Assembly of MHC region of cheetah

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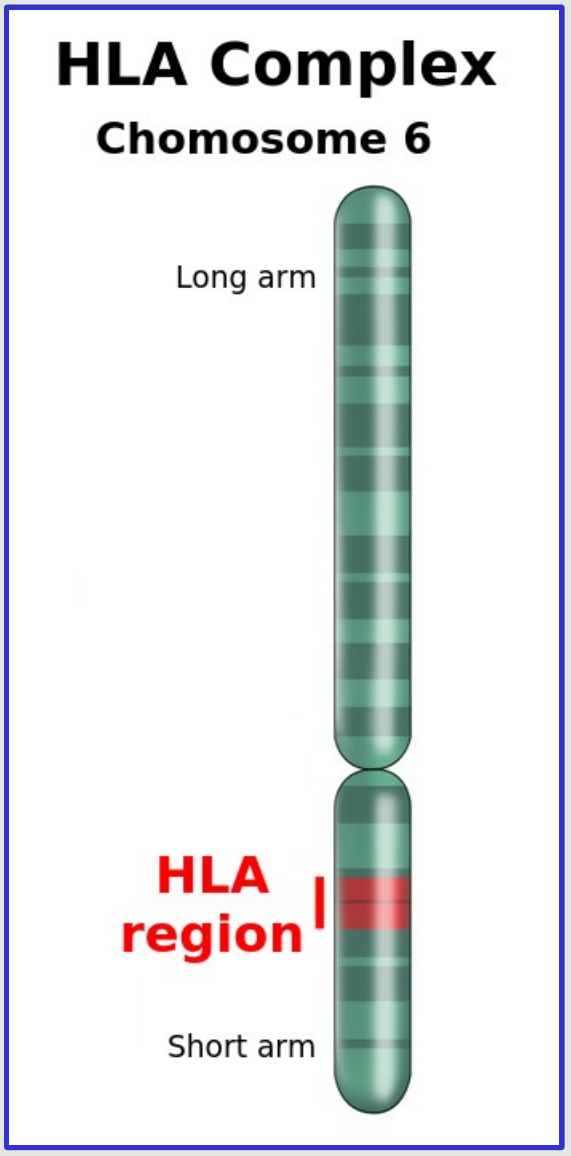
Purpose

MHC region assemblies of cheetah genome using information about sequence and structure of cat's MHC (gene sequences and order, BAC clones).

MHC — ***Major histocompatibility complex*** — a group of genes that determine histocompatibility antigens

HLA — ***Human leukocyte antigen***, system is the name of the loci of genes that encode for MHC in humans

FLA — ***Feline leukocyte antigen***, cat's homolog of HLA



MHC in human: 140 genes spanning 3.6 Mbp.

MHC proteins:

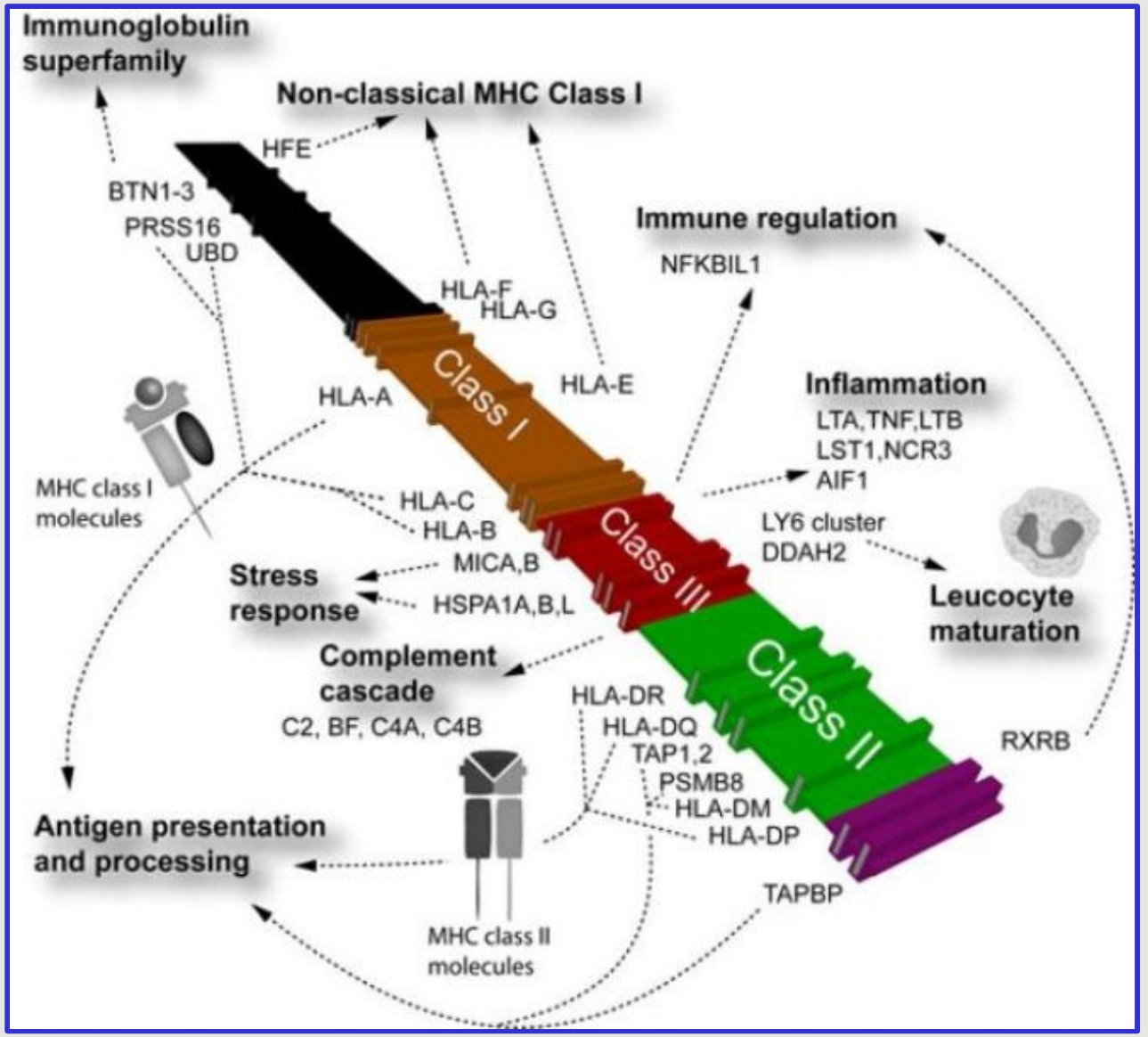
Class I

Class II

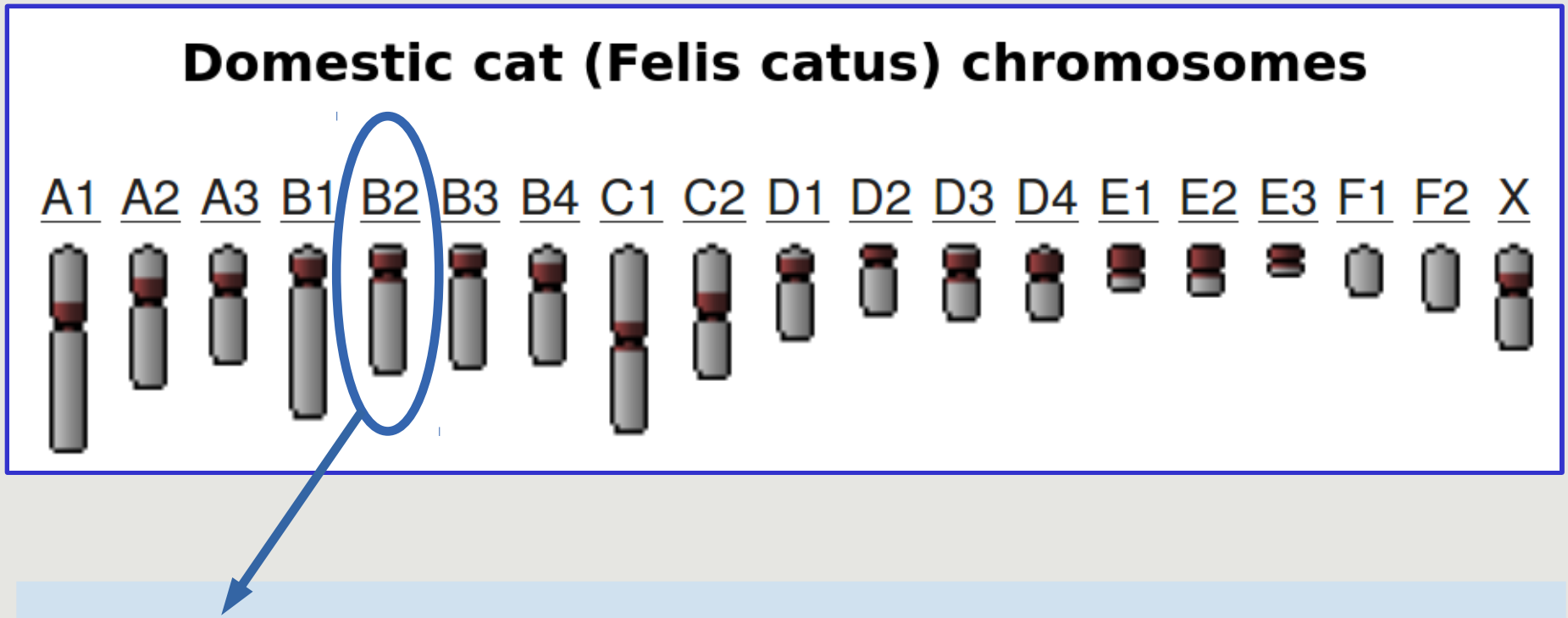
Class III

Well conserved among species, except the antigen binding class I genes

Difficult for assembling



Domestic cat MHC



Cat chromosome B2:

- is homologous with human Chr. 6

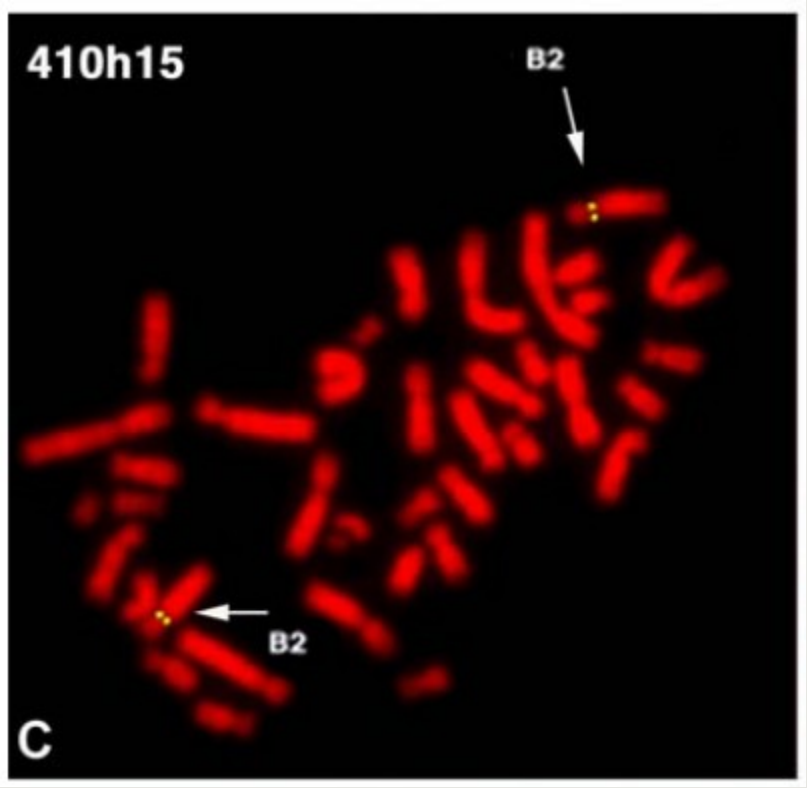
- the p-arm and distal q-arm of B2 are inverted relative to the gene order of human Chr. 6

MHC assembling in domestic cat

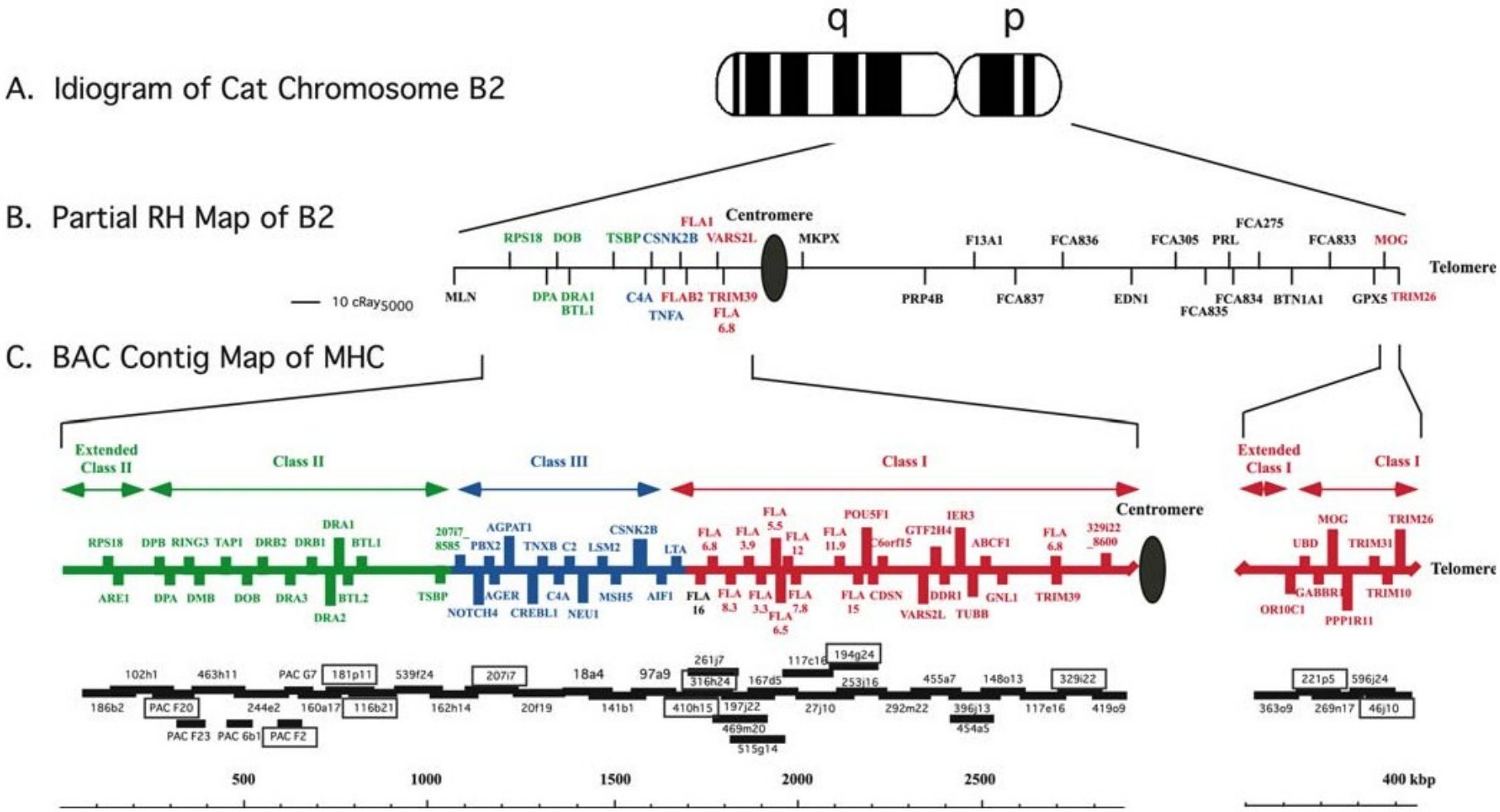
Construction a BAC contig map of the domestic cat MHC (194 BAC clones)

Determination the order of regions across Chr. B2

using an expanded set of markers in radiation hybrid (RH) mapping and fluorescent in situ hybridization (FISH) analyses (31 markers)

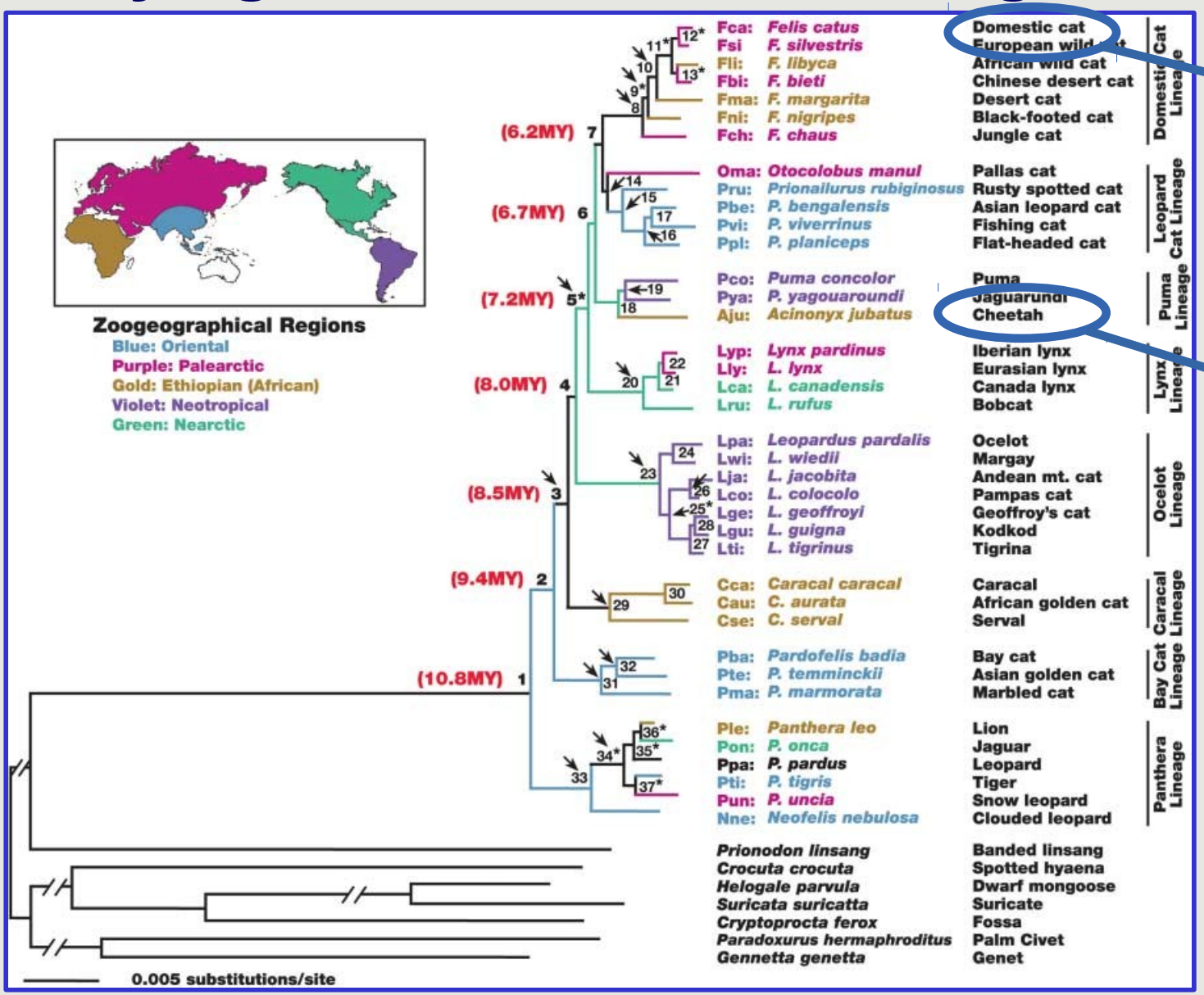


Genomic organization of the domestic cat major histocompatibility complex (MHC)



TW Beck et al. *Immunogenetics* (2005) 56: 702–709

Phylogenetic relations among felid species



Domestic cat

Distance about 6,7 MY

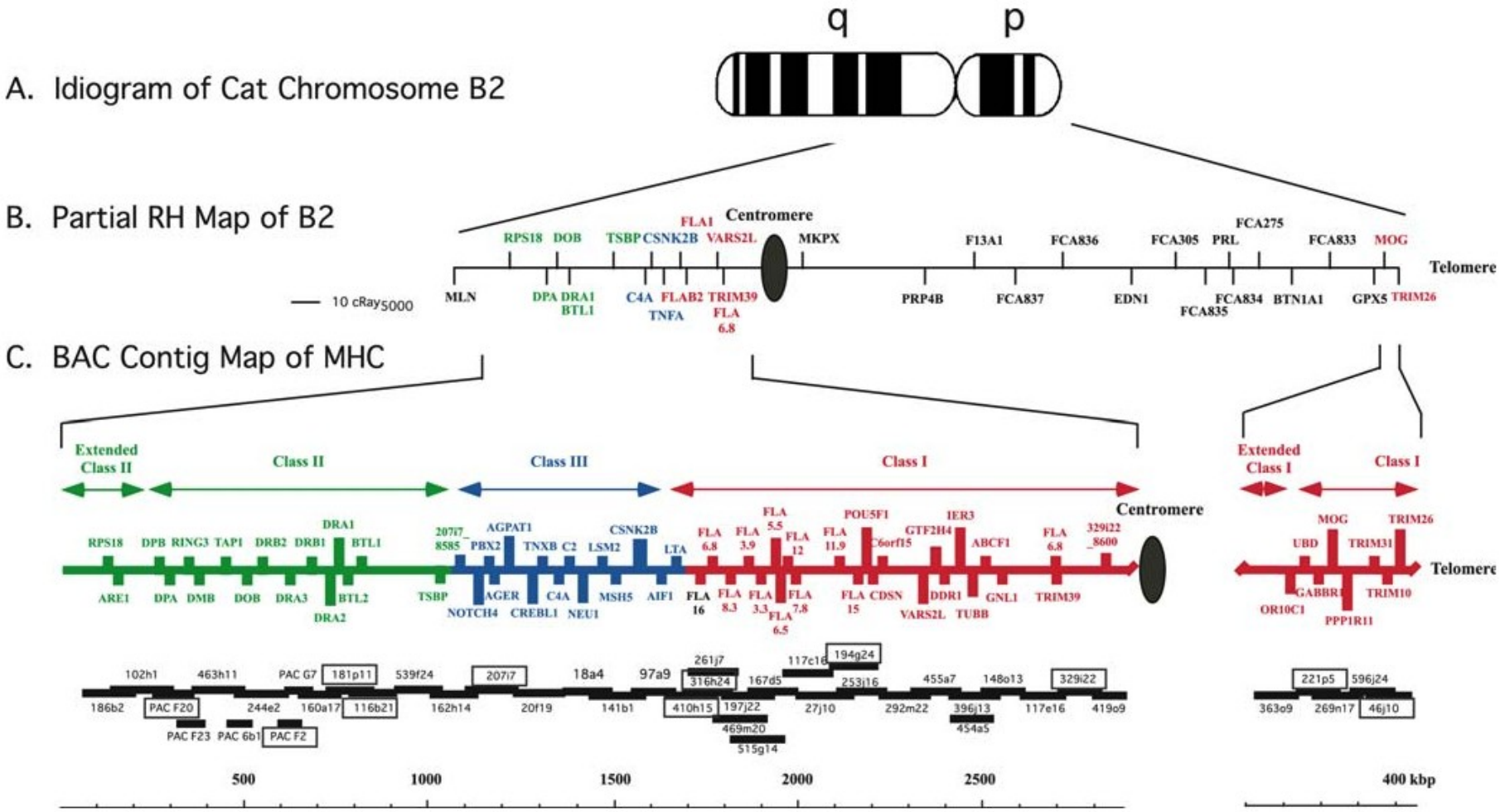
Cheetah

A rather high level of genomic synteny between *Felidae* species

Warren E. Johnson et al. *Science* 311, 73 (2006)

YS Cho et al. *Nature Communications 4:2433* (2013)

Genomic organization of the domestic cat major histocompatibility complex (MHC)



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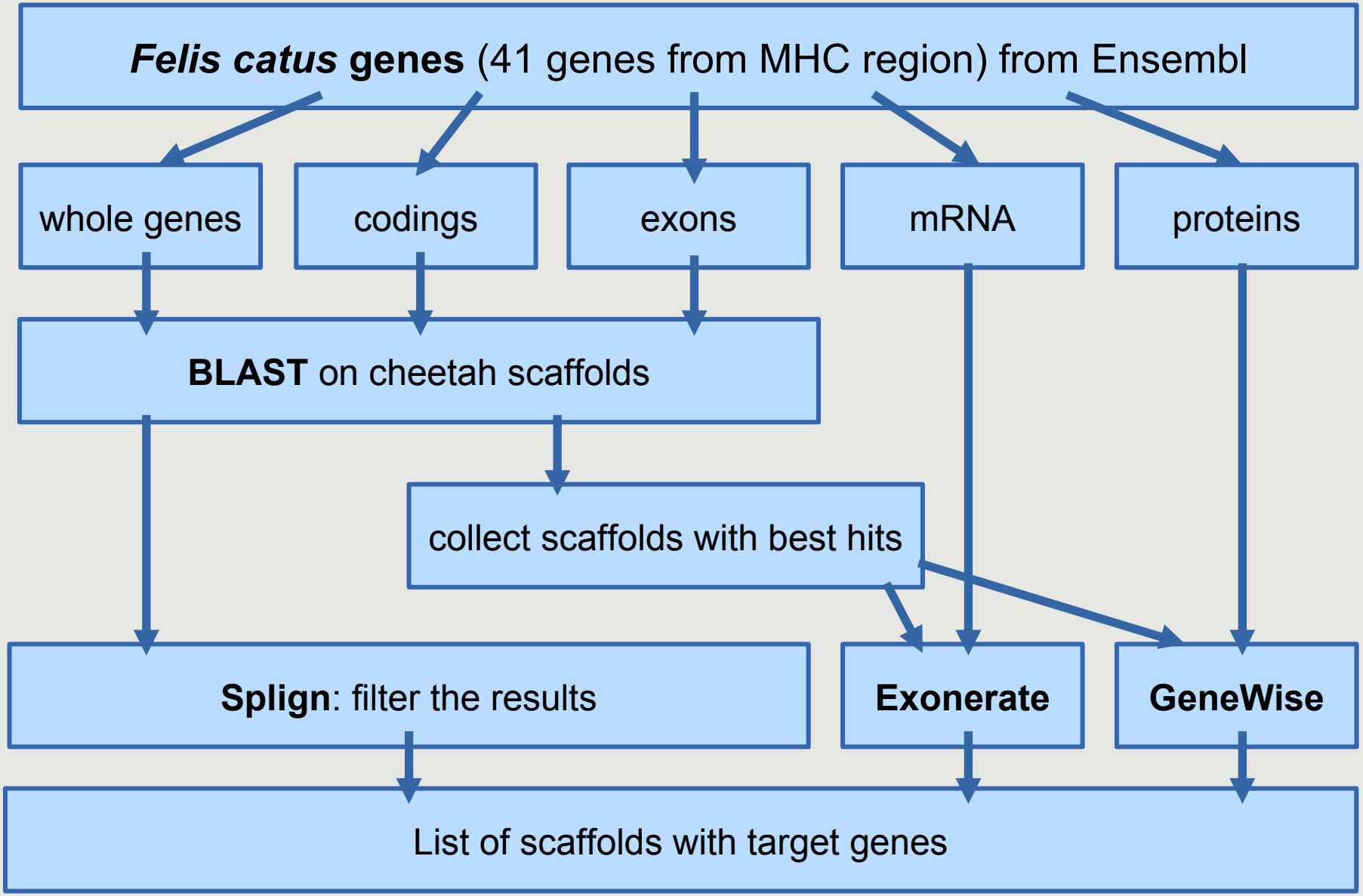
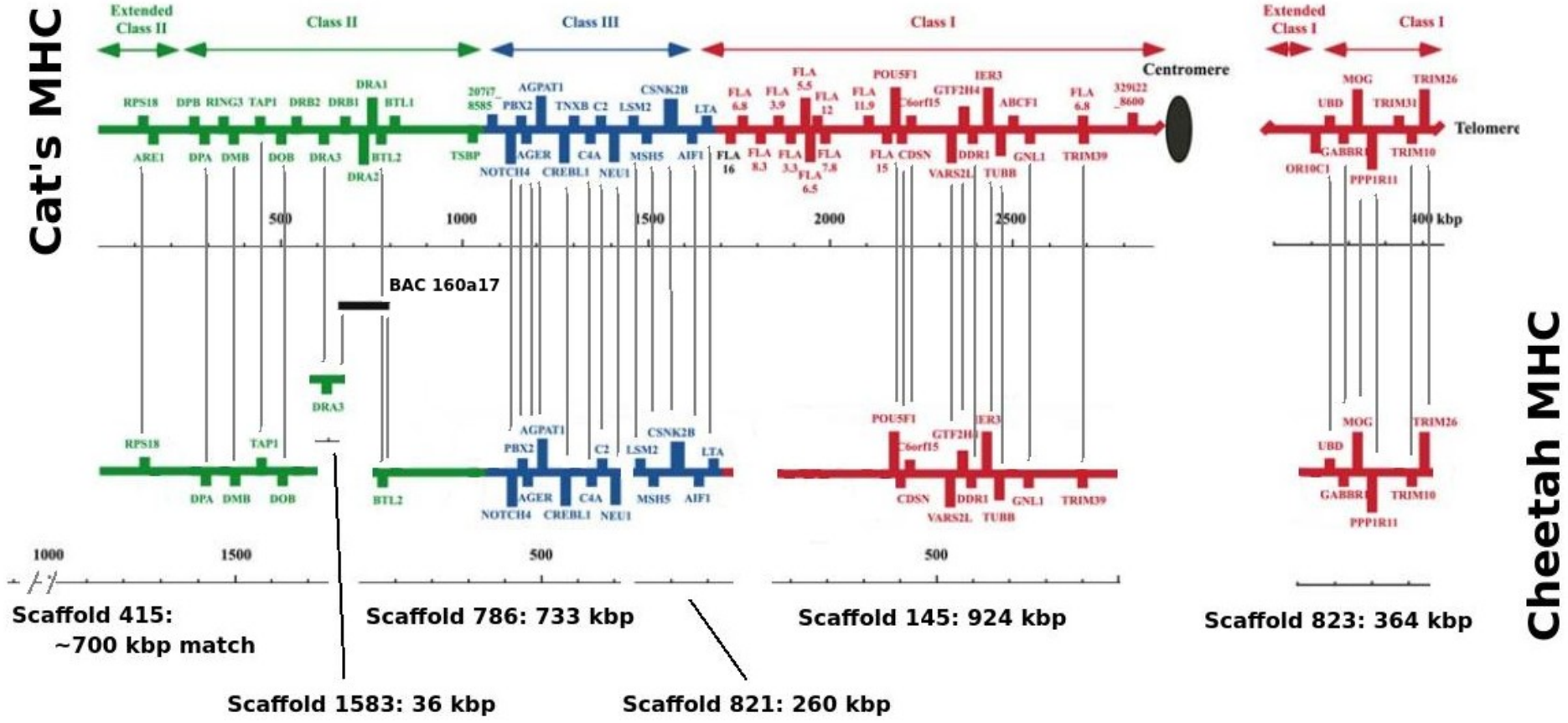
Pipeline


Felis catus **genes** (41 genes from MHC region) from Ensembl
whole genes
codings
exons
mRNA
proteins
BLAST on cheetah scaffolds
collect scaffolds with best hits
Splign: filter the results
Exonerate
GeneWise
List of scaffolds with target genes

Results



Total scafflods size about 3 Mbp

Future plans

- Fill the gaps between scaffolds
- Formalize the gene finding pipeline (python scripts to filter and combine results)
- Repeat this pipeline with the tiger MHC region
- *De novo* gene annotation (using Augustus, Glimmer or another tool)
- Comparison of MHC regions between cat, cheetah, tiger and other species (for example, dog, rat, mouse): genes, pseudogenes, SNP frequency, CpG content, CpG islands...

Thank you!