

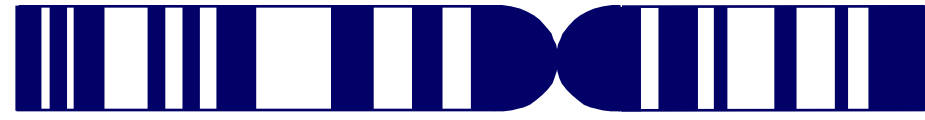
ChickRH

- Cartographie d'irradiation chez la poule :
 - Cartographie dense de SNP
 - localisation d'EST absentes de la séquence génomique
- Participants :
 - INRA UMR Génétique Cellulaire Toulouse
 - Centre National de Génotypage (CNG) Evry.

CARTOGRAPHIE

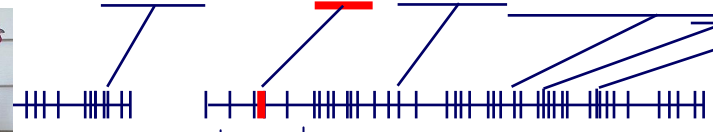
Carte cytogénétique

Sonde ADN



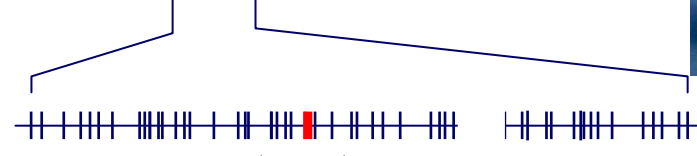
Carte génétique

Polymorphisme, phénotypes



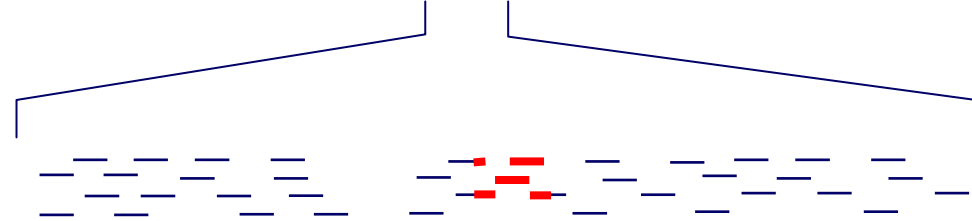
Cartes d'hybrides irradiés

PCR



Contigs de BAC

BAC



Séquence génomique

Gènes

Variation nucléotidique (SNP)



Séquençage de transcrits

ARNm et EST

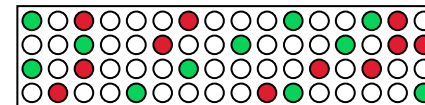
Splicing (cells)

ARNm

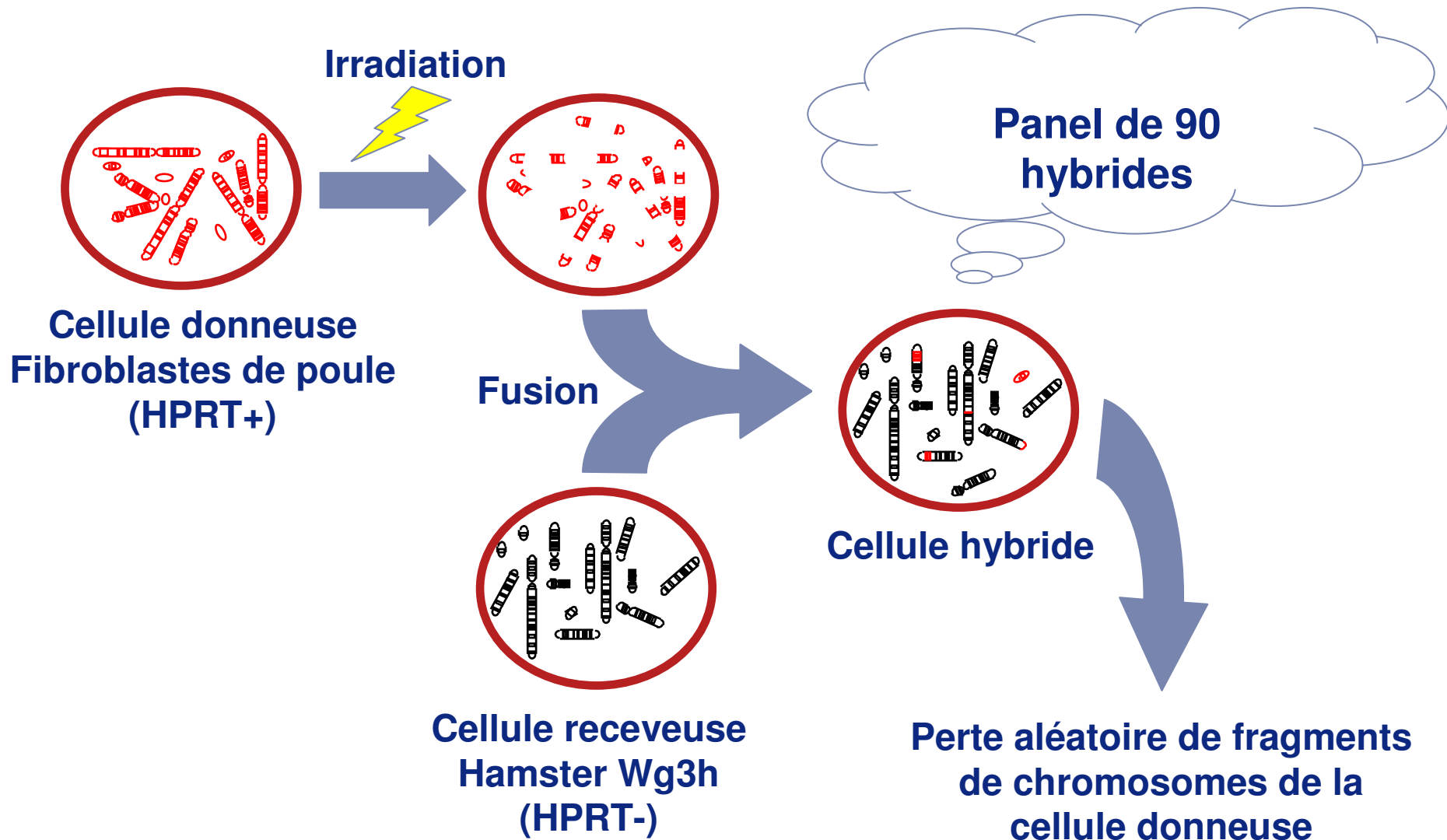


EXPRESSION

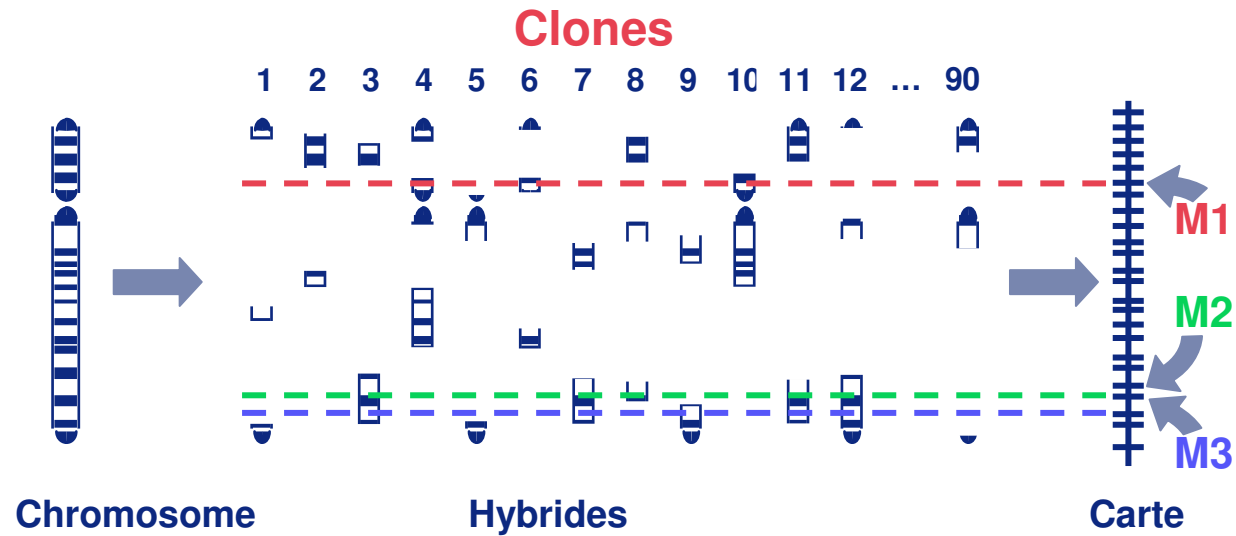
Analyses d'expression



Panel d'hybrides irradiés

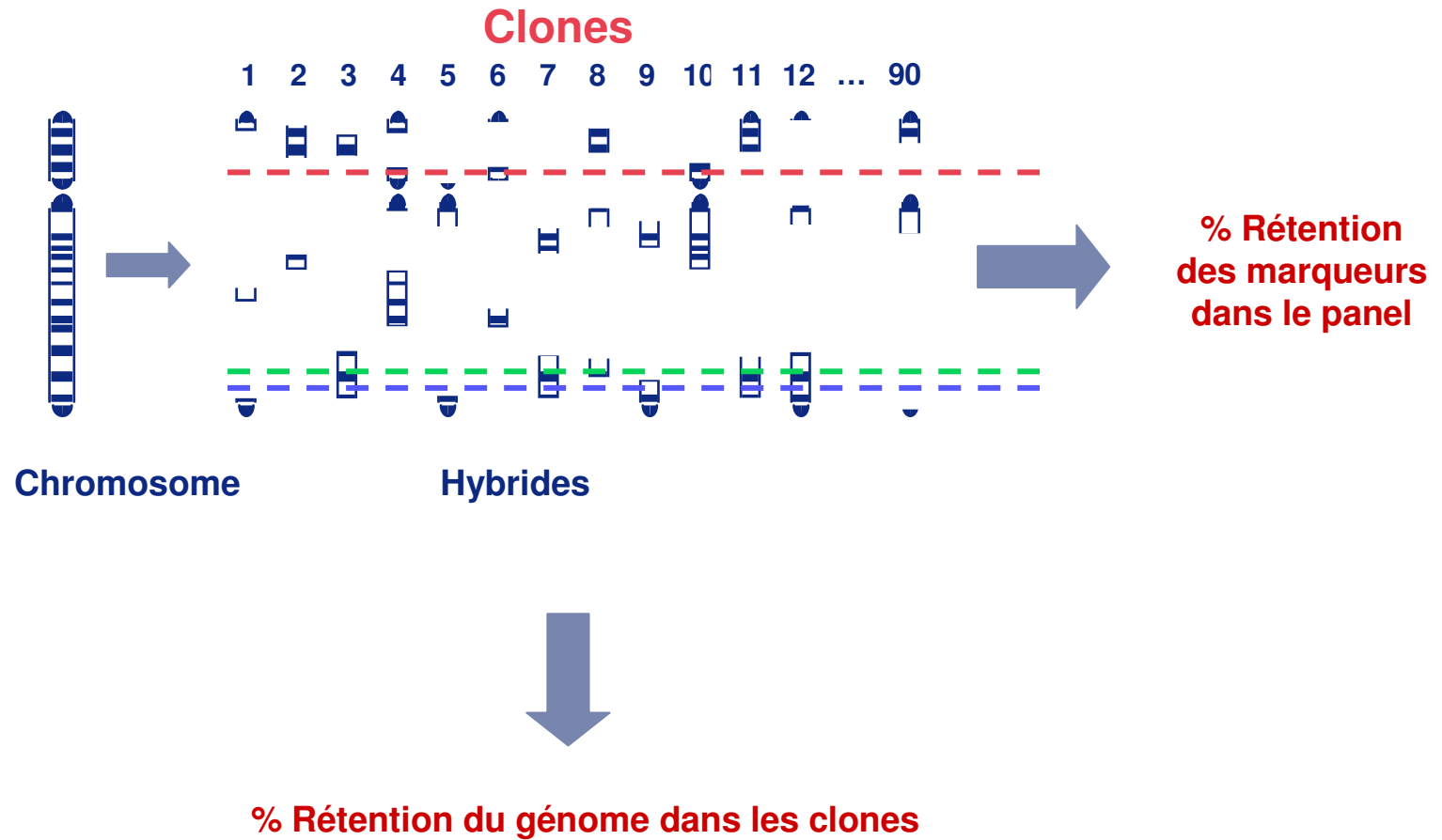


Génotypage et cartes



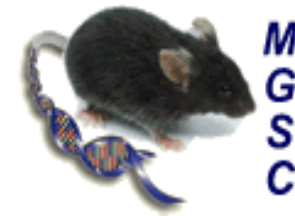
Résultats PCR														
Hybr.	1	2	3	4	5	6	7	8	9	10	11	12	...	90
M1	-	-	-	+	-	+	-	-	-	+	-	-		-
M2	-	-	+	-	-	-	+	+	-	-	+	-		-
M3	-	-	+	-	-	-	+	-	+	-	+	-		-

Génotypage et cartes

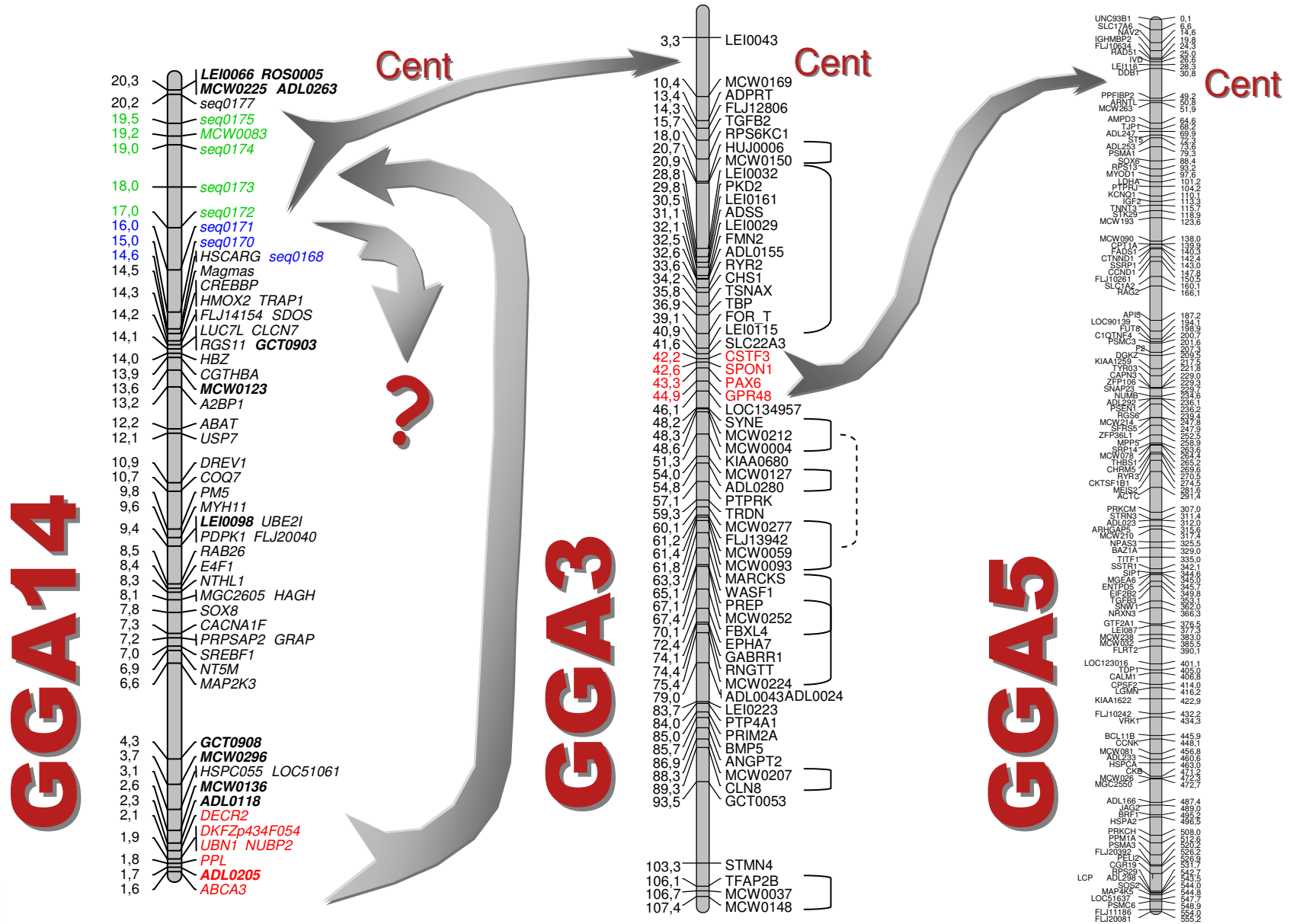


Premiers vertébrés séquencés

- Humain
- Chimpanzé
- Macaque
- Souris
- Rat
- Chien
- Opossum
- Poule
- Takifugu
- Tetraodon



Assemblage : mars 2004 et cartes RH



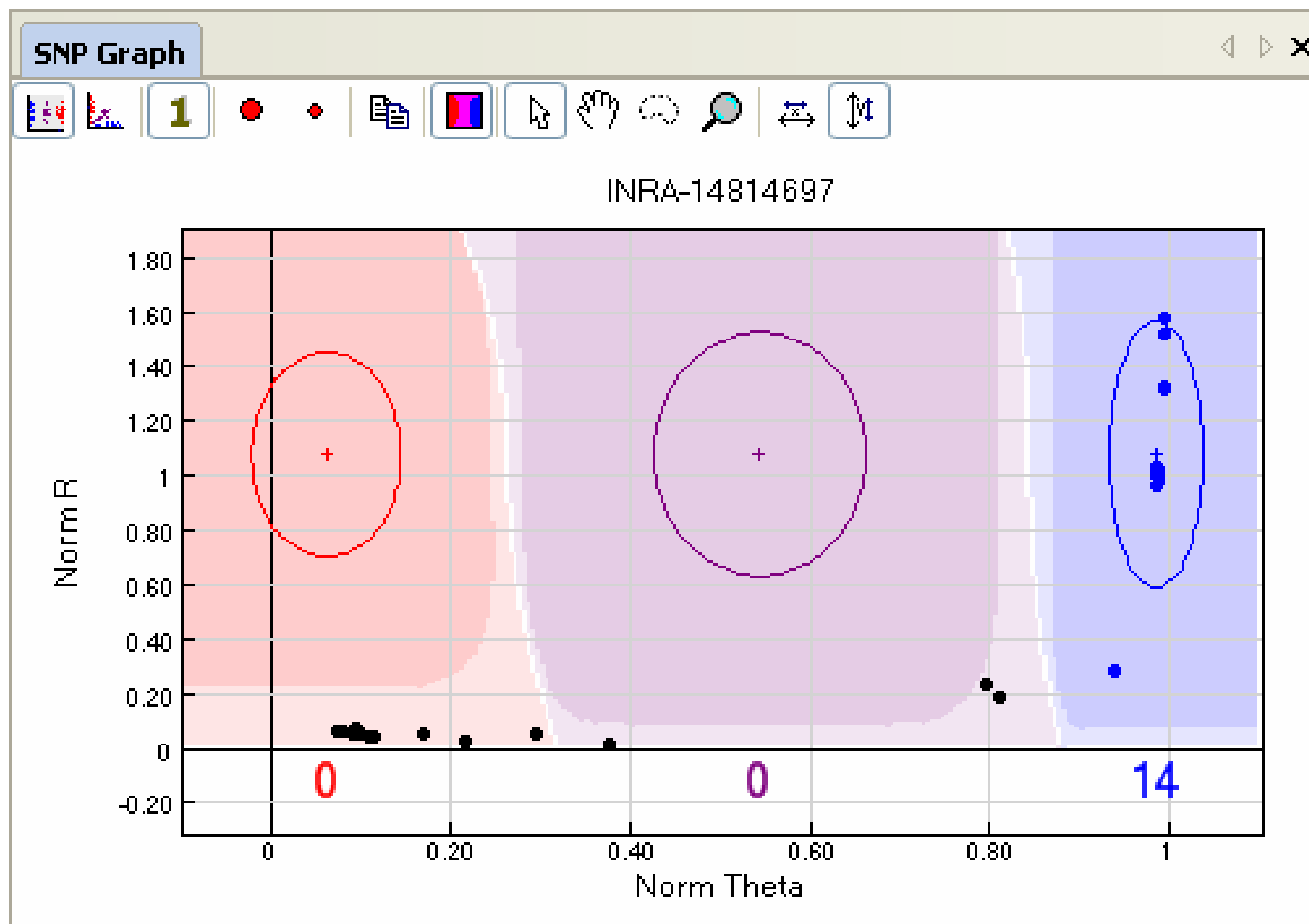
Cartes RH de poule : le passé

- Marqueurs utilisés (ère pré-séquence)
 - Microsatellites des cartes génétiques
 - EST : similarités de séquence avec des régions HSA définies
- Marqueurs utilisés (ère post-séquence)
 - STS de l'assemblage

Cartes RH de poule : le présent (1)

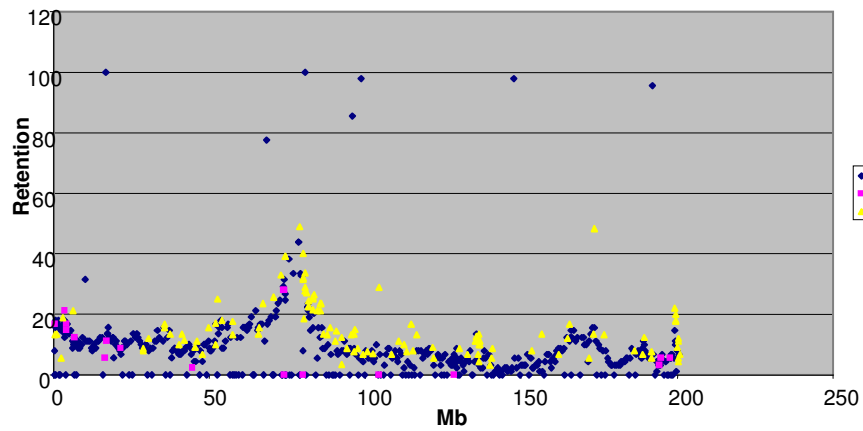
- Marqueurs utilisés (ère pré-séquence)
 - Microsatellites des cartes génétiques
 - EST : similarités de séquence avec des régions HSA définies
- Marqueurs utilisés (ère post-séquence)
 - STS de l'assemblage
 - Technologie de génotypage Illumina
 - 9212 marqueurs

Génotypage RH Illumina

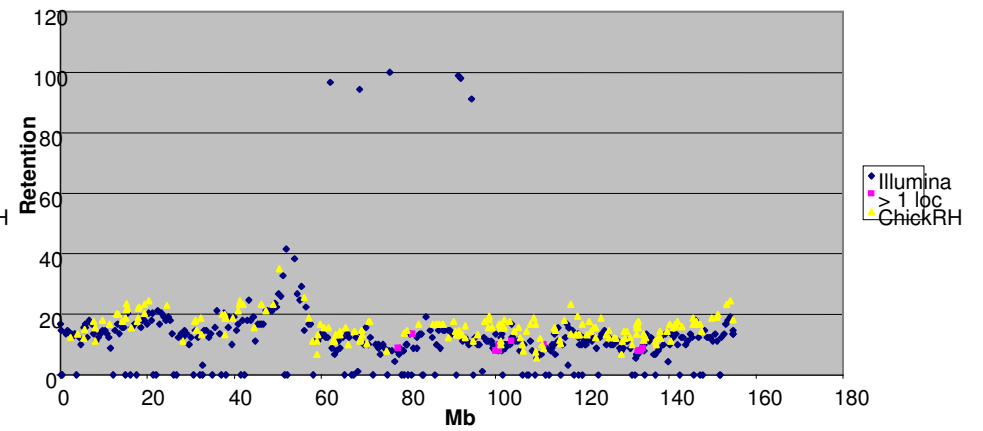


Rétention des marqueurs

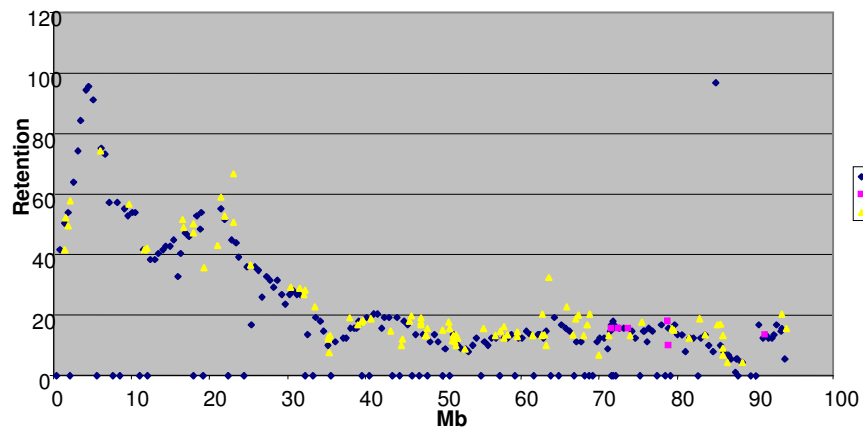
GGA1



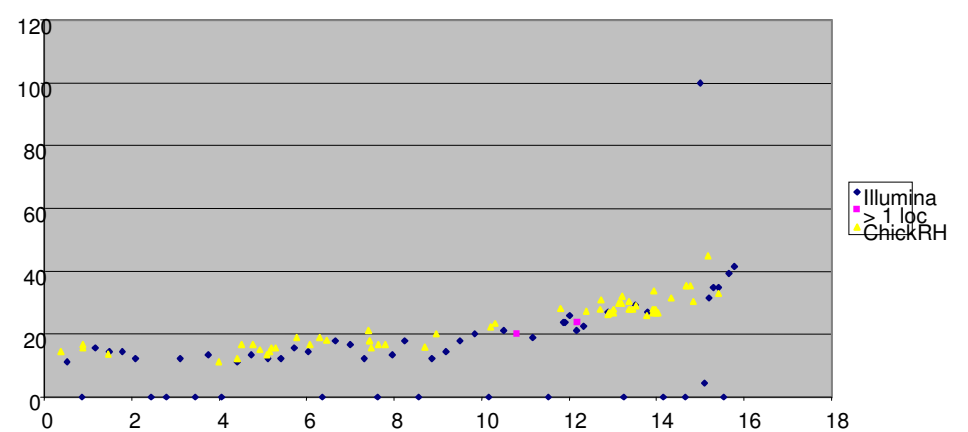
GGA2



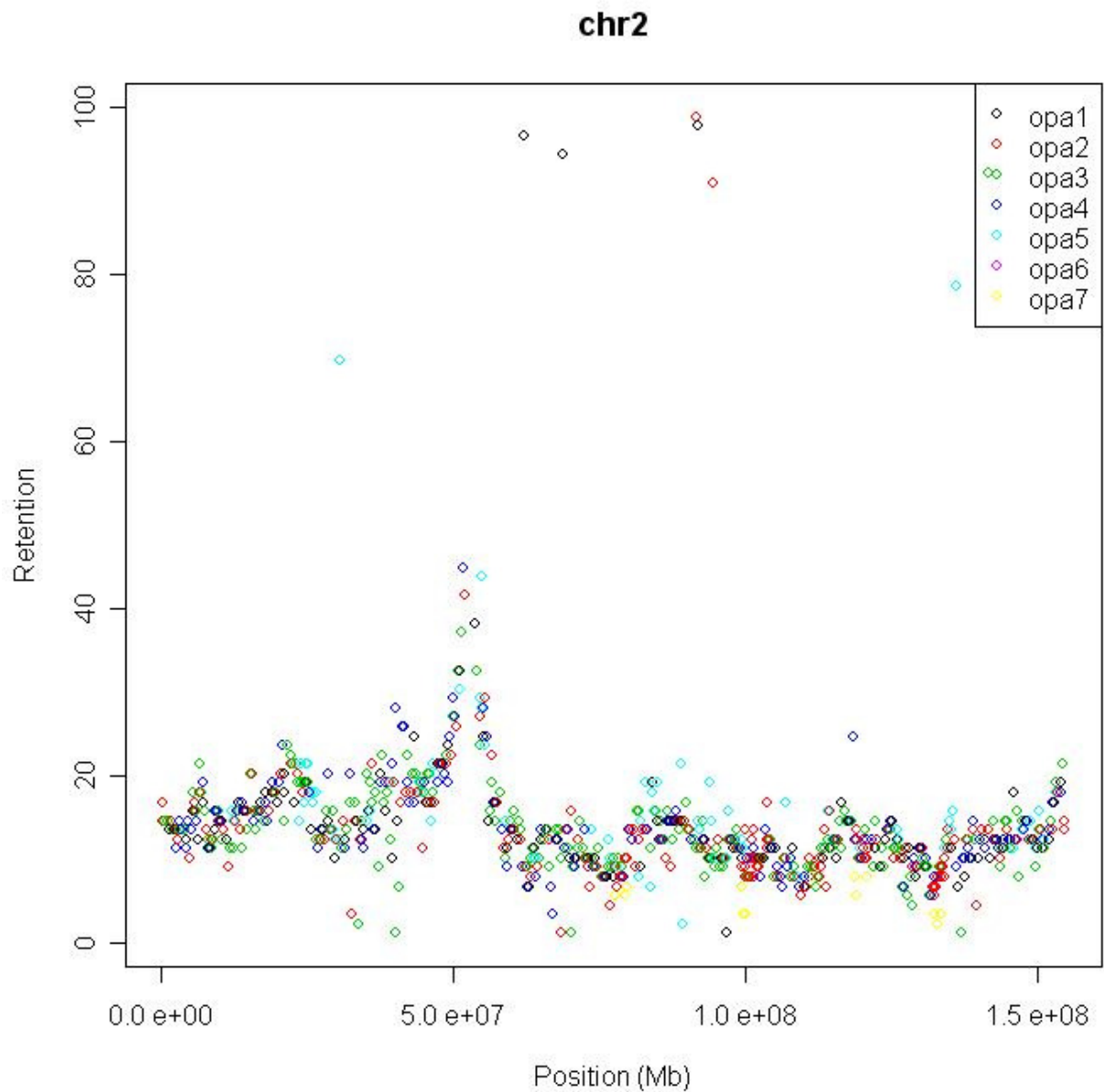
GGA4



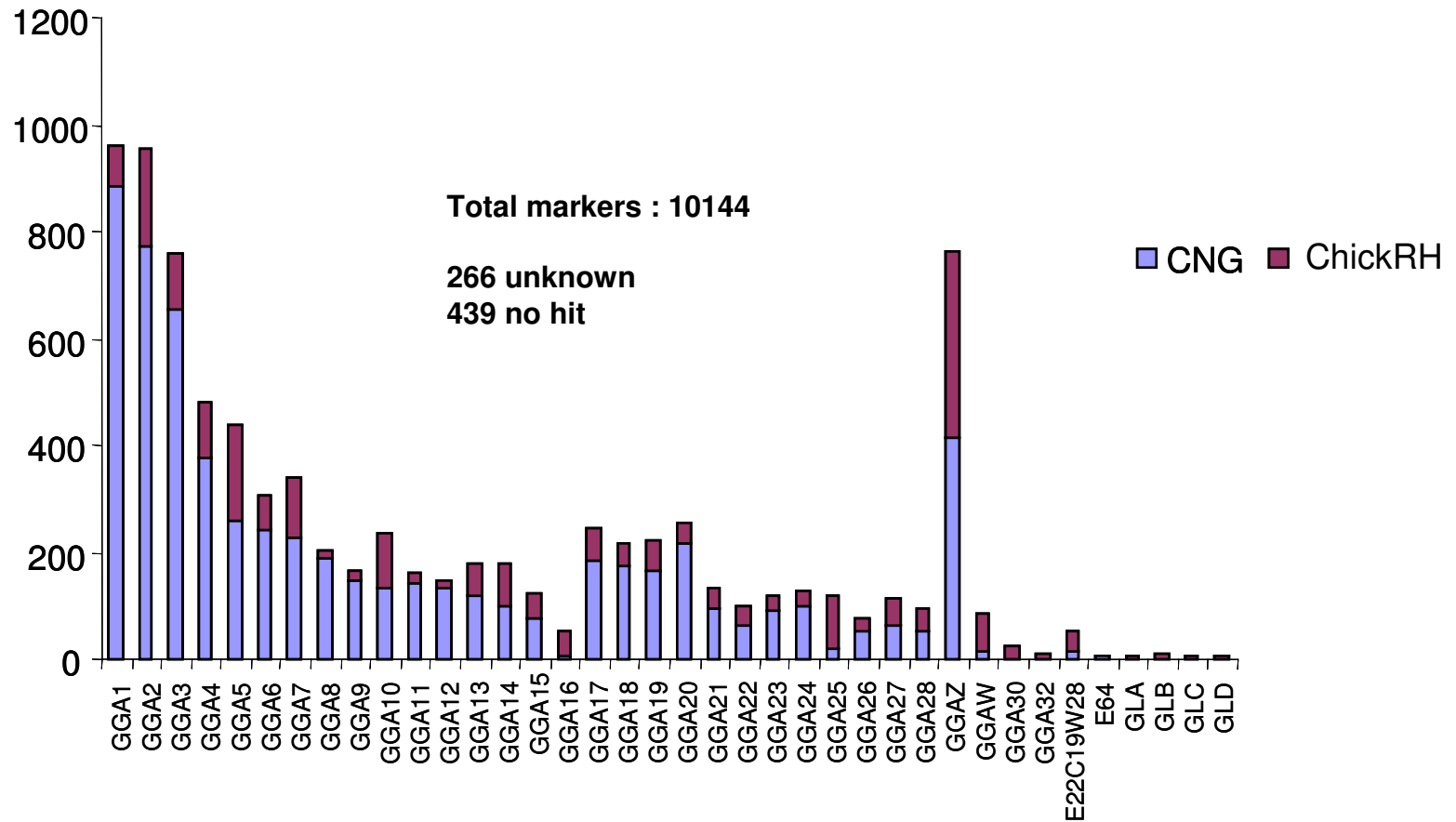
GGA14



Rétention: marqueurs des 7 OPA (GGA2)

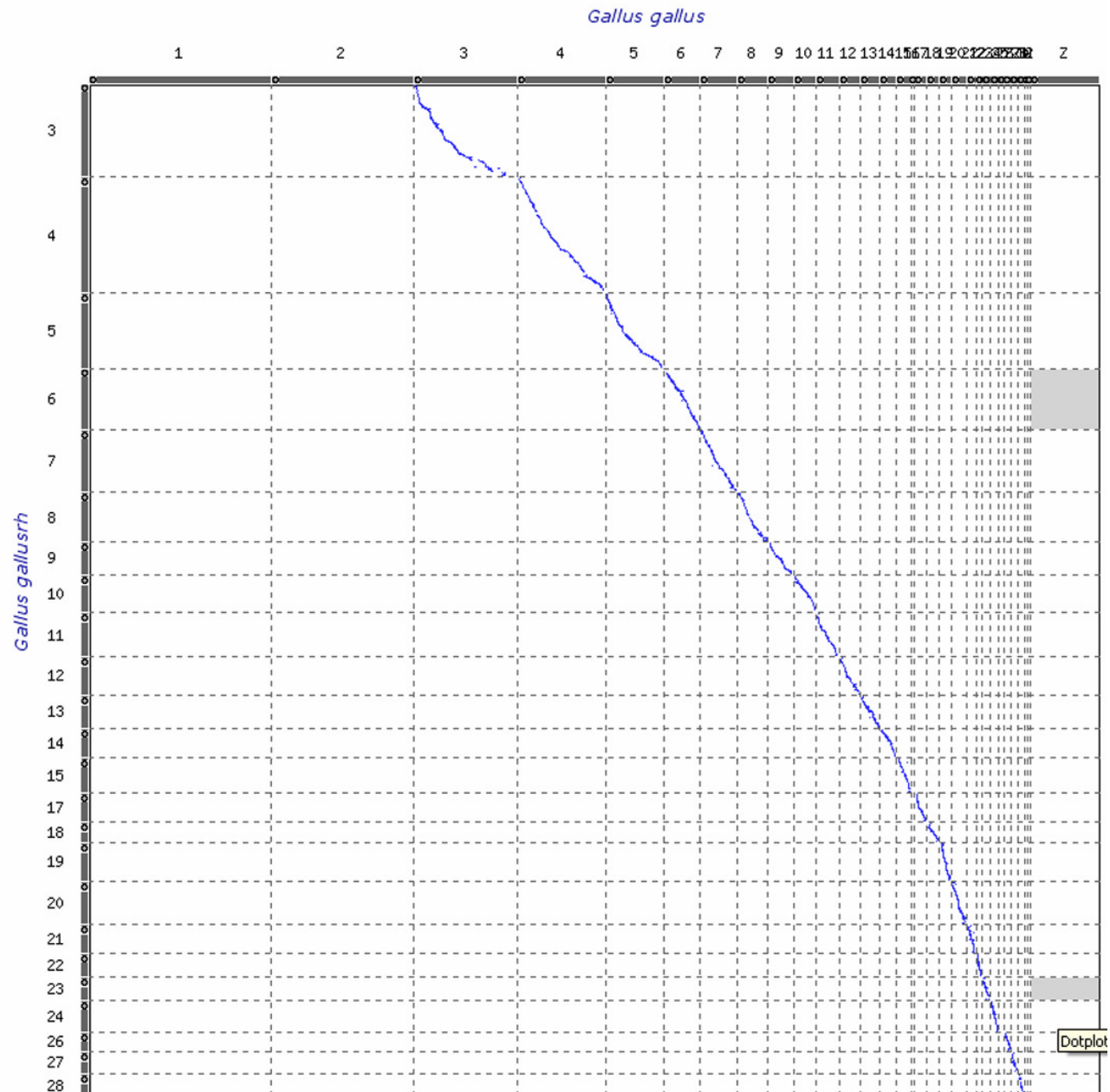


RH linkage groups at lod 7




1 686 markers are unlinked or in very small linkage groups (1 000 CNG + 600 ChickRH)


Concordance RH - Séquence



Viewing maps in Narcisse



A mirror view of conserved syntenies
Rel 1.5.0--



INRA
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE

Narcisse New session Help release Notes Credits

Zoom Data Display Session

Synteny levels ?

0
 1
 2
 3

 4
 5

Involved lower levels ?

0
 1
 2

Upload your data ?

Add a genome ?

Reference: Gallus gallus

target1: Gallus gallusrh mapping

target2: Gallus gallusfw mapping

Dynamic Legend ?

Markers

organism chickfw (3b)

symbol rs13675356

name rs13675356

start 178.1 (178.1)

end 179.1 (179.1)

Coucou 1 (1)

type default

Gallus gallusrh
method:mapping

CR

rs15255758
rs14309211
rs14308531
rs15253361
rs14309254
Chic..0789
rs14309403
rs15257939
rs15259172
rs14310908
rs16218442
rs14311981
rs14319575
rs15277048
rs15273962
rs16225707
rs14316120
rs15267074
rs14085746
rs14084943
rs13733203
rs14082468
rs15015185
rs14081750
RBL2597
RBL1566
rs14320247
rs15282865
rs13717657
rs15283903
Chic..0622
rs15289287
rs15292870
rs15295355
rs16228791
Chic..1477
Chic..0780
Chic..0130
Chic..1486
rs14333371
rs15311568
rs14334468
rs14334712
rs15316882
rs15319731
rs15325781
RBL11768
rs13675356
rs15330163
rs14345265
rs14345884
rs16260924
rs14347175
rs15338509
rs14350398
rs16269462
rs14353730

Gallus gallus
chromosome:3

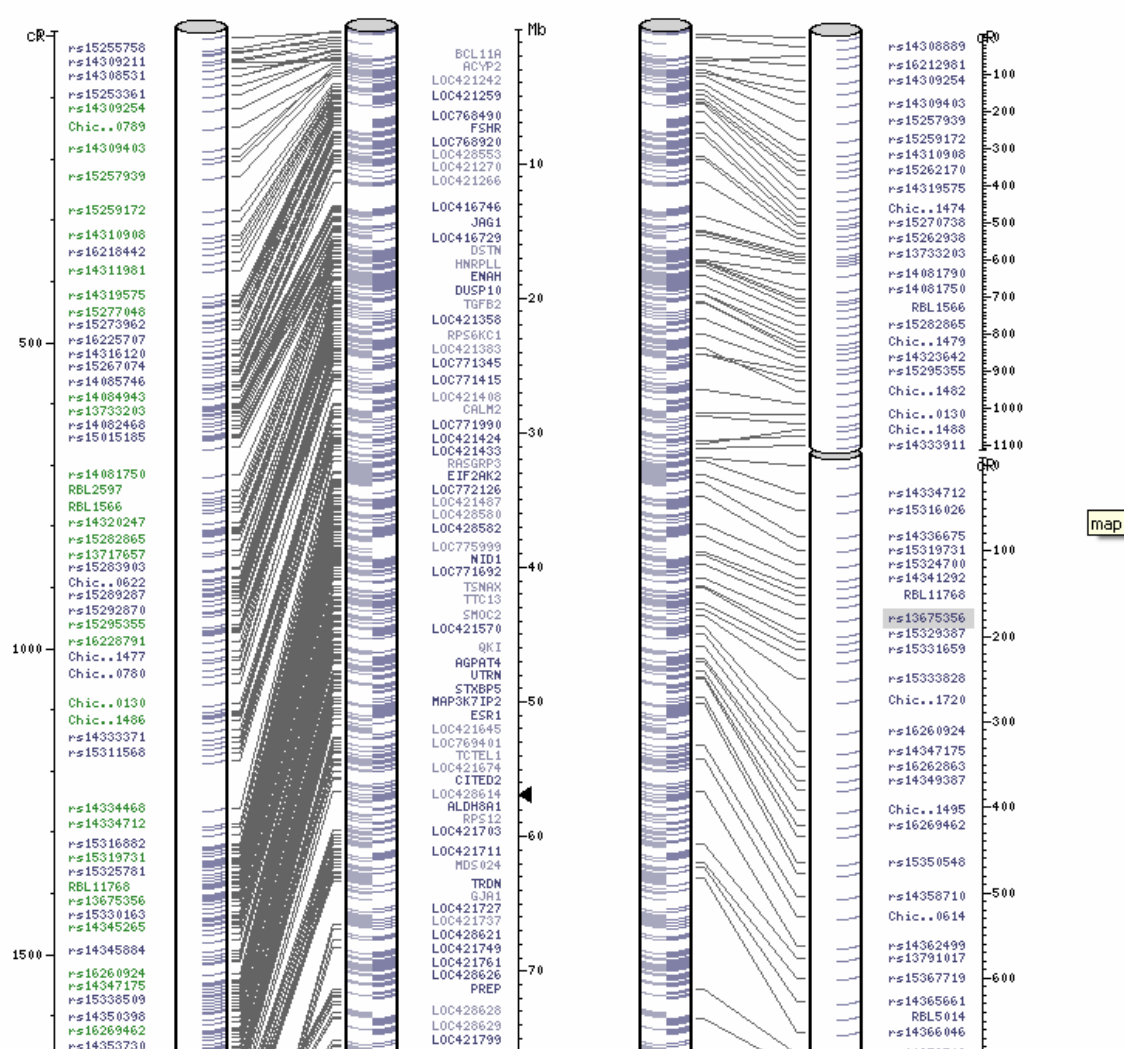
Mb

BCL11A
RCYP2
LOC421242
LOC421259
LOC768490
FSHR
LOC768920
LOC428553
LOC421270
LOC421266
LOC416746
JAG1
LOC416729
DSTN
HNRPLL
ENAH
DUSP10
TGFB2
LOC421358
RPS6K1
LOC421383
LOC771345
LOC771415
LOC421408
GALM2
LOC771990
LOC421424
LOC421433
RPS6RP3
EIF2AK2
LOC772126
LOC421487
LOC428560
LOC428582
LOC775999
NID1
LOC771692
TSNAX
TTC13
SNOC2
LOC421570
QKI
AGPAT4
UTRN
STMBP5
MAP3K7IP2
ESR1
LOC421645
LOC769401
TC TEL1
LOC421674
CITED2
LOC428514
ALDH8A1
RPS12
LOC421703
LOC421711
NDS024
TRDN
GJA1
LOC421727
LOC421757
LOC428621
LOC421749
LOC421761
LOC428626
PREP
LOC428628
LOC428629
LOC421799

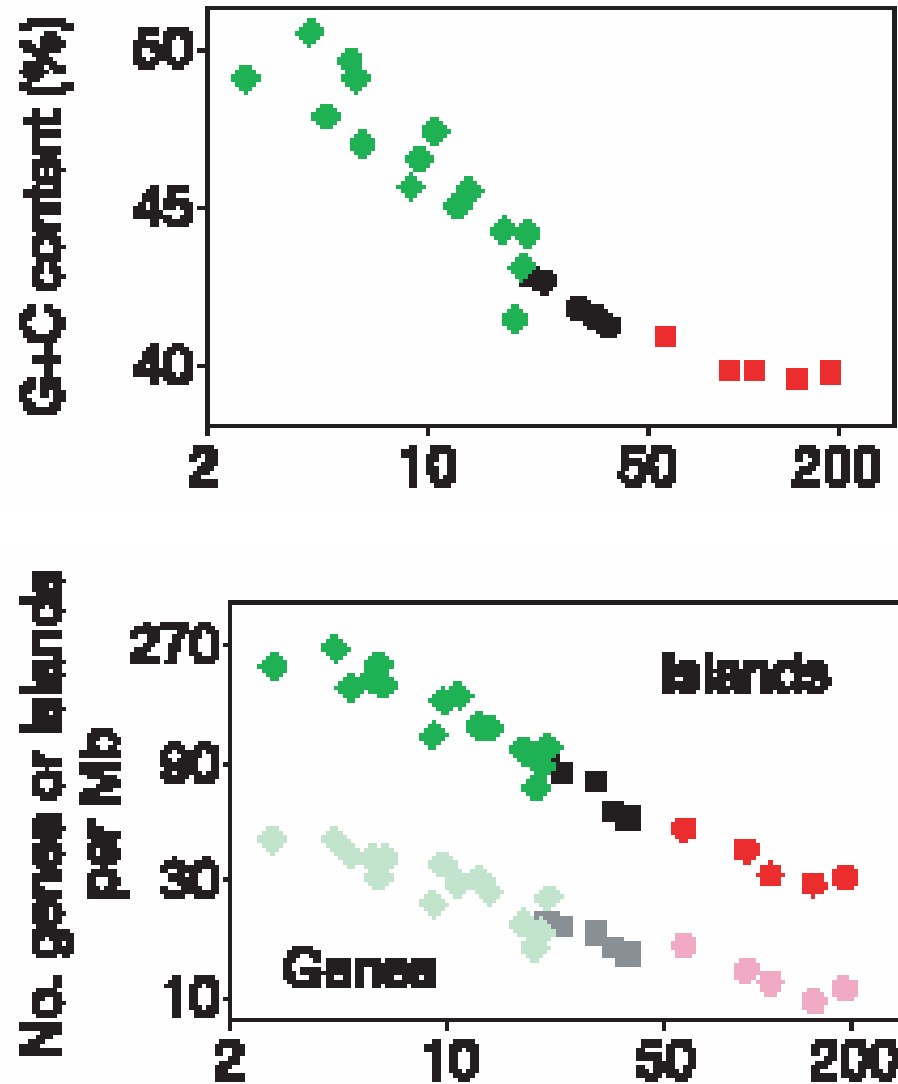
Gallus gallusfw
method:mapping

CR

rs14308889
rs16212981
rs14309254
rs14309403
rs15257939
rs15259172
rs14310908
rs15262170
rs14319575
Chic..1474
rs15270758
rs15262938
rs13733203
rs14081790
rs14081750
RBL1566
rs15282865
Chic..1479
rs14323642
rs15295355
Chic..1482
Chic..0130
Chic..1488
rs14333911
rs14334712
rs15316026
rs14336675
rs15319731
rs15324700
rs14341292
RBL11768
rs13675356
rs15329387
rs15331659
rs15333828
Chic..1720
rs16260924
rs14347175
rs16262863
rs14349367
Chic..1495
rs16269462
rs15350548
rs14358710
Chic..0614
rs14362499
rs13791017
rs15367719
rs14365661
RBL5014
rs14366046
rs14372716



Macro-microchromosomes



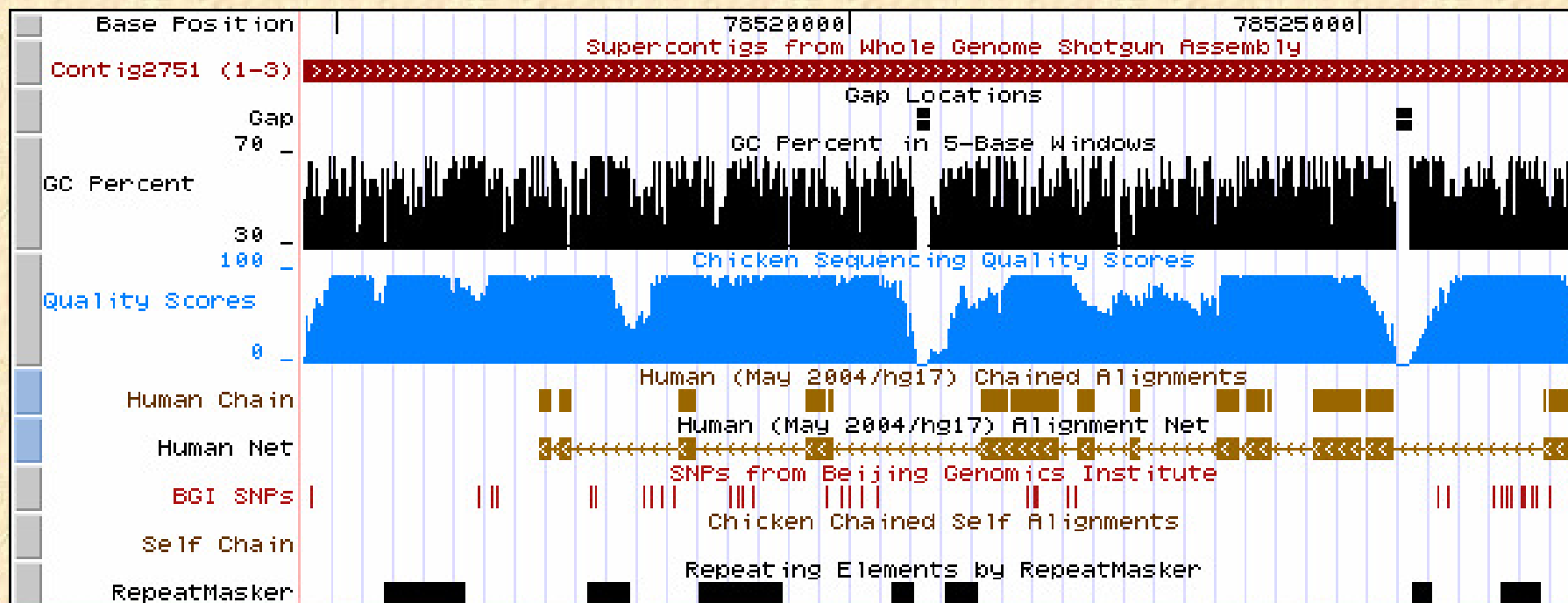
Cartes RH de poule : le présent (2)

- Marqueurs utilisés (ère pré-séquence)
 - Microsatellites des cartes génétiques
 - EST : similarités de séquence avec des régions HSA définies
- Marqueurs utilisés (ère post-séquence)
 - STS de l'assemblage
 - Technologie de génotypage Illumina
 - 9212 marqueurs
 - **STS et SNP du chrUn**

UCSC Genome Browser on Chicken Feb. 2004 Assembly

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

position chrUn:78,514,668-78,527,166 jump clear size 12,499 bp. configure



move start

< 2.0 >

Click on a feature for details. Click on base position to zoom in around cursor. Click on left mini-buttons for track-specific options.

move end

< 2.0 >

default tracks

hide all

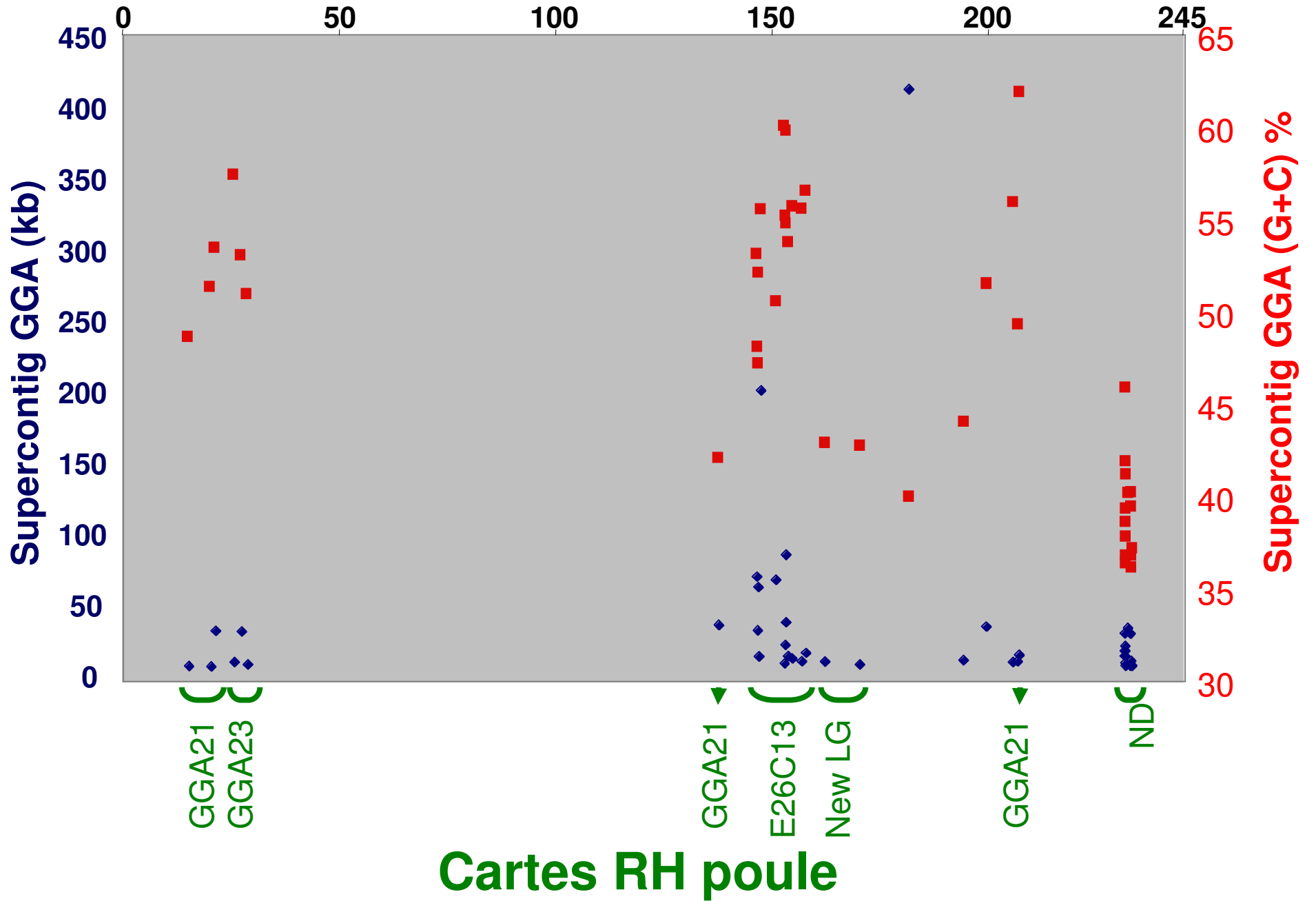
configure

refresh

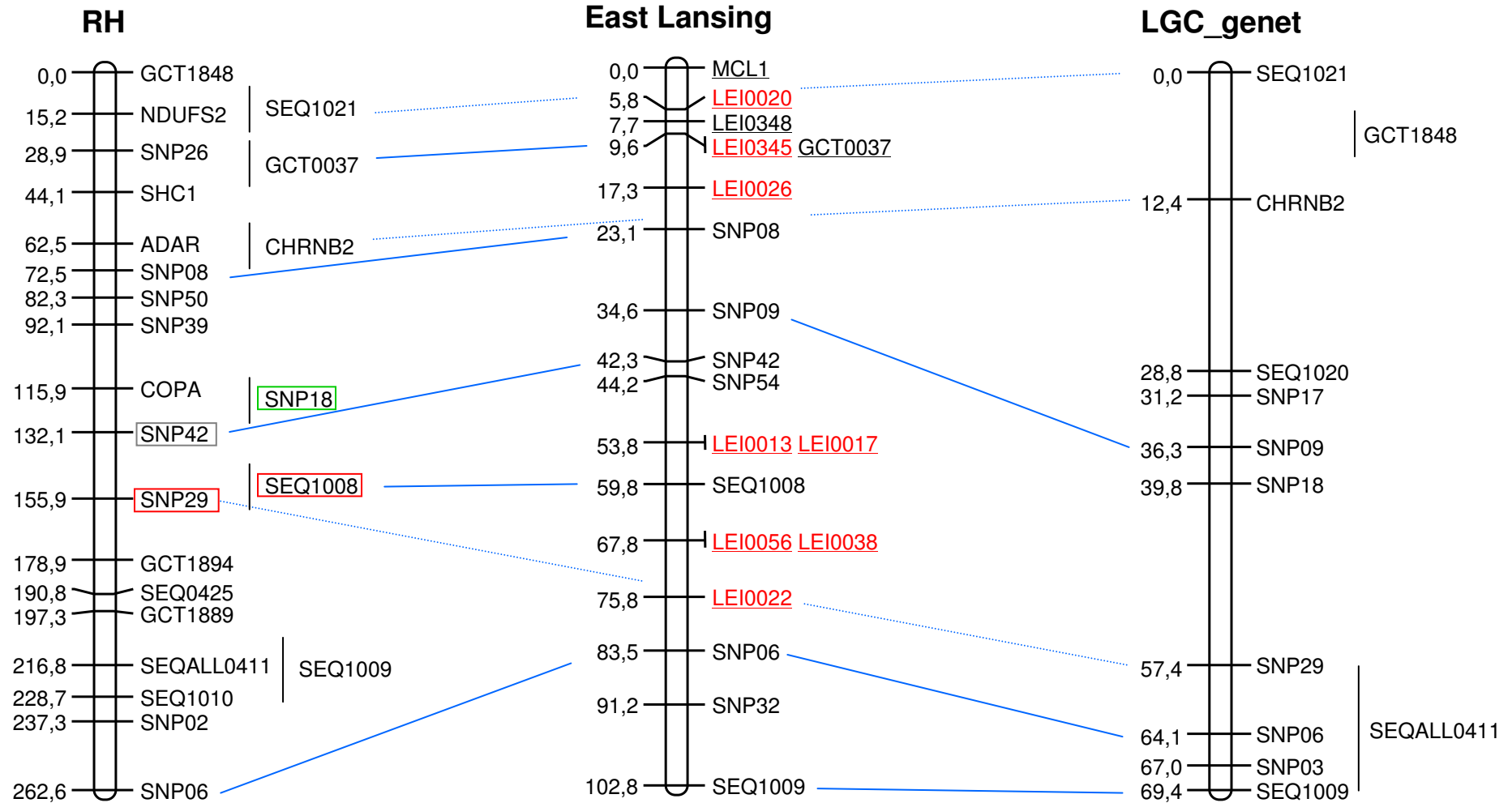
Chromosome Color Key:

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y M Un

Position sur HSA1 (Mb)



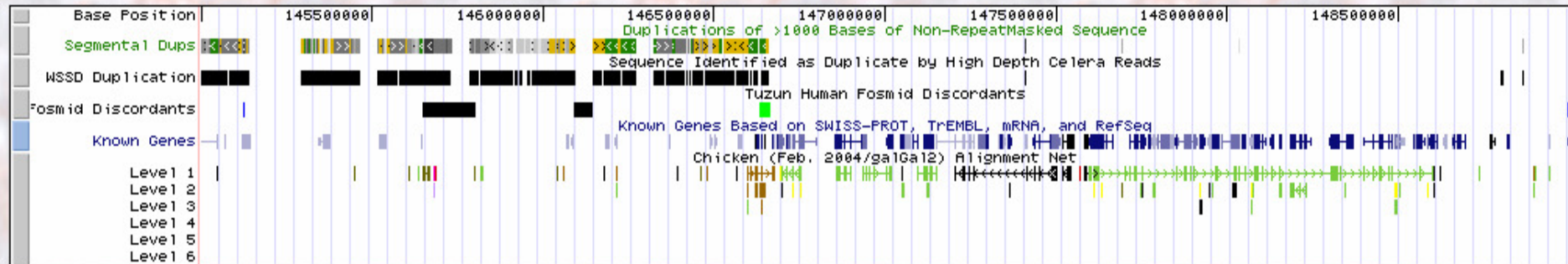
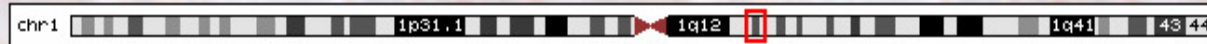
GGA25 RH et Génétique



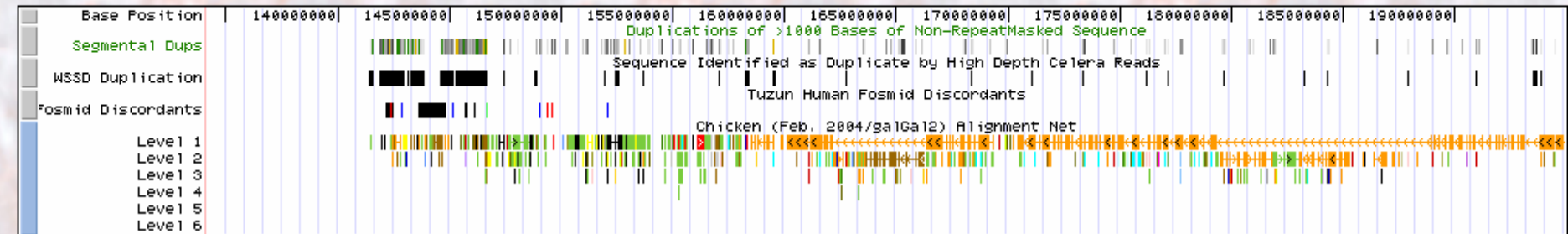
UCSC Genome Browser (UW Duplication overlay) on Human May 2004 Assembly

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

position chr1:145,000,000-149,000,000 size 4,000,001 bp. image width: 1000 jump



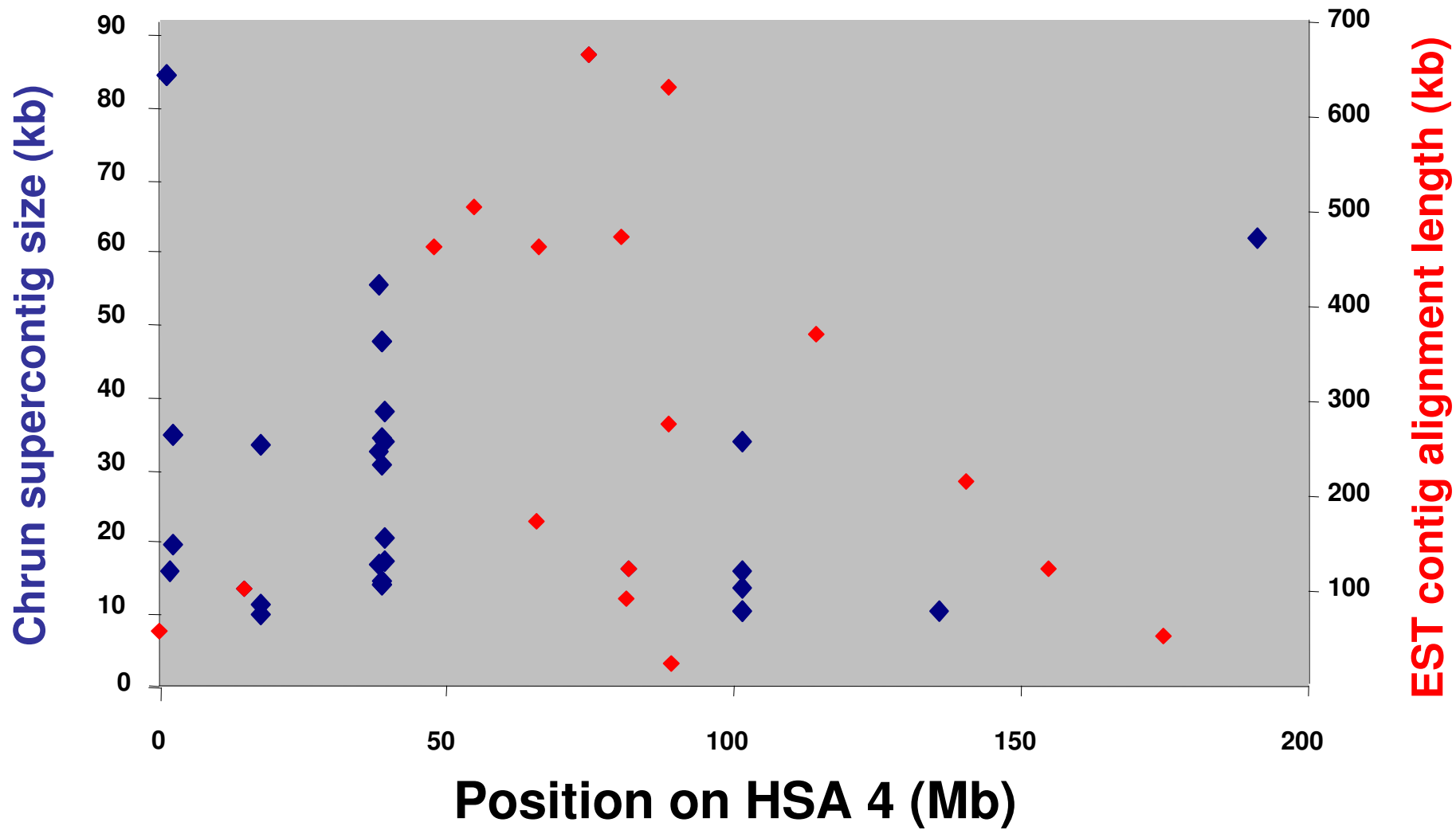
position chr1:134,174,993-194,925,010 size 60,750,018 bp. image width: 1000 jump

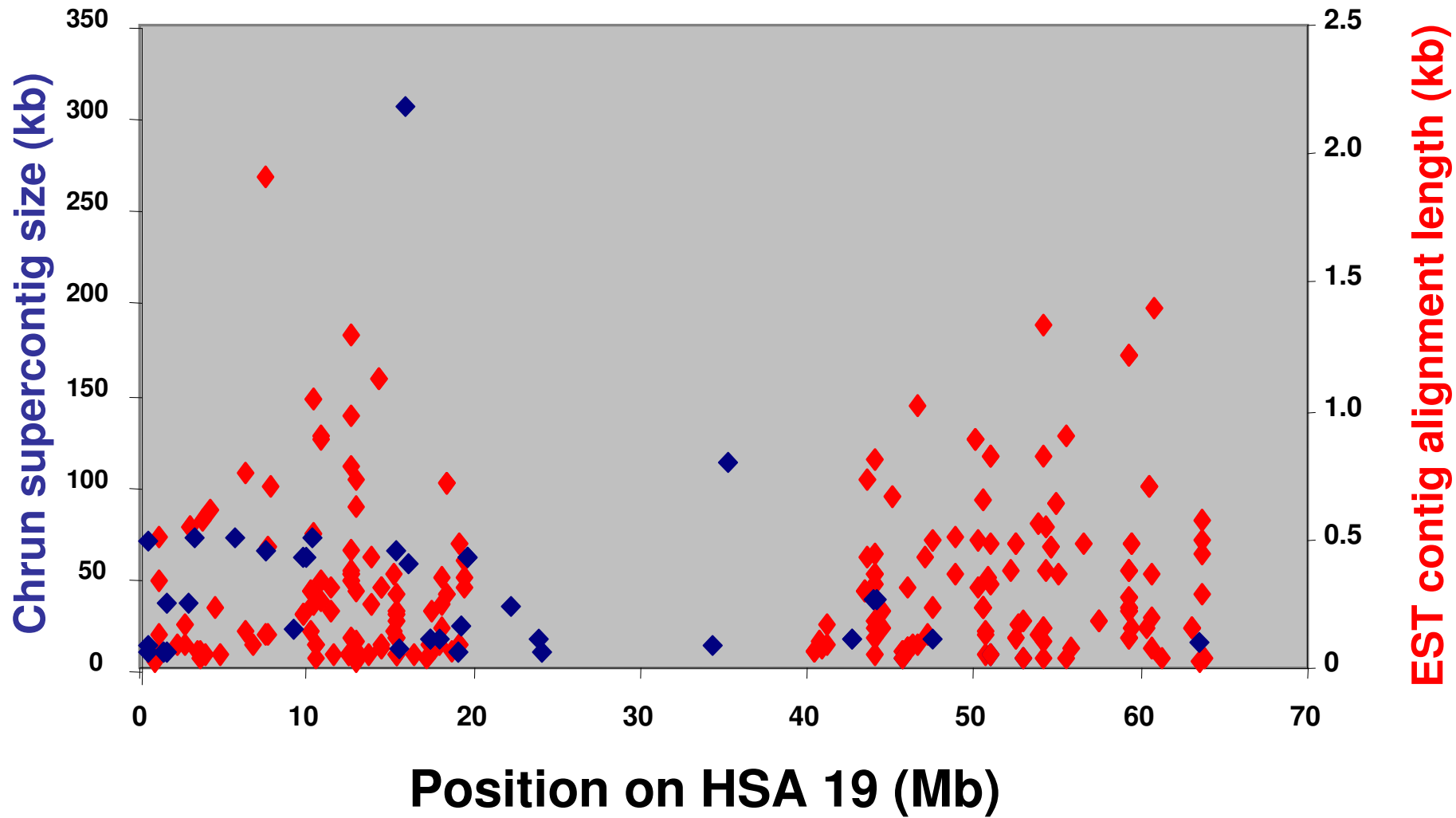


<http://humanparalogy.gs.washington.edu>

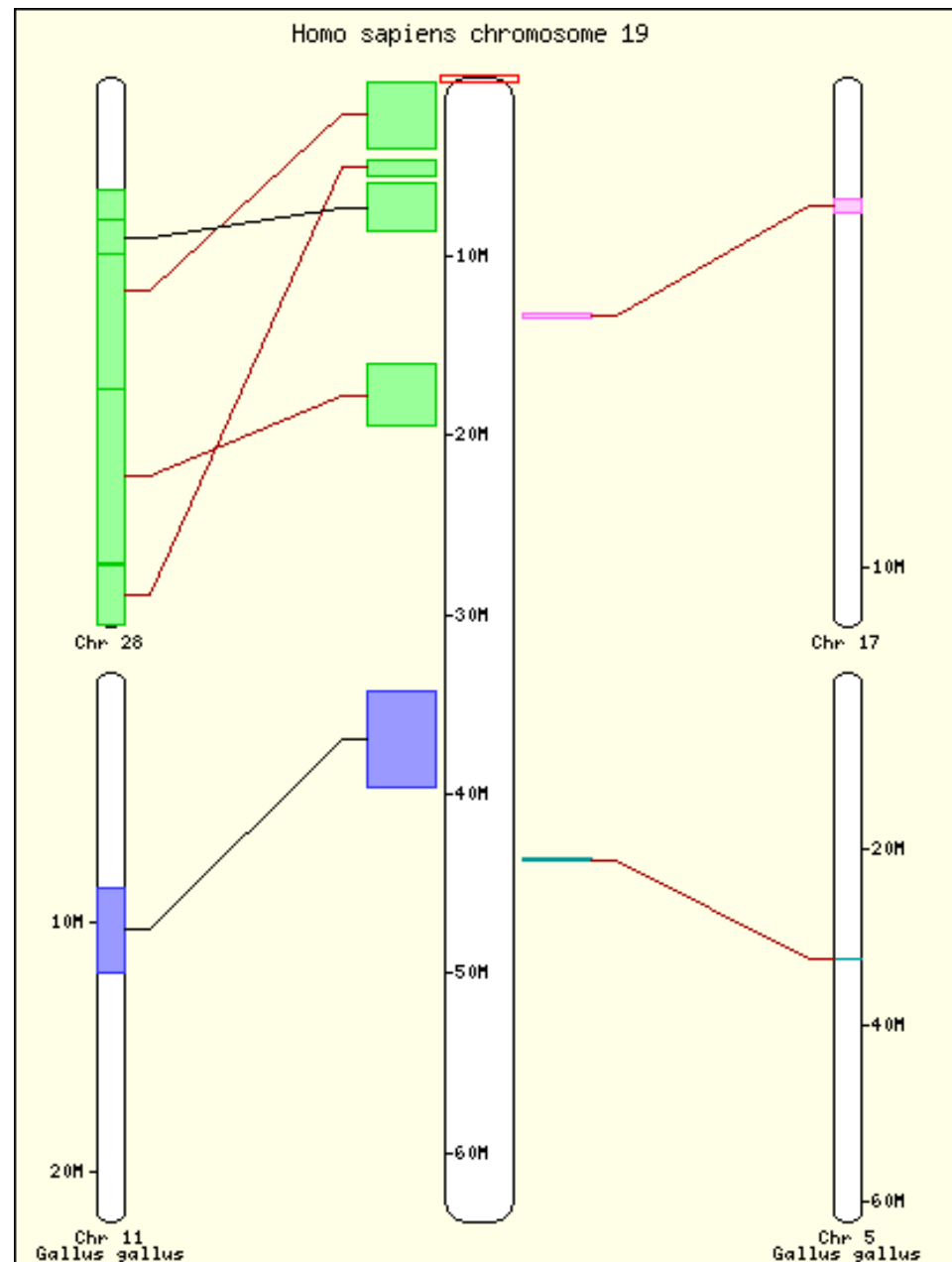
Cartes RH de poule : le présent (3)

- Marqueurs utilisés (ère pré-séquence)
 - Microsatellites des cartes génétiques
 - EST : similarités de séquence avec des régions HSA définies
- Marqueurs utilisés (ère post-séquence)
 - STS de l'assemblage
 - Technologie de génotypage Illumina
 - 9212 marqueurs
 - STS et SNP du chrUn
 - EST absents de l'assemblage « no hit mapping »

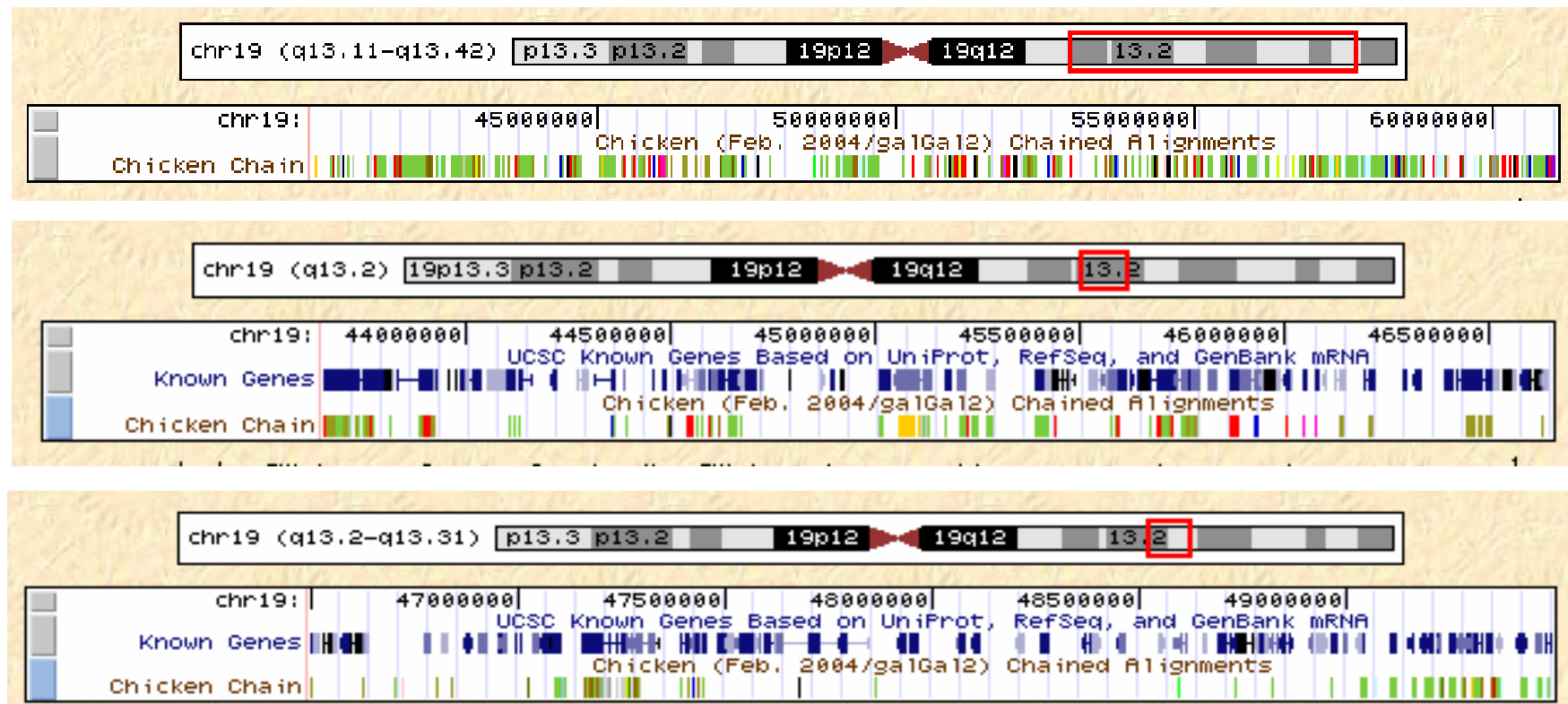




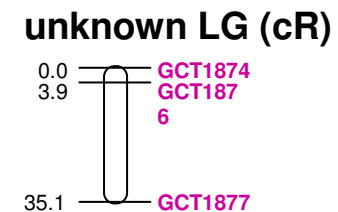
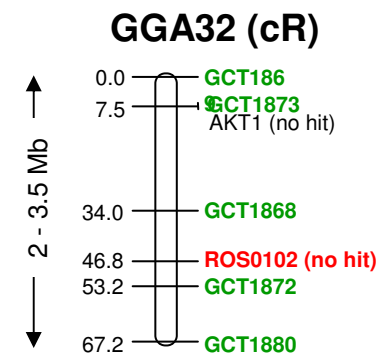
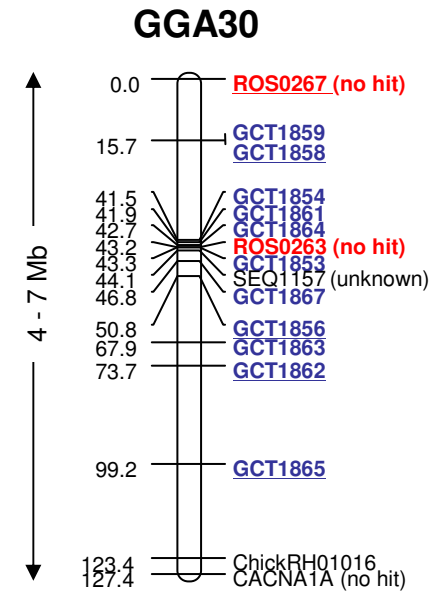
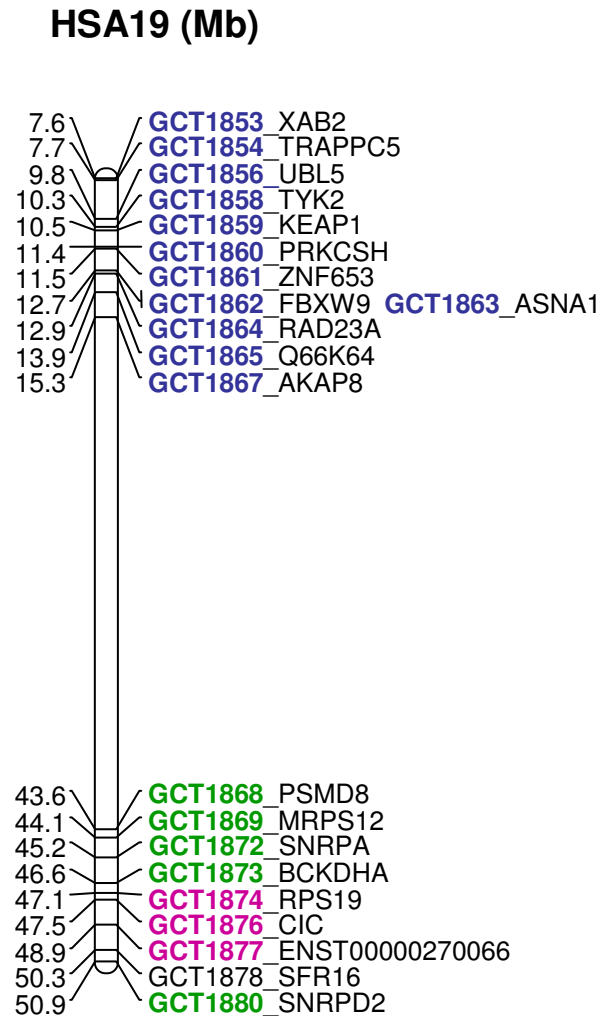
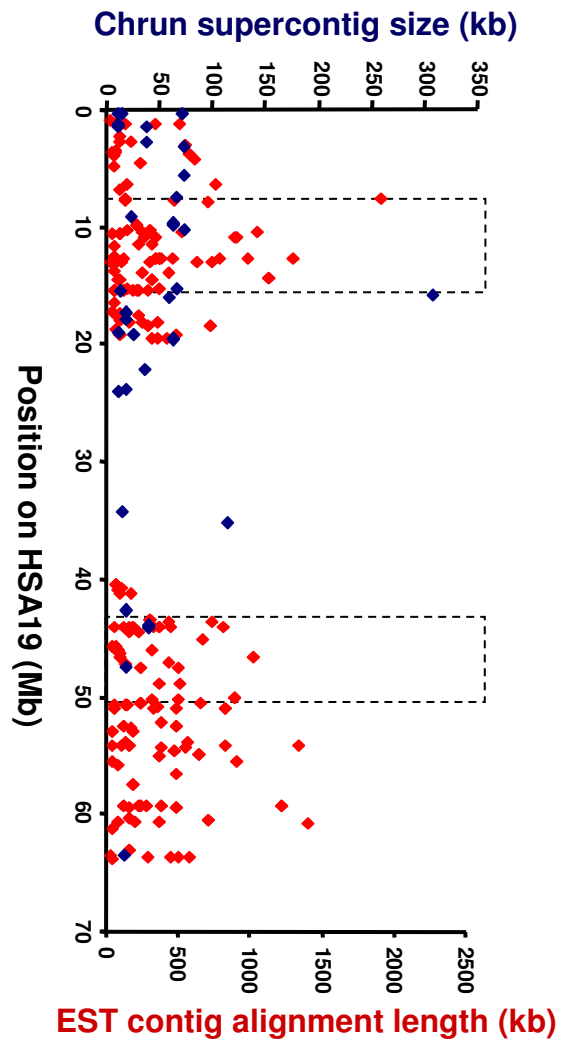
Conservation de synténie HSA19-GGA



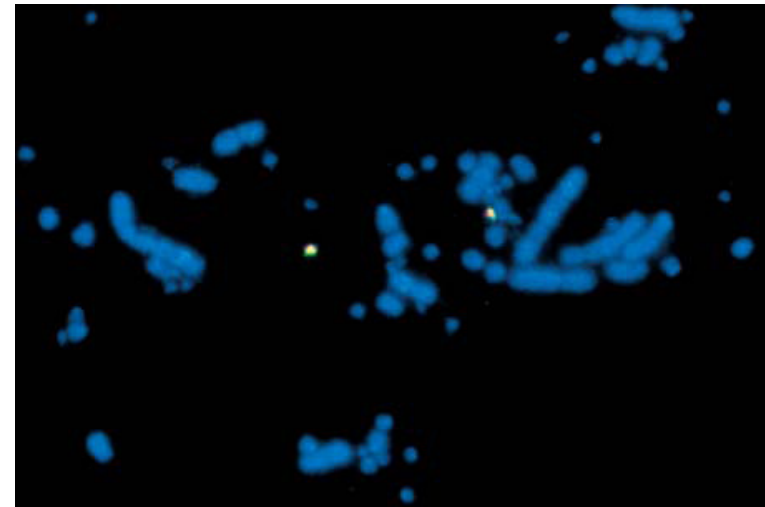
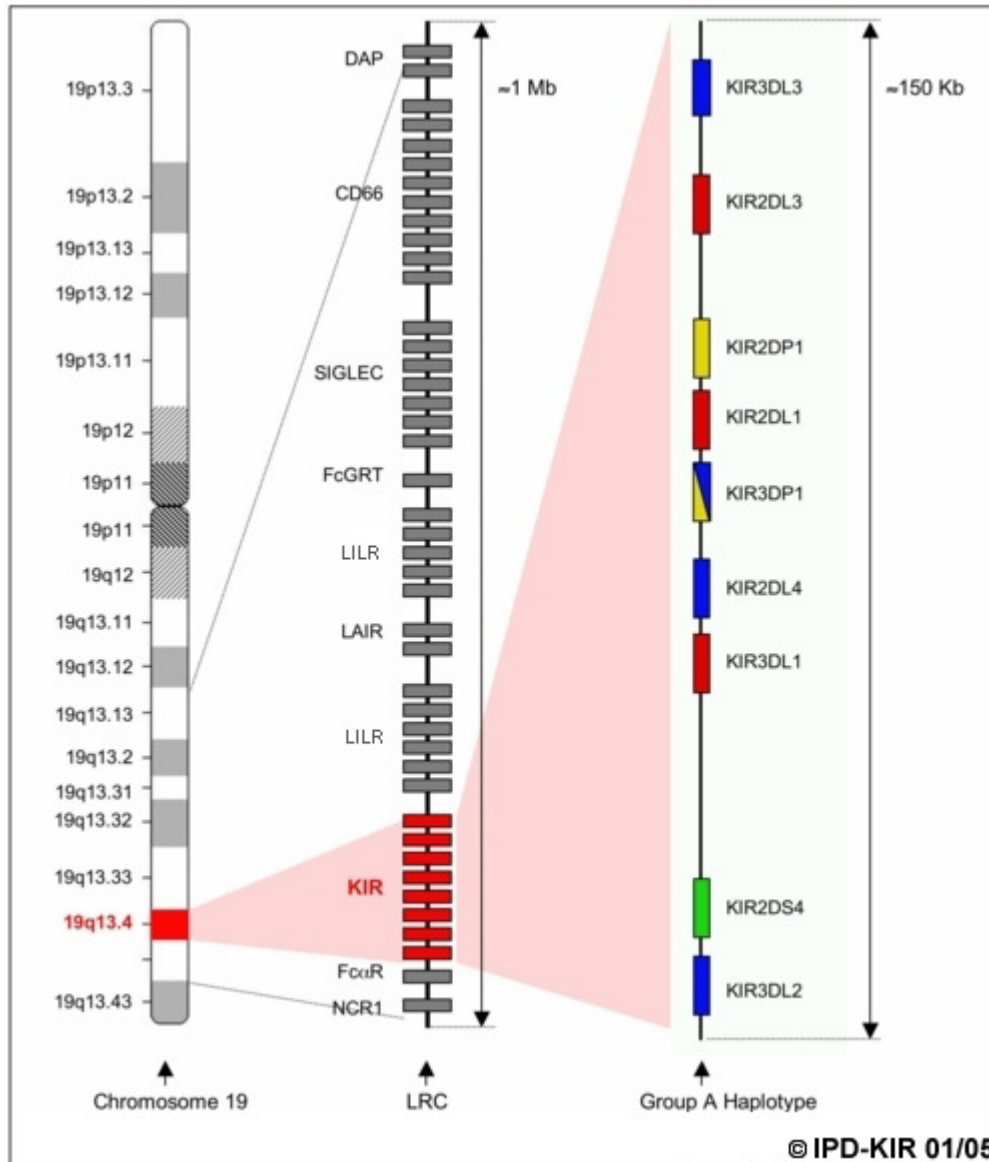
Human chromosome 19



Cartographie EST « no hit »



HSA19 et GGA31

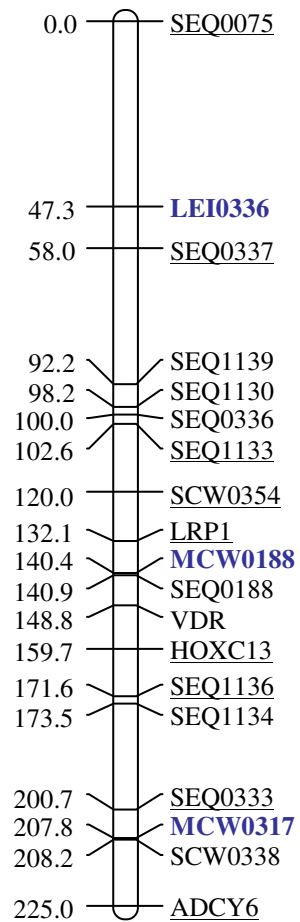


Gènes CHIR sur GGA31 (E64)

No Hit EST mapping: similar to HSA12

E22C19W28_E50C23

RH map (cRays)



Gallus_gallus-2.1
 (05-30-2006)
 IS- PCR
 Chr:Mb

Chrun

Chrun

Chrun

E22C19W28-E50C23 : 0.887
 E22C19W28-E50C23 : 0.864
 E22C19W28-E50C23 : 0.853
 E22C19W28-E50C23 : 0.708

Chrun

Chrun

No hit

E22C19W28-E50C23 : 0.505

No hit

Chrun

Chrun

Chrun

E22C19W28-E50C23 : 0.005
 No hit
 E22C19W28E50C23 : 0.444

No hit

Location on the
 Human genome
 Chr:Mb

No similarity

No similarity

HSA1:3.951

HSA12 : 55.319

HSA12 : 48.174

No similarity

HSA12 : 51.149

HSA12 : 60.560

No similarity

No similarity

HSA6:167.082

No data

HSA12 : 34.170

HSA12 : 52.776

HSA12 : 52.203

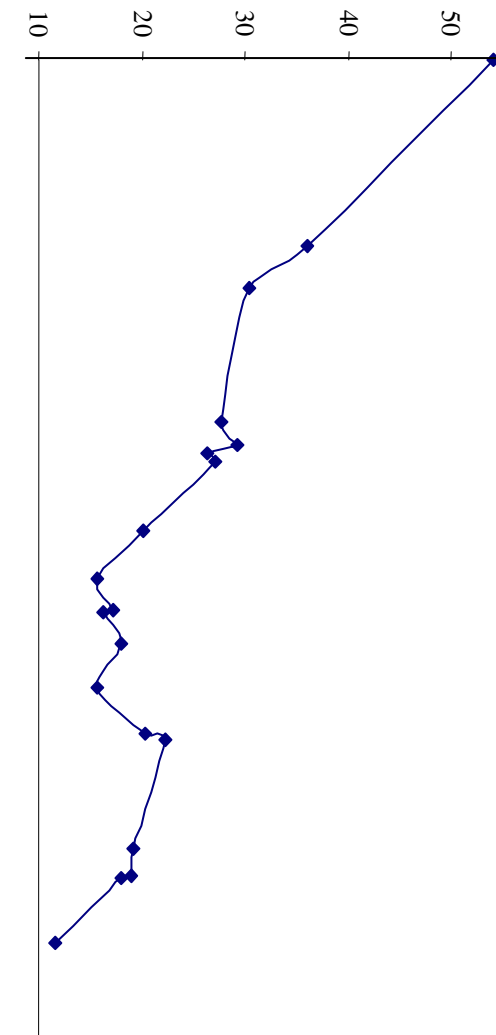
HSA12 : 54.638

No similarity

HSA4 : 74.873

HSA12 : 47.457

Retention frequency of the markers along the RH map



En cours

- Génotypage SNP Illumina de SNP chrUn
 - Tous contigs avec une similarité de séquence HSA
 - > 384 marqueurs
- Définition d'un jeu Illumina « no hit »
 - Contigs SIGENAE absents de l'assemblage poule
 - Localisation sur la séquence HSA (BLAST)
 - Alignement multiple HSA, MMU, RNO, GGA
 - Définition d'OPA Illumina: positions divergentes

Ensuite

- A terminer
 - Réalisation des cartes RH des microchromosomes
 - Confrontation avec l'assemblage 2009
- Perspectives
 - SNP sur microchromosomes
 - Séquençage 454 d'une fraction enrichie (programme Pyresavi)

Participants

UMR GC

Labo et cartes

**Mireille Morisson
Aurélie Tircazes
Suzanne Bardes
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Katia Feve
Valérie Fillon
Sophie Leroux
Frédérique Pitel
Marie Gerus
Marine Douaud**

UMR GC

Cartes et représentations

**Caroline Hourcade
Thomas Faraut**

CNG

**Ivo Gut
Mario Foglio**

SIGENAE

**Patrice Dehais
Christophe Clopp**

