Supplementary Materials

1. Sequence of the bovine PCR product

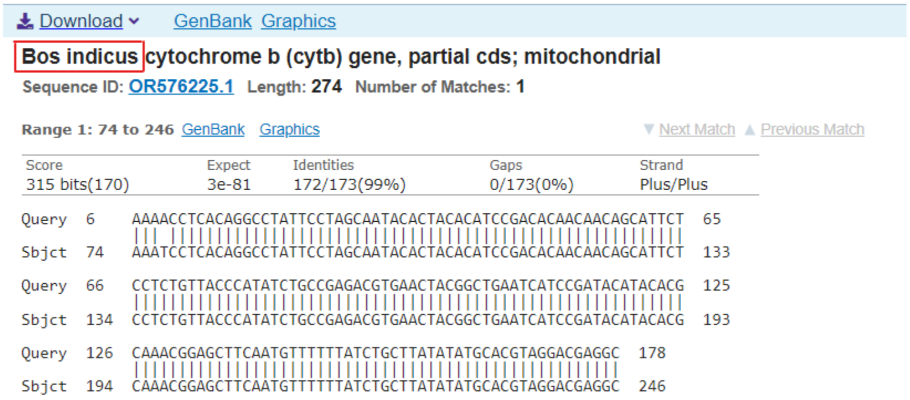
GCGGGGTTCCCTCCTGGGAATCTGCCTAATCCACAAAAACCTCACAGGCCTATTCCTAGCAATACACTACACATCCGACACAACAACAGCATTCTCCTCTGTTACCCATATCTGCCGAGACGTGAACTACGGCTGAATCATCCGATACATACACGCAAACGGAGCTTCAATGTTTTTATCTGCTTATATATGCACGTAGGACGAGGCTTATATTACGGGTCTTACACTTTTCTAGAG

2. Sequence of the pig PCR product

ATGCGGGGATCCCTCCTAGGCATCTGCCTAATCGGGCAAATCCTAACAGGCCTGTTCTTAGCAATACATTACACACCAGACACAACAACAGCTTTCTCATCAGTTACACACATCTGTCGAGACGTAAATTACGGATGAGTTATTCGCTACCTACATGCAAACGGAGCATCCATATTCTTTATTTGCCTATTCATCCACGTAGGCCGAGGTCTATACTACGGATCCTATATATTCCTAGAAACATGAAACATTGGAGTAGTCCTACTATTTACCGTCATAGCAACAGCCTTCGTAGGCTACGTCCTGCCCTGAGGACAAATATCATTCTGAGGAGCTACGGTCATCACAAATCTACTATCAGCCACA

4. Sequence of the canine PCR product

CTGCGGGAATCCTTACTAGGAGTATGCTTGATTTTCTACAGATTCTAACAGGTTTATTCTTAGCTATGCACTATACATCGGATACAGCCACAGCTTTTTCATCAGTCACCCAAATG



Bos indicus **cytochrome b (cytb) gene, partial cds; mitochondrial**

Sequence ID: OR576225.1 Length: 274 Number of Matches: 1

Range 1: 74 to 246 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
315 bits(170)	3e-81	172/173(99%)	0/173(0%)	Plus/Plus

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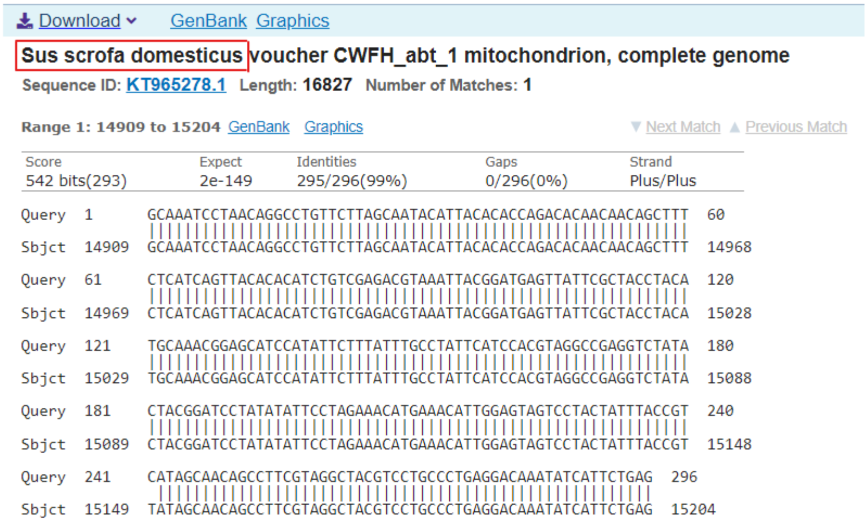
Query  6    AAAACCTCACAGGCCTATTCCTAGCAATACACTACACATCCGACACAACAACAGCATTCT  65
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  74   AAATCCTCACAGGCCTATTCCTAGCAATACACTACACATCCGACACAACAACAGCATTCT  133

Query  66   CCTCTGTTACCCATATCTGCCGAGACGTGAACTACGGCTGAATCATCCGATACATACACG  125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  134  CCTCTGTTACCCATATCTGCCGAGACGTGAACTACGGCTGAATCATCCGATACATACACG  193

Query  126  CAAACGGAGCTTCAATGTTTTTATCTGCTTATATATGCACGTAGGACGAGGC  178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  194  CAAACGGAGCTTCAATGTTTTTATCTGCTTATATATGCACGTAGGACGAGGC  246
```

S1: Alignment of the sequenced bovine DNA with reference sequence.



Sus scrofa domesticus voucher CWFH_abt_1 mitochondrion, complete genome

Sequence ID: KT965278.1 Length: 16827 Number of Matches: 1

Range 1: 14909 to 15204 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
542 bits(293)	2e-149	295/296(99%)	0/296(0%)	Plus/Plus

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Query  1      GCAAATCCTAACAGGCCTGTTCTTAGCAATACATTACACACCAGACACAACAACAGCTTT  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  14909  GCAAATCCTAACAGGCCTGTTCTTAGCAATACATTACACACCAGACACAACAACAGCTTT  14968

Query  61     CTCATCAGTTACACACATCTGTCGAGACGTAAATTACGGATGAGTTATTCGCTACCTACA  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  14969  CTCATCAGTTACACACATCTGTCGAGACGTAAATTACGGATGAGTTATTCGCTACCTACA  15028

Query  121    TGCAAACGGAGCATCCATATTCTTTATTTGCCTATTCATCCACGTAGGCCGAGGTCTATA  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  15029  TGCAAACGGAGCATCCATATTCTTTATTTGCCTATTCATCCACGTAGGCCGAGGTCTATA  15088

Query  181    CTACGGATCCTATATATTCCTAGAAACATGAAACATTGGAGTAGTCCTACTATTTACCGT  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  15089  CTACGGATCCTATATATTCCTAGAAACATGAAACATTGGAGTAGTCCTACTATTTACCGT  15148

Query  241    CATAGCAACAGCCTTCGTAGGCTACGTCCTGCCCTGAGGACAAATATCATTCTGAG  296
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  15149  TATAGCAACAGCCTTCGTAGGCTACGTCCTGCCCTGAGGACAAATATCATTCTGAG  15204
```
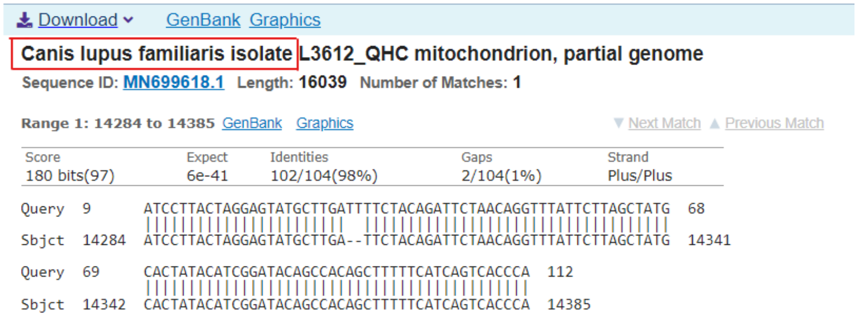

S2: Alignment of the sequenced pig DNA with reference sequence.



Canis lupus familiaris isolate L3612_QHC mitochondrion, partial genome

Sequence ID: MN699618.1 Length: 16039 Number of Matches: 1

Range 1: 14284 to 14385 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
180 bits(97)	6e-41	102/104(98%)	2/104(1%)	Plus/Plus

```
Query  9      ATCCTTACTAGGAGTATGCTTGATTTTCTACAGATTCTAACAGGTTTATTCTTAGCTATG  68
              |||||||||||||||||||||||  |||||||||||||||||||||||||||||||||||
Sbjct  14284  ATCCTTACTAGGAGTATGCTTGA--TTCTACAGATTCTAACAGGTTTATTCTTAGCTATG  14341

Query  69     CACTATACATCGGATACAGCCACAGCTTTTTCATCAGTCACCCA  112
              ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  14342  CACTATACATCGGATACAGCCACAGCTTTTTCATCAGTCACCCA  14385
```

S3: Alignment of the sequenced canine DNA with reference sequence.