

Supplementary Material 5 - BLAST search result for D2140 scat sequence

BLASTN 2.2.32+

Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

Reference for database indexing: Aleksandr Morgulis, George Coulouris, Yan Raytselis, Thomas L. Madden, Richa Agarwala, Alejandro A. Schaffer (2008), "Database Indexing for Production MegaBLAST Searches", Bioinformatics 24:1757-1764.

RID: UDRJX1BE01N

Database: Nucleotide collection (nt)
 31,070,346 sequences; 100,143,135,861 total letters
 Query= D2140_contig_Nepal

Length=227

		Score (Bits)	E Value
Sequences producing significant alignments:			
gb KJ776749.1	Canis lupus familiaris haplotype CSWB D-loop, ...	420	6e-114
gb KP665928.1	Canis lupus familiaris isolate 23 D-loop, comp...	420	6e-114
gb KP665927.1	Canis lupus familiaris isolate 22 D-loop, comp...	420	6e-114
gb KP665926.1	Canis lupus familiaris isolate 21 D-loop, comp...	420	6e-114
gb KP665925.1	Canis lupus familiaris isolate 20 D-loop, comp...	420	6e-114
gb KM061588.1	Canis lupus familiaris isolate Cf_ws3 mitochon...	420	6e-114
gb KM061584.1	Canis lupus familiaris isolate Cf_uno mitochon...	420	6e-114
gb KM061577.1	Canis lupus familiaris isolate Cf_tdz5 mitoch...	420	6e-114
gb KM061575.1	Canis lupus familiaris isolate Cf_tdz19 mitoch...	420	6e-114
gb KM061570.1	Canis lupus familiaris isolate Cf_tdz13 mitoch...	420	6e-114
gb KM061563.1	Canis lupus familiaris isolate Cf_stp79 mitoch...	420	6e-114
gb KM061559.1	Canis lupus familiaris isolate Cf_stp65 mitoch...	420	6e-114
gb KM061549.1	Canis lupus familiaris isolate Cf_psy4 mitoch...	420	6e-114
gb KM061532.1	Canis lupus familiaris isolate Cf_pl25 mitoch...	420	6e-114
gb KM061530.1	Canis lupus familiaris isolate Cf_pl16 mitoch...	420	6e-114
gb KM061509.1	Canis lupus familiaris isolate Cf_L56 mitochon...	420	6e-114
gb KM061499.1	Canis lupus familiaris isolate Kos_9 mitochond...	420	6e-114
gb KM061487.1	Canis lupus familiaris isolate Cf_jam7 mitoch...	420	6e-114
gb KM061482.1	Canis lupus familiaris isolate Cf_jam10 mitoch...	420	6e-114
gb KM061479.1	Canis lupus familiaris isolate Cf_cau6 mitoch...	420	6e-114
gb KJ139084.1	Canis lupus familiaris isolate 1477_ON1 D-loop...	420	6e-114
gb KC540940.1	Canis lupus familiaris haplotype Dog_D14 contr...	420	6e-114
gb KC540917.1	Canis lupus haplotype Wolf_W1 control region, ...	420	6e-114
gb KM201268.1	Canis lupus familiaris haplotype Be73/19 D-loo...	420	6e-114
gb KJ934230.1	Canis lupus familiaris haplotype H8 D-loop, pa...	420	6e-114
gb KJ934225.1	Canis lupus familiaris haplotype H3 D-loop, pa...	420	6e-114

gb KJ522809.1	Canis lupus familiaris mitochondrion, complete...	420	6e-114
gb KJ637070.1	Canis lupus familiaris haplotype Be22_1 mitoch...	420	6e-114
gb KJ637068.1	Canis lupus familiaris haplotype Be19_9 mitoch...	420	6e-114
gb KJ637067.1	Canis lupus familiaris haplotype Be19_8 mitoch...	420	6e-114
gb KJ637065.1	Canis lupus familiaris haplotype Be19_6 mitoch...	420	6e-114
gb KJ637064.1	Canis lupus familiaris haplotype Be19_5 mitoch...	420	6e-114
gb KJ637063.1	Canis lupus familiaris haplotype Be19_4 mitoch...	420	6e-114
gb KJ637062.1	Canis lupus familiaris haplotype Be19_3 mitoch...	420	6e-114
gb KJ637061.1	Canis lupus familiaris haplotype Be19_2 mitoch...	420	6e-114
gb KJ637060.1	Canis lupus familiaris haplotype Be19_14 mitoc...	420	6e-114
gb KJ637058.1	Canis lupus familiaris haplotype Be19_13/15 mi...	420	6e-114
gb KJ637056.1	Canis lupus familiaris haplotype Be19_12 mitoc...	420	6e-114
gb KJ637055.1	Canis lupus familiaris haplotype Be19_10/11 mi...	420	6e-114
gb KJ637054.1	Canis lupus familiaris haplotype Be19_10 mitoc...	420	6e-114
gb KJ637053.1	Canis lupus familiaris haplotype Be19_1 mitoch...	420	6e-114
gb KF002337.1	Canis lupus familiaris isolate Y22 mitochondri...	420	6e-114
gb KF002336.1	Canis lupus familiaris isolate Y20 mitochondri...	420	6e-114
gb KF002306.1	Canis lupus familiaris isolate m705 mitochondr...	420	6e-114
gb KF002291.1	Canis lupus familiaris isolate L8 mitochondrio...	420	6e-114
gb KF002273.1	Canis lupus familiaris isolate H64 mitochondri...	420	6e-114
gb KF002268.1	Canis lupus familiaris isolate H51 mitochondri...	420	6e-114
gb KF002266.1	Canis lupus familiaris isolate H44 mitochondri...	420	6e-114
gb KF002263.1	Canis lupus familiaris isolate H3 mitochondrio...	420	6e-114
gb KF002262.1	Canis lupus familiaris isolate H22 mitochondri...	420	6e-114
gb KJ472767.1	Canis lupus familiaris mitochondrion, complete...	420	6e-114
gb KF857179.1	Canis lupus mitochondrion, complete genome	420	6e-114
gb KF757308.1	Canis lupus familiaris isolate PQ11 D-loop, pa...	420	6e-114
gb HQ261490.1	Canis lupus familiaris haplotype A15 control r...	420	6e-114
gb HQ452429.1	Canis lupus familiaris haplotype A189 control ...	420	6e-114
gb KC985190.1	Canis lupus familiaris D-loop, partial sequenc...	420	6e-114
gb JX173682.1	Canis lupus familiaris isolate CAN1 D-loop, pa...	420	6e-114
gb JN182095.1	Canis lupus familiaris isolate greyhound3 cyto...	420	6e-114
gb JN182116.1	Canis lupus familiaris isolate husky3 cytochro...	420	6e-114
emb HE687017.1	Canis lupus familiaris mitochondrial partial ...	420	6e-114
gb HQ452468.1	Canis lupus familiaris haplotype A171 control ...	420	6e-114
gb HQ452422.1	Canis lupus familiaris haplotype A175 control ...	420	6e-114
gb JF342891.1	Canis lupus familiaris haplotype HV1 A11 mitoc...	420	6e-114
gb JF342882.1	Canis lupus familiaris haplotype HV1 A11 mitoc...	420	6e-114
gb JF342858.1	Canis lupus familiaris haplotype HV1 A11 mitoc...	420	6e-114
gb JF342857.1	Canis lupus familiaris haplotype HV1 A11 mitoc...	420	6e-114
gb JF342835.1	Canis lupus familiaris haplotype HV1 A11 mitoc...	420	6e-114
gb JF342833.1	Canis lupus familiaris haplotype HV1 A11 mitoc...	420	6e-114
gb JF342827.1	Canis lupus familiaris haplotype HV1 A11 mitoc...	420	6e-114
gb JF342820.1	Canis lupus familiaris haplotype HV1 A11 mitoc...	420	6e-114
gb JF342814.1	Canis lupus familiaris haplotype HV1 A169* mit...	420	6e-114
gb JF342808.1	Canis lupus familiaris haplotype HV1 A11 mitoc...	420	6e-114
dbj AB605594.1	Canis lupus familiaris mitochondrial gene for...	420	6e-114
dbj AB605582.1	Canis lupus familiaris mitochondrial gene for...	420	6e-114
dbj AB605581.1	Canis lupus familiaris mitochondrial gene for...	420	6e-114
dbj AB605575.1	Canis lupus familiaris mitochondrial gene for...	420	6e-114
dbj AB605570.1	Canis lupus familiaris mitochondrial gene for...	420	6e-114
dbj AB605568.1	Canis lupus familiaris mitochondrial gene for...	420	6e-114
dbj AB605558.1	Canis lupus familiaris mitochondrial gene for...	420	6e-114

dbj AB605516.1	Canis lupus familiaris mitochondrial gene for...	420	6e-114
dbj AB605492.1	Canis lupus familiaris mitochondrial gene for...	420	6e-114
gb HQ452457.1	Canis lupus familiaris haplotype A226 control ...	420	6e-114
dbj AB622564.1	Canis lupus familiaris DNA, hypervariable reg...	420	6e-114
dbj AB622563.1	Canis lupus familiaris DNA, hypervariable reg...	420	6e-114
dbj AB622562.1	Canis lupus familiaris DNA, hypervariable reg...	420	6e-114
dbj AB622561.1	Canis lupus familiaris DNA, hypervariable reg...	420	6e-114
gb HQ997560.1	Canis lupus familiaris isolate 231 D-loop, par...	420	6e-114
gb HQ997531.1	Canis lupus familiaris isolate 201 D-loop, par...	420	6e-114
gb HQ997493.1	Canis lupus familiaris isolate 121 D-loop, par...	420	6e-114
gb HQ997454.1	Canis lupus familiaris isolate 052 D-loop, par...	420	6e-114
gb HQ997424.1	Canis lupus familiaris isolate 004 D-loop, par...	420	6e-114
gb HM560932.1	Canis lupus familiaris haplotype Be61 D-loop, ...	420	6e-114
gb HQ845274.1	Canis lupus familiaris isolate K_38 breed Dwar...	420	6e-114
gb HQ845266.1	Canis lupus familiaris isolate K_30 breed Chih...	420	6e-114
gb HQ644192.1	Canis lupus familiaris isolate 87G ATP synthas...	420	6e-114
gb HQ644148.1	Canis lupus familiaris isolate h21M ATP synthas...	420	6e-114
gb HM561541.1	Canis lupus familiaris isolate K9_18 breed Fox...	420	6e-114
gb HM561539.1	Canis lupus familiaris isolate K9_16 breed Sou...	420	6e-114
gb AF531667.2	Canis familiaris isolate A14 control region, p...	420	6e-114
gb HM560892.1	Canis lupus familiaris haplotype Be21 D-loop, ...	416	7e-113

ALIGNMENTS

>gb|KJ776749.1| Canis lupus familiaris haplotype CSWB D-loop, partial sequence;
mitochondrial

Length=398

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Minus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCCCTCCCTA	60
Sbjct 277	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCCCTCCCTA	218
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 217	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	158
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 157	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	98
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 97	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 51	

>gb|KP665928.1| Canis lupus familiaris isolate 23 D-loop, complete sequence;
mitochondrial

Length=1270

Score = 420 bits (227), Expect = 6e-114

Identities = 227/227 (100%), Gaps = 0/227 (0%)

Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	79
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 140	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	199
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 246	

>gb|KP665927.1| Canis lupus familiaris isolate 22 D-loop, complete sequence;

mitochondrial

Length=1270

Score = 420 bits (227), Expect = 6e-114

Identities = 227/227 (100%), Gaps = 0/227 (0%)

Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	79
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 140	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	199
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 246	

>gb|KP665926.1| Canis lupus familiaris isolate 21 D-loop, complete sequence;

mitochondrial

Length=1270

Score = 420 bits (227), Expect = 6e-114

Identities = 227/227 (100%), Gaps = 0/227 (0%)

Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCCCTA	60
Sbjct 20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCCCTA	79
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 140	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	199
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct 200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	246

>gb|KP665925.1| Canis lupus familiaris isolate 20 D-loop, complete sequence;
mitochondrial
Length=1270

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCCCTA	60
Sbjct 20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCCCTA	79
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 140	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	199
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct 200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	246

>gb|KM061588.1| Canis lupus familiaris isolate Cf_ws3 mitochondrion, complete genome
Length=16710

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCCCTA	60
Sbjct 15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCCCTA	15539

Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	15706

>gb|KM061584.1| Canis lupus familiaris isolate Cf_uno mitochondrion, complete genome

Length=16730

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query	1	TTGAATCACCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCCCTA	60
Sbjct	15480	TTGAATCACCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCCCTA	15539
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	15706

>gb|KM061577.1| Canis lupus familiaris isolate Cf_tdz5 mitochondrion, complete genome

Length=16730

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query	1	TTGAATCACCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCCCTA	60
Sbjct	15480	TTGAATCACCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCCCTA	15539
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120

Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCACACAGTAATCGAATG 	180
Sbjct	15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCACACAGTAATCGAATG	15659
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGTCCTCGAGAAC 227 	
Sbjct	15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGTCCTCGAGAAC 15706	

>gb|KM061575.1| Canis lupus familiaris isolate Cf_tdz19 mitochondrion, complete genome

Length=16730

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCCTA 60 	
Sbjct	15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCCTA 15539	
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120 	
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 15599	
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCACACAGTAATCGAATG 	180
Sbjct	15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCACACAGTAATCGAATG 15659	
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGTCCTCGAGAAC 227 	
Sbjct	15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGTCCTCGAGAAC 15706	

>gb|KM061570.1| Canis lupus familiaris isolate Cf_tdz13 mitochondrion, complete genome

Length=16730

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCCTA 60 	
Sbjct	15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCCTA 15539	
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120 	
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 15599	
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCACACAGTAATCGAATG 	180

Sbjct	15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	15706

>gb|KM061563.1| Canis lupus familiaris isolate Cf_stp79 mitochondrion, complete genome

Length=16730

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct	15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	15706

>gb|KM061559.1| Canis lupus familiaris isolate Cf_stp65 mitochondrion, complete genome

Length=16730

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct	15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659

Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227
 |||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct 15660 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 15706

>gb|KM061549.1| Canis lupus familiaris isolate Cf_psy4 mitochondrion, complete genome

Length=16730

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct 15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query 121	TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 15600	TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 15706	

>gb|KM061532.1| Canis lupus familiaris isolate Cf_pl25 mitochondrion, complete genome

Length=16730

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct 15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query 121	TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 15600	TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 15706	

>gb|KM061530.1| Canis lupus familiaris isolate Cf_pl16 mitochondrion, complete genome
Length=16730

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCTCCCCCTA	60
Sbjct 15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCTCCCCCTA	15539
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query 121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 15706	

>gb|KM061509.1| Canis lupus familiaris isolate Cf_L56 mitochondrion, complete genome
Length=16730

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCTCCCCCTA	60
Sbjct 15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCTCCCCCTA	15539
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query 121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 15706	

>gb|KM061499.1| Canis lupus familiaris isolate Kos_9 mitochondrion, complete

genome

Length=16730

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct 15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query 121	TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 15600	TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC 227	
Sbjct 15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC 15706	

>gb|KM061487.1| Canis lupus familiaris isolate Cf_jam7 mitochondrion, complete genome

Length=16730

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct 15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query 121	TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 15600	TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC 227	
Sbjct 15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC 15706	

>gb|KM061482.1| Canis lupus familiaris isolate Cf_jam10 mitochondrion, complete genome

Length=16730

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct 15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query 121	TTACATAGGACATATTAACCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 15600	TTACATAGGACATATTAACCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 15706	

>gb|KM061479.1| Canis lupus familiaris isolate Cf_cau6 mitochondrion, complete genome
 Length=16730

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct 15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query 121	TTACATAGGACATATTAACCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 15600	TTACATAGGACATATTAACCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 15706	

>gb|KJ139084.1| Canis lupus familiaris isolate 1477_ON1 D-loop, partial sequence;
 mitochondrial

gb|KJ139085.1| Canis lupus familiaris isolate 1737_ON4 D-loop, partial sequence;
 mitochondrial

gb|KJ139086.1| Canis lupus familiaris isolate 1739_ON3 D-loop, partial sequence;
 mitochondrial

Length=582

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	79
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query 121	TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 140	TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG	199
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct 200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	246

>gb|KC540940.1| Canis lupus familiaris haplotype Dog_D14 control region, partial sequence; mitochondrial

Length=536

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	79
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query 121	TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 140	TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG	199
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct 200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	246

>gb|KC540917.1| Canis lupus haplotype Wolf_W1 control region, partial sequence; mitochondrial

gb|KC540933.1| Canis lupus familiaris haplotype Dog_D6 control region, partial sequence; mitochondrial

Length=536

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	79
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 140	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	199
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct 200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	246

>gb|KM201268.1| Canis lupus familiaris haplotype Be73/19 D-loop sequence; mitochondrial Length=1070

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	79
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 140	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	199
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct 200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	246

>gb|KJ934230.1| Canis lupus familiaris haplotype H8 D-loop, partial sequence; mitochondrial Length=650

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCCCTA	60
Sbjct 20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCCCTA	79
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 140	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	199
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct 200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	246

>gb|KJ934225.1| Canis lupus familiaris haplotype H3 D-loop, partial sequence;
mitochondrial

Length=650

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCCCTA	60
Sbjct 20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCCCTA	79
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 140	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	199
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct 200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	246

>gb|KJ522809.1| Canis lupus familiaris mitochondrion, complete genome

Length=16730

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCCCTA	60
Sbjct 15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCCCTA	15539

Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCACACAGTAATCGAATG	180
Sbjct	15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCACACAGTAATCGAATG	15659
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	15706

>gb|KJ637070.1| Canis lupus familiaris haplotype Be22_1 mitochondrial, partial genome

Length=16530

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct	15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCACACAGTAATCGAATG	180
Sbjct	15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCACACAGTAATCGAATG	15659
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	15706

>gb|KJ637068.1| Canis lupus familiaris haplotype Be19_9 mitochondrial, partial genome

Length=16530

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct	15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599

Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC	227
Sbjct	15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC	15706

>gb|KJ637067.1| Canis lupus familiaris haplotype Be19_8 mitochondrial, partial genome
Length=16530

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct	15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC	227
Sbjct	15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC	15706

>gb|KJ637065.1| Canis lupus familiaris haplotype Be19_6 mitochondrial, partial genome
Length=16530

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct	15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180

Sbjct 15600 TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 15659

Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227
 |||||||

Sbjct 15660 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 15706

>gb|KJ637064.1| Canis lupus familiaris haplotype Be19_5 mitochondrial, partial genome

Length=16530

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1 TTGAATCACCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA 60
 |||||||

Sbjct 15480 TTGAATCACCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA 15539

Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120
 |||||||

Sbjct 15540 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 15599

Query 121 TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 180
 |||||||

Sbjct 15600 TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 15659

Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227
 |||||||

Sbjct 15660 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 15706

>gb|KJ637063.1| Canis lupus familiaris haplotype Be19_4 mitochondrial, partial genome

Length=16530

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1 TTGAATCACCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA 60
 |||||||

Sbjct 15480 TTGAATCACCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA 15539

Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120
 |||||||

Sbjct 15540 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 15599

Query 121 TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 180
 |||||||

Sbjct 15600 TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 15659

Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227

Sbjct 15660 CATATCACTTAGCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 15706

>gb|KJ637062.1| Canis lupus familiaris haplotype Be19_3 mitochondrial, partial genome

Length=16529

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA 60

Sbjct 15479 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA 15538

Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120

Sbjct 15539 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 15598

Query 121 TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 180

Sbjct 15599 TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 15658

Query 181 CATATCACTTAGCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227

Sbjct 15659 CATATCACTTAGCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 15705

>gb|KJ637061.1| Canis lupus familiaris haplotype Be19_2 mitochondrial, partial genome

Length=16530

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA 60

Sbjct 15480 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA 15539

Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120

Sbjct 15540 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 15599

Query 121 TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 180

Sbjct 15600 TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 15659

Query 181 CATATCACTTAGCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227

Sbjct 15660 CATATCACTTAGCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 15706

>gb|KJ637060.1| Canis lupus familiaris haplotype Be19_14 mitochondrial, partial genome
Length=16530

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct 15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query 121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC 227	
Sbjct 15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC 15706	

>gb|KJ637058.1| Canis lupus familiaris haplotype Be19_13/15 mitochondrial, partial genome
Length=16530

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct 15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query 121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC 227	
Sbjct 15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC 15706	

>gb|KJ637056.1| Canis lupus familiaris haplotype Be19_12 mitochondrial, partial genome

Length=16530

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCCTA	60
Sbjct 15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCCTA	15539
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query 121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC	227
Sbjct 15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC	15706

>gb|KJ637055.1| Canis lupus familiaris haplotype Be19_10/11 mitochondrion, partial genome

Length=16530

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCCTA	60
Sbjct 15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCCTA	15539
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query 121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC	227
Sbjct 15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC	15706

>gb|KJ637054.1| Canis lupus familiaris haplotype Be19_10 mitochondrion, partial genome

Length=16530

Score = 420 bits (227), Expect = 6e-114

Identities = 227/227 (100%), Gaps = 0/227 (0%)

Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCTCCCTA	60
Sbjct 15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCTCCCTA	15539
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query 121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC 227	
Sbjct 15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC 15706	

>gb|KJ637053.1| Canis lupus familiaris haplotype Be19_1 mitochondrion, partial genome

Length=16530

Score = 420 bits (227), Expect = 6e-114

Identities = 227/227 (100%), Gaps = 0/227 (0%)

Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCTCCCTA	60
Sbjct 15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCTCCCTA	15539
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query 121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC 227	
Sbjct 15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC 15706	

>gb|KF002337.1| Canis lupus familiaris isolate Y22 mitochondrion, partial genome

Length=8018

Score = 420 bits (227), Expect = 6e-114

Identities = 227/227 (100%), Gaps = 0/227 (0%)

Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCTCCCTA	60
---------	---	----

Sbjct	7456	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAACCCCTCCCCCTCCCTA	7515
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	7516	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	7575
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	7576	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	7635
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct	7636	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 7682	

>gb|KF002336.1| Canis lupus familiaris isolate Y20 mitochondrion, partial genome
Length=8018

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAACCCCTCCCCCTCCCTA	60
Sbjct	7456	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAACCCCTCCCCCTCCCTA	7515
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	7516	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	7575
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	7576	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	7635
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct	7636	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 7682	

>gb|KF002306.1| Canis lupus familiaris isolate m705 mitochondrion, partial genome
Length=8018

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAACCCCTCCCCCTCCCTA	60
Sbjct	7456	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAACCCCTCCCCCTCCCTA	7515
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120

Sbjct	7516	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	7575
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTACAGTAATCGAATG	180
Sbjct	7576	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTACAGTAATCGAATG	7635
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	7636	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	7682

>gb|KF002291.1| Canis lupus familiaris isolate L8 mitochondrion, partial genome
Length=8018

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCAGGTAAACCCTCTCCCTCCCCTA	60
Sbjct	7456	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCAGGTAAACCCTCTCCCTCCCCTA	7515
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	7516	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	7575
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTACAGTAATCGAATG	180
Sbjct	7576	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTACAGTAATCGAATG	7635
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	7636	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	7682

>gb|KF002273.1| Canis lupus familiaris isolate H64 mitochondrion, partial genome
gb|KF002289.1| Canis lupus familiaris isolate L43 mitochondrion, partial genome
Length=8018

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCAGGTAAACCCTCTCCCTCCCCTA	60
Sbjct	7456	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCAGGTAAACCCTCTCCCTCCCCTA	7515
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	7516	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	7575
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTACAGTAATCGAATG	180

Sbjct 7576 TTACATAGGACATATTAAC TCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 7635

Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227
 |||||||

Sbjct 7636 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 7682

>gb|KF002268.1| Canis lupus familiaris isolate H51 mitochondrion, partial genome
 gb|KF002277.1| Canis lupus familiaris isolate H85 mitochondrion, partial genome
 gb|KF002288.1| Canis lupus familiaris isolate L36 mitochondrion, partial genome
 gb|KF002297.1| Canis lupus familiaris isolate m432 mitochondrion, partial genome
 gb|KF002313.1| Canis lupus familiaris isolate m752 mitochondrion, partial genome
 gb|KF002326.1| Canis lupus familiaris isolate R41 mitochondrion, partial genome
 gb|KF002327.1| Canis lupus familiaris isolate R42 mitochondrion, partial genome

Length=8018

Score = 420 bits (227), Expect = 6e-114

Identities = 227/227 (100%), Gaps = 0/227 (0%)

Strand=Plus/Plus

Query 1 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAACCCCTCTCCCCTCCCCTA 60
 |||||||

Sbjct 7456 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAACCCCTCTCCCCTCCCCTA 7515

Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120
 |||||||

Sbjct 7516 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 7575

Query 121 TTACATAGGACATATTAAC TCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 180
 |||||||

Sbjct 7576 TTACATAGGACATATTAAC TCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 7635

Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227
 |||||||

Sbjct 7636 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 7682

>gb|KF002266.1| Canis lupus familiaris isolate H44 mitochondrion, partial genome
 gb|KF002279.1| Canis lupus familiaris isolate H94 mitochondrion, partial genome
 gb|KF002285.1| Canis lupus familiaris isolate L22 mitochondrion, partial genome
 gb|KF002316.1| Canis lupus familiaris isolate Ny78 mitochondrion, partial genome

Length=8018

Score = 420 bits (227), Expect = 6e-114

Identities = 227/227 (100%), Gaps = 0/227 (0%)

Strand=Plus/Plus

Query 1 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAACCCCTCTCCCCTCCCCTA 60
 |||||||

Sbjct 7456 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAACCCCTCTCCCCTCCCCTA 7515

Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120
 |||||||

Sbjct	7516	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	7575
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTACAGTAATCGAATG	180
Sbjct	7576	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTACAGTAATCGAATG	7635
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	7636	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	7682

>gb|KF002263.1| Canis lupus familiaris isolate H3 mitochondrion, partial genome
Length=8018

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCAGGTAAACCCTCTCCCTCCCCTA	60
Sbjct	7456	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCAGGTAAACCCTCTCCCTCCCCTA	7515
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	7516	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	7575
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTACAGTAATCGAATG	180
Sbjct	7576	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTACAGTAATCGAATG	7635
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	7636	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	7682

>gb|KF002262.1| Canis lupus familiaris isolate H22 mitochondrion, partial genome
Length=8018

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCAGGTAAACCCTCTCCCTCCCCTA	60
Sbjct	7456	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCAGGTAAACCCTCTCCCTCCCCTA	7515
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	7516	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	7575
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTACAGTAATCGAATG	180
Sbjct	7576	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTACAGTAATCGAATG	7635

```

Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227
       ||||||| |
Sbjct 7636 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 7682

```

>gb|KJ472767.1| Canis lupus familiaris mitochondrion, complete genome
Length=16730

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

```

Query 1 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA 60
       ||||||| |
Sbjct 15480 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA 15539

Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120
       ||||||| |
Sbjct 15540 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 15599

Query 121 TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 180
       ||||||| |
Sbjct 15600 TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 15659

Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227
       ||||||| |
Sbjct 15660 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 15706

```

>gb|KF857179.1| Canis lupus mitochondrion, complete genome
Length=16729

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

```

Query 1 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA 60
       ||||||| |
Sbjct 15480 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA 15539

Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120
       ||||||| |
Sbjct 15540 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 15599

Query 121 TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 180
       ||||||| |
Sbjct 15600 TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 15659

Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227
       ||||||| |
Sbjct 15660 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 15706

```

>gb|KF757308.1| Canis lupus familiaris isolate PQ11 D-loop, partial sequence; mitochondrial
Length=582

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	79
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 140	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	199
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 246	

>gb|HQ261490.1| Canis lupus familiaris haplotype A15 control region, partial sequence; mitochondrial
Length=610

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 48	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	107
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 108	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	167
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 168	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	227
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 228	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 274	

>gb|HQ452429.1| Canis lupus familiaris haplotype A189 control region, partial sequence; mitochondrial

Length=582

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	79
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query 121	TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 140	TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG	199
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 246	

>gb|KC985190.1| Canis lupus familiaris D-loop, partial sequence; mitochondrial
 Length=418

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Minus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 279	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	220
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 219	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	160
Query 121	TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 159	TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG	100
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 99	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 53	

>gb|JX173682.1| Canis lupus familiaris isolate CAN1 D-loop, partial sequence;
 mitochondrial
 Length=413

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)

Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCCTCTCCCTCCCTA	60
Sbjct 76	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCCTCTCCCTCCCTA	135
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 136	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	195
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 196	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	255
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct 256	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	302

>gb|JN182095.1| Canis lupus familiaris isolate greyhound3 cytochrome b gene, partial cds; tRNA-Thr and tRNA-Pro genes, complete sequence; and D-loop, partial sequence; mitochondrial

gb|JN182129.1| Canis lupus x Canis lupus familiaris isolate phyl cytochrome b gene, partial cds; tRNA-Thr and tRNA-Pro genes, complete sequence; and D-loop, partial sequence; mitochondrial

Length=1433

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCCTCTCCCTCCCTA	60
Sbjct 204	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCCTCTCCCTCCCTA	263
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 264	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	323
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 324	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	383
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct 384	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	430

>gb|JN182116.1| Canis lupus familiaris isolate husky3 cytochrome b gene, partial cds; tRNA-Thr and tRNA-Pro genes, complete sequence; and D-loop, partial sequence; mitochondrial

Length=1373

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 204	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	263
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 264	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	323
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 324	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	383
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct 384	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	430

>emb|HE687017.1| Canis lupus familiaris mitochondrial partial D-loop, breed: Bucovina Shepherd Dog

Length=840

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 227	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	286
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 287	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	346
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 347	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	406
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct 407	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	453

>gb|HQ452468.1| Canis lupus familiaris haplotype A171 control region, partial sequence; mitochondrial

Length=582

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	79
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 140	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	199
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct 200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	246

>gb|HQ452422.1| Canis lupus familiaris haplotype A175 control region, partial sequence; mitochondrial

Length=582

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	79
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 140	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	199
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct 200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	246

>gb|JF342891.1| Canis lupus familiaris haplotype HV1 A11 mitochondrion, partial genome

Length=16736

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60

Sbjct	15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query	121	TTACATAGGACATATTAACCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	15600	TTACATAGGACATATTAACCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC 227	
Sbjct	15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC 15706	

>gb|JF342882.1| Canis lupus familiaris haplotype HV1 A11 mitochondrion, partial genome

Length=16736

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct	15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query	121	TTACATAGGACATATTAACCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	15600	TTACATAGGACATATTAACCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC 227	
Sbjct	15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCAGCCTCGAGAAC 15706	

>gb|JF342858.1| Canis lupus familiaris haplotype HV1 A11 mitochondrion, partial genome

Length=16736

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct	15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120

Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	15706

>gb|JF342857.1| Canis lupus familiaris haplotype HV1 A11 mitochondrion, partial genome

gb|JF342865.1| Canis lupus familiaris haplotype HV1 A11 mitochondrion, partial genome

gb|JF342877.1| Canis lupus familiaris haplotype HV1 A11 mitochondrion, partial genome

Length=16736

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCCCTA	60
Sbjct	15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCCCTA	15539
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	15706

>gb|JF342835.1| Canis lupus familiaris haplotype HV1 A11 mitochondrion, partial genome

Length=16735

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCCCTA	60
Sbjct	15479	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCCCTA	15538

Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	15539	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15598
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCACACAGTAATCGAATG	180
Sbjct	15599	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCACACAGTAATCGAATG	15658
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	15659	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	15705

>gb|JF342833.1| Canis lupus familiaris haplotype HV1 A11 mitochondrial, partial genome

Length=16737

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct	15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCACACAGTAATCGAATG	180
Sbjct	15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCACACAGTAATCGAATG	15659
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	15706

>gb|JF342827.1| Canis lupus familiaris haplotype HV1 A11 mitochondrial, partial genome

Length=16736

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct	15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599

Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	15706

>gb|JF342820.1| Canis lupus familiaris haplotype HV1 A11 mitochondrial, partial genome
Length=16736

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct	15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	15600	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	15659
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	15660	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	15706

>gb|JF342814.1| Canis lupus familiaris haplotype HV1 A169* mitochondrial, partial genome
Length=16736

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	60
Sbjct	15480	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTCTCCCCTCCCTA	15539
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	15540	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	15599
Query	121	TTACATAGGACATATTAACACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180

Sbjct 15600 TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 15659

Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227
 |||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 15660 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 15706

>gb|JF342808.1| Canis lupus familiaris haplotype HV1 A11 mitochondrion, partial genome

Length=16736

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCCCTCCCTA 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 15480 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCCCTCCCTA 15539

Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120
 |||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 15540 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 15599

Query 121 TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 180
 |||||||||||||||||||||||||||||||||||||||||||||

Sbjct 15600 TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 15659

Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227
 |||||||||||||||||||||||||||||||||||||||||

Sbjct 15660 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 15706

>dbj|AB605594.1| Canis lupus familiaris mitochondrial gene for tRNA-Pro, D-loop, complete and partial sequence, isolate: Cf106

Length=710

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCCCTCCCTA 60
 |||||||||||||||||||||||||||||||||||||||||

Sbjct 86 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCCCTCCCTA 145

Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120
 |||||||||||||||||||||||||||||||||||||||||

Sbjct 146 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 205

Query 121 TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 180
 |||||||||||||||||||||||||||||||||||||

Sbjct 206 TTACATAGGACATATTAACCTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 265

Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227

Sbjct 266 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 312

>dbj|AB605582.1| Canis lupus familiaris mitochondrial gene for tRNA-Pro, D-loop, complete and partial sequence, isolate: Cf94

Length=710

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA 60
 |||||||

Sbjct 86 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA 145

Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120
 |||||||

Sbjct 146 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 205

Query 121 TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 180
 |||||||

Sbjct 206 TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 265

Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227
 |||||||

Sbjct 266 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 312

>dbj|AB605581.1| Canis lupus familiaris mitochondrial gene for tRNA-Pro, D-loop, complete and partial sequence, isolate: Cf93

Length=710

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA 60
 |||||||

Sbjct 86 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA 145

Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120
 |||||||

Sbjct 146 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 205

Query 121 TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 180
 |||||||

Sbjct 206 TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG 265

Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227
 |||||||

Sbjct 266 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 312

>dbj|AB605575.1| Canis lupus familiaris mitochondrial gene for tRNA-Pro, D-loop, complete and partial sequence, isolate: Cf87
Length=710

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 86	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	145
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 146	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	205
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 206	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	265
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 266	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 312	

>dbj|AB605570.1| Canis lupus familiaris mitochondrial gene for tRNA-Pro, D-loop, complete and partial sequence, isolate: Cf82
Length=710

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 86	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	145
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 146	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	205
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 206	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	265
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 266	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 312	

>dbj|AB605568.1| Canis lupus familiaris mitochondrial gene for tRNA-Pro, D-loop, complete and partial sequence, isolate: Cf80

Length=710

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 86	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	145
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 146	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	205
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 206	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	265
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 266	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 312	

>dbj|AB605558.1| Canis lupus familiaris mitochondrial gene for tRNA-Pro, D-loop, complete and partial sequence, isolate: Cf70

Length=710

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 86	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	145
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 146	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	205
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 206	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	265
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 266	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 312	

>dbj|AB605516.1| Canis lupus familiaris mitochondrial gene for tRNA-Pro, D-loop, complete and partial sequence, isolate: Cf28

Length=710

Score = 420 bits (227), Expect = 6e-114

Identities = 227/227 (100%), Gaps = 0/227 (0%)

Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 86	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	145
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 146	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	205
Query 121	TTACATAGGACATATTAACACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 206	TTACATAGGACATATTAACACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG	265
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 266	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 312	

>dbj|AB605492.1| Canis lupus familiaris mitochondrial gene for tRNA-Pro, D-loop, complete and partial sequence, isolate: Cf04

Length=710

Score = 420 bits (227), Expect = 6e-114

Identities = 227/227 (100%), Gaps = 0/227 (0%)

Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 86	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	145
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 146	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	205
Query 121	TTACATAGGACATATTAACACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 206	TTACATAGGACATATTAACACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG	265
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 266	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 312	

>gb|HQ452457.1| Canis lupus familiaris haplotype A226 control region, partial sequence; mitochondrial

gb|KJ139135.1| Canis lupus familiaris isolate 1810_MIN3 D-loop, partial sequence; mitochondrial

gb|KJ139136.1| Canis lupus familiaris isolate 1707_CAL3 D-loop, partial sequence; mitochondrial

Length=582

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCCTTCTCCCCCTCCCTA	60
Sbjct 20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCCTTCTCCCCCTCCCTA	79
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 140	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	199
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 246	

>dbj|AB622564.1| Canis lupus familiaris DNA, hypervariable region 1 (control region), partial sequence, haplotype: NVLU052
 Length=660

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCCTTCTCCCCCTCCCTA	60
Sbjct 25	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCCTTCTCCCCCTCCCTA	84
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 85	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	144
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 145	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	204
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 205	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 251	

>dbj|AB622563.1| Canis lupus familiaris DNA, hypervariable region 1 (control region), partial sequence, haplotype: NVLU051
 Length=660

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 25	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	84
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 85	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	144
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 145	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	204
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 205	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 251	

>dbj|AB622562.1| Canis lupus familiaris DNA, hypervariable region 1 (control region), partial sequence, haplotype: NVLU050

Length=660

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct 25	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	84
Query 61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct 85	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	144
Query 121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct 145	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	204
Query 181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct 205	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 251	

>dbj|AB622561.1| Canis lupus familiaris DNA, hypervariable region 1 (control region), partial sequence, haplotype: NVLU049

Length=660

Score = 420 bits (227), Expect = 6e-114
 Identities = 227/227 (100%), Gaps = 0/227 (0%)
 Strand=Plus/Plus

Query 1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60

Sbjct	25	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	84
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	85	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	144
Query	121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	145	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	204
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct	205	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 251	

>gb|HQ997560.1| Canis lupus familiaris isolate 231 D-loop, partial sequence;
mitochondrial

Length=673

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct	20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	79
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120
Sbjct	80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query	121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	140	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	199
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227	
Sbjct	200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 246	

>gb|HQ997531.1| Canis lupus familiaris isolate 201 D-loop, partial sequence;
mitochondrial

Length=673

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct	20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	79
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	120

Sbjct	80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query	121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	140	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	199
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	246

>gb|HQ997493.1| Canis lupus familiaris isolate 121 D-loop, partial sequence;
mitochondrial

Length=673

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct	20	TTGAATACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	79
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATCC	120
Sbjct	80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATCC	139
Query	121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	140	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	199
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	246

>gb|HQ997454.1| Canis lupus familiaris isolate 052 D-loop, partial sequence;
mitochondrial

gb|HQ997468.1| Canis lupus familiaris isolate 087 D-loop, partial sequence;
mitochondrial

Length=672

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct	20	TTGAATACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	79
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATCC	120

Sbjct	80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	139
Query	121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	140	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	199
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	246

>gb|HQ997424.1| Canis lupus familiaris isolate 004 D-loop, partial sequence;
mitochondrial

gb|HQ997592.1| Canis lupus familiaris isolate 442 D-loop, partial sequence;
mitochondrial

Length=673

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct	20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	79
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATCC	120
Sbjct	80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATCC	139
Query	121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	140	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	199
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	200	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	246

>gb|HM560932.1| Canis lupus familiaris haplotype Be61 D-loop, partial sequence;
mitochondrial

Length=1070

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct	20	TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	79
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATCC	120
Sbjct	80	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATCC	139

```

Query 121 TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG 180
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 140 TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG 199
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Query 181 CATATCAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 200 CATATCAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 246
|||||||||||||||||||||||||||||||||||||||||||||||||||

```

>gb|HQ845274.1| Canis lupus familiaris isolate K_38 breed Dwarf Schnauzer control region, partial sequence; mitochondrial
Length=1272

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

```

Query 1 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA 60
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 20 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA 79
|||||||||||||||||||||||||||||||||||||||||||||||||||
Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120
|||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 80 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 139
|||||||||||||||||||||||||||||||||||||||||||
Query 121 TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG 180
|||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 140 TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG 199
|||||||||||||||||||||||||||||||||||||||
Query 181 CATATCAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227
|||||||||||||||||||||||||||||||||||||||
Sbjct 200 CATATCAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 246
|||||||||||||||||||||||||||||||

```

>gb|HQ845266.1| Canis lupus familiaris isolate K_30 breed Chihuahua control region, partial sequence; mitochondrial
Length=1248

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

```

Query 1 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA 60
|||||||||||||||||||||||||||||||||||||||||||
Sbjct 20 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA 79
|||||||||||||||||||||||||||||||||||
Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120
|||||||||||||||||||||||||||||||||||
Sbjct 80 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 139
|||||||||||||||||||
Query 121 TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG 180
|||||||||||||||||||||||||||||||||||

```

Sbjct 140 TTACATAGGACATATTAACACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG 199

Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227

|||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 200 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 246

>gb|HQ644192.1| Canis lupus familiaris isolate 87G ATP synthase F0 subunit 6 (ATP6), cytochrome c oxidase subunit III (COX3), and NADH dehydrogenase subunit 4 (ND4) genes, partial cds; tRNA-His, tRNA-Ser, and tRNA-Leu genes, complete sequence; NADH dehydrogenase subunit 5 (ND5) gene, partial cds; and D-loop, partial sequence; mitochondrial

Length=3228

Score = 420 bits (227), Expect = 6e-114

Identities = 227/227 (100%), Gaps = 0/227 (0%)

Strand=Plus/Plus

Query 1 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCAGGTAAACCCTTCTCCCTCCCCTA 60

|||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 2610 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCAGGTAAACCCTTCTCCCTCCCCTA 2669

Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120

|||||||||||||||||||||||||||||||||||||||||||||

Sbjct 2670 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 2729

Query 121 TTACATAGGACATATTAACACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG 180

|||||||||||||||||||||||||||||||||||||||||||||

Sbjct 2730 TTACATAGGACATATTAACACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG 2789

Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227

|||||||||||||||||||||||||||||||||||||||||

Sbjct 2790 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 2836

>gb|HQ644148.1| Canis lupus familiaris isolate h21M ATP synthase F0 subunit 6 (ATP6), cytochrome c oxidase subunit III (COX3), and NADH dehydrogenase subunit 4 (ND4) genes, partial cds; tRNA-His, tRNA-Ser, and tRNA-Leu genes, complete sequence; NADH dehydrogenase subunit 5 (ND5) gene, partial cds; and D-loop, partial sequence; mitochondrial

Length=3228

Score = 420 bits (227), Expect = 6e-114

Identities = 227/227 (100%), Gaps = 0/227 (0%)

Strand=Plus/Plus

Query 1 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCAGGTAAACCCTTCTCCCTCCCCTA 60

|||||||||||||||||||||||||||||||||||||||||

Sbjct 2609 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCAGGTAAACCCTTCTCCCTCCCCTA 2668

Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC 120

Sbjct	2669	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATATCC	2728
Query	121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	2729	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	2788
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	2789	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	2835

>gb|HM561541.1| Canis lupus familiaris isolate K9_18 breed Fox Terrier control region, partial sequence; mitochondrial
Length=1591

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct	117	TTGAATACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	176
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATCC	120
Sbjct	177	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATCC	236
Query	121	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	180
Sbjct	237	TTACATAGGACATATTAACTCAATCTCATAATTCACTGATCTATCAACAGTAATCGAATG	296
Query	181	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	227
Sbjct	297	CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC	343

>gb|HM561539.1| Canis lupus familiaris isolate K9_16 breed South African Boerboele control region, partial sequence; mitochondrial
Length=1591

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

Query	1	TTGAATACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	60
Sbjct	117	TTGAATACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA	176
Query	61	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATCC	120
Sbjct	177	TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATCC	236

```

Query 121 TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG 180
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 237 TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG 296
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227
|||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 297 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 343
|||||||||||||||||||||||||||||||||||||||||||||||||||

```

>gb|AF531667.2| Canis familiaris isolate A14 control region, partial sequence
Length=609

Score = 420 bits (227), Expect = 6e-114
Identities = 227/227 (100%), Gaps = 0/227 (0%)
Strand=Plus/Plus

```

Query 1 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA 60
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 47 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA 106
|||||||||||||||||||||||||||||||||||||||||||||||||||
Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATCC 120
|||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 107 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATCC 166
|||||||||||||||||||||||||||||||||||||||||||
Query 121 TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG 180
|||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 167 TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG 226
|||||||||||||||||||||||||||||||||||||||
Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227
|||||||||||||||||||||||||||||||||||||||
Sbjct 227 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 273
|||||||||||||||||||||||||||||||

```

>gb|HM560892.1| Canis lupus familiaris haplotype Be21 D-loop, partial sequence;
mitochondrial
Length=1070

Score = 416 bits (225), Expect = 7e-113
Identities = 226/227 (99%), Gaps = 0/227 (0%)
Strand=Plus/Plus

```

Query 1 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA 60
|||||||||||||||||||||||||||||||||||||||||||
Sbjct 20 TTGAATCACCCCTACTGTGCTATGTCAGTATCTCCAGGTAAACCCTTCTCCCTCCCTA 79
|||||||||||||||||||||||||||||||||||
Query 61 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATCC 120
|||||||||||||||||||||||||||||||||||
Sbjct 80 TGTACGTCGTGCATTAATGGTTGCCCATGCATATAAGCATGTACATAATATTATCC 139
|||||||||||||||||||
Query 121 TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG 180
|||||||||||||||||||||||||||||||
Sbjct 140 TTACATAGGACATATTAACTCAATCTCATATTCACTGATCTATCAACAGTAATCGAATG 199
|||||||||||||||

```

```
Query 181 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 227
       |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  200 CATATCACTTAGTCCAATAAGGGCTTAATCACCATGCCTCGAGAAC 246
```

Database: Nucleotide collection (nt)

Posted date: Jul 5, 2015 11:00 AM

Number of letters in database: 1,358,888,053

Number of sequences in database: 31,070,346

Lambda K H
1.33 0.621 1.12

Gapped

Lambda K H
1.28 0.460 0.850

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 0, Extension: 0

Number of Sequences: 31070346

Number of Hits to DB: 1316254

Number of extensions: 589

Number of successful extensions: 589

Number of sequences better than 10: 494

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 494

Number of HSP's successfully gapped: 494

Length of query: 227

Length of database: 100143135861

Length adjustment: 32

Effective length of query: 195

Effective length of database: 99148884789

Effective search space: 19334032533855

Effective search space used: 19334032533855

A: 0

X1: 13 (25.0 bits)

X2: 32 (59.1 bits)

X3: 54 (99.7 bits)

S1: 13 (25.1 bits)

S2: 22 (41.7 bits)