

# Ensembl Gene Annotation (e!93) Cat (felis catus)

Assembly: Felis\_catus\_9.0, GCA\_000181335.4

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This document describes the annotation process of an assembly. The first stage is Assembly Loading where databases are prepared and the assembly loaded into the database.

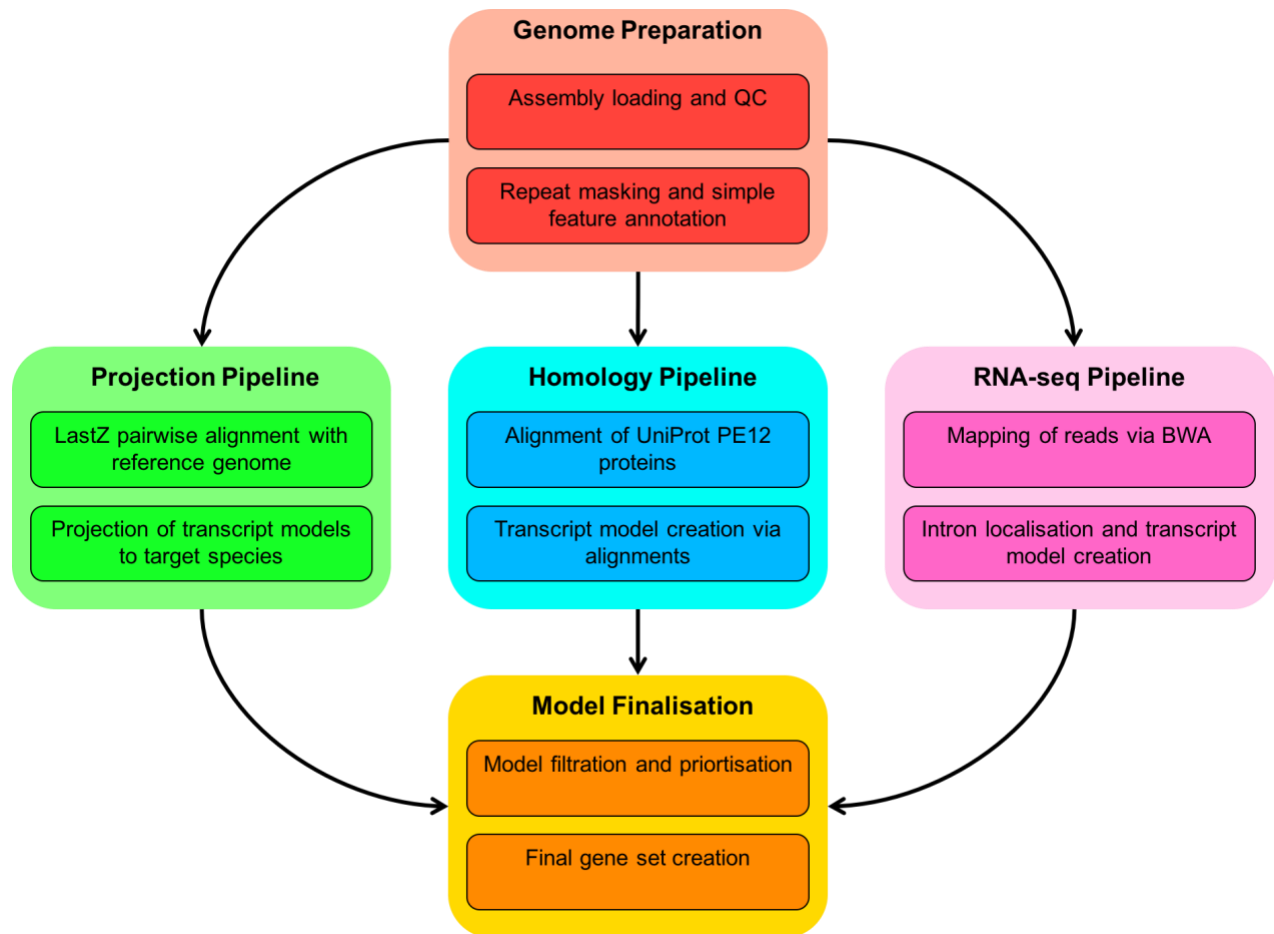


Fig. 1: Flowchart of the protein-coding annotation pipeline. Small ncRNAs, lg genes, TR genes, and pseudogenes are computed using separate pipelines.

## Section 1: Genome Preparation

The genome phase of the Ensembl gene annotation pipeline involves loading an assembly into the Ensembl core database schema and then running a series of analyses on the loaded assembly to identify an initial set of genomic features. The most important aspect of this phase is identifying repeat features (primarily through RepeatMasker) as soft masking of the genome is used extensively later in the annotation process.

### Repeat Finding

After the genomic sequence has been loaded into a database, it is screened for sequence patterns including repeats using RepeatMasker [1] (version 4.0.5 with parameters, using as the search engine), Dust [2] and TRF [3]. For the cat annotation, the Repbase mammal's library was used with RepeatMasker.

### Low complexity features, ab initio predictions and BLAST analyses

Transcription start sites are predicted using Eponine-scan [4]. CpG islands longer than 400 bases and tRNAs are also predicted. The results of Eponine-scan, CpG, and tRNAscan [5] are for display purposes only; they are not used in the gene annotation process.

Genscan [6] is run across repeat-masked sequence to identify ab initio gene predictions. The results of the Genscan analyses are also used as input for UniProt [7], UniGene [8] and Vertebrate RNA alignments by NCBI-BLAST [9]. Passing only Genscan results to BLAST is an effective way of reducing the search space and therefore the computational resources required.

Genscan predictions are for display purposes only and are not used in the model generation phase.

## Section 2: Protein-Coding Model Generation

Various sources of transcript and protein data are investigated and used to generate gene models using a variety of techniques. The data and techniques employed to generate models are outlined here. The numbers of gene models generated are described in gene summary.

### Projection mapping pipeline

For all species a whole genome alignment is generated against a suitable reference assembly using LastZ [10]. Syntenic regions identified using this alignment are then used to map protein coding annotation from the most recent GENCODE [11] gene set. For the cat annotation, the human assembly, GRCh38, was used as a reference and The GENCODE 27 gene set was used to map protein coding annotation.

The mapped transcripts are then assessed for non-canonical splice sites and frameshifts; this can happen when mapping coordinates from one assembly to another. Mapped transcripts featuring two or more non-canonical splice sites/frameshifts are passed into a realignment pipeline. Here they are re-aligned to the original sequence in the region they are mapped to. If possible, a model with canonical splicing is built otherwise the transcript model is discarded.

### Protein-to-genome pipeline

Protein sequences are downloaded from UniProt and aligned to the genome in a splice aware manner using GenBlast [12]. The set of proteins aligned to the genome is a subset of UniProt proteins used to provide a broad, targeted coverage of the cat proteome.

The set consists of the following:

Self (cat) SwissProt/TrEMBL PE 1 & 2  
Human SwissProt/TrEMBL PE 1 & 2  
Mouse SwissProt/TrEMBL PE 1 & 2  
Other mammals SwissProt/TrEMBL PE 1 & 2  
Other vertebrates SwissProt/TrEMBL PE 1 & 2

Note: PE level = protein existence level

For the cat annotation, a cut-off of 50 percent coverage and identity and an e-value of  $e^{-1}$  were used for GenBlast with the exon repair option turned on. The top 5 transcript models built by GenBlast for each protein passing the cut-offs are kept.

Protein group	Count
Self SwissProt/TrEMBL PE 1 & 2	14533
Human SwissProt/TrEMBL PE 1 & 2	49427
Mouse SwissProt/TrEMBL PE1 & 2.	69046
Other mammals SwissProt/TrEMBL PE 1 & 2	227966
Other vertebrates SwissProt/TrEMBL PE 1 & 2	166791

Table 1: Counts of transcript models built by GenBlast for each protein group

## RNA-seq pipeline

RNA-seq data is downloaded from ENA (<https://www.ebi.ac.uk/ena/>) and used in the annotation. A merged file containing reads from all tissues/samples is created. The merged data is less likely to suffer from model fragmentation due to read depth. The available reads are aligned to the genome using BWA [13], with a tolerance of 50 percent mismatch to allow for intron identification via split read alignment. Initial models generated from the BWA alignments are further refined via exonerate. Protein coding

models are identified via a BLAST alignment of the longest ORF against the UniProt vertebrate PE 1 & 2 data set.

In the case where multiple tissues/samples are available we create a gene track for each such tissue/sample that can be viewed in the Ensembl browser and queried via the API.

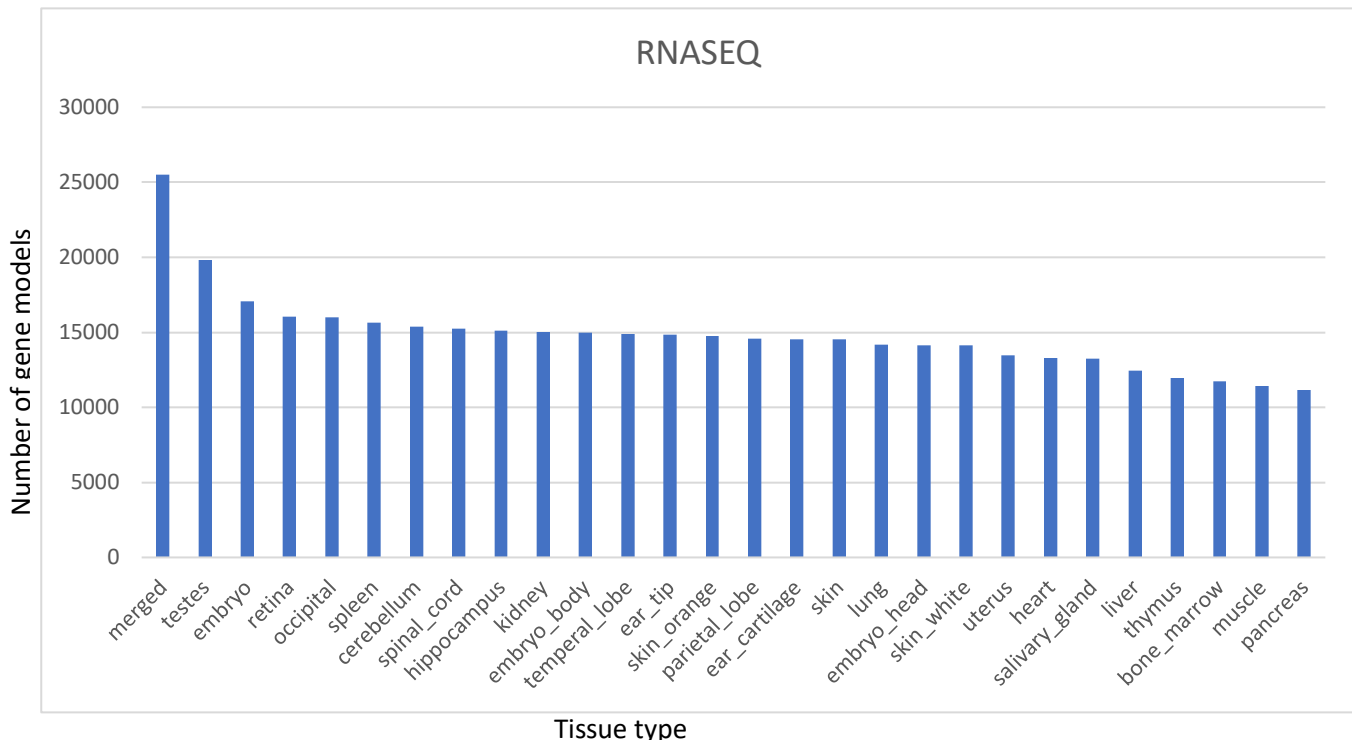


Fig 2: Counts of RNA-Seq transcript models for each sample

## Section 3: Filtering the Protein-Coding Models

The filtering phase decides the subset of protein-coding transcript models, generated from the model-building pipelines, that comprise the final protein-coding gene set. Models are filtered based on information such as what pipeline was used to generate them, how closely related the data are to the target species and how good the alignment coverage and percent identity to the original data are.

### Prioritising models at each locus

The LayerAnnotation module is used to define a hierarchy of input data sets, from most preferred to least preferred. The output of this pipeline includes all transcript models from the highest ranked input set. Models from lower ranked input sets are included only if their exons do not overlap a model from an input set higher in the hierarchy. Note that models cannot exist in more than one layer. For UniProt proteins, models are also separated into clades, to help selection during the layering process. Each UniProt protein is in one clade only, for example mammal proteins are present in the mammal clade and are not present in the vertebrate clade to avoid aligning the proteins multiple times.

When selecting the model or models kept at each position, we prioritize based on the highest layer with available evidence. In general, the highest layers contain the set of evidence that is considered the most trustworthy, in terms of both alignment/mapping quality, and also in terms of relevance to the species being annotated. So, for example, when a primate is being annotated, well aligned evidence from either the species itself or other closely related vertebrates would be chosen over evidence from more distant species. Regardless of what species is being annotated, well-aligned human proteins are usually included in the top layer as human is the current most complete vertebrate annotation. For further details on the exact layering used please refer to section 6.

## Addition of UTR to coding models

The set of coding models is extended into the untranslated regions (UTRs) using RNA-seq data (if available) and alignments of species-specific RefSeq cDNA sequences. The criteria for adding UTR from cDNA or RNA-seq alignments to protein models lacking UTR (such as the projection models or the protein-to-genome alignment models) is that the intron coordinates from the model missing UTR exactly match a subset of the coordinates from the UTR donor model.

## Generating multi-transcript genes

The above steps generate a large set of potential transcript models, many of which overlap one another. Redundant transcript models are collapsed and the remaining unique set of transcript models are clustered into multi-transcript genes where each transcript in a gene has at least one coding exon that overlaps a coding exon from another transcript within the same gene.

## Pseudogenes

Pseudogenes are annotated by looking for genes with evidence of frame-shifting or lying in repeat heavy regions. Single exon retrotransposed pseudogenes are identified by searching for a multi-exon equivalent elsewhere in the genome. A total number of genes that are labelled as pseudogenes or processed pseudogenes will be included in the core db, please check Final Gene set Summary.

## Immunoglobulin and T-cell Receptor genes

Translations of different human IG gene segments are downloaded from the IMGT database [14] and aligned to the genome using GenBlast.



For the cat annotation, a cut-off of 80 percent coverage, 70 percent identity and an e-value of  $e^{-1}$  were used for GenBlast with the exon repair option turned on. The top 10 transcript models built by GenBlast for each protein passing the cut-offs are kept. In cases where multiple sequences aligned to the same locus, we selected the alignment with the highest combined percent identity and coverage.

## Section 4: Creating the Final Gene Set

### Small ncRNAs

Small structured non-coding genes are added using annotations taken from RFAM [15] and miRBase [16]. Rfam and miRBase annotations were searched against the genomic sequence using NCBI-BLAST. The resulting alignments were then filtered using RNA-fold (miRBase hits) and Infernal [17] (Rfam hits).

### lincRNAs

Candidate long intergenic non-coding RNAs (lincRNAs) should not overlap a protein-coding gene nor have a Pfam domain. The RNA-seq data sets, which were filtered against the protein-coding gene set, are used to predict lincRNAs and the Pfam analysis from InterProScan is run against the filtered gene set.

For the primate clade annotation, it was difficult to ascertain the validity of 2-exon models as lincRNA candidates so they were excluded from the set of potential lincRNAs.

### Cross-referencing

Before public release the transcripts and translations are given external references (cross-references to external databases). Translations are searched for signatures of interest and labelled where appropriate.

## Stable Identifiers

Stable identifiers are assigned to each gene, transcript, exon and translation. When annotating a species for the first time, these identifiers are auto-generated. In all subsequent annotations for a species, the stable identifiers are propagated based on comparison of the new gene set to the previous gene set.

## Section 5: Final Gene Set Summary

Gene Class	Count
IG_C_gene	9
IG_V_gene	15
lincRNA	2708
miRNA	354
misc_RNA	608
Mt_rRNA	2
Mt_tRNA	22
processed_pseudogene	89
protein_coding	19409
pseudogene	589
ribozyme	11
rRNA	717
scaRNA	36
snoRNA	624
snRNA	1480
sRNA	4
TR_C_gene	2
TR_J_gene	4
TR_V_gene	7

Table 2: counts of the gene classes

<b>Transcript Class</b>	<b>Count</b>
IG_C_gene	9
IG_V_gene	15
lincRNA	4758
miRNA	345
misc_RNA	608
Mt_rRNA	2
Mt_tRNA	22
processed_pseudogene	89
protein_coding	33912
pseudogene	589
ribozyme	11
rRNA	717
scaRNA	36
snoRNA	624
snRNA	1480
sRNA	4
TR_C_gene	2
TR_J_gene	4
TR_V_gene	7

Table 3: counts of the transcript classes

## Section 6: Appendix - Further information

The Ensembl gene set is generated automatically, meaning that gene models are annotated using the Ensembl gene annotation pipeline. The main focus of this pipeline is to generate a conservative set of protein-coding gene models, although non-coding genes and pseudogenes may also be annotated.

Every gene model produced by the Ensembl gene annotation pipeline is supported by biological sequence evidence (see the “Supporting evidence” link on the left-hand menu of a Gene page or Transcript page); ab initio models are not included in our gene set. Ab initio predictions and the full set of cDNA and EST alignments to the genome are available on our website.

The quality of a gene set is dependent on the quality of the genome assembly. Genome assembly can be assessed in a number of ways, including:

1. Coverage estimates
  - A higher coverage usually indicates a more complete assembly.
  - Using Sanger sequencing only, a coverage of at least 2x is preferred.
2. N50 of contigs and scaffolds
  - A longer N50 usually indicates a more complete genome assembly.
  - Bearing in mind that an average human gene may be 10-15 kb in length, contigs shorter than this length will be unlikely to hold full-length gene models.
3. Number of contigs and scaffolds
  - A lower number top level sequences usually indicates a more complete genome assembly.
4. Alignment of cDNAs and ESTs to the genome
  - A higher number of alignments, using stringent thresholds, usually indicates a more complete genome assembly.

## Assembly Information

Species name	Common name	Assembly name	Genbank accession ID	Assembly level
<i>Felis catus</i>	Cat	Felis_catus_9.0	GCA_000181335.4	Chromosome

Table 4: Assembly info

## Statistics of Interest

Species name	Common name	Total bases	Bases masked	Bases unmasked
<i>Felis catus</i>	Cat	2,491,009,630	10774527	2480235103
%			43.253655	56.746445

Table 5: Number of bases unmasked and repeat masked

Species name	Common name	Eponine	CpG	tRNAscan
<i>Felis catus</i>	Cat	92740	36781	211585

Table 6: Counts of low complexity features

## Layers in detail

Each group within a layer has two numbers attached to the end of it. The first number is the alignment coverage of the original evidence that was aligned. The second number is the percent identity between the original evidence that was aligned and the translation that was created. So, for example, human\_pe12\_sp\_95\_80 can be read as: “A human protein with protein existence level one or two, that was present in SwissProt and that

had an alignment coverage of greater than or equal to 95 percent when aligned to the Ensembl transcript and had a percent identity of greater than or equal to 80 percent when aligned to the Ensembl transcript". Note that the alignment percent identity and coverage values are in bins, so if you see two groups such as human\_pe12\_sp\_95\_95 and human\_pe12\_sp\_95\_80, they are mutually exclusive (so the second group covers  $\geq 80$ , but  $< 95$  percent identity. Most of the names refer to different alignments of UniProt proteins via GenBlast. The realign names refer to the projection models (if projection was carried out), while the 28 rnaseq\_merged and rnaseq\_tissue refer to models built from the merged RNA-seq track or the tissue RNA-seq tracks respectively (if RNA-seq data were aligned). Below you can view the exact layering rules used to select the transcripts for each protein-coding gene. Note that regardless of whether certain evidence types were not used in the annotation (e.g. if a species does not have RNA-seq data or if no projection was carried out), they will still be listed in the layers below (as we use different layering templates based on which clade the species belongs to), but would be ignored by the layering code.

#### **Layer 1**

IG\_C\_gene, IG\_J\_gene, IG\_V\_gene, IG\_D\_gene, TR\_C\_gene, TR\_J\_gene,  
TR\_V\_gene, TR\_D\_gene

#### **Layer 2**

realign\_95, realign\_80, rnaseq\_merged\_95, rnaseq\_merged\_80, self\_pe12\_sp\_95,  
self\_pe12\_tr\_95, self\_pe12\_sp\_80, self\_pe12\_tr\_80, human\_pe12\_sp\_95,  
human\_pe12\_tr\_95, primates\_pe12\_sp\_95, primates\_pe12\_tr\_95,  
mammals\_pe12\_sp\_95, mammals\_pe12\_tr\_95

#### **Layer 3**

rnaseq\_tissue\_95, human\_pe12\_sp\_80, human\_pe12\_tr\_80, primates\_pe12\_sp\_80,  
primates\_pe12\_tr\_80, mammals\_pe12\_sp\_80, mammals\_pe12\_tr\_80

#### **Layer 4**

rnaseq\_tissue\_80, realign\_50

#### **Layer 5**



human\_pe12\_sp\_50, human\_pe12\_tr\_50

## More information

More information on the Ensembl automatic gene annotation process can be found at:

- Publication

Aken B et al.: The Ensembl gene annotation system. Database 2016.

- Web

[Link to Ensembl gene annotation documentation](#)

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