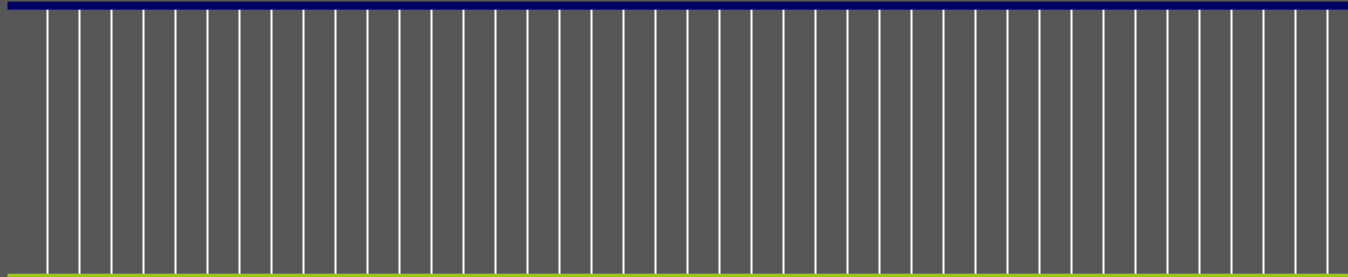


Alineamiento de genomas completos

Objetivo

Para dos genomas, *A* y *B*, mapear cada posición de *A* en su posición correspondiente de *B*

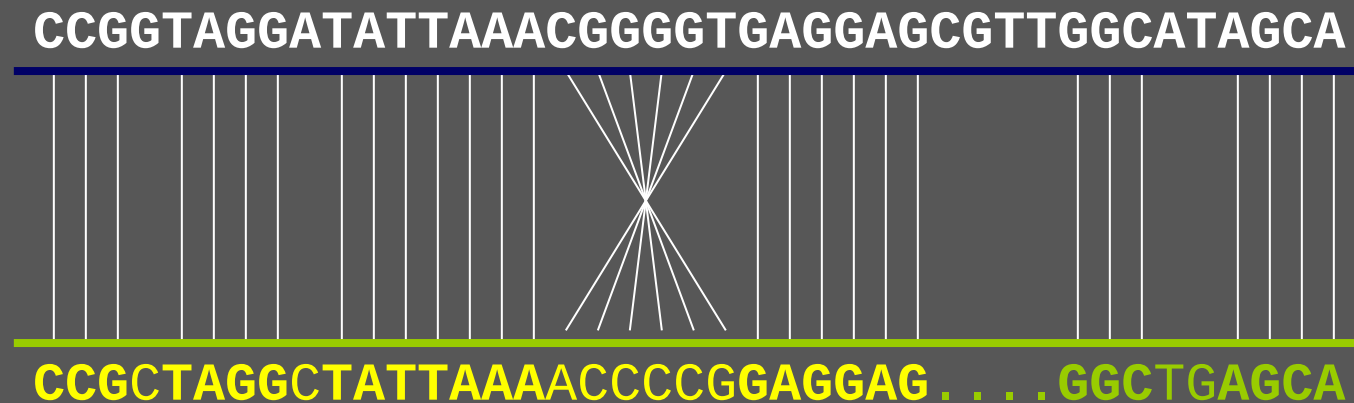
CCGGTAGGCTATTAAACGGGGTGAGGAGCGTTGGCATAGCA

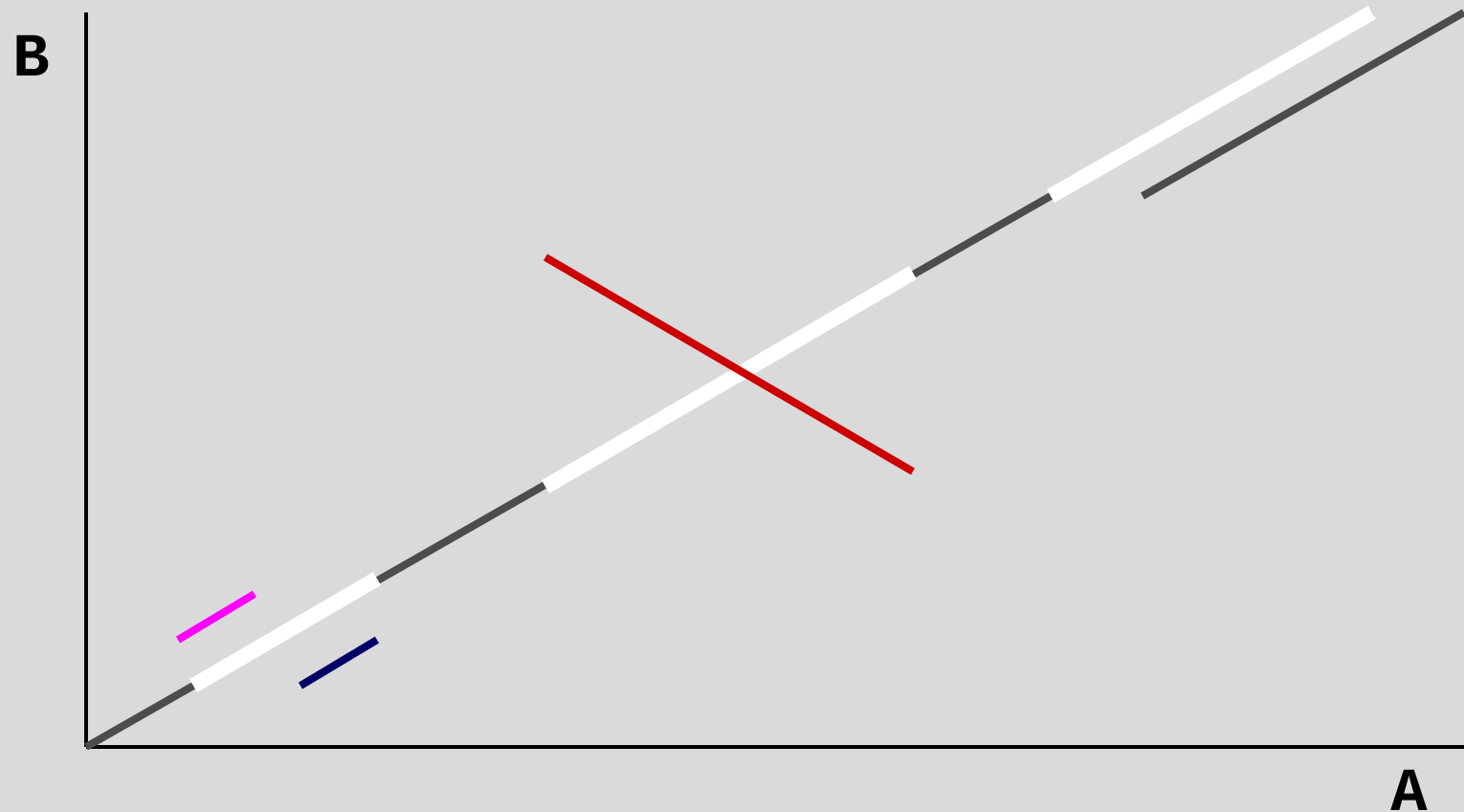
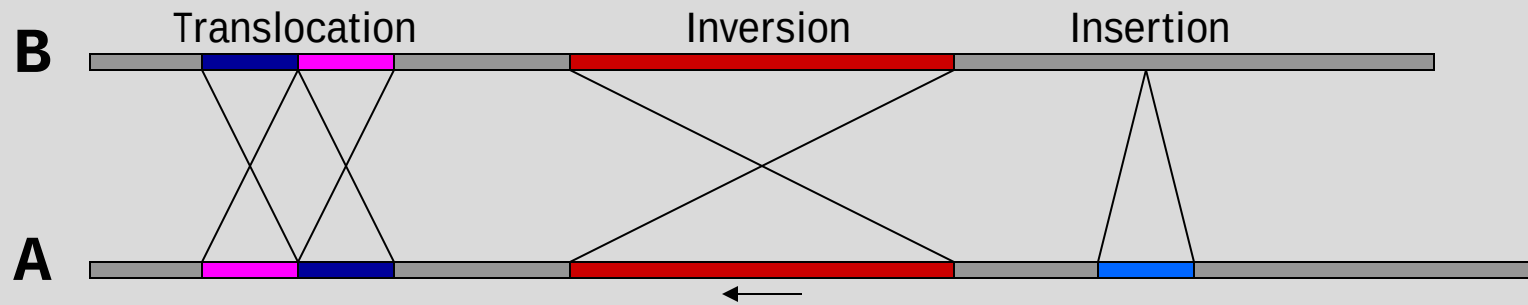


CCGGTAGGCTATTAAACGGGGTGAGGAGCGTTGGCATAGCA

Pero no tan rápido...

Puede haber inserciones, deleciones,
translocaciones, inversiones,
duplicaciones, SNPs...





El objetivo, por tanto, del alineamiento de genomas completos es encontrar y alinear las piezas similares entre dos genomas



LAST software

Query sequences

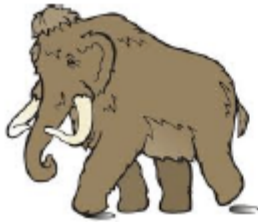
cgcgctctattaa
ctg**agcaagtaatg**gtag
atattctgtat
ctatgctatgc
ctagctagctgtgt
cgcgatgtaat
ctgatcgtgta
cctgcgaaaata
cgctgctgaacc
cgctgctgaacc
aatgctgatgtcg
ctgatcgtgtagtcgtaa

Reference sequences

ct**agctatgtgatga**
ctcgttagctgtgtcgtgtg
ctcgtagctgatcgtgt
ctgatcgtacgtatatataa
aatatagtttcctattc
ctg**cctgcatgatcta**gcat
tgtagtcgtagctatgtcgaaac

agctatgtgatg
||| | || |||
agcaa-gtaatg

cctgcatgatcta
||||| || ||
cctgc--gaaata



Mammoth DNA reads

aactgatgctgta

ctatgctagtgtgc

cgcaaaagtgtgta

ccggctatttcg

gcggcgtagctg

cccgatgctagta

gtcgtagctgat

atgatcgtagct

gaggcgtagctg

g c g g c g t a g c t g

████████████████████

Example 1



Elephant genome

tgtagtcgtagctatgctagctgtcgtaatatattatatgctagttactcgaac

ctgctagctagctgcgtcgtctcttattatatatatattgcgcgcgtgtc

ctgacgtacgtagctagtcgtcggcgcgcgatgctgtgta

cgctgatgctgtgtagtgatcgctgatgctgcagtgc

ctgctcgtcgtatatattatctgtcgtagctgt

tgtgatcgtatatattatctgctgcgtatg

ctgatcgtagctagctttttattgcc

cgca--tgtgta

cgcaaaagtgtgta

atgctatttctat

atgcaatt-ctat

Example 3

Metagenome DNA reads

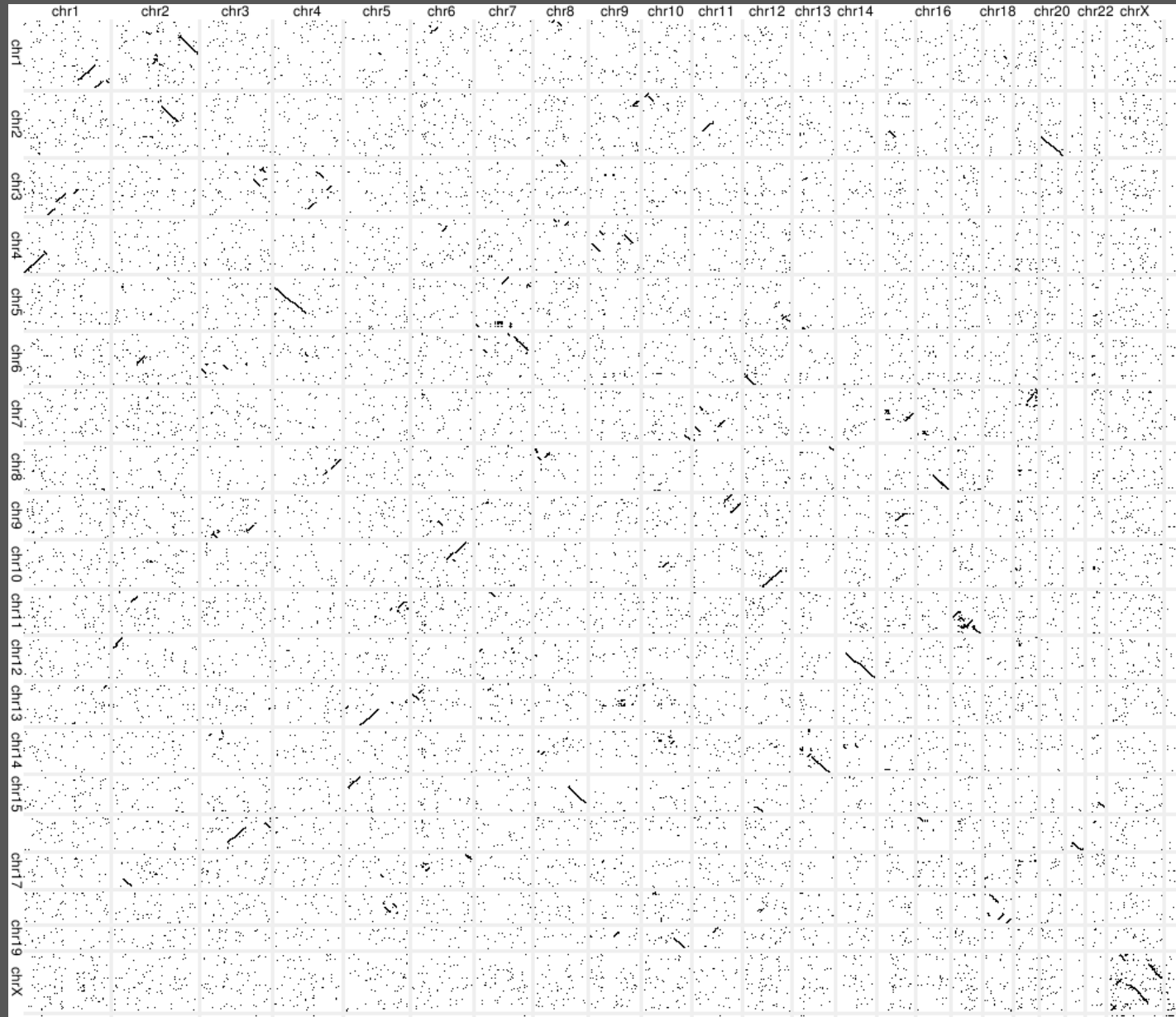
aactgatgctgta
ctatgctagtgtgc
cgcaaaagtgta
ccggctatatctg
gcggcgtagctg
cccgatgctagta
gtcgtagctgat
atgatcgtagct
gcggcgtagctg
gcggcgtagctg
aaaaaaaaaaaa

p g r y
| | | |
gtaactgagtc

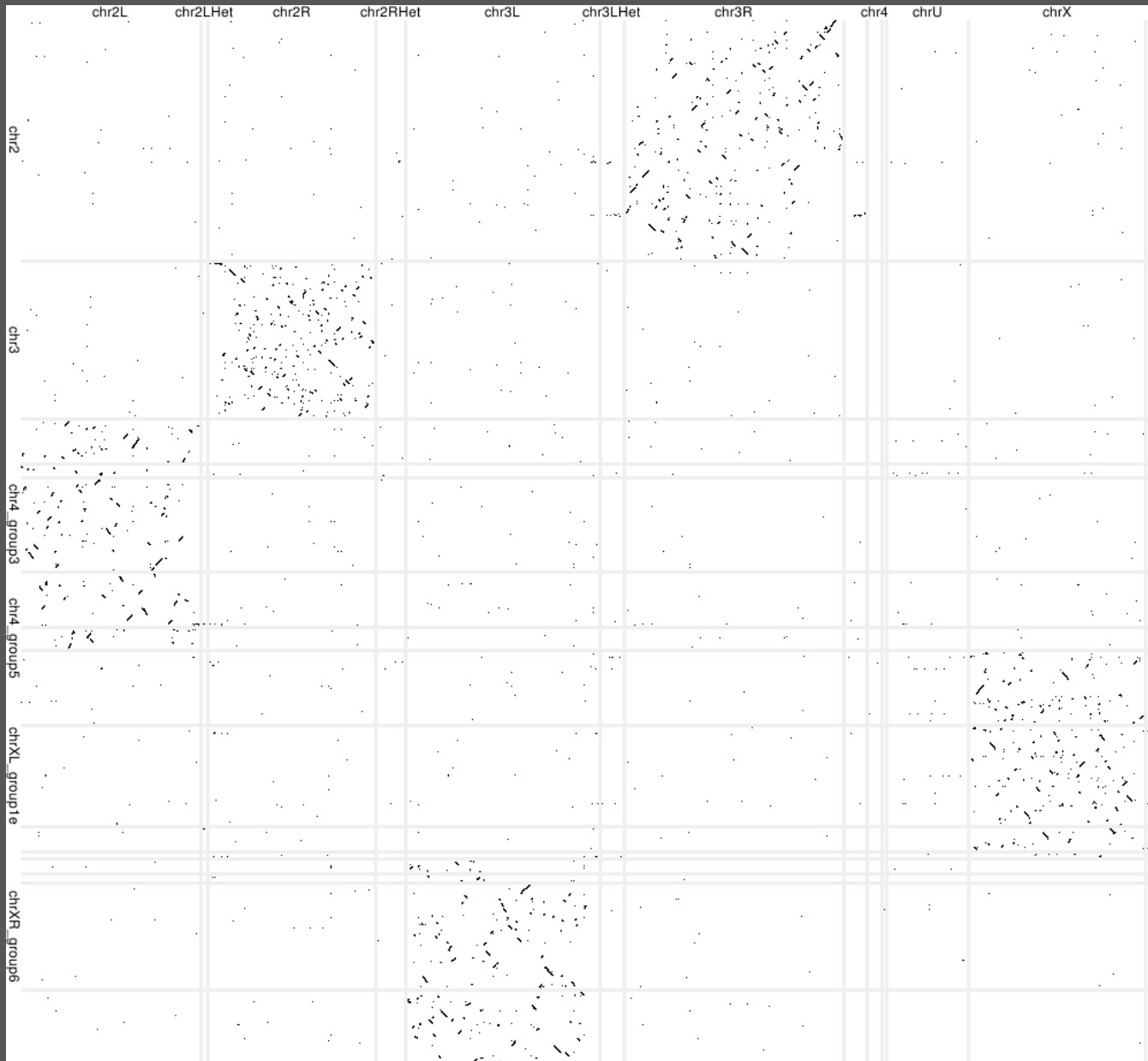
Protein database

mtghedfiklppagwyttagtlff
myedefaagpkmvvcgrrcw
mwyaggqddhivinnaiievkky
mhpgrycyfhhgapa
mmrnhfagpilvpqerratelsss
mhivilfagaafviprcwt

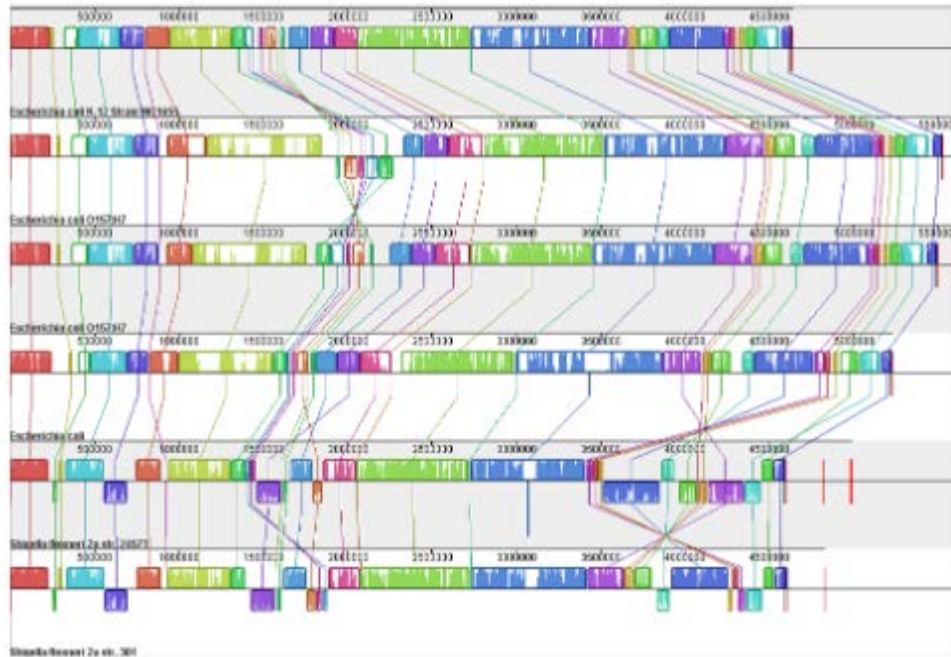
Matriz de puntos entre humanos (hg18) y ratón (mm9)



Matriz de puntos entre *D. melanogaster* y *D. pseudoobscura*



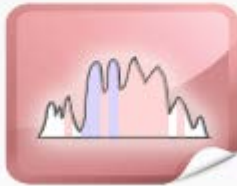
Mauve Alignment of 9 Enterobacteria (*Shigella* and *E. coli*)



Shigella flexneri 2a str. 301

Precomputed Alignments

VISTA Browser



<http://pipeline.lbl.gov/cgi-bin/gateway2>



VISTA

Tools for Comparative Genomics

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Clade

Genome

Release

Position

Vertebrate

Human

Feb. 2009

chr9:107,543,285-107,690,436

Submit

☒ VISTA-Point

☐ VISTA Browser (Requires Java2)

 [Java 2 installation instructions](#)

 [Help](#)

Whole Genome Comparative Analysis of the *Human Feb. 2009 Genome*

From this page you can access the results of:

the **multiple alignments**

- [Human Feb. 2009](#), [Chimp Mar. 2006](#), [Callithrix jacchus v.2.0.2](#), [Rhesus Jan. 2006](#) and [Pongo pygmaeus abelii v.2.0.2](#) genomes.

UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr22:31,217,701-34,573,570 3,355,870 bp.

enter position, gene symbol or search terms

go

chr22 (q12.2-q12.3) 22p13 22p12 22p11.2 22q11.21 q11.23 22q12.1 22q12.2 22q12.3 22q13.1 22q13.2 22q13.31 13.33

