

APPENDIX 5. First five hits of the BLASTn analyses of the contig fragments >50 bp recovered in the *Pliomys* sequence generated using BWA relaxed parameters (REL) that were not recovered using the stringent parameters (STR). Position of the fragments within the mitogenome, length of the sequences, and hits statistics are indicated.

16S									
135bp									
CTTTTATAGCGAATAAATCCAAATTCGAAAAAACCAATTGTTGGCCCTAAAGACGATGACCAATAAAGAAAGCGTTAAAGGCTCAACACTATAACACCCCTTAATCCCATAAACCAACAAATGACTTCCCTATATG/									
Description									
Scientific Name									
Max Score									
Total Score									
Query Cover									
E value									
Per. Ident									
Acc. Len									
Accession									
Microtus chrotorrhinus mitochondrion, complete genome									
Microtus chrotorrhinus									
180									
180									
100.00 %									
1.00E-40									
90.44 %									
16297									
NC_057557.1									
Neodon medogensis mitochondrion, complete genome									
Neodon medogensis									
176									
176									
100.00 %									
1.00E-39									
89.71 %									
16332									
MN487087.1									
Neodon medogensis mitochondrion, complete genome									
Neodon medogensis									
176									
176									
100.00 %									
1.00E-39									
88.71 %									
16331									
NC_081578.1									
Neodon sikimensis mitochondrion, complete genome									
Neodon sikimensis									
173									
173									
100.00 %									
1.00E-38									
88.41 %									
16330									
NC_035503.1									
Neodon sp. na BGI-2019 mitochondrion, complete genome									
Neodon sp. na XW-2022									
173									
173									
100.00 %									
1.00E-38									
88.41 %									
16337									
MN487097.1									
ND1									
61bp									
TTATGAATTCACCTACCTATACCACACCCAGTAGCAAAACCTTAACCTAGGGAATTCAT1									
Description									
Scientific Name									
Max Score									
Total Score									
Query Cover									
E value									
Per. Ident									
Acc. Len									
Accession									
Myodes glareolus isolate 2189 mitochondrion, complete genome									
Myodes glareolus									
82.4									
82.4									
98.00 %									
5.00E-12									
90.00 %									
16353									
MN103094.1									
Myodes glareolus isolate 1111 mitochondrion, complete genome									
Myodes glareolus									
82.4									
82.4									
98.00 %									
5.00E-12									
90.00 %									
16355									
MN103094.1									
Myodes glareolus isolate 1110 mitochondrion, complete genome									
Myodes glareolus									
82.4									
82.4									
98.00 %									
5.00E-12									
90.00 %									
16354									
MN103063.1									
Myodes glareolus isolate 1009 mitochondrion, complete genome									
Myodes glareolus									
82.4									
82.4									
98.00 %									
5.00E-12									
90.00 %									
16355									
MN103062.1									
Myodes glareolus voucher 1190 mitochondrion, complete genome									
Myodes glareolus									
82.4									
82.4									
98.00 %									
5.00E-12									
90.00 %									
16353									
KM892819.1									
ND2									
99bp									
CCTTATCTATATGTTATCAATATCATGAAGCTGTTAGACGCCAAATACTAA1TATATCAGCTATCACCTCAGTTCTGTATCGGAGGCTTGGAAATGGAC									
Description									
Scientific Name									
Max Score									
Total Score									
Query Cover									
E value									
Per. Ident									
Acc. Len									
Accession									
Synaptomys cooperi mitochondrion									
Synaptomys cooperi									
107									
107									
100.00 %									
3.00E-19									
83.84 %									
16346									
MT492450.1									
Dicrostonyx torquatus mitochondrion, complete genome									
Dicrostonyx torquatus									
101									
101									
98.00 %									
5.00E-17									
82.65 %									
16343									
MN792983.1									
Dicrostonyx torquatus mitochondrion, complete genome									
Dicrostonyx torquatus									
101									
101									
98.00 %									
5.00E-17									
82.65 %									
16343									
MN792981.1									
Dicrostonyx torquatus mitochondrion, complete genome									
Dicrostonyx torquatus									
101									
101									
98.00 %									
5.00E-17									
82.65 %									
16343									
MN792980.1									
Dicrostonyx torquatus mitochondrion, complete genome									
Dicrostonyx torquatus									
101									
101									
98.00 %									
5.00E-17									
82.65 %									
16343									
MN792979.1									
261bp									
ATATCACTTATATGAAATAAGATACCCATAGCCCTCCCATATCTCACTAA1TCTTATATCAACAGSAGGGCTCCCAACCTCTCACAGSAGTTCTTACCAAAATAGGCCATCATCAGAGAACCTCTAAAAACAATAATCTAATCTTAGCCACACTAATAGCAATAACTGCCCTTATCAACCTGTTCTTCTACACCCGACTAGTCTATTCAACCTCACTAACCCACATTAACCTCCAAA 1									
Description									
Scientific Name									
Max Score									
Total Score									
Query Cover									
E value									
Per. Ident									
Acc. Len									
Accession									
Arvicola amphibius isolate DM22 mitochondrion, complete genome									
Arvicola amphibius									
332									
332									
98.00 %									
5.00E-86									
86.67 %									
16356									
MN122834.1									
Arvicola amphibius isolate DM16 mitochondrion, complete genome									
Arvicola amphibius									
323									
323									
98.00 %									
3.00E-83									
87.89 %									
16356									
MN122828.1									
Arvicola amphibius mitochondrion, complete genome									
Arvicola amphibius									
323									
323									
98.00 %									
3.00E-83									
87.89 %									
16355									
MT381921.1									
Neodon sherylaensis mitochondrion, complete genome									
Neodon sherylaensis									
320									
320									
96.00 %									
1.00E-82									
88.10 %									
16335									
NC_081585.1									
Myodes glareolus isolate 1588 mitochondrion, partial genome									
Myodes glareolus									
319									
319									
97.00 %									
3.00E-82									
87.80 %									
16281									
MN103036.1									
COXI									
453bp									
CGATGCTAGGAAACAGCCCTCAGCATCCTAATTCGAGCAGAGATTAGACAACCGGGCGCCCTATTAGGCGATGACCAAGATCTACAATGTGATTGTCACAGCCCGACCGCA1TTCGTATAATCTTCTCTCATAGTTATACCAATAAATGTTGGTGCTTCGGGAATGTAGTGTAGTCCCTCATATGTTGGGCTCCGACATAGCATCCCGAGTAATAACAATATAAGCTTCTGACTTTTACCCCATCATCTCTGCTACTATTGGCATCATCAATAGTGGAGGCTGGAGCGGGAACAGGTTGAAGCTGTTTACCCCCACTAGCTGGTAATCTAGCACACGAGGAGCATCAGTGGAGCTTAACCATCTTCTCACTCCACCTGGCAGGTGATCTCCTATCTCTAGGAGCAATTAATTTTATCACTACAATATCAACATAAAACCGCCAGCTATAAGA									
Description									
Scientific Name									
Max Score									
Total Score									
Query Cover									
E value									
Per. Ident									
Acc. Len									
Accession									
Ondatra zibethicus voucher HBL008351 cytochrome oxid									
Ondatra zibethicus									
556									
556									
100.00 %									
1.00E-153									
87.20 %									
657									
JF456977.1									
Ondatra zibethicus mitochondrion, complete genome									
Ondatra zibethicus									
552									
552									
100.00 %									
6.00E-152									
86.98 %									
16351									
MN485774.1									
Ondatra zibethicus voucher NMW 85327 cytochrome oxid									
Ondatra zibethicus									
552									
552									
100.00 %									
6.00E-152									
86.98 %									
658									
OR530669.1									
Ondatra zibethicus voucher USNM:MAMM 570625 cytochrome oxid									
Ondatra zibethicus									
547									
547									
100.00 %									
7.00E-151									
86.75 %									
16350									
MT084805.1									
281bp									
CTTATTATCTGATGATCAGTACTCATCACCGCGCTTCTCCTACTCCTTCCCTTCGSGTCTAGCTGGCGGATTATACCATCTCTCCAGACCGGAAACCTAAACACACCATCTTTTGATTCGAGCTGGAGGAGGCGCAACCAATCCTCTACCAGCACCTATTTTGATTCCTCGGTCAACCAGAAAGTCTATATCCTCATCTCTCCAGCGTTCGGGATTATTTACACATCGTTACTTACTACTCAGTAAAAAAGAACCAATTCGGCTA 1									
Description									
Scientific Name									
Max Score									
Total Score									
Query Cover									
E value									
Per. Ident									
Acc. Len									
Accession									
Microtus ochrogaster mitochondrion, complete genome									
Microtus ochrogaster									
311									
311									
99.00 %									
6.00E-80									
86.74 %									
16292									
NC_027945.1									
Cricetulus kamensis voucher SGI1503 cytochrome c oxid									
Cricetulus kamensis									
309									
309									
98.00 %									
2.00E-79									
86.69 %									
1545									
MH161651.1									
Cricetulus kamensis voucher PL1565 cytochrome c oxid									
Cricetulus kamensis									
303									
303									
98.00 %									
1.00E-77									
86.33 %									
1545									
MH161639.1									
Cricetulus kamensis voucher PL1549 cytochrome c oxid									
Cricetulus kamensis									
303									
303									
98.00 %									
1.00E-77									
86.33 %									
1545									
MH161638.1									
Cricetulus kamensis voucher PL1532 cytochrome c oxid									
Cricetulus kamensis									
303									
303									
98.00 %									
1.00E-77									
86.33 %									
1545									
MH161637.1									
189bp									
CTTCACAGTAGGAGGTCTCACAGGCATCGTACTATCCAACTCTTCTAGACATCGTCTTCACGACACATATATGATGATGAGCCCACTCCACATCGCTTATCAATAGCTCCCGGTATTTGCTATTATAGCGGGATTCTGCCACTGATTCGCGCTGTTACAGGTTACACACTAGAC 1									
Description									
Scientific Name									
Max Score									
Total Score									
Query Cover									
E value									
Per. Ident									
Acc. Len									
Accession									
Eothenomys custos isolate YN15160 cytochrome oxidase									
Eothenomys custos									
268									
268									
99.00 %									
4.00E-67									
91.49 %									
1539									
KY997257.1									
Eothenomys custos isolate YN15191 cytochrome oxidase									
Eothenomys custos									
268									
268									
99.00 %									
4.00E-67									
91.49 %									
1539									
KY997256.1									
Eothenomys custos isolate YN15174 cytochrome oxidase									
Eothenomys custos									
268									
268									
99.00 %									
4.00E-67									
91.49 %									
1539									
KY997255.1									
Eothenomys custos isolate YN15159 cytochrome oxidase									
Eothenomys custos									
268									
268									
99.00 %									
4.00E-67									
91.49 %									
1539									
KY997254.1									
Eothenomys custos isolate YN15143 cytochrome oxidase									
Eothenomys custos									
268									
268									
99.00 %									
4.00E-67									