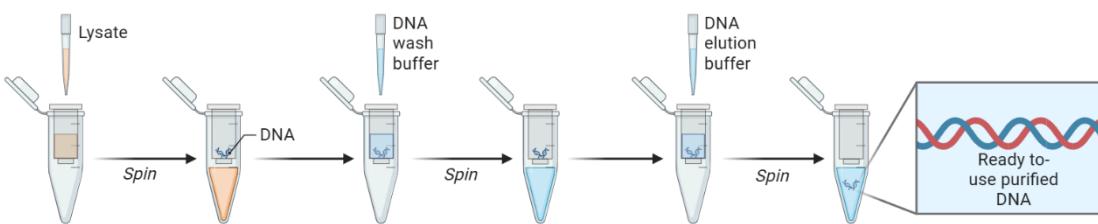


# Analysis of sequencing data

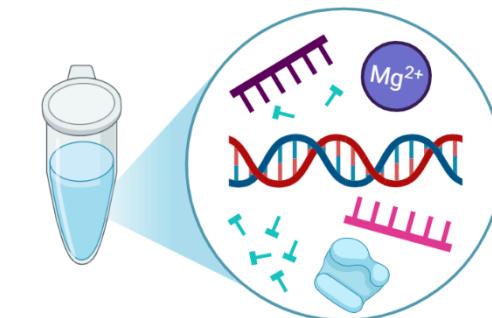
Summer school 2025

Mateja Dolinar

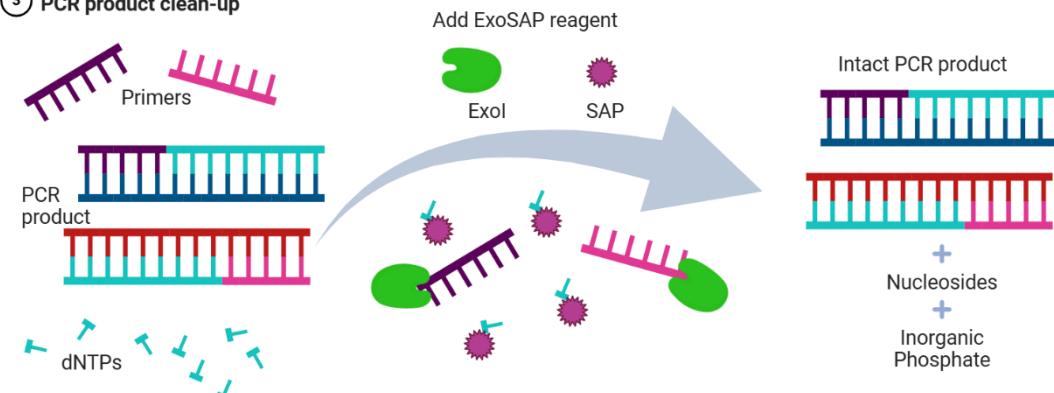
### ① DNA isolation



### ② PCR reaction

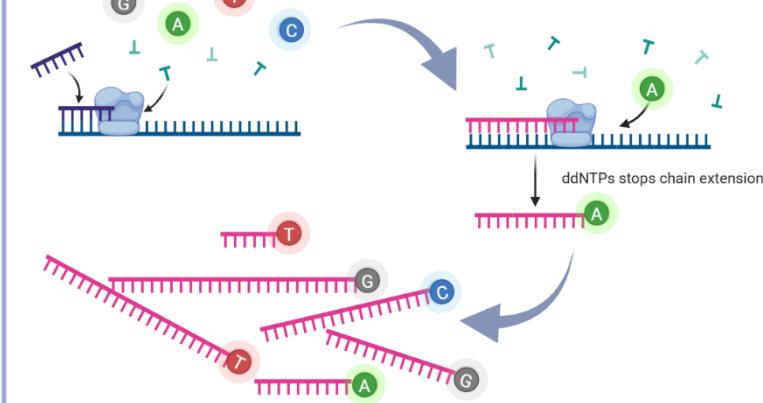


### ③ PCR product clean-up



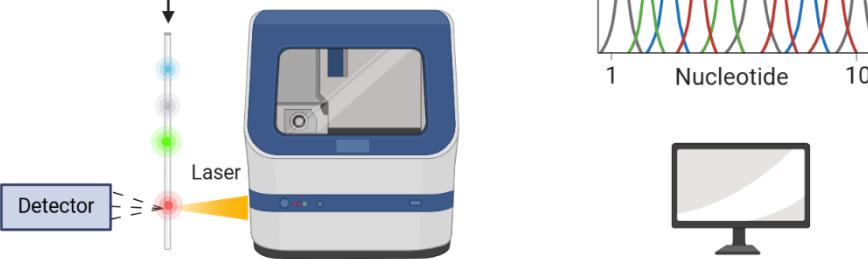
### ④ Sanger sequence reaction

#### Reagents



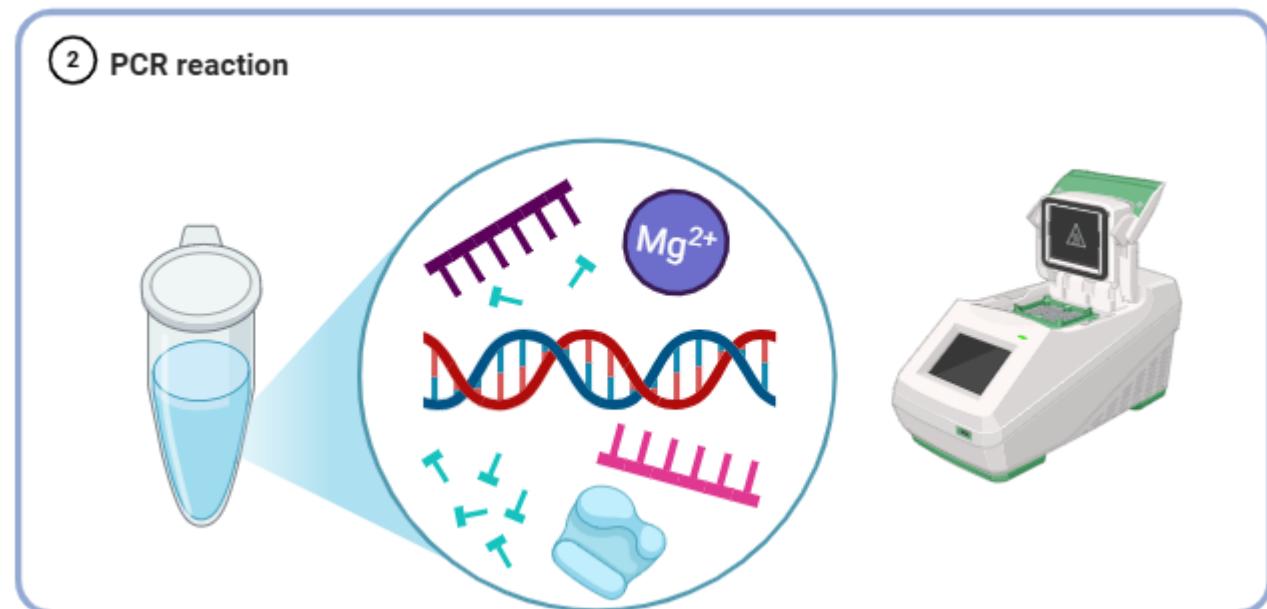
### ⑤ Sanger sequencing and analysis

DNA Sample



# Identification of mammals: PCR reaction

- mtDNA region
  - conserved within a species, but different enough between species for identification of mammals
  - easy to amplify with universal primers because some regions are conserved across many animals
- universal mtDNA primers for mammals:  
FwdM: GACGAGAAGACCCTATGGAGC  
RevM: TCCGAGGTACCCCAACC



# Sanger sequencing



## Files

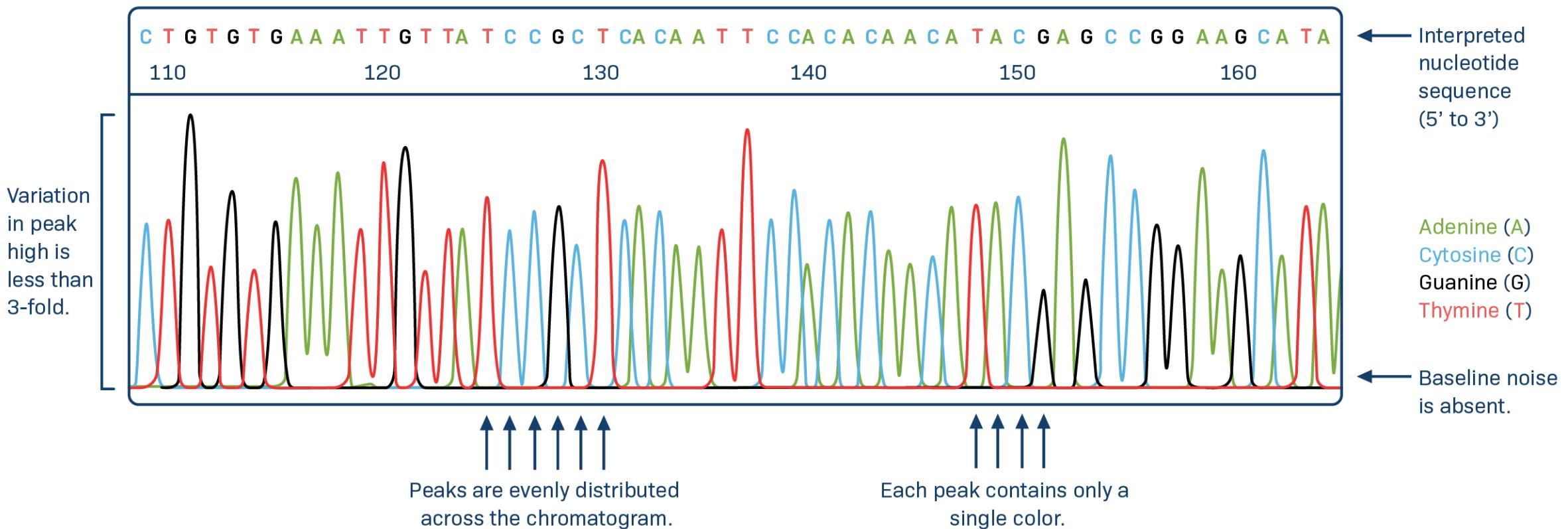
**\*.ab1**

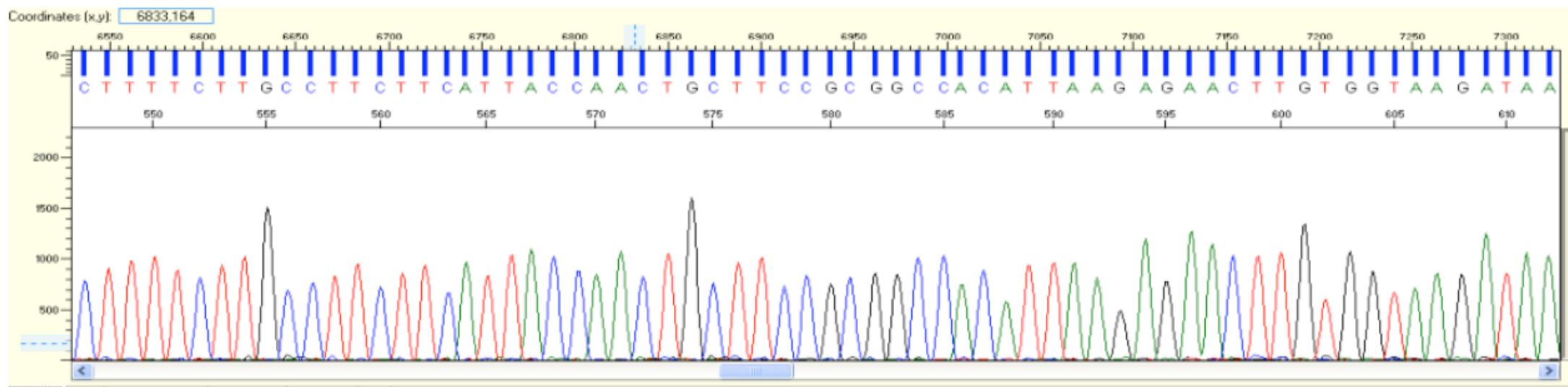
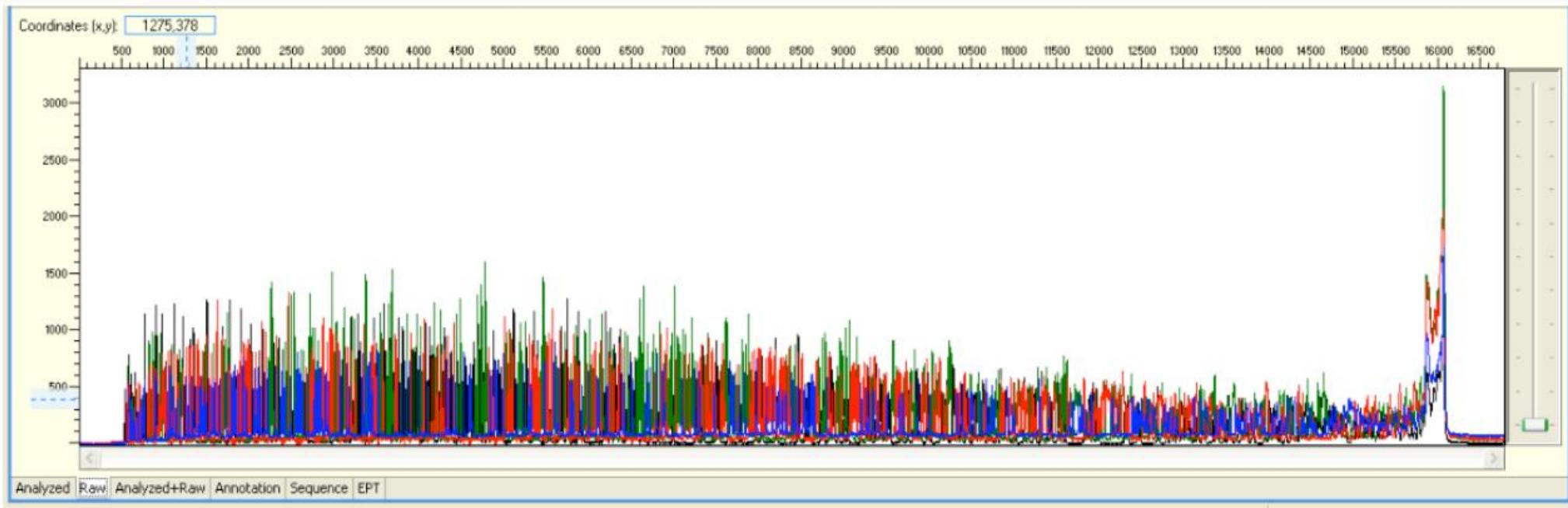
(DNA chromatogram files)

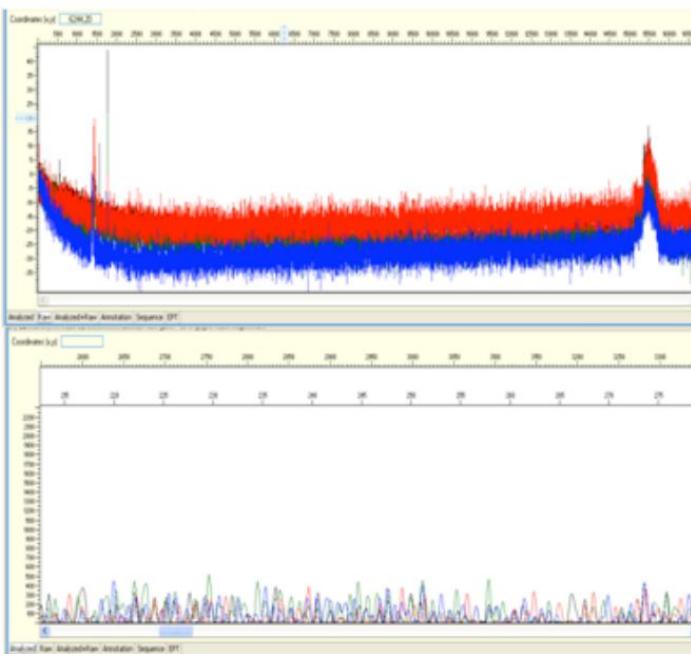
**\*.seq**

(sequence in FASTA format)

# Chromatogram

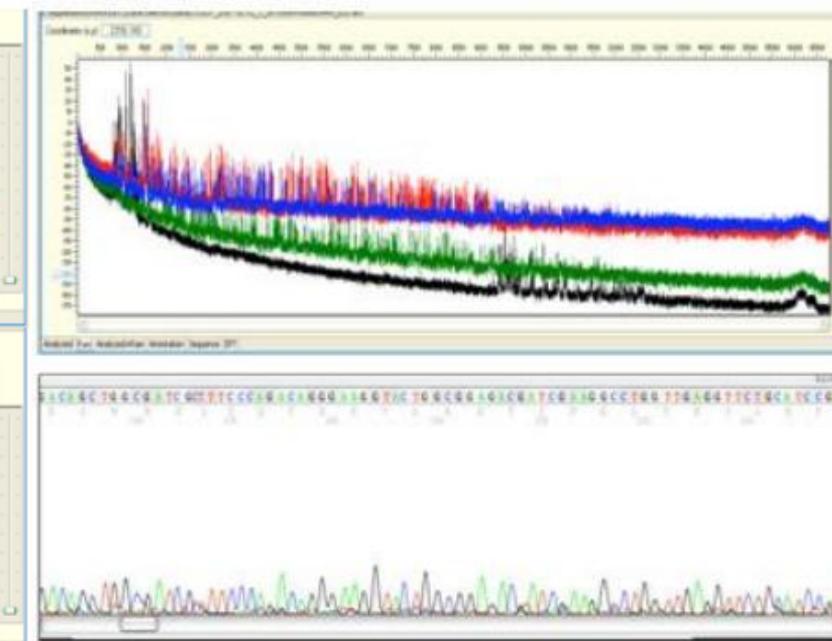






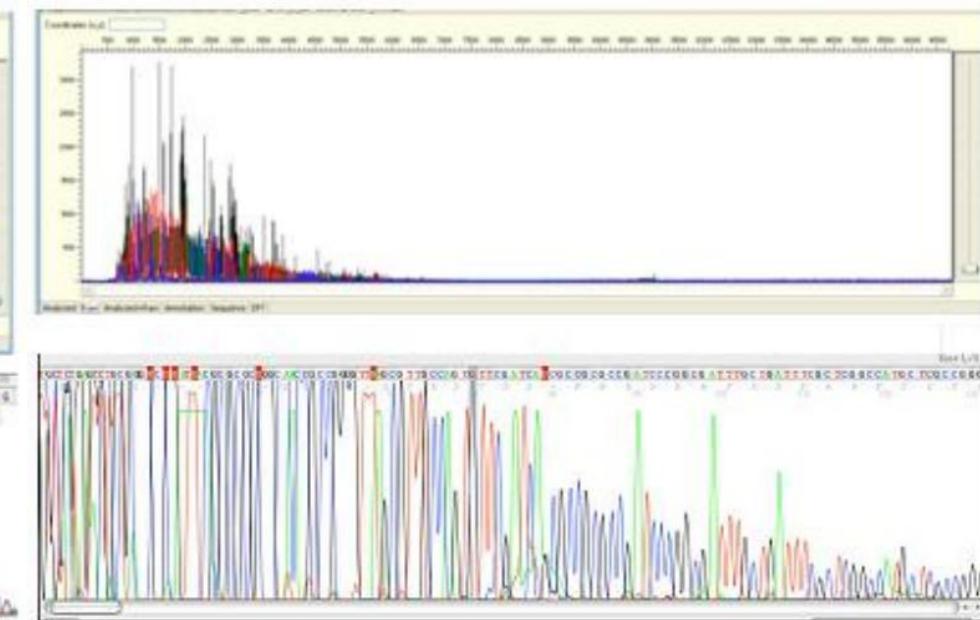
no signal (only noise)

no priming site present  
inefficient primer binding  
insufficient amount of  
DNA template  
Inhibitory contaminant in  
the samples (e.g. salts,  
phenol, EDTA, ethanol)



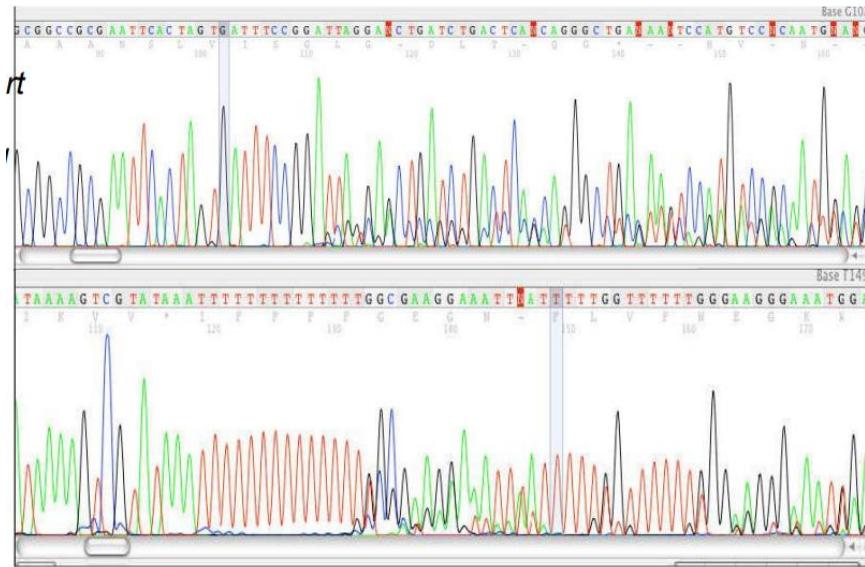
weak signal (signal fade before the  
end of the read)

insufficient amount of DNA  
template  
insufficient amount of primer  
Inhibitory contaminant in the  
samples (e.g. salts, phenol, EDTA,  
ethanol)



short sequence

primer or template ratio is incorrect  
contaminant is present in template  
repetitive region (repeat regions,  
especially GC and GT repeats, can cause  
the signal to fade either due to depletion  
or slippage or secondary structure)  
secondary structure (GC and AT rich  
templates can cause the DNA to loop and  
form hairpins)

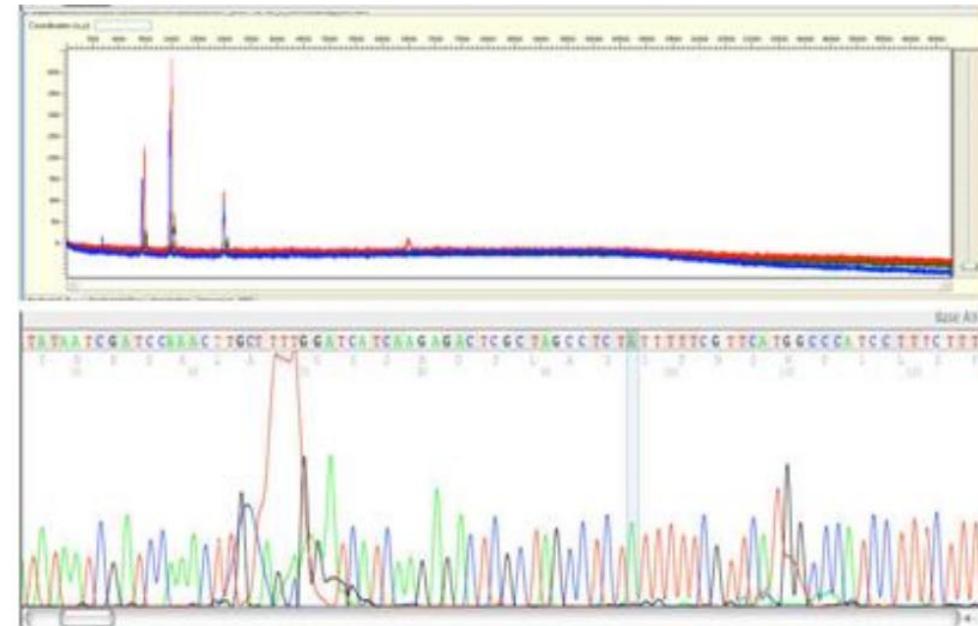


multiple sequences

multiple PCR products

primer-dimer contamination

multiple primers in reaction



artifacts

peaks of excess dye present in the raw data trace

large broadened peaks that obscure the sequence

dye blobs caused by unincorporated BigDye Terminator (BDT), usually seen in failed or weak sequences; real sequence can still be read underneath these blobs

# Sequence

- NCBI (nucleotide database)
  - mitochondrial reference genome
- Ensembl

ensembl.org/info/website/tutorials/sequence.html



BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog

Using this website

Annotation and prediction

Data access

API & software

About us

In this section

- Retrieving sequences
- Gene Expression
- Compare genes across species
- Variants for my gene
- Diseases and Phenotypes
- The GRCh37 assembly in Ensem
- Use my own data

Search documentation...

Go

## Retrieving sequences

### Gene sequence (ENSG...)

Ensembl protein coding genes can be described as a set of splice variants resulting from alignments of cDNA and protein sequence to the genome and/or manual annotation by the Havana project. Human Ensembl genes are the GENCODE set. Read more about Ensembl genes in our [help page](#) or [documentation](#), including noncoding genes such as ncRNA and pseudogenes.

[Gene sequence view](#) shows all possible exons highlighted and in red for all transcripts (splice variants) in one particular gene.

GCCTGACTTCCGGGTGG:  
GGGCTTGTGGCGCGAGC'  
GCGCCTCTGCTGCGCT'  
AGGGGACAGATTGTGA'  
CACCTCTGGAGCGGGTT'  
CCAGTCCAGCGTGGCG(

← Exon  
in red

Find out more, including how to draw sequence variation:

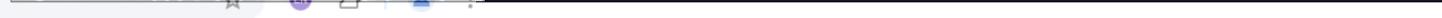
- [Gene sequence help page](#)

← → ⌂ ncbi.nlm.nih.gov/nuccore

An official website of the United States government [Here's how you know](#) ↘

**NIH** National Library of Medicine  
National Center for Biotechnology Information

Nucleotide Nucleotide   Advanced Help



Using Nucleotide Login/Register

Search all species...

Quick Start Guide

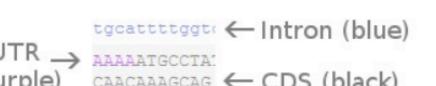
FAQ

Transcript sequence (ENST...)

An Ensembl transcript is a single splice variant that can be coding or noncoding. A coding transcript is comprised of UnTranslated Region (UTR) at the 5' and 3' ends, and the CoCoding sequence (CDS). To see the sequence of the UTR and CDS, you must select a splice variant, and be in the Transcript tab.

Exons and Introns

Exons view shows UTR, CDS, introns and flanking sequence for one transcript.



More about Exons view:

- [Help page](#)

# Sequence

Nucleotide Nucleotide  Search Log in Help

Species Summary 20 per page Sort by Default order Send to: Filters: [Manage Filters](#)

Animals (1,198)  
Fungi (14)  
Customize ...

Molecule types genomic DNA/RNA (1,189)  
mRNA (21)  
Customize ...

Source databases INSDC (GenBank) (1,182)  
RefSeq (30)  
Customize ...

Sequence Type Nucleotide (1,212)

Genetic compartments Mitochondrion (1,140)

Sequence length Custom range...

Release date Custom range...

Revision date Custom range...

[Clear all](#)

ORGANELLE

Was this helpful? Like Dislike

**Dog mitochondrial reference genome**

*Canis lupus familiaris* (dog)

Included in the dog reference assembly ([Dog10K\\_Boxer\\_Tasha](#))

RefSeq: NC\_002008.4 Length: 16,727 bp circular

[Gene](#) (37) [RefSeq.protein](#) (13) [PubMed](#) (1)

[Genome Data Viewer](#) [Primer-BLAST](#) [Download](#)

[See all archival \*Canis lupus familiaris\* complete mitochondrial genomes \(1,353\)](#)

Items: 1 to 20 of 1212

<< First < Prev Page  of 61 [Next >](#) [Last >>](#)

[Canis familiaris mitochondrion mtDNA control region I](#)

1. 407 bp linear DNA

Search See more...

Results by taxon

Top Organisms [\[Tree\]](#)

- Canis lupus (1169)
- Rhipicephalus sanguineus (6)
- Laupala eukolea (5)
- Pneumocystis canis (4)
- Nyctereutes procyonoides (3)
- All other taxa (25)

[More...](#)

Find related data

Database: Select

Find items

Search details

`("Canis lupus familiaris"[Organism] OR dog[All Fields]) AND mtDNA[All Fields]`



Nucleotide

Nucleotide

Search

[Advanced](#)

[Help](#)

GenBank

Send to:

Change region shown

## Canis lupus familiaris mitochondrion, complete genome

NCBI Reference Sequence: NC\_002008.4

[FASTA](#) [Graphics](#)

Go to:

LOCUS NC\_002008 16727 bp DNA circular MAM 03-APR-2023

DEFINITION Canis lupus familiaris mitochondrion, complete genome.

ACCESSION NC\_002008

VERSION NC\_002008.4

DBLINK BioProject: [PRJNA927338](#)

KEYWORDS RefSeq.

SOURCE mitochondrion Canis lupus familiaris (dog)

ORGANISM [Canis lupus familiaris](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Carnivora; Caniformia; Canidae;

Canis.

REFERENCE 1 (bases 1 to 16727)

AUTHORS Kim,K.S., Lee,S.E., Jeong,H.W. and Ha,J.H.

TITLE The complete nucleotide sequence of the domestic dog (Canis familiaris) mitochondrial genome

JOURNAL Mol. Phylogenet. Evol. 10 (2), 210-220 (1998)

PUBMED [9878232](#)

REFERENCE 2 (bases 1 to 16727)

CONSRM NCBI Genome Project

TITLE Direct Submission

JOURNAL Submitted (22-JUN-2007) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

REFERENCE 3 (bases 1 to 16727)

AUTHORS Kim,K.S., Lee,S.E., Jeong,H.W., Jeong,S.Y., Sohn,H.S. and Ha,J.H.

Customize view

### Analyze this sequence

[Run BLAST](#)

[Pick Primers](#)

[Highlight Sequence Features](#)

[Find in this Sequence](#)

### Related information

[Assembly](#)

[BioProject](#)

[Protein](#)

[PubMed](#)

[Taxonomy](#)

[Full text in PMC](#)

[Gene](#)

[Identical GenBank Sequence](#)

[PubMed \(Weighted\)](#)

## FASTA ▾

Send to: ▾

## Canis lupus familiaris mitochondrion, complete genome

NCBI Reference Sequence: NC\_002008.4

[GenBank](#) [Graphics](#)

>NC\_002008.4 Canis lupus familiaris mitochondrial, complete genome  
GTTAATGTAGCTTAATTAATAAGCAAGGCACTGAAAATGCCAAGATGAGTCGCACGACTCCATAAACAT  
AAAGGTTGGTCTAGCCTTCTATTAGTTTAGTACACTACATGCAAGCCTCCACGCCAGTGAA  
GAATGCCCTAAAATCACCAGTGATCTAAAGGAGCAGGTATCAAGCACACTCTTAAGTAGCTCATAACAC  
CTTGCTAACGCCACCCCCACGGGATACAGCAGTGATAAAAATTAAGCCATAAACGAAAGTTGACTAAC  
CCATACTAAATAGGGTTGTTAAATTCTGTGCCAGCCACCGCGGTACGATTAACCCAAACTAATAGGC  
CTACGGCGTAAAGCGTGTCAAGATACTTTACACTAAAGTTAAAACCTTAACTAAGCCGTAAGCTAC  
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GGGATTAGATACCCCACTATGCTAGCCCTAACATAGATAATTTACAACAAAATAATTGCCAGAGGGAA  
CTACTAGCAATAGCTAAAACCTCAAAGGACTTGGCGGTGCTTATATCCCTCTAGAGGAGCCTGTTCTAT  
AATCGATAAACCCCGATAAACCTCACCAACCTTCGCTAATTCACTATACCGCCATCTTCAGCAAAC  
CCTCAAAAGGTAGAACAGTAAGCACAATCATTACATAAAAAAGTTAGGTCAAGGTGTAACCTATGAGG  
TGGGAAGAAATGGGCTACATTTCTACCCAAAGAACATTCACTGTTACGAAATGTTTATGAAATTAAAAGTGA  
GGAGGATTTAGTAGTAAATTAGAAATAGAGAGCTTAATTGAATAGGCCATGAAGCACGCACACACGCC  
CGTCACCCCTCCTCAAGTAATAAGACACAACCATAACCATATTAACCTTAACCTAAACAGAGGAGACAA  
GTCGTAACAAGGTAAGCATACCGGAAGGTGTGCTGGATTAATCAAAGTGAGCTTAACCTAACGCGTCTG  
GCCTACACCCAGAAGATTCTTACCTTATGCCACTTGAACAAAAGCTAGCCCAACTAACCCCAAACCT  
AAGTATTACAGACACATAAAATAAAACATTAGTTAAACAATAAAAGTATAGGAGATAGAAATTAAATT  
GGAGCGATAGAGATAGTACCGTAAGGGAATGATGAAAGACATCTTAACAGTATTAAACAGCAAAGATTAC  
CCCTTCTACCTTGCATAATGAACCTAGCCAGAAACAACCTAACAAAGAGAACTTAAGCTAACGCTCCCG  
AAACCAAGACGAGCTACCCATAAACAACTAACAAAGGATCAACTCATCTATGTAGCTAAAGTAGT  
TTGTGGGTAGAGGTGAAAAGCCTAACGAGCCTGGTGTAGCTGGTTACCCACAGACAGAAATTAGTCA  
ACTTTAAATTTACCTAADDADDAATADADTTTADATGTAADATTTAADDATATAGCTAACGDAAGGTA  
CAGCTAACGAGGAAATGAGCTAACGAGGAACTAACGAGGAACTAACGAGGAACTAACGAGGAACTAACGAGGAA

- Complete Record
  - Coding Sequences
  - Gene Features

## Choose Destination

- File
  - Collections
  - Clipboard
  - Analysis Tool

Download 1 item.

## Format

- FASTA
  - Summary
  - GenBank
  - GenBank (full)
  - FASTA**
  - ASN.1
  - XML
  - INSDSeq XML
  - TinySeq XML
  - Feature Table
  - Accession List
  - GI List
  - GFF3

Protelis

PubMed

## Taxonomy

Full text in PMC

8

Math 108 - B

# FASTA format

- starts with ">"
- a description of the sequence (all in a single line)
- the sequence

## **Canis lupus familiaris mitochondrion, complete genome**

NCBI Reference Sequence: NC\_002008.4

[GenBank](#) [Graphics](#)

```
>NC_002008.4 Canis lupus familiaris mitochondrion, complete genome
GTTAATGTAGCTTAATTAATAAAAGCAAGGCACTGAAAATGCCAAGATGAGTCGCACGACTCCATAAACAT
AAAGGTTGGTCTAGCCTCCTATTAGTTTAGTAGACTTACACATGCAAGCCTCCACGCCAGTGA
GAATGCCCTTAAATCACCAGTGTCTAAAGGAGCAGGTATCAAGCACACTCTTAAGTAGCTATAACAC
CTTGCTAACCCACACGGGATACAGCAGTGATAAAAATTAAGCCATAACGAAAGTTGACTAAG
CCATACTAAATAGGGTTGGTAAATTCGTGCCAGCCACCGCGGTACATCGATTAACCCAAACTAATAGGC
CTACGGCGTAAAGCGTGTCAAGATACTTTACACTAAAGTTAAACTAAGCCGTAAAAAGCTAC
AGTTATCATAAAATAAACCACGAAAGTGACTTATAATAATCTGACTACACGATAGCTAACGACCCAAACT
GGGATTAGATAACCCACTATGCTTAGCCCTAACATAGATAATTTACAACAAAATAATTGCCAGAGGA
CTACTAGCAATAGCTTAAACTCAAAGGACTTGGCGGTGCTTATATCCCTAGAGGAGCCTGTTCTAT
AATCGATAAACCCCGATAAACCTCACCACTTCGCTAATTCACTATACCGCCATCTCAGCAAAC
CCTCAAAAGGTAGAACAGTAAGCACAATCATTACATAAAAAAGTTAGGTCAAGGTGTAACCTATGAGG
TGGGAAGAAATGGGCTACATTTCTACCCAAGAACATTCACTGAAATGTTTATGAAATTAAAAACTGAA
GGAGGATTAGTAGTAAATTAGAACATAGAGAGCTTAATTGAATAGGGCCATGAAGCAGCACACACCGCC
CGTCACCCCTCAAGTAATAAGACACAACCATAACCATATTAACTTAACTAAAACACAAGAGGAGACAA
GTCGTAACAAGGTAAGCATAACCGGAAGGTGTGCTTGGATTAATCAAAGTGTAGCTTAACAAAGCGTCTG
```

# FASTA format

- starts with ">"
- a description of the sequence (all in a single line)
- the sequence

## **Canis lupus familiaris mitochondrion, complete genome**

NCBI Reference Sequence: NC\_002008.4

[GenBank](#) [Graphics](#)

```
>NC_002008.4 Canis lupus familiaris mitochondrion, complete genome
GTTAATGTAGCTTAATTAATAAAAGCAAGGCAGTGAAATGCCAAGATGAGTCGCACGACTCCATAAACAT
AAAGGTTGGTCTAGCCTCCTATTAGTTTAGTAGACTTACACATGCAAGCCTCCACGCCAGTGA
GAATGCCCTAAAATCACCAGTGATCTAAAGGAGCAGGTATCAAGCACACTCTTAAGTAGCTATAACAC
CTTGCTAACCCACACCCCCACGGGATACAGCAGTGATAAAAATTAAGCCATAACGAAAGTTGACTAAG
CCATACTAAATAGGGTTGGTAAATTCTGTGCCAGCCACCGCGGTACATCGATTAACCCAAACTAATAGGC
CTACGGCGTAAAGCGTGTCAAGATACTTTACACTAAAGTTAAAACCTTAACTAAGCCGTAAAAAGCTAC
AGTTATCATAAAATAAACCACGAAAGTGACTTATAATAATCTGACTACACGATAGCTAACGACCCAAACT
GGGATTAGATAACCCACTATGCTTAGCCCTAACATAGATAATTTACAACAAAATAATTGCCAGAGGA
CTACTAGCAATAGCTTAAACTCAAAGGACTTGGCGGTGCTTATATCCCTAGAGGAGCCTGTTCTAT
AATCGATAAACCCCGATAAACCTCACCACTTCGCTAATTCACTATACCGCCATCTCAGCAAAC
CCTCAAAAGGTAGAACAGTAAGCACAATCATTACATAAAAAAGTTAGGTCAAGGTGTAACCTATGAGG
TGGGAAGAAATGGGCTACATTTCTACCCAAGAACATTCACTGGCGGTGCTTATATCCCTAGAGGAGCCTGTTCTAT
GGAGGAGTTAGTAGTAAATTAGAACATAGAGAGCTTAATTGAATAGGGCCATGAAGCAGCACACACCGCC
CGTCACCCCTCTCAAGTAATAAGACACAACCATAACCATATTAACTTAACTAAAACACAAGAGGAGACAA
GTCGTAACAAGGTAAGCATAACCGGAAGGTGTGCTTGGATTAATCAAAGTGTAGCTTAACAAAGCGTCTG
```

# FASTA format

- starts with ">"
- a description of the sequence (all in a single line)
- the sequence

## **Canis lupus familiaris mitochondrion, complete genome**

NCBI Reference Sequence: NC\_002008.4

[GenBank](#) [Graphics](#)

```
>NC 002008.4 Canis lupus familiaris mitochondrion, complete genome
GTTAATGTAGCTTAATTAAATAAAAGCAAGGCACTGAAAATGCCAAGATGAGTCGCACGACTCCATAAACAT
AAAGGTTGGTCCTAGCCTTCTATTAGTTTAGTAGACTTACACATGCAAGCCTCCACGCCAGTGA
GAATGCCCTTAAATCACCAGTGTCTAAAGGAGCAGGTATCAAGCACACTCTTAAGTAGCTCATAACAC
CTTGCTAACCCACACGGGATACAGCAGTGATAAAAATTAAGCCATAACGAAAGTTGACTAAG
CCATACTAAATAGGGTTGGTAAATTCGTGCCAGCCACCGCGGTACATCGATTAACCCAAACTAATAGGC
CTACGGCGTAAAGCGTGTCAAGATACTTTACACTAAAGTTAAACTAAGCCGTAAAAAGCTAC
AGTTATCATAAAATAAACCACGAAAGTGACTTATAATAATCTGACTACACGATAGCTAACGACCCAAACT
GGGATTAGATAACCCACTATGCTTAGCCCTAACATAGATAATTTACAACAAAATAATCGCCAGAGGA
CTACTAGCAATAGCTTAAACTCAAAGGACTTGGCGGTGCTTATATCCCTAGAGGAGCCTGTTCTAT
AATCGATAAACCCCGATAAACCTCACCCACCTTCGCTAATTCACTATACCGCCATCTCAGCAAAC
CCTCAAAAGGTAGAACAGTAAGCACAATCATTTACATAAAAAGTTAGGTCAAGGTGTAACCTATGAGG
TGGGAAGAAATGGGCTACATTTCTACCCAAGAACATTCACTGTTTATGAAATTAAAAACTGAA
GGAGGATTAGTAGTAAATTAGAATAGAGAGCTTAATTGAATAGGGCCATGAAGCAGCACACACCGCC
CGTCACCCCTCTCAAGTAATAAGACACAACCATAACCATATTAACTTAACTAAAACACAAGAGGAGACAA
GTCGTAACAAGGTAAAGCATACCGGAAGGTGTGCTTGGATTAATCAAAGTGTAGCTTAACAAAGCGTCTG
```

# Trim the sequence

- to keep only the relevant mitochondrial region used for species identification
- change file extension from .fasta to .txt
- remove blank spaces from a sequence
  - [http://imed.med.ucm.es/Tools/SMS/filter\\_dna.html](http://imed.med.ucm.es/Tools/SMS/filter_dna.html)
- find the position of the F-primer, and remove (trim) the sequence from the beginning up to 20 bases upstream of the F-primer
- find the R-primer, and remove (trim) the sequence starting 20 bases downstream of the R-primer to the end of the sequence – converts a DNA sequence (R-primer) into reverse-complement
  - [https://www.bioinformatics.org/SMS/rev\\_comp.html](https://www.bioinformatics.org/SMS/rev_comp.html)

Primers are always written in the 5' to 3' direction. The **forward primer** binds directly on the 3' end of the coding strand, so you can search for it as-is.

The **reverse primer** binds on the opposite strand, also in the 5' to 3' direction, so you need to take its **reverse complement** to find it in your forward sequence.

# MEGA



<https://www.megasoftware.net/>

MEGA: Molecular Evolutionary Genetics Analysis version 1.01

Kumar S, Tamura K, Nei M (1993)  
The Pennsylvania State University (135 pp.)

 [Web Link](#)

 [Download PDF](#)

Currently, many computer programs are available for estimating evolutionary distances and reconstructing phylogenetic trees from molecular data. However, most of them are written for specific methods and cannot be interconnected easily because of their inflexible input and output file formats. MEGA presents an interactive, user-friendly platform for estimating evolutionary distances, reconstructing phylogenetic trees, and computing basic statistical quantities that are of evolutionary interest. MEGA has been developed specifically for use on IBM and IBM-compatible personal computers.

MEGA is designed to facilitate extensive sequence data analysis from an evolutionary perspective using a single program package. At the same time, the overlap between the methods implemented in MEGA and those in other existing evolutionary analysis programs has been consciously avoided. This is reflected in the exclusion of the maximum likelihood method (PHYLIP) and in the absence of extensive options for the maximum parsimony method (PAUP and MacClade). Limitations on the memory size and relatively slower speeds of desktop computers (and the presence of many commercial and non-commercial programs) prompted the decision not to include sequence alignment methods in MEGA.



- Edit/Build Alignment
- Edit/View Sequencer Files (Trace)...
- Open Saved Alignment Session...
- Show Web Browser
- Query Databanks
- Do BLAST Search

Done Loading



## Alignment Editor

## Select an Option

- Create a new alignment
- Open a saved alignment session
- Retrieve a sequence from a file

Help

Cancel

OK

Done Loading



## Data Type for Alignment

Are you building a DNA or protein sequence alignment?

DNA

Protein

Cancel

## RECENT PUBLICATIONS



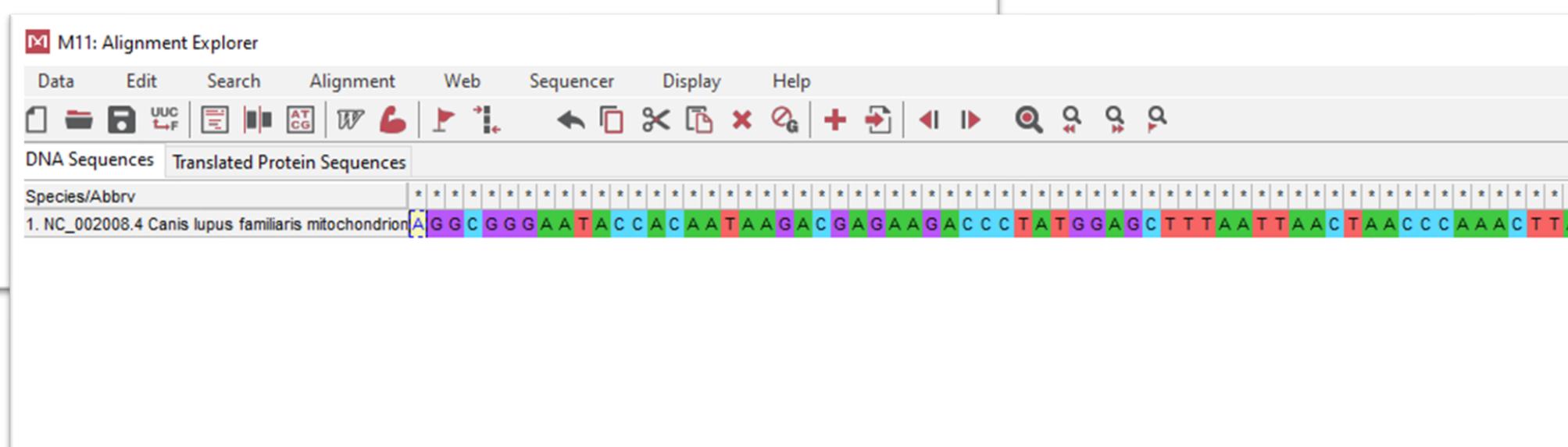
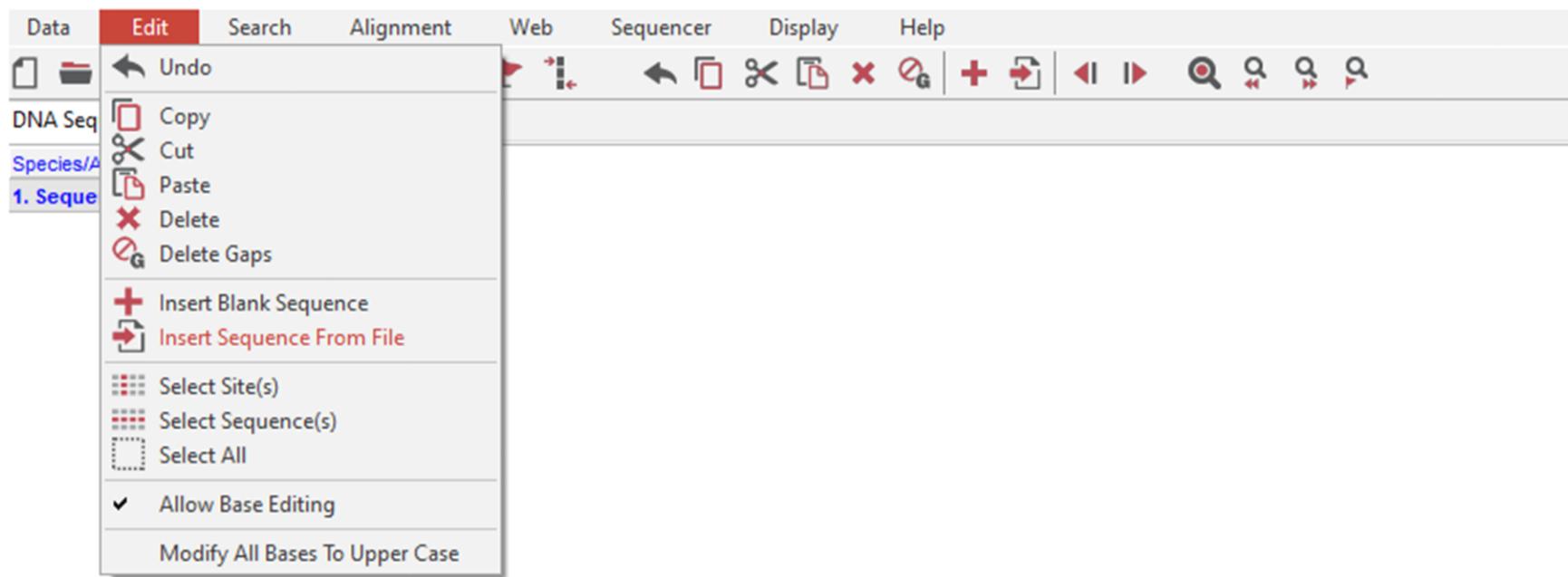
HELP DOCS EXAMPLES CITATION REPORT BUG UPDATES MEGA

## RECENT PUBLICATIONS



HELP DOCS EXAMPLES CITATION REPORT BUG UPDATES MEGA LINKS TOOLBAR PREFERENCES

## M11: Alignment Explorer



## M11: Alignment Explorer (sekvence za poravnavo - pes\_konj\_osel\_ovca\_govedo.fasta)

Data Edit Search Alignment Web Sequencer Display Help



DNA Sequences

|

Translated Protein S

|

Align DNA

|

Align Codons

|

Species/Abbrv

1. NC 091244.1 Equus caballus isolate H 3958 breed thoroughbred mitochondrial genome  
 2. NC 001788.1 Equus asinus mitochondrion complete genome  
 3. NC 006853.1 Bos taurus mitochondrion complete genome  
 4. NC 002008.4 Canis lupus familiaris mitochondrion complete genome  
 5. NC 001941.1 Ovis aries mitochondrion complete genome

AACACACAAACCTAACCTTCAGGGACAAACAAAACCTTTGATTGAATCAGCAATTTCGGTTGGGGTGACCTC  
 AACATACAAACCTAACCCCTCAGGGACAAACAAAACCTTTGATTGAATCAGCAATTTCGGTTGGGGTGACCTC  
 AGAGAATAGATTAAACCATTAAAGGAATAACAACAAATCTCCATGAGTTGGTAGTTTCGGTTGGGGTGACCTC  
 GATACTAGATACCTACAAGGCATAACATAACACCATTATTATGAGTTAGCAATTAGGTTGGGGTGACCTC  
 GGAAAATAAATTCAACCACCAAGGGATAACAAACACTCCTTATGAGTTAACAGTTTCGGTTGGGGTGACCTC

## M11: Alignment Explorer (sekvence za poravnavo - pes\_konj\_osel\_ovca\_govedo.fasta)

Data Edit Search Alignment Web Sequencer Display Help



DNA Sequences

|

Translated Protein Sequences

Species/Abbrv

1. NC 091244.1 Equus caballus isolate H 3958 breed thoroughbred mitochondrial genome  
 2. NC 001788.1 Equus asinus mitochondrion complete genome  
 3. NC 006853.1 Bos taurus mitochondrion complete genome  
 4. NC 002008.4 Canis lupus familiaris mitochondrion complete genome  
 5. NC 001941.1 Ovis aries mitochondrion complete genome

AACACACAAACCTAACCTTCAGGGACAAACAAAACCTTTGATTGAATCAGCAATTTCGGTTGGGGTGACCTC  
 AACATACAAACCTAACCCCTCAGGGACAAACAAAACCTTTGATTGAATCAGCAATTTCGGTTGGGGTGACCTC  
 AGAGAATAGATTAAACCATTAAAGGAATAACAACAAATCTCCATGAGTTGGTAGTTTCGGTTGGGGTGACCTC  
 GATACTAGATACCTACAAGGCATAACATAACACCATTATTATGAGTTAGCAATTAGGTTGGGGTGACCTC  
 GGAAAATAAATTCAACCACCAAGGGATAACAAACACTCCTTATGAGTTAACAGTTTCGGTTGGGGTGACCTC

## ClustalW Options

## ▼ Alignment

## Pairwise Alignment

Gap Opening Penalty: 80,00  
 Gap Extension Penalty: 100,00

## Multiple Alignment

Gap Opening Penalty: 80,00  
 Gap Extension Penalty: 100,00

## Matrix

Help Cancel OK

Done Loading

Site # 66

 with  w/o gaps
 

Site # 66

 with  w/o gaps
 

Selected genetic code: Standard

M11: Alignment Explorer (sekvence za poravnavo - pes\_konj\_osel\_ovca\_govedo.fasta)

Data Edit Search Alignment Web Sequencer Display Help

UUC F

DNA Sequences Translated Protein Sequences

Species/Abbrv

Species/Abbrv	1. NC 091244.1 Equus caballus isolate H 3958 breed thoroughbred mitochondrial genome	2. NC 001788.1 Equus asinus mitochondrial complete genome	3. NC 006853.1 Bos taurus mitochondrial complete genome	4. NC 002008.4 Canis lupus familiaris mitochondrial complete genome	5. NC 001941.1 Ovis aries mitochondrial complete genome
	GGGAAATGACCTAAATAAAGACGAGAAGACCCCTATGGAGCTTTAACTTAACTTGATTCAACAAACAAACACAC	GGCGGGAAATAATCAAATAAGACGAGAAGACCCCTATGGAGCTTTAACTTAACTTGATTCAACAAACAAACATA	GGCGGGAAATGCACAAATAAGACGAGAAGACCCCTATGGAGCTTTAACTTAACTTGATTCAACAAACAAAGAGAAATAGATTT	GGCGGGAAATACCAACAAATAAGACGAGAAGACCCCTATGGAGCTTTAACTTAACTTGATTCAACAAACAAACTTATGGATACT	GGCGGGATAAAATCAAACAAAGACGAGAAGACCCCTATGGAGCTTTAACTTAAAGTAACCTAAACCCAAACTTATGGATACT

Site # 163   with  w/o gaps Selected genetic code: Standard

# Molecular Evolutionary Genetics Analysis

File      Analysis      Help



Edit/Build Alignment

Edit/View Sequencer Files (Trace)...

Open Saved Alignment Session...

Show Web Browser

Query Databanks

Do BLAST Search

INSTANCE

DIVERSITY

PHYLOGENY

USER TREE

ANCESTORS

SELECTION

RATES

CLOCKS

DISEASE

