGTGTCCTGTGCACTCAGTGTAACCACAGGCA 3216
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Sbjct 11185 TCTGGCAGCCTTCTGTTGTCTTACCTGTGTCCTGTGCACTCAGTAACCACAGGCA 11126

Query 3217 GACCTCTGCCAATTGCTGACATTAACCTATTGAATCCTGGCAGAGAAGAATAAGTTTGCA 3276
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Sbjct 11125 GACCTCTGCCAGCTGCTAACATTAACCTGTTGAATTCTAGCAGAGAAGAACAACCTTTGCA 11066

Query 3277 GACTGGAATTTGCATGTCTGGGCCAGATACGAGACCAGGAGGCAAGCCATATTT-ACCT 3335
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Sbjct 11065 GACAGGAATTTGCATGTCTGGGCCAGATACAAGACCAAGAGGCAAGGCCGTATTTTATCT 11006

Query 3336 GTTCTCCCCAGTTGTG-GCAAATCACCCACATTCTGGTTAAACCAGATGTTTCACACCC 3394
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Sbjct 11005 GCCCTCCCCAATTGTGAGCGAATCACACACCTTCTGGTTCAAACCAGATGTTTCACACCC 10946

Query 3395 ATGACTGCAATGCCACACATCAACAGTTGCTTACAAAGAACACAAAGTGGTTTTTCACAT 3454
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Sbjct	14226	GTTTTTGGCCAGACATTTGTGTTGCTGAGGGAGAAATCATGGCAGAACTGTGTCATTCCATA	14167
Query	590	-GGaaaaaaaa-----TCAGGCTAAAAGGGAAGAGTTTGTGTGAAAACAGTTCTGTTTTTA	642
Sbjct	14166	CTGAAAAAAAAAAAAAATTTCAGGCTAAAAGGAGAGGAGTTGCTTGAAAACAGTTCTGTTGTA	14107
Query	643	GAAACCAGTCCTTGGAGTCTCATCGCCAGACACA--GTCTTATGaaa	687
Sbjct	14106	GAAACCAGCCTTTGGAGTCTACTCTCCAGACACAACCTTCTTAGGAAA	14060
Score = 479 bits (530), Expect = 1e-130			
Identities = 667/914 (72%), Gaps = 33/914 (3%)			
Strand=Plus/Minus			
Query	4311	TGCTAGGGTTAATTGCTCAGCCTGAGAGGCTCTCCAGGCTGGCAGGTCACACTAGAGCCA	4370
Sbjct	10410	TGCCAGGGTCAAGTGCGTAGGCTGAGAGGTTCTCTAATTGGCAGGCCACACCAAGGCCA	10351
Query	4371	AGAGTGAAGGGTCCATTTCAGTAAGGTCACTGCCATGATCAGTTCTCAACCACTTTAACTC	4430
Sbjct	10350	AGAGCGAAGGTGCAGTCCAGTGAGGCCAGTATAATGATCAGTTCTCAACTGCTTTGACTT	10291
Query	4431	AGTTTTTCTGTTGCTGCTTTGTTGGTTAGTGGTTGTTTGTCTTCTACCCATTTGGGAGAA	4490
Sbjct	10290	GGTTTTTCTGTTTGAATTCTTTGGTTCCTGGTGTATTGTTTCAACCCATTTGGGAAGA	10231
Query	4491	GGGTAGGAAAGGAACTAAGGTGATCAACTATTCCATATGTGTCAGGCCCTGTACTTGT-C	4549
Sbjct	10230	GGGTAGGGAAGAAGCTAACATGATTGACTATTTTCGTATGTGCCAGGCTCAGTGCTTGTAC	10171
Query	4550	TTTTCAAACACTTATTCACACTCTGAGGGACTCTCTCAGGTCCAGCAACTGTGTAGCTAT	4609
Sbjct	10170	TTTTC-AACACTCAAGCATA--CTGAAGGA-TTTTTCACCTTCAGCAACTGTGTGGTTAT	10115
Query	4610	GATGTGAAATAGCAGCTTCTCTCTATGCATTCACTGGGAATGGTTTGTCTGATCACACA	4669
Sbjct	10114	AATGTGAAACTG---TGGTTTCTATATATTCCTGGGAAAGGTTTGTCTGATGACTCT	10059
Query	4670	ATTTTTTCCAGTTCTTCCGACGTTAGGTGTTGCATGGTAAGAAACAGGTGGTTAATTATT	4729
Sbjct	10058	A-ATTTTCCCGTGTTTTGAACATTGAGTAGTAGATGGTGAGAGACAGGTTGTTAAGTGTT	10000
Query	4730	GAGACAGTTCTTATTGGGAATTGTCTCTTCTCCTCTCTCCTCTCAGGCAGATGCTAAAGG	4789
Sbjct	9999	TA-CCAGTACTTATTGGGAGTTACCTCTTCTTCTTCAGATTTTCATGCAAGTGGTCAACA	9941
Query	4790	ATGTCTGTAGTTT-TTTCATGGCATTGTTGCTAAAGATGCACATTCATTAATTCATCAAAT	4848
Sbjct	9940	GTGTCTGGAATTTCTTTTATGCTATTTTATTGAAAATGCATATTCATAATTCATAAAAT	9881
Query	4849	AGCtttttttGAGACATTATTATGA---GTGAGGTGTTGTGCTATGATATGCTTTATATA	4905
Sbjct	9880	CGC-CTCTTTGAGTCATTATGATGATATGCTACGTTTTGTG--ATTA-ATGCTTTACATA	9825
Query	4906	CCATATCTTATTTTCATCCTCACCACAAAGCTATGAGGTAGGTACTATCATTATCTTAATT	4965
Sbjct	9824	TCATATCTTATTTTATCTTCACCACCAAGCTGTGAGGTAGGTACTGTCTAGCTTCATT	9765
Query	4966	TTAC-AATGAAGAGACTGAGGCTCAGGAAACATAATGCAAGGTCACACTCAGTTAATAAG	5024
Sbjct	9764	TTCCAAATGAGGAGATCGAAGCTCAGAGATTATAACGCAAGACCACA--CAGTCAATAAG	9707
Query	5025	TTGAGAGCTAGGATTCAAACCCAGGT-TTATCTGACTCAGTTACACTACACTTCTCCAC	5083
Sbjct	9706	TGGGGAACGGGATTCAA--CAGCTGTTA--GATGCAACTGCATTATACTTCTCCAC	9652
Query	5084	ATAGCACATTGTGGGCCCGTCACAGCTCTTGAGGACAAAATTCATCCTTAGAAAAGTTTT	5143
Sbjct	9651	GTA CTGTATTTTGGGCCCTCACAGGCCTTGAGAACAAAATTTCTCCTTAGGGAA-ATTT	9593
Query	5144	CTTACTCCACTTTTTgtctgatact---actgctgctgttgctgctgctactactattac	5199
Sbjct	9592	CCTACTCTACATTTTGCTAATAGTACGAACAACCGCTGCCTCTACTACTACTATTGT	9533
Query	5200	tactactgctactg	5213

Score = 405 bits (448), Expect = 2e-108
Identities = 406/522 (77%), Gaps = 25/522 (4%)
Strand=Plus/Minus

Score = 374 bits (414), Expect = 3e-99
Identities = 785/1174 (66%), Gaps = 156/1174 (13%)
Strand=Plus/Minus

Query	14584	AATGAGTGTTAACTAGCCTTTCTTCTTATCATGATCATCTTCATTGTCAATTATCGGCAT- 	14642
Sbjct	1144	AATAAATGTTAACTTTTTTTCTTCGTATCATCGTCATCATTATT---ATTATCTGCATG	1088
Query	14643	---ATTATATAAATTATCTCATTATTCTTCTTAACTACAGGA-----CT--- 	14684
Sbjct	1087	AATATTATATACATTATCTCAATTAATCCTTGTAACTCCAGAAAAAAAAAAAACTCCAG	1028
Query	14685	---TAGCAACTATTATTTTATTTCCAGTTTACAATGAGGAAACCAGTATCTTATTTT 	14740
Sbjct	1027	AAGGTGGCATTATATTATTTTCATCCCCAGTTTATAAATGAGGAAACCAATATCTTGTGTG	968
Query	14741	ATCCAAGCTTGTGGGTACTGAGAATATAAAGAGGAATTCAATATGGTTCTAGGCAACTT 	14800
Sbjct	967	ATCTAAGCCTGAGGGTACTGAGAATACAAAGGAGAACCAATATGGTCCCAGGCCACTTT	908
Query	14801	TGGGG-TCTTCCCTATCTAGTGGGAGGGACCGAGGCACACATAAGCCCTCATGGTCCAAT 	14859
Sbjct	907	TGGGGATCTCCTCT-TCTAGTGGGAGGGACCAAGGCACCCATAAATACTCA-GGTCCAAT	850
Query	14860	AGGTGCTGTGGTAGAGGA-----ACGTATCTGGG 	14888
Sbjct	849	GGGTGCTGTAACAGAGGACTGTACCAGTGCAACTGAGGACTGGATGACCACGTATCTGGG	790
Query	14889	GAAGTTGAGGAAGTCTCCACGAATGAAGGAGGC-----TTGAGCAGCATCTTGAGGGAT 	14942
Sbjct	789	GAAGTAG-GGAAGGCTTTGCAGGTGAAAGACATACATATTTGAGCTGAATCTAATGGGT-	732
Query	14943	GGCAGGTTATGTGAGGAGGAACAGTGGAGG-----CAGGGGAAGACATTCCAGGCCAAAGT	14997

Sbjct	731	-GCAGGGCTTGCAAGGAGGAGCAGTGGAGGAGGGGCAGGGTAGGGCATTCCAGTCAGGCG	673
Query	14998	GAGCAGTATTTGTGTGACAGGGCCTAGTGCATGTTTCAAAGGGCAGGACA-ATTGTAGCT	15056
Sbjct	672	GAAGTGCATT-GCGTGACAGTGCACGGTGCTGGCTCTTACGGGAAGGATGCATCTTTGGT	614
Query	15057	GGG-TGCACCACTGGCAGCAGCAGGAGGGGAGTGGACAGTATTTGGGGTCAGCT-ATTC	15114
Sbjct	613	GGGCTGTGTGATTGGCGGCACCAGAAGGGAAGTGGAAAAGGTGGTCAGGTCAGCTTATTC	554
Query	15115	AGAGCCCTATTGGCCAAGCTGAAGGTTT-----TGTTCTGTGAGCAAGAGGGAGCCACTG	15169
Sbjct	553	AGGGCTTTTGCTGGCCAAGCTGAGAGTTTACACTTGTTCTGTGAGCAAAAGGGAGTCACCC	494
Query	15170	GAGCTTTTTTA---TTAAGGCAGATTCTGGGACAGACTAGG-----AAGACAGTC	15214
Sbjct	493	AAGGTTTTTTAAATTAATAACAGAGGAGTGACAGACCAGGTTTAGGTGAGGAAGACAATT	434
Query	15215	CTTAC-----CAGGGTGTTGAAAGATTGGAGGGAAGAGAGGCCAGCTGCATGCGGACCAA	15269
Sbjct	433	CCTACAGCACCAGGATAAGGAAGGGCTGGAGGGGAAAGAGGCTAAAAGCAGGGAGATGAG	374
Query	15270	TTGGGAGACCATCTCCAGGGTCTGGGCAAGAAGTGGAAACAGGCTCTGAACCACGACCGTG	15329
Sbjct	373	TTAGAAGGCCATCTCAAGTGTCCAGGCAAGTAGTG-----CTAA-----GTG	332
Query	15330	GCAGTGAGAGCCGAGAGGAGGGGATGACTCAAGGCACATGTCAACAGGTAGAAACCTCAG	15389
Sbjct	331	-CAGGGAG-----GGGGTGACTCCAGGTACATGTCAATAGGTAGAAGCCATAG	284
Query	15390	GGCTGGCTGTCTATGGGG---TCAAGGAGAGGGAAAAGGTGACAAGGACCCTGAGGTTCC	15445
Sbjct	283	GGCTGTGTGTCTATGGGGGGGGTCAAAGAGAAGGAAAAGGTGACGATGACTCTGAGGCTTT	224
Query	15446	AGCTTGGGTCCGTGGTGATACTGTCAACTGAGGCA-----GGGAACACAAGACTG	15495
Sbjct	223	GGCTTGGGTAAAGTGATGATACTGGTAACCAAGACATTGAGGAGAGGGGGCCGTAAAGACTA	164
Query	15496	TTAGTAGAGAGGGAGAGTGAGGGGAGACAGATGACAAGGTCTGTTTGGACTTGCTGGGTT	15555
Sbjct	163	TTAGTAGGGAGGGGGAATGAGTGACAGACAGGTGACAAGTTCAGCCAGGACATGTTGGGTT	104
Query	15556	TGGAGTGC---TGG---AT---AGCGGACATGTCCAGCAAGAACTGGGAATCTTGGCTT	15606
Sbjct	103	TGGGGTGCCAGTGGGACATCCAAGTGGACATGTCCAGCAGGAAGCTGGAAATCTGGGCTT	44
Query	15607	TGAGCCCAGCTGAGACATGGGGGCTGGAAGCCA	15640
Sbjct	43	AGAGGCCAGATGAGAGATGGGGTCTGGGAAGCCA	10

Query 11294 TACAGAGGAGGCACCAGACTCAGACAGGCTGAATAACTTGGCCAAGGTCACATAGCTAGT 11353
 |||| ||||| ||| ||||| |||| | ||||| ||||| | ||| ||
 Sbjct 7954 TACACAGGAGGCATCAGGCTCAGAGAGGCTAAGTAACTTGCTCAAGGTCATACAGCTGGT 7895

Score = 62.6 bits (68), Expect = 3e-05
 Identities = 86/117 (73%), Gaps = 5/117 (4%)
 Strand=Plus/Minus

Query 6516 TAATTCATTTAATCCTCA-CACAGCCCTACAGGA-GCAAGTACTATTATTCCCCACGT 6573
 ||||| ||||| |||| | | || || || || || |||| ||||| ||| |
 Sbjct 4672 TAATTCATTTAATTCCTCAGTATA---CTTCATGAGGTAGGTACCATTATTGTCCAATTT 4616

Query 6574 TACAGAGCAGGCATCAGGCTGAGAGAGGCTAAGTCATTTGCTCAAGATCATATAGCT 6630
 || |||| |||| ||||| ||| ||||| || ||| |||| ||| ||||
 Sbjct 4615 TAGAGAGGTGGCACCAGGCTCAGACAGGCTAAGTAACTTGGCCAAGGTCACACAGCT 4559

Score = 59.0 bits (64), Expect = 3e-04
 Identities = 117/171 (68%), Gaps = 3/171 (1%)
 Strand=Plus/Minus

Query 725 TTTATTGGGTATTTACTATGTGCCAGGAAGTGTCTAAGTGTCTACACAGATTATCTCA 784
 ||||| ||||| ||||| ||||| || ||||| || | |||| |||
 Sbjct 4725 TTTATTGAACATTTACTATGTGCCAGGTACCATTCTAAGTACTTTGTGTGTATTAATTCA 4666

Query 785 TTTAATCCTCATCATAACCCAATGACGTCAACTCTATTATTAGCTCCATTTAACAGATGA 844
 ||||| |||| || || |||| || | |||| | | |||| ||| |
 Sbjct 4665 TTTAATTCTCAGTAT-ACTTCATGAGGTAGGTACCATTATTGTCCAATTTTAGAGAGGT 4607

Query 845 AGGAATTGAGGCTCTGGGATGTTAAGAAAAGTGCCCAAGGTCACACAGCTA 895
 | | ||||| | | |||| || || ||||| ||||| |||||
 Sbjct 4606 GGCA--CCAGGCTCAGACAGGCTAAGTAACTTGGCCAAGGTCACACAGCTA 4558

Query	2	CCGCCCCGCGCCCCCTCTGATTGGCTGTACCACCCCGCTCTGTACAGCTCTTTTGTCTCA	61
Sbjct	118596	 CCGCCCCCGCACTTCGCTGATTGGCCGCACTAGCCCGCTC-GTCACAGCTCTTTTGTCTCA	118538
Query	62	GTGGGTAGAGGCTAAAAGCAGCGCGGCTGCCGTGGGAACCGCGTTGCCTCCACTCGGCT	121
Sbjct	118537	 GCTGGCAGAGGATAAAAAGCCCGCGCGGCTGCCTTAGGAACGGCGCTGCCTCGTCTCTGCT	118478
Query	122	ACTT-TGGCTGTGCGGCGGTGCGAAGCAGCTCAGGCGTGCGGCCCGGGTAACCTCCTAG	180
Sbjct	118477	 ACCCCTGGTTGGGCGGCCCTGCGAAGCAGCTCCTTCGGGCAGCCCCGGGTCGCTT---AG	118421
Query	181	TTACCGAGGAGGCGCCCGT-CTTTCTCTCTTTGCAAGACGGCGGCGCCAGGACGCGGAC	239
Sbjct	118420	 CGGCCAAGGAGGCTTCAGTTCTTTGCCGCGCT----GCAAGGCGGAGACCAGAAGCGGAA	118365
Query	240	TCCACAGCTATAGATGCCGT-----TCTCCATCACCAGGTC-CAGGTAGAGAAAGG	289
Sbjct	118364	 TCCACAGCTGGCGACGCGGGAGCATCTGCTGTCCACCAGCGGAGCACAGGTAAGAATGG	118305
Query	290	GG-TGCGATTGCCTAGCACCGAA---GGTG-----CTGGGTGGCTCC	327
Sbjct	118304	 GGGTGTGATTGCCCGCGCGGGAGAGGGGTGGGGGAAGACCCACCAGTACTGGGCGGCTCC	118245
Query	328	CCGCTTGG-----GGCA-----AAGAGCACTCCAGTAGCTGGGCTGCA	365
Sbjct	118244	 CAGCTTGGAGAATCGGTGACTGTGAGGCAGGGGTAGGAGTACTCTCGTGGCCCGGCTGCG	118185
Query	366	--GAGAGAGGAGGTAGGGTTCAACTGGATGCTGCCGAATGGGTAGGGTTTGCCTGAATTG	423
Sbjct	118184	 CTGAGGGAGGAGGTGGGGTTACCTTGATACTGCGGGCTAGGTAGGATTTGCCTGGATT-	118126
Query	424	AGAATGGGGGAGAATTTGGGGGCAGGGGCAGGCTTGAAAGATGGAGGGTTGAAATCGCG	483
Sbjct	118125	 ----TGGGGG-----TGGGAGGAGGGGCGAG---GGGTAGCGGGGGGA--GGAATCTCG	118081
Query	484	AACTGCTGCCTTA-AACCCCTTTTGCCTCTGCTCATCTCGTCTGGAGAAAATATGTGAA	542
Sbjct	118080	 AGCTGTTTGGCTTCGAACATCCTTTGCATCTCCTCATCTCTTTCTGGGAGGAATATGTGGG	118021
Query	543	TGG-----CCGGCTCATTTTCCCTTTCTCCGTGACAGGTCATCGAAGCCAAAGCCGAAG	596
Sbjct	118020	 TGGGTGTGTCCAACCTCTATTCCCTTTCTCCGTGGCAGGCCATCAAAGCCGCATCTGAAC	117961
Query	597	TTAAGCTCCGTGTGGCTGATTTCAGAGCTGGTAGGCCACGGTTCCTCGGGGAGGGGGGC	656
Sbjct	117960	 TTGAATTCTGTGCAGCTGATTGCAGAGCTGGTAGGCCGACGGCTTCCCGGGG-----	117909
Query	657	GGTGGGATTTAATGGAGGAGGGA-----CTCG-CTTTGGCTTGCAATCAGCAGGTGGGA	709
Sbjct	117908	 ---GAAATGTAATGCTGGAGGGTGGGGGCTGGTCTCTGGCTTATAGTCAGGAGGGGGCA	117852
Query	710	GTGGAATTTTTTACCTGGCGACAGCAGAGGTGACTGGGATGGGGGTG--GGG---AGGT	764
Sbjct	117851	 GAGAGAATTTTTTCGCTGGCAACAGCGGAGGTGGTGGGTAGCAGGATGACGGGTGAAGCT	117792
Query	765	GGGAATGAGGCTGCCCTTTTCT---CTAC--CACAGT---CAGTCTTGACGCTGTGAG	816
Sbjct	117791	 GCTTCTAACCCTTCCCTTCTCTGGCCTTCTCCGTGTGGCGCAATCTTGAAACCTCA-AG	117733

Query	817	GACCCTAATCCGCGAACCTCAGTGGACAGAGGCCTACAGGACCTTGAGGCTG-GATTTCT	875
Sbjct	117732	GACCCGGATCTGCGACCCCTGTGGACAGAGGTTGACCGTACCCCGAGAGAGCTTTCT	117673
Query	876	CA-GCACTG-ACTGAAGGCAGAGGCTGGAACGAAACAAAGGCGTACACTTGTTCCTGAG	933
Sbjct	117672	CACGGAGGGCACTGGTTGCAGAGGCTGGAAGTGAAATAAAGACGCGCTCTGTTCAGAG	117613
Query	934	ATCACGTAAGAATC--AGAAATGAGAAT-----TTTGAGAAGGG	970
Sbjct	117612	TTCGTGTAAGAATCTGAGAAATAACAAGGGGACGGGCGTGGGGGGCACTTTGAGAAGGG	117553
Query	971	GGTGTGGTGGAGACGTTAGGCCCTTGAGATTAATGAGATTTTATTT-ATTTTCACAAATCT	1029
Sbjct	117552	GGTGTGGTTGAGACCAGAGACCATGAGGTTAATGAGATCTTATTTTATTTCCACAAATCT	117493
Query	1030	---ATCAGATTTAGACCGTGACACTCTACTTAGAGAGCCAGTCTCAGCTCCACACACCA	1086
Sbjct	117492	GCGATCA---TT-----GT---ACTCTATTTGGAGAGCCCAATATCAGCTCCAGACACTG	117444
Query	1087	TTACACCTAGAATGTGAAGCAACAGTTGCCCTCTGTATTGGAGGATTAGCTCGCGGAGAT	1146
Sbjct	117443	CTACACCTAGAATTTGAAGCAACAGTTACCGTCCCTCTTGGAGGACTGGTGGGAGG-GAT	117385
Query	1147	AAATGCGGCTCTGAAAAGCACCGTACTGGCCAAGGGACACTGGCTATTGCTCTG--AGGC	1204
Sbjct	117384	GGATGTGGCTGCAAAAAGCACCTTGCTAGCACGCAGGCATCGGGTA--GCTCTGGGAGGT	117327
Query	1205	CGTAGTTGTCTTTTCTTGCAGGGCG-TTTTTAGTGCAGTGGGCAGATACAAAATGCAGT	1263
Sbjct	117326	TGTAAGTGTCATCTCCTACAGGATTATTTTAGGGTAGTGGGCAAATATAAAATGTACT	117267
Query	1264	GTAGGGTATTTCAGAAAGGAGAGCACTGGGCTGCAGATTGCCACTGTGTAGCCTGCTACT	1323
Sbjct	117266	GCAGGATATTACGGTAGGAAGAGAA-----TGCACT-----GCAGCCCGCTCCC	117222
Query	1324	TTACTGACCCCTTCCCCTTTTTTCCCTTTTCTTTACAGTTCTACTGAGATACAAGGGA	1383
Sbjct	117221	TTATTAACCAGCC-CCCCTTT-----CTTTT--TTACAGCCCTGCTGAGATA---GGAA	117173
Query	1384	GGCAGAGCCCTGGAACATTGCTTTGGAGATTCTCGGTGCAAACTAGGCTTTTCTGCAAAA	1443
Sbjct	117172	GGCAGAGCC-----ACCTC-CTCTCCTC-TCCACCTGCAGATTAAGCTTTTCTAAAAAG	117120
Query	1444	CCTGAGCATTTTGTATATTTCAGATAACCAAGTCATTGTGAGTCATGGCTAGCATCATTGC	1503
Sbjct	117119	CCTAGGCATCTTCTTATATTTCAGATAACCTATCGTCGTCAGTCATGGCTAGCATCATTGC	117060
Query	1504	ACATATGTTGAACAGTCGGGGCCAGAATGCACCCTTGCCACCTTGGGCCCATTCCATGCT	1563
Sbjct	117059	ACGTGTCGGTAACAGCCGGCGGCTGAATGCACCCTTGCCGCTTGGGCCCATTCCATGCT	117000
Query	1564	GAGGTCCCTGGGAGGAGCCTTGGTCCCTTAATGGCCCACTTGGCAGAGAGAAACATAAA	1623
Sbjct	116999	GAGGTCCCTGGGAGAGTCTCGGTCTATAATGGCCAGCATGGCAGACAGAAACATGAA	116940
Query	1624	GTTGTTCTCGGGAAGGGTGGTGCCAGTCCAGGGGAAGAAACCTTTGAAAACCTGGCTGAA	1683
Sbjct	116939	GTTGTTCTCGGGAGGGTGGTGCCAGCCCAAGGGGAAGAAACCTTTGAAAACCTGGCTGAC	116880
Query	1684	TCAAGTCAATGGGATCTTGCCAGATTGGAATACCTCTGAGGAGGAAAACTCAAGCGCTT	1743
Sbjct	116879	CCAAGTCAATGGCGTCTTGCCAGATTGGAATATGTCTGAGGAGGAAAAGCTCAAGCGCTT	116820
Query	1744	GATGCAGACCCTTAGGGGCCCTGCCAGGAGGTCATGCGCTTGCTTCAGGCAGCCAACCC	1803
Sbjct	116819	GATGAAAACCTTAGGGGCCCTGCCCGGAGGTCATGCGTGTGCTTCAGGCGACCAACCC	116760
Query	1804	CAGCCTAAGTGTGGCAGATTTCTTGCGGGCCATGAAACTGGTGTTTGGGGAGTCTGAAAG	1863
Sbjct	116759	TAACCTAAGTGTGGCAGATTTCTTGCGAGCCATGAAATTGGTGTTTGGGGAGTCTGAAAG	116700
Query	1864	TAGCGTGACTGCCCATGGTAAATTTTTTAACACCCTGCAGGCGCAAGGAGAGAAAACATC	1923
Sbjct	116699	CAGTGTGACTGCCCATGGTAAATTTTTTAACACCCTACAAGCTCAAGGGGAGAAAGCCTC	116640
Query	1924	CCTGTATGTGATCCGTTTAGAGGTGCAGCTCCAGAATGCTATTACGGCAGGAGTCGTAGC	1983

Sbjct	116639	 CCTTTATGTGATCCGTTTAGAGGTGCAGCTCCAGAACGCTATTACAGGCAGGCATTATAGC	116580
Query	1984	TGAGAAAGATGCAAACCCAGACTCGCTTGCACCAACTCCTTCTAGGGGCTGAGCTGAACAG	2043
Sbjct	116579	 TGAGAAAGATGCAAACCCGACTCGCTTGCAGCAGCTCCTTTTAGGCGGTGAGCTGAGTAG	116520
Query	2044	GGACCTGCGCTTCAGGCTTAAGGAGCTTCTCAGGATGTATGCAAATGAGCAGGAGTGTCT	2103
Sbjct	116519	 GGACCTCCGACTCAGACTTAAGGATTTTCTCAGGATGTATGCAAATGAGCAGGAGCGGCT	116460
Query	2104	TCCCGGTTTCTGGAGCTAATCAGAATGATAAGGGCTGAAGAGGATTGGGATGGCACTTT	2163
Sbjct	116459	 TCCCAACTTTCTGGAGTTAATCAGAATGGTAAGGGAGGAAGAGGATTGGGATGATGCTTT	116400
Query	2164	TATTAAACGAAAGCGACCCAAAAGATCTGAGTCAGTTGTGGAGAGGGCAGCTAACCCGT	2223
Sbjct	116399	 TATTAAACGGAAGCGTCCAAAAAGGTCTGAGTCAATGGTGGAGAGGGCAGTCAGCCCTGT	116340
Query	2224	GGCATCGCAGGGCCTGCAGCCGATAGTGACTGGCAATGCTAATTGCAACTTGATAGAGAT	2283
Sbjct	116339	 GGCATTTCAGGGCTCCCCACCGATAGTGATCGGCAGTGCTGACTGCAATGTGATAGAGAT	116280
Query	2284	CGATGATTCCCTTGATGATTGAGATGAGGATGTGATCTTGGTGGAGCCTCAGGACCCCTC	2343
Sbjct	116279	 AGATGATACCCCTCGACGACTCCGATGAGGATGTGATCCTGGTGGAGTCTCAGGACCCCTC	116220
Query	2344	AGTCATATCGGTGGCTTCTCCTCCCCCTGTGTG-CAGGGCCAGACCTCAGGATCAGGTGC	2402
Sbjct	116219	 ACTTCCATCCTGGGGTGCCCCCTCCCC-TCAGAGACAGGGCCAGACCTCAGGATGAAGTGC	116161
Query	2403	TGGTCAATGATTCCCCCAACAATTCCTGGGCCCGGTTTCTTCCACCAGTGGTGGTTCTG	2462
Sbjct	116160	 TGGTCATTGATTCCCCCACAATTCAGGGCTCAGTTTCTTCCACCAGTGGTGGTTCTG	116101
Query	2463	GGCATCAGAGTGATGGTCTGGGGATAAGCGTAAGGCCAGGAAGCGAAAAATACACAATCC	2522
Sbjct	116100	 GCTATAAGAATAACGGTCTGGGGAGATGCGTAGAGCCAGGAAGCGAAAAACACACAATCC	116041
Query	2523	GCTGTTTATTTTGTGGTGAAGAGGGCCACACAAAAGAAATTTGTG---GTGAAAAACAACA	2579
Sbjct	116040	 GCTGTTTCGTATTGTGGTGAAGAGGGCCACTCAAAGAAACCTGTGACAACGAGAGTGACA	115981
Query	2580	AAGCCCAGGTTTTTTGAGAATCTCATTATCACCCCTTCAGGAACCTGACACATACAGAGGAGG	2639
Sbjct	115980	 AGGCCCAGGTTTTTTGAGAATTTGATCATCACTCTCCAGGAGCTGACCCATACTGAGATGG	115921
Query	2640	AGGAGACAAAAGAGGTCTCTGGTGGACGCAATGACCTCTCTGAGCTGCGGAAAGGAGCTA	2699
Sbjct	115920	 AGAGGTCAAGAGTGGCCCTGGCGAATACAATGACTTCTCTGAGCCACTGTAAGGGACCA	115861
Query	2700	GCCCCAGCCCTAAATGAACCGTTGTCTATATTTAGCGTACAGTGGGGGGAAGACTGGGG	2759
Sbjct	115860	 -CCCCAGGTTTCAGTGAACCCCTACCTATATTAGCATCCAGTAGTGGGAAAACCTGGGG	115802
Query	2760	AGGGG-----TTTTTCATTGCATGCATTAATCCTCAGAGCAACTTTCTTTTGG	2806
Sbjct	115801	 TGGGGGTGGGGGTGGGACTTCTAACTGCATGAATTAATCCACAAAGCGGCTATCTTTTGG	115742
Query	2807	GGTGGAGGACAAAAAGCTTTTGATGCCAGCACAGGGGAGGGGAATGGCCTGACCTTTCTG	2866
Sbjct	115741	 GGTGGAGTAGAAAGGGTCTTGGATACCAGCACATTGGAGGGAGATAGCCTGACC--TCTG	115684
Query	2867	TCTCTGCTC--TCTCCCT---ACCTAAGGGTCCATTTTCTGTGTGTGTCTAATTCTTTGA	2921
Sbjct	115683	 TCCTTGCTCCTTCTCCCTGCAGCCTACGGGTCTGTTTTCTGTGTGTGCCATTTCCTTGA	115624
Query	2922	TGGGTTTACTCTCTTTGTGAAACTGGTGCAA-----	2952
Sbjct	115623	 CAGCTTTA--TTCTTTGTGAAAGTGGTATAATTATTGTTAAATATTTGAACAATAAAAA	115566
Query	2953	--GTACAAAAACTAATGTAC-AGCTACCTGAAACCCCTCCACCCATATATAATCATTGTCA	3009
Sbjct	115565	 AGGTACAAAAAGTGAAGTACAAATTACCCAAATCTCTCCACCCCTATATAATCATTGTCA	115506
Query	3010	AGCCTTTTGATGAATGCCTTTCTAGATACTTCCCTATACCTGTGTACCCAGATAGATTTAT	3069

Sbjct	115505	ACCCTTTGTATGAGT-----GATATTTCCCTATACCTATGTACCCAGATAGATATAT	115455
Query	3070	GTATAGATAAAAAAGTGATCAAATAAAAAAGTGCTGTTGTATATTGTGTATTTTTCACCAAA	3129
Sbjct	115454	GCATAGAT-AAAAGTGATGAAAT-ATAAGTGCTGTTCTAT-CTGTAT-TTTTTCACCAAA	115399
Query	3130	C 3130	
Sbjct	115398	C 115398	

C. Highly conserved introns in placental mammals are not limited to domesticated genes but can be found in diverse genes located either on autosomes or sex chromosomes

Query was Homo ZFX intron 1 (located in the 5'UTR)

>gb|AAGU03060905.1| *Loxodonta africana* (AFROTHERIA) cont3.60904, whole genome shotgun sequence

Length=100138

Score = 1348 bits (1494), Expect = 0.0
Identities = 1463/1929 (75%), Gaps = 191/1929 (9%)
Strand=Plus/Minus

Query	1	TGAGTCCCGGGTGCCGCCGCGCGGGGCTAGTGCGCGCACAGCGGCTGGTCTCGG	60
Sbjct	84575	TGAGTCCCGGGCGCTG-----GCGGGGCTAGCACGCGCAGCGGCTGGTCCCGG	84524
Query	61	CCTGGTcggcggcccgcaaggcgccctcccgcgctaggccggggcggtggcgcgcgcg	120
Sbjct	84523	CCTGGTCGGCGGCCCGCAAGGCGCCTTCCGCGCTAGGCCGGGCGGCGTGGCGCGCGCG	84464
Query	121	ccgAGCAGGCCCGGAGGAGCCGAGTTAGGCCCCGGGAGGAGCCCGGCTGCCCCGAGCG	180
Sbjct	84463	CCGAGCAGGCCCGGAGGAGCCGAGTTAGGCCCCGGGAGGAGCCCGGCTGCCCCGATCG	84404
Query	181	GCGGCGGAGGCGCGCTCCGTAAGCGGGCGGGGTTGGGGGAGGGTCGCCCGGTTGTGCCG	240
Sbjct	84403	GTGGCGGAGGCGCGTTCCGTAAGCGGGCGGGGTTGGGGGAGGGTCGCCCGTAGCCCGT	84344
Query	241	GAGGCGGTCGAGGGGCCCCGGGTCGGCTCCGCGGCCGACCTGGGGCACCAGCGCCGGGGTG	300
Sbjct	84343	GAGGCGGTCGAGGGGCTCCGGGTCGACGCCACGGCCGGCCCTGGGCACTGCGCGGGGTCG	84284
Query	301	AGGCCTGGCGAGGAGGCGAAGGCTGCAGGCGTGAGGTGAAGGCCGAGGCCGGCCGGGCC	360
Sbjct	84283	AGGCCTGGTCGAGGAGGCGAAGGCTGCAGGCGTGAGGTGAAGGCCGAGGCCGGCCGGGCC	84224
Query	361	GATTTTCGCTATGTAAATATCGGTGAggggggggagggagcggggACAAGATGGCGGCG	420
Sbjct	84223	GATTTTCGCTATGTAAATATCGGTGA--GGGGGGAGGGACGGGGGACAAGATGGCGGCG	84166
Query	421	GCTCGGCGCCTGCTGCAGGGGACGATAGAGGGGGTTGCCGGGAGGGGAGCCGCCATCTT	480
Sbjct	84165	GCTCGGCGCCTGCTGCAGGGGACGTTGAGGGGGTTGCCGGGAGGGGAGCCGCCATCTT	84106
Query	481	GGAGGCGGTGTCTGGAGAGAAAATTCGCTACAGCCCGTGAgggggggtgggagagcggg	540
Sbjct	84105	GAAGGCGGTGTCTGGAGAGAAAATTCGCTACAGCCCGTGAGGGGGGTGCGAGAGCG--	84048
Query	541	cggcgggcggcagcgcgccggtgacgggccccgagggccccggcgcgcggtgtgcgcg	600
Sbjct	84047	----GGCGGTAGCGCGCCGGTGAAGGGCCCGGAGGCCCGCGCGATGGCGTGTGCGCG	83992
Query	601	cggagggggcgTGCTCGCTCCCCGTGGCGGCCATTGCCCTTGCCGCCATGATGAGCGCTCG	660
Sbjct	83991	CGGAGGGGCGTGTCTGTTCCCCACAGCGGCCATTGCCCTGCGCCCATGATGAGAGTTTG	83932
Query	661	GGCTCCAGGCGCTCGGCGGCAGCGCCACCTTCCTGCCTTGCTTCCGCGAGCCCCGTGACT	720
Sbjct	83931	GGCTCCAGGTCCTCGGCGGCAGCGCCACCTTCCTGTCTGCTGCGCAACCCCGTGACT	83872
Query	721	GGCTGCAGTTTCCGCTGCGTTTCAGCTGAGCTGCCGCGAGCGGC---CACCGCCGCGCC	777
Sbjct	83871	GACTGCTGTTTCCGCTGCATTTTAACTGAGCTGCCGCGAGCGGCCGTCGCTGCCGCTGCC	83812
Query	778	CGGACGCCGGGACCGTTTACCCCTCAGCGCCCTGGCCCTGCGCCTTCCCCCGCGCCTGT	837
Sbjct	83811	CAGGCGCCGAGCCCG-----GGGGTGTGG-----GCCACTGCGTTTGT	83773
Query	838	AGCCACCCGAGGGCAGTCGGGCGAGGTGGCATTCGGACACCTGGGCTTACCAGGGCATA	897
Sbjct	83772	AGC-----TCACTC-----CGTATCGG-CATCTCGCCTCACCAAGGCAGA	83734
Query	898	CGGGACCCAGGAAATGTTATTTTGTCTTAAGTCAAATCATATGTGGCTGCTAAGGTGCT	957

Sbjct	83733	-----	83688
		TGGGACATCAAGAAATTTTA-----AAGTTATGAGTGCCTCTTAGGGTGCT	
Query	958	TTGATGTCAGTTGTTTTTCCAACAATCTTTGCCGCCCGAGTATCTGAATAAAGGAAGAA	1017
Sbjct	83687	CTCTGTGTGCTTG-TTTTCCAACAATCATTGTCTCTCCAGTATCTGAATAAAGAAATAA	83629
Query	1018	AAATAAAGATTGATGGGA---AAGTTTTTGCCATTCTTTTGTCTATAG-GGaaaa---	1069
Sbjct	83628	AAATGAAATTTGATGGCAAAGAAGTTCTAATCACTCTTTTGTCCAATAGAAGAAAAGTGC	83569
Query	1070	aaaTTGCACAACACGAGAGCGGAGGAATAAAATT-TTGAATC-ATTCGTACTCATTATG	1127
Sbjct	83568	AGATTGCACAACACCAAAGCGGAGGAATAAAATTGTGGAGTCTTTTATTGTCGTTTATT	83509
Query	1128	TGGAACAACACTTTCTTGA-----AAAACGATTTAAGTA-----GTGAT-CTGTT	1170
Sbjct	83508	TGGAACAGCTGTGTTGACGAGCTCTTTTAAACTA-TTAATTAATCCCCTTATACTGTT	83450
Query	1171	GG-----TGGTAttt---ttttAAATCG--AGGAATAAG-GGCAGAC	1206
Sbjct	83449	TGCTCTTTAATGAGTTTCATACTATTTACTGTTTTTCAGGGTTAAGAAAAGACAAAGGT	83390
Query	1207	TTTTTTATTTTCTTATTGGAGGACAACCTTAGTGTGGTGCA-TATTTATTGTGCATTGGC	1265
Sbjct	83389	TTTTTTATTTT-TAATTGAAGGACAGCATAATCTAATGAAGTATTATTGTTCCTGTACC	83331
Query	1266	TGTCATGGTATTTTCGATTTTTCATTTGTGAAGTTTAAGGCGGAGTTTCATCCCCTAACG	1325
Sbjct	83330	TGTCATGGTATTTAAATT---ATTGAAAAGTTTAAGATTGAGTACCATCCCATAACG	83275
Query	1326	TACTTTTTTGATTGCACACTGTGCAACTTCTTGATAAACTCGGAGCCTACTGTTAGCGA	1385
Sbjct	83274	TAC--TGTTGATTGCGCAGTATACCACCTTCCTGGTACAGTCGGAGCCCACTGTTTGCGA	83217
Query	1386	TGCACCGTGCTAGATGCTAAGAAACATTAAAAAGGTTCTTGTAATGCAGACGGTGGCTGC	1445
Sbjct	83216	TGCACTCTGCTAGGTG-TTAGAAAGATTAAACGGTTGTGGTAATGCAGACGGTGGCTGC	83158
Query	1446	AAGAAGTCTC-ATGTTTAGAGGTAGGTGGGGCAAGGTGAAATGCAGTAAAGTG-----	1497
Sbjct	83157	AAGAAG-CTCGTTGTCCAGAAGTAGATGAGACCAGGTGAAATGCACT-AAGTGCTGCGGA	83100
Query	1498	AGAGGTACAACATAATTACTGGGATTTCCGAGGGAAGCAAGGTTGCCA-TTGGAGGATCAG	1556
Sbjct	83099	AAAGGTACACCCAGTTACTGGGGGTCCAGACGAAGGCGGGGTTTTATTGGAGCATCA-	83041
Query	1557	GGAGGGAC-GGGTTCCTGAAGTATTAATAGGT-GGCATTTTGAGAAGGTTACCGAGGGAT	1614
Sbjct	83040	----GGACAGGGTTCCTGGTGTA----GGGTAGGC----GAGAAGGTTTCTGAAGGAT	82995
Query	1615	GGGTAGGACTTTGTAGGTAGAGGTGGAGGTGGAGAAAGGACGTTTCAAGGGTGAAGCTT	1674
Sbjct	82994	GGGTAGGACTTTGTGAGGTAGAGGTGG-GGTGGGGAAGGGCATTTCAGGGTGAAGCTT	82936
Query	1675	CTTCAGTAAACAGTAAGTATTTACAGTTTGGCAAAAGTGGATGGTATAGGTAGGGGAGTG	1734
Sbjct	82935	CTTCAGAAAACAGCAAGTGTTTACCGTTTGGCTGGAATCGATGGTATAG-----	82887
Query	1735	GTGGGAATTCAGGCTAGAAAAGTTAGATTGCAGAAGGGCTTGCTTGCCAGGT-GGAGGGG	1793
Sbjct	82886	-----ACATGCTAGAAATGGTAG-TTGCCAAAGAGCTGGCCTGCTATGTGGGAGGGG	82836
Query	1794	CTTATACTCAATGGGGTAG---GCAGCGGGGTGCCCTCAACTAGAAAGAGTGATGGCACA	1850
Sbjct	82835	CTTCTACTCTGCGTGGGAGAGAGAGCGAAGG-GCCTTCTACCAGCGAGTGAAGATACA	82777
Query	1851	CCTGAGCTG 1859	
Sbjct	82776	CCTGAGCTG 82768	

>gb|AAGV020292018.1| *Dasypus novemcinctus* (XENARTHRA) cont2.292017, whole genome shotgun sequence
Length=2385

sequence by: Sort alignments for this subject

E value Score Percent identity
Query start position Subject start

position

Score = 495 bits (548), Expect = 6e-137
Identities = 629/844 (74%), Gaps = 51/844 (6%)
Strand=Plus/Plus

Query	523	gggggggtgggagagcgggcgggcgggcagcgggcgccggtgacggggccc-ggaggcccg	581
Sbjct	3	GGGGGTGG-AGAGCGGGCG-CAGCGGCAGCG---CCCGTGACGGGTCCCAGGAGACCCG	57
Query	582	gcgcggcgcggtgtgcgcgcggagggcgTGCTC-GCTCCCCGTGGCGGCCATTGCCCTT	640
Sbjct	58	-CGCGC--GCGTGAGCGCGCAGAGAGGCGTGCTCCGCTCCCCACCGCGACATTGCCCTT	114
Query	641	GCCGCCATGATGAGCGCTCGGGCTCCAGGCGCTCGGCGGCAGCGCCACCTTCTGCCTTG	700
Sbjct	115	GCCGCCATGATGAGCGCTCGAGTTCCAGGCGCTCGGCGGCAGCGCCACCTTCTGCCTTG	174
Query	701	CCTCCCGCAGCCCCGTGACTGGCTGCGATTTCGCTGCGTTTCAGCTGAGCTGCCGCAGG	760
Sbjct	175	CCTCCCCAGCCGCTGACTGGCTGCTGCTTCCGCTGCATTTTAACTGAGCTGCCGCAGG	234
Query	761	CGGCCACCGCGCCCGCCGACG--CCGGGACCGTTTACCCCTCAGCGCCCTGGCCCTG	818
Sbjct	235	CAG---CCGCCGTCGCTCGGCGCTCCGCGCCAACTCGTCCCTCCGTGTCCCCGGCCCCG	291
Query	819	CGCCTTCCCCCGCGCCTGTAG-CCACCCGAGGGCAGTCGGGCGAGGTGGCATTCCGGACA	877
Sbjct	292	CGCC-TGTCCCGCTTTGTAGCCACGCGAGGGCCGCTCTGGGCGGTGGCAATCCGGGCA	350
Query	878	CCTGGGCTTACCAGGGCATAACGGGACCC-CAGGAAATGTTATTTTGGCTTAAGTCAAATC	936
Sbjct	351	TCTGGGCTCATCGATGCCAAAGGAACCCCTGAGGAAATTTTCTTTTAAATAAAGGC	410
Query	937	ATATGTGGCTGCTAAGGTGCTTTCGATGCAGTTGTTTTCACAAATC----TTTGCCGC	992
Sbjct	411	ATACGTGGCTGCTAGGGTGTCTTGTATGCGGTTG-TTTCTAGCAATCACTGATTGCCCC	469
Query	993	CCCGAGTA----TCTGAATAAAGGAAGAAAAATAAGATTGATGGGAAAGTTTGGCCAT	1048
Sbjct	470	CTCATGTACCAGCCTGAATAAAGAACAAAAATGAAATTTGACGGGAAAGAAATTTCTCAT	529
Query	1049	-TCTTTTGTCTTATAGGAAAAA-----aTTGCACAACACGAGAGCGGAGGAATAAAA	1101
Sbjct	530	CACTCTTGTCGAATAGGAACAGAAGTGCAGATTGCACTGCAAGAAAGCGGAGGAATAAAA	589
Query	1102	TTTTGAATCA--TTCGTACTCATTTATGTGGAAACAACCTTCTTGAAAAA--CGATTTA	1156
Sbjct	590	TTTTGAAGGAGTCTTGTCTCGTTTATTTGGAACAACCTTCTTGAAAACTCCATTTA	649
Query	1157	----AGTAGTGATCTGTTGGTGGTAttttttAAATCGAGG-----AATAAGGGCAGACT	1207
Sbjct	650	AAGTATTACTGATCTCCCTATCCTATTACTTTTTTCGACGGTTAAGAAAAGGACGAAGT	709
Query	1208	TTTTTATTTCTTATTTGGAGGACAACCTTAGTGTGGTGC-ATATTTATTGTGCAATTTGCCT	1266
Sbjct	710	TTTTCATTTCTAATTGAAGCACATCATAATGTGATGCAATATTTATTGTTTATATACCT	769
Query	1267	GTCATGGTATTTTCGATTTTTCATTTGTGAAGTTTAAAGCGGAGTTTCATCCCTAACGT	1326
Sbjct	770	GTCACGGTACTTAAATTCTCTATT--TTAAGTTTTAAGGTTGAGTTTCAACCCTTGAAGT	827
Query	1327	ACTT 1330	
Sbjct	828	ACTT 831	

Score = 235 bits (260), Expect = 9e-59
Identities = 286/386 (74%), Gaps = 43/386 (11%)
Strand=Plus/Plus

Query	1418	AGGTTCTTGTAAATGCAGACGGTGGCTGCAAGAAGTCTCATGTTTA-GAGGT-AGGTGGGG	1475

Sbjct	1363	AGGTTCTTATAATGCAGACGGTG---CAAGAATT-TCGTTTTCTCAGGTTAGATGAGA	1417
Query	1476	CAAGGTGAAATGCAGTA AAA-----GTGAGAGGTACA AACTAATTACTGGGATTTC CGAGG 	1529
Sbjct	1418	CAAGGTGAAATGC ACTAAA TACC GCGGAAGAGGTAC AGCCAATTACTGGGATTTCAGAGG	1477
Query	1530	G AAGCAAG GTTGCCATT-GGAGGAT CAGGGAGGGACGGGTTCCTGAAGTATTA ATAGGTG 	1588
Sbjct	1478	AAGGCAGGTTTTCCATT TTGAGCATCAGG AAAGA----G TTCCTGATGTA-----GGTG	1527
Query	1589	GCATTTTGAGAAGGTT ACCGAGGGATGGGTAGGACTTTGT TAGGTAGAGGTGGAGGTGGA 	1648
Sbjct	1528	GCATTTTGAGAAGGTTAGT GAAGGACGGGAAGGACTTTGT TAGGCCAAAGGTGGGGGTGGG	1587
Query	1649	GAAAGGACGTTTCAAGG TG AAGCTTCTTCAGTAA ACAGTAAGTATTTACAGTTTG GCAA 	1708
Sbjct	1588	GAAAGGGCATTTT CAAGAG-----TTTTTAGAAA ACAGCAAGTATTTACAATT TG GCTG	1640
Query	1709	AAGTGGATGGTATAGGTAGGGAGTGGTGGGAATTCAGGCTAGAAAA GTTAGATTGCAGA 	1768
Sbjct	1641	TAGTGGATAGTATAGGTAGTGAA--GTGGCAATTC-----CAGGTAGGTTGTGAA	1688
Query	1769	AGGGCTTGCTTGCCAGGTGGAGGGGC 1794 	
Sbjct	1689	AGAGCTTGCTTGCCAGGTGGAGAGGC 1714	

Score = 100 bits (110), Expect = 5e-18
Identities = 81/97 (83%), Gaps = 2/97 (2%)
Strand=Plus/Plus

```
>gb|AAEX02025623.1| Canis familiaris (LAURASIATHERIA) cont2.025622, whole genome shotgun
sequence
Length=145932
```

Sbjct	141194	GCTCGGCGCCTGCTGCAGGGAACGATTGAGGGGGTTGTCTGGGAGGGGGAGCCGCCATCTT	141135
Query	481	GGAGGCGGTGTCTGGAGAGAAAATTCCGCTACAGCCCGTGAgggggggtgggagagcggg 	540
Sbjct	141134	GAAGGCGCGCTCTGAAGAGAAAAATTCCGCTACAGCCCGTGAGGGGGGGTCGGAGAGCGGG	141075
Query	541	cggcggcgcgcagcggcgccgggtgaacgggccccggaggcccggcgcgcgcgctgtgcgcg 	600
Sbjct	141074	CGGCGGCG---GCGGCTCCGGTGACGGGCCCCGAGGCCCGGCACGGCACGCCTGTGCGCG	141018
Query	601	cggA-ggggcgTGCTCGCTCCCCGTGGCGGCCATTGCCCTTGCCGCCATGATGAGCGCTC 	659
Sbjct	141017	CGGAGGGGGCGTGCTTGCTCCCACAGCGGCCATTGCCCTTGCCGCCATGATGGGCGCTC	140958
Query	660	GGGCTCCAGGCGCTCGGCGGCAGCGCCACCTTCTCGCTTGCCCTCCCGCAGCCCCGTGAC 	719
Sbjct	140957	AGGCTCTAGGCGCTCGGCGGCAGCGCCACCTTGCTGCCCTGCCTCCCGCAGCCCCGTGAC	140898
Query	720	TGGCTGCAGTTTTCCGCTGCGTTTTAGCTGAGCTGCCGAGGCGGCCACCGCCGCCGCCCG 	779
Sbjct	140897	TGGCTGCTGCTTCCGCTGCATTTTAAGTAGAGTGCCGAGGCGGCCATC-----	140849
Query	780	GACGCCGGGACCGTTTCACCCCTCAGCGCCCCCTGGCCCTGCGCC--TTCCCCCGCCTGTA 	838
Sbjct	140848	-----TCGT----CCCTGGGCGTCCCTGGCCCTGCGCCTTTCTCCCGCTCCTGGA	140803
Query	839	GCCACCCGAGGGCAGTCGGGGCAGGTGGCATTCCGGACACCTGGGCTTACCAGGGCATAC 	898
Sbjct	140802	GCAACCCGAGGGATGTCTGGGACGGGTGGCAGCCAGGCATCTGGGCTCGCTACGGCAAAT	140743
Query	899	GGGACCCCGAGAAATGTTATTTTTGCTTAAGTCAAATCATATGTGGCTGCTAAGGTGCTT 	958
Sbjct	140742	GGAACCCACGACATTTTATTTTTACT----CCACGTCGTACGTGGCTATTATGGTGCCC	140687
Query	959	TCGATGCAGTTGTTTTTCCAACAATCTTTGCCGCCCCGAGTATCTGAATAAAGGAAGAAA 	1018
Sbjct	140686	TCGATGC---GGTTTTGCAGCACTCTCTGCTTTCTCTAGTACCCGAATAAAGAAATAAA	140631
Query	1019	AATAAAGATTGATGGGAA-AGTTTTTGCCATTCTTTTGCTTA--TAGGGaaaa----aa 	1071
Sbjct	140630	AATAAAATTCGATAGGAACAGTTCTCATCACGCTTTTATCCAACGGAGGGGAAAGTGTA	140571
Query	1072	aTTGCACAACACGAGAGCGGAGGAATAAAATTTT----GAATCATTCGTACTCATTTATG 	1127
Sbjct	140570	TTTGCACAACACGAAAACAGAGCAGTAATTTTSTAAGGAGTCTTTTGAAGTCAATTTATT	140511
Query	1128	TGAAACAACACTTCTTGAAAA--ACGATTTAAG----TAGTGATCTGTTGGTGGTA----	1177
Sbjct	140510	TGAAAGCAACTTCTTAGAAAAGGTCCATTTAAGCTATTAGTGATCTGTTGGTATTAACTT	140451
Query	1178	---ttttttaaATCGAGGAATA--AGGCAGACTTTTTTATTTTCTTATTGGAGGACA 	1231
Sbjct	140450	TTTTTTTTTTTTTTTGGAGGAGTAAGGAGGTGAGA-AAGTTATTTCCTTA-----	140402
Query	1232	ACTTAGTGTGGTGCA-TATTTATTGTGCATTTGCCTGTCATGG--TATTCGATTTTTCA 	1288
Sbjct	140401	-----GTCGTGCAGTATTTATT---CATCTGCTTGCCATGGTTTTTTTAGTTTCTTTA	140352
Query	1289	TTTG---TG--AAGTTTTAAGGCGGAGTTTCATCCCCTAACGTACTTTTTTGATTGCACA 	1343
Sbjct	140351	TTTGACTTGAAAAATCTTAGGTGGCATTCCGTCCTCGAGAGGAC--TTTTGATTGCACA	140294
Query	1344	CTGTGCAACTTTCTTGATAAACTCGGAGCCTACTGTTAGCGATGCACCGTGCTAGATGCT 	1403
Sbjct	140293	CTGCAGAACTCCCTG-TAAACTTGGAACCCAGTGTTAGCGATGCACTGTGCTCGCTGAT	140235
Query	1404	-AAGAAACATTAAAAAGGTTCTTGTAATGCAGACGGTGGCTGCAAGAAGTCTCATGTTTA 	1462
Sbjct	140234	AAAGAAAGATTAGAAAGGTTCTTGGGATGCAGACGGTGGCTGCAAGAAGTTCGTTGTTCA	140175
Query	1463	GAGGTAGGTGGGGCAAGGTGAAATGCAGTAAAGTG-----AGAGGTACAAC 	1509
Sbjct	140174	GAGGCGGAGGAGTCCTGGTGAATTGCACTCAAGTGCTGCTGGGGGGAAAAAGGTACAGCC	140115
Query	1510	AATTACTGGGATTTCCGAGGGAAGCAAGGTTGCCATTGGAGGATCAGGGAGGGACGGGTT 	1569
Sbjct	140114	AATTACGGGGGTTCCAGAGGAAGGCAGAGTTTCCATT--TGGAGC-GTGAGGAAGGTTT	140055

Query	1570	CCTGAAGTATTAATAGGTGGCATTTTGAGAAGGTTACCGAGGGATGGGTA--GGACTTT	1626
Sbjct	140057	CCTGAAG-----TAGGTGACATTTT--TGAGGTACTTAAGGATGGGGAGGGGGGCTTT	140006
Query	1627	GTT-AGGTAGAGGT-GGAGGTGGAGAAAGGACGTTTCAAGGGTGAAGCTTCTTC---AG	1680
Sbjct	140005	GTTAAAGCATAAGTAGCCGGTGGGGAAAGGGCATTTCAGGGTGAAGTTCTTCACAAAG	139946
Query	1681	T-----AAACAGTAAGTATTTACAGTTTGGCAAAAGTGGATGGT	1719
Sbjct	139945	TAGCAAGTATTTGAGAAAAACAAACCAGCCAGTATTTGTAGTTTGGCAGGAGTCGATGGT	139886
Query	1720	ATAGGTAGGGGAGTGGTGGGAATTCAGGCTAGAAAAGTTAGATTGCAGAAGGGCTTGCTT	1779
Sbjct	139885	GAAGGTAGGGAGGTGATGAGATTCTTGCTAGAGAAG----GTGC--AAGGGTTTGCTT	139833
Query	1780	GCCAGGTGGAGGGGCTTATACTCAATGGGGTAGGCAGCGGGGTGCCCTCAACTAGAAGA	1839
Sbjct	139832	GCCAGGTGGAGGGGCTTATA--CGTTGGAGGTGGC--CAGGGCAGCCCTTGCGTAGAAGG	139777
Query	1840	GTGATGGCACACCTGAGCTGCACCTTGTTATTTACTTA	1877
Sbjct	139776	ATGATAATACACCTGAGCTG-GGCTTTATATTCACTTA	139740

>gb|AAGW02040882.1| *Oryctolagus cuniculus* (EUARCHONTOGLIRES) cont2.40881, whole genome
shotgun sequence
Length=2750

Score = 1041 bits (1154), Expect = 0.0
Identities = 1284/1717 (74%), Gaps = 121/1717 (7%)
Strand=Plus/Minus

Query	175	CGAGCGGCGGCGGAGGCGCGCTCCGTAAGCGGGCGGGGGTTGGGGGAGGGTCGCCCGGTT	234
Sbjct	2675	CGATCTGCGGCGTAGGCGTGTTCA-TAAACGGGCGGTGGTTGCGGGAGGGTCGCACAGCG	2617
Query	235	GTGCCGGAGGCGG-TCGAGGGGCCCGGGTC-GGCTCCGCGGCC-GACCTGGGGCACCGC	291
Sbjct	2616	GGTCTTGAGGCGGGTTGAGGGGCCCGGATCAGGCGTCGCAGCCTGTCCCGAGGCACTGA	2557
Query	292	GCCGGGGTGAGGCC-TGGCGAGGAGGCGAAG-GCTGCAGGCGTGAGGTGAAGGCCGAGG	349
Sbjct	2556	GAGGGGGTGAGACCCTGGCGAGGAGGCGAAGAGCTGCAGGCGTGAGGTGAAGGCCGAGG	2497
Query	350	CCGGCCGGGCGGATTTTCGCTATGTAAATATCGGTGAggggggggaggggacgggggACA	409
Sbjct	2496	CCGGCCGGGCGGATTTTCGCTATGTAAATATCGG--AGGGGGGGGAGGGACGGGGGACA	2439
Query	410	AGATGGCGGCGGCTCGGCGCCTGCTGCAGGGGACGATAGAGGGGGTTGCCGGGAGGGGA	469
Sbjct	2438	AGATGGCGGCGGCTCGGCGCCTGCTGCAGGGGACGACTGAGGGGGTTGCCGGGAGGGGA	2379
Query	470	GCCGCCATCTTGAGGCGGTGCTGAGAGAGAAATCCGCTACAGCCCGTGAgggggggt	529
Sbjct	2378	GCCGCCATCTTGAAGGCGGCGTCTGAGAGAGAAATCCGCTACAGCCCGTGAGGGGGGT	2319
Query	530	gggagagcgggcgggcgggcgagcgggcgccggtgacggggcccgaggcccgcgcgcg	589
Sbjct	2318	GGGAGAGCGGGCTGCAGCGCGGCGCGCGGTGACGGGACCGGAGGCCCTGCGCAGCG	2259
Query	590	gcgtgtgcgcgcggagggggtGCTCGCTCCCCGTGGCGGCCATTGCCCTTGCCGCCATG	649
Sbjct	2258	GCGTGTGCGCGCGGAGGGGCTGCTCGCTCCCCACGGCGGCCATTGCCTCGGCCGCCATG	2199
Query	650	ATGAGCGCTCGGGCTCCAGGCGCTCGGCGGCAGCGCCACCTTCCTGCCTTGCCCTCCGCA	709
Sbjct	2198	ATGAGCTCTCGGGCTCTAAGCGCTCGGCGGCAGCGCCACCTTCCTGCCTTGCCCTCCGCA	2139
Query	710	GCCCCGTGACTGGCTGCAGTTTCCGCTGCGTTTACGTGAGCTGCCGCAGGCGGCCACCG	769
Sbjct	2138	GCCCCGTGACTGGCTGCTGCTTCCGTTGCGTTTACGTGAGCTGCCGCAGGCGGCCACCG	2079
Query	770	CCGCCGCCCGGACGCGGGGACCGTTTC-ACCCTCAGCGCCCTGGCCCTGCGC-CTTCCC	827
Sbjct	2078	CCGGCGCCCGGGCGCCAGAGCCCTCTCGCCCTCAGCGCCCGGGGCCGCGCTTTTTC	2019

Query 828 CCGCGCCTGTAGCCACCCGAGGGCAGTC-GGGGCAGGTGGCATTCCGGACACCTGGGCTT 886
 ||||| || || ||||| || ||||| ||||| || ||||| |||||
 Sbjct 2018 TTGCGCTTGCCGCGCCCCGAGGGCCATCGGGGGCCGGTGGCAGCCAGACACTTAGGCTC 1959

Query 887 ACCAGGGCATACGGGACCCAGGAAATGTTATTTTGGCTTAAGTCAAATCA--TATGTGG 944
 || ||| | ||||| ||||| || ||||| | ||||| || |||||
 Sbjct 1958 CCCGAGGCGGAAGGACCCCTGGGAATTTTAAATTTTGGT----TTAAATCAGTTAAGTGG 1903

Query 945 CTGCTAAGGTGCTTTCGATGCAGTTGTTTTTCCAACAATCTTTGCCGCCCGAGTATCTG 1004
 || | | ||| || ||||| ||||| || | ||| ||||| | ||||| |||
 Sbjct 1902 CTTTCAGGATGCCCTCTGTGCGGTTG-TTTGCCTGCCATCCTTGCCCTTCTCGAGTGTGCG 1844

Query 1005 AATAAAGGAAGAAAAATAAAGATTGATGGGAAAGTTTTTGCCATTCTTTTGTCTATAGG 1064
 ||| ||||| || ||||| ||||| || ||||| ||||| |||||
 Sbjct 1843 AAT-----AAATAAAGTGGGTGGGAAAGTTCCCAACCACTCTCCTGTCCAATAGG 1794

Query 1065 G---aaaaaaaTTGCACAACACGAGAGCGGAGGAATAAAATT---TTGAATCATTCGTA 1117
 | || | ||||| ||||| ||||| || ||| || ||||| |||||
 Sbjct 1793 GGGAAAGTATGTTGCACAGAACGAAAGCGGAAGAGTAAGGTTCGGAGGGAGTCATTGTGA 1734

Query 1118 CTCATTTATGTGGAACAACCTTCTTGAAAACGATTTAAGTAGTGA-TCTGTTGGTGGT 1176
 ||| || ||||| ||||| ||||| || || ||||| ||||| |||||
 Sbjct 1733 GTCACCTGGGTGGAACAACCTTCTTGAAAAGC----TGCGT--TGACGCTGTTAG-CGT 1681

Query 1177 AtttttttAAATCGAGGAATAAG-GGCAGAC-TTTTTATTTTCTTATTGGAGGACAAC 1234
 | | | ||||| || ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct 1680 AGCTGGCT---CTGAGGAATAAGAAGAGGACAGTTTAATTTTCTTACT-GAGGAAAA-- 1627

Query 1235 TAGTGTGGTG-CATATTTATGTGCATTTGCCTGTGCATGGTATTTTCGATTTTTCATTGT 1293
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct 1626 -AACGTGGTGAGGTATTTATGTTCATTTACTTGTGCATGGCGTTTC-ATTTTTTTTTTTT 1569

Query 1294 GAAGTTTTAAGGCGGAGTTTCATCCCTAACGTACTTTTTTGATTGCACACTGTGCAACT 1353
 |||| | ||||| || | || ||||| | || ||||| |||||
 Sbjct 1568 ----TTTTTTTTGAAGTTTC--CCGGTGGCG-----TTTGATGG--CAGTGTAAGT 1523

Query 1354 TTCTTGATAAACTCGGAGCCTACTGTTAGCGATGCACCGTGCATAGATGC---TAAGAAAC 1410
 || || | ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct 1522 TTGCTGGT-GACTCGGAGCCCGGTGTGAGCCGGGCATTGTACTGGGTGCTGGTCAGAA-- 1466

Query 1411 ATTAAAAAGGTTCTTGAATGCAGACGGTGGCTGCAAGAAG-TCTCATGTTTAGAGGTAG 1469
 || | | ||||| | || ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct 1465 ATGACAGGGGTTCTGGAGACGCGGACCCCTGGCCGCCAGGGGCTCCGTGGTTCAGGGTTAG 1406

Query 1470 GTGGGGCAAGGTGAATGCAGTAAAGTG-AGAGGTACAATAATTACTGGGATTTCCGAG 1528
 || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct 1405 ATGACTCAAGGTGAGGTGC-GGCAAGTGTGCGGGGAAGGACTGAC---GTGTCCCGCG 1350

Query 1529 GGAAGCAAGGTTGCCATTGGAGGATCAGGGAGGGACGGGTTCTGAAGTATTAATAGGTG 1588
 | |||| |||| || ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct 1349 G-----AAGGCTGCGTTCGGAGGCTCAGGG-----TCTGA-----ACTTGGTG 1312

Query 1589 GCATTTTGAGAAGGTTACCGAGGGATGGGTAGGACTTTGTTAGGTAGAGGTGGAGGTGGA 1648
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct 1311 GCATTTTCGGAAGGTTGCC-----GGGTAGGACTTTGTTAGGTGGAGTTGAAAGTGGG 1259

Query 1649 GAAAGGACGTTTCAAGGGTGAAGCTTCTTCAGTAAACAGTAAGTATTACAGTTTGGCAA 1708
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct 1258 GAAAGGGCGTTTCAAGGGTGAAGCTTCTT-----CCGAAAGTGTT--CAGCGTGGCTC 1208

Query 1709 AAGTGGATGGTATAGGTAGGGGAGTGGTGGGAATTACAGCTAGAAAAGTTAGATTGCAGA 1768
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct 1207 CAGTGGGAGCTATAGGTA-GGGAGTGGTAGGGATTGCACCTAGAAAAGGTGGATTGCAGA 1149

Query 1769 AGGGCTTGCTTGCCAGGTGGAGGGGCTTATACTCAATGGGGTAGGCAGCGGGGGTGCCCT 1828
 | ||| | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct 1148 GGAGCTGGCGTG-CAGGTGGAAGGGCTTATA-TCAGTGGGGGACATAGCGGGGGAGCCCT 1091

Query 1829 CAACTAGAAGAGTGATGGCACACCTGAGCTGCACCTT 1865
 | |||| ||||| | |||| ||||| ||||| ||||| |||||
 Sbjct 1090 CGACTAGCAGAGTGGGGACACATCTGTCCTGTGCCTT 1054

Q was intron 1 from the Homo ZNF436 (KRAB-ZNF) gene, located on the Chr.1 (autosomal)
>gb|AAGU03057289.1| Loxodonta africana cont3.57288, whole genome shotgun sequence

Length=158909

Score = 944 bits (1046), Expect = 0.0
Identities = 1018/1330 (76%), Gaps = 56/1330 (4%)
Strand=Plus/Minus

Query	4	CAGGAGGTAAGTCTGTTCGTCCCCACTCGGGTTTTCGGCTTCTACCTTCAACCGGACA	63
Sbjct	95677	CAGGAGGTAAGTCTGTTCATTTCCAACCTCGGGTTTTCGGCTTTCACCTTCAGCCGGACA	95618
Query	64	GGGACTGCTAACATCCTGAAGGCCGCCCGGATCAGGGCCTCAGACGCCAGGGTCCCTT	123
Sbjct	95617	GG-ACTGTTAATA-----CCCAACAGTCTCAGGCTCTCAGAGGCC-----TT	95576
Query	124	CGGTGCGGGAGGCCGCTGGGAGCCCTGTAGCAGACAAGCCCTCTGGGACGCTAAGGAGG	183
Sbjct	95575	CTGTGCTGGGGGCCGCCAGAAACAATTTTAGCAGACAACCCCAAGGGAGGATAAAGGATG	95516
Query	184	GCCCGcccccccccGCAGGGGCCTGGCTATCTCCTCCTTACACGCC---CTACAC---CG	236
Sbjct	95515	GCCCTTCCCTGCC-CTGGGCTCTGGCTCTCTCCTCTCTGCATACCTCTCCTACCCTCCCG	95457
Query	237	CCACCC---GCTTCTGAGTCCCC-CAGGGTTTTTCGCCTCCCCGCCGCTGGACGCCACTCA	292
Sbjct	95456	CTACTCCCGGCTTCTGGGTCCCTCAGGGTTTTCACTCTCCCTCCTCTGGGCACGACTCT	95397
Query	293	GCCCGCCGCTCGA-GGGGCGCCCCCTTGAGAAGGACGCAGTCGCACGCCCTACAGGGTT	351
Sbjct	95396	GCCCGTCCCTCAAAGGGGCGCCCTCCTCAGAAGGACGCGGTTAGCCGCTCTGACAGGGTT	95337
Query	352	AA-AGCGCCGAAGCCAAGACACCGCCAGGCTCTACTGCCGACCGCACTCCCGAGTCGCCC	410
Sbjct	95336	AACAGCGATGGGGCCGGGCACTGTCAGGCCATAACGCCGGCTGT---CCGAGTCAGCC	95281
Query	411	CGGCGCGGGGCGGCGCGGGGCCTCTCGGGAGTTGTATTGCGTACAGAGCCGCGCCG---C	467
Sbjct	95280	GGACCTTTGGTAG-----GGCCAGTCGGGAGTTGTAGTATGCACAGCAGGGTGCCGATGC	95226
Query	468	CGCAGGCGCTGTTGGGAGATGTAGTGCCTGGGCGGGGCTCAAAGTTCCAGCGCGCCTCC	527
Sbjct	95225	CGCAGGCGCTGCCGGGAGATGTAGT-CGTAGGCGGGGCTCAAAGTTCCAGCGCTGCTGCC	95167
Query	528	GAGTCTCCCTTGGGAGTGGGCGGCTGCCGCTTCCCTCTCCAGCCTGTGCTGTCAAG-CA	586
Sbjct	95166	GAGTCGCCCCGGGAGTGGGCGGCTGCTGCTTCCCTGTACGCCTGGGTGTCAAATCA	95107
Query	587	GGGGCTCATTTCTAGCTCAGCTCAACACAGGCCAGCGCCTAAATTGGC-CTGACTTCGCAG	645
Sbjct	95106	AGGTCA-ATCCAGCAGAGCTCAACTCCGGCCGGCGCCTAAATGGGGTCGGATGTGCGGG	95048
Query	646	ATAATAAGGCCCGACTCAAGAGAAGCTTCTAGGGACGTGAGGCGAAGCAGGGCAGCCTCT	705
Sbjct	95047	TTAA---GGTCCGACTCAAAGAAGCTTCTAGGGACGTGAGGAGAGGGAGGGCAGCTTCC	94991
Query	706	A--GCTTAATCGTGCTGCAG-TCTCCATAAGAAAAAAGCGAGA-ATACTCCGCCCTGACT	761
Sbjct	94990	TCGGCTGAATCGAACTGGGGTCTCCAAGAGAAGAAAGCGAAAGATACTCCGCCCTGGCT	94931
Query	762	GGGAGGACGCGCTTACTTTTTCACCTTTTGTCTTTTCCCTCCTTGGCTTTTGGCCTCT	821
Sbjct	94930	AGGAGGACACACTGCTTTCTTACCTTTTGTCTTTTCCCTCCCCGGCTTTTGGCCTCT	94871
Query	822	GGCTAGCTTTTGTACGCGGGAGTGGAACCCAACCTCCCGCAGGCCATGGGGGCAGGCAC	881
Sbjct	94870	GACTGTCTTTGTACGCCGAATGGAACCCAAGTCCCGCAGGCCACGGGAGCAGGCGC	94811
Query	882	AGGCGCACTAGAGGCTCTTGCCAGGCTGTGGGAGGCGGGCATAGTGTCCGCCTCTGAT	941
Sbjct	94810	AGGCGTGATACTCGTGCTCGGCCACGCCAGGAGGCGGGCCTAGTGCCGGTAGTAAT	94751
Query	942	TGGCAGAGTGGTTCACGAACCTTCGCTCGCTGATTGGCTGAGGCAGCTGCCGGAAGGACC	1001
Sbjct	94750	TGGCAGAACGTTATGTGAGCATCGCTCTTTGATTGGCTGGTCCAGCTGCCGGAAGGGCC	94691
Query	1002	CGGCCTCGAGATGGCAGAGCGGAGGCGTTCCCTGGGCTGAGCTGAGCACCTCCTCCCTGA	1061
Sbjct	94690	CGGCCTCGGGATGGAAGAGCTGAGGCGTTCTGTGGGTGGGCTAAGAGCCTCCTCCCTGA	94631

Query	1062	GACAGCAGCGGTCTAACCCCCGGCGCGGGAGGGACCCAGCCAGGGGGCTGTCCTAGTAGA	1121
Sbjct	94630	GACAGAAGCGCGCTGACCCCTGGCCCGGGAGGGACCGAGCTAGGGGGCTGTCCTCCTAAA	94571
Query	1122	TTCCGGCATTGCCTCCACCCCGCTGTGGCGGAGACGCAGAGGGCGGGTCGCGCTCGAGGG	1181
Sbjct	94570	TTCCGACAGTGCCTCCGCCCCGCGGTGGCGGAGACGCAGAGGGCGGGTTTCGCTCAAGGG	94511
Query	1182	TCAGGGAGGAGAG-TGACCCGGCCTGGTCCAGGGCCCTCCCTGCCGCTTGGGGCCAG	1240
Sbjct	94510	TCAGGAAGGAGAGTTGACCCAGCCCCGTTGCAGGGCCCTCCCCGCTCGTCTTGCGGCCAG	94451
Query	1241	AACTCCAGCCCTGGGGAGTGGGCAGGGCCTGTTTTCCGTGCCTACGCCCTGCTTTTCGC	1300
Sbjct	94450	AACTCCAGCCCTGGGGAGTGGGCAGGGCCTGTTTTCCGTGCCTACGCCCTGCTTTTCCC	94391
Query	1301	CTCCTTCAGC	1310
Sbjct	94390	CTCCTTCAGC	94381