

CELLULES SOUCHES PLURIPOTENTES INDUITES (iPS) : APPLICATIONS AUX PATHOLOGIES GÉNÉTIQUES ET LIMITES

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Montpellier ACLF 2016

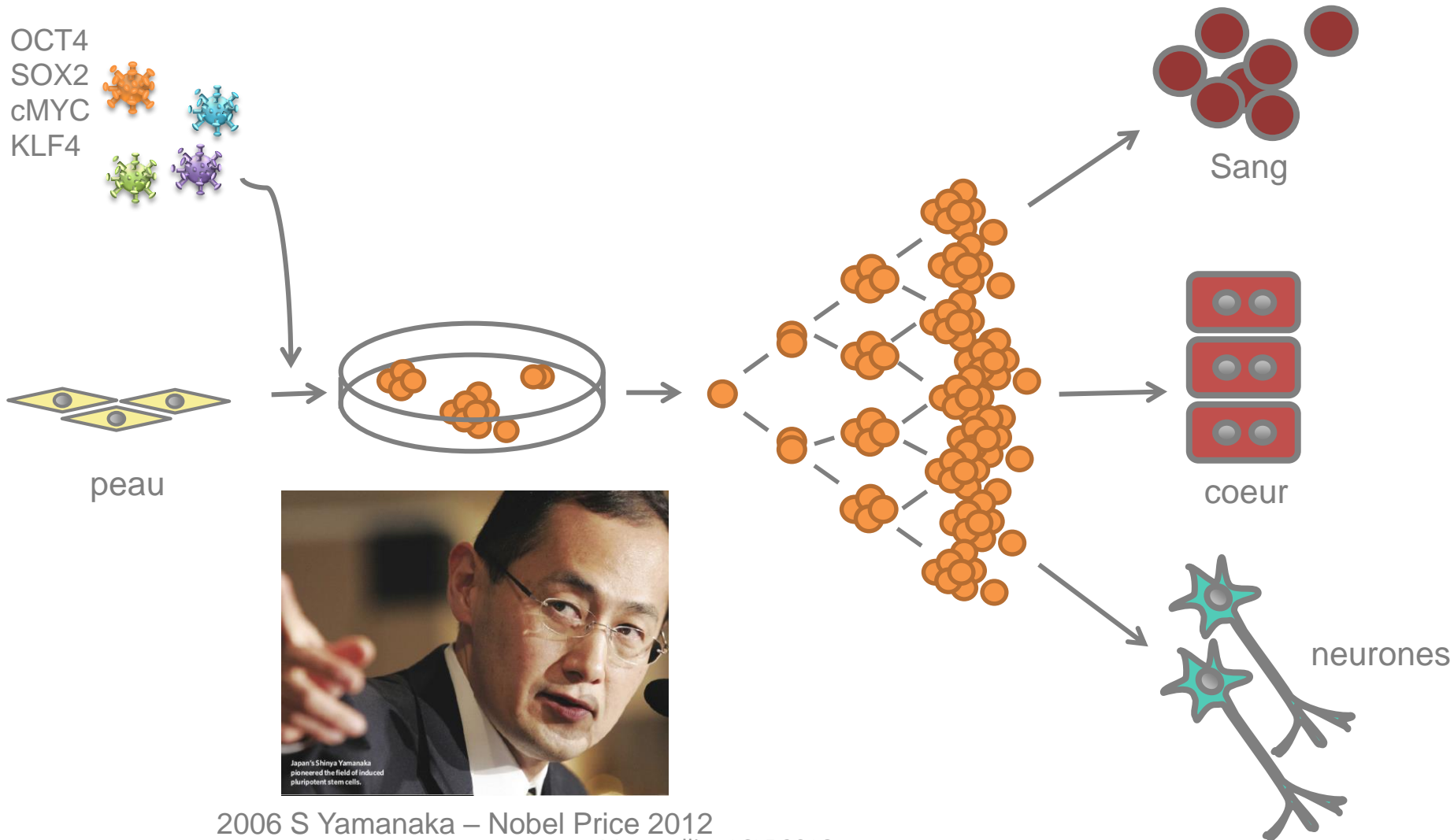
 **Inserm**

Université de Montpellier
FACULTÉ
de MÉDECINE
Montpellier-Nîmes



CELLULES
SOUCHES
PLURIPOTENTES

Induced pluripotent stem cells (iPS)



2006 S Yamanaka – Nobel Price 2012
Montpellier ACLF 2016

K. Takahashi and S. Yamanaka. *Cell*, 126:663, 2006.

Applications

1. Modélisation in vitro du développement normal et des **maladies génétiques**
2. Une source illimité de cellules pour la **thérapie cellulaire** potentiellement **autologues**
3. Un moyen de **rajeunir des cellules âgées** voire **sénescentes**

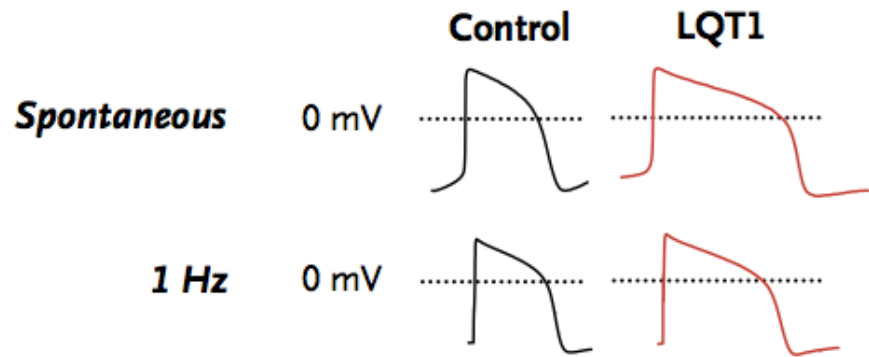
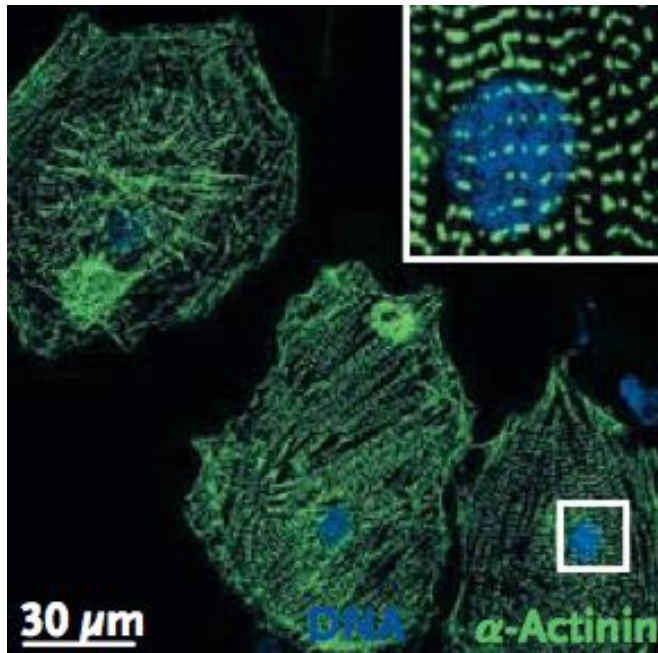


MODELLISATION DE PATHOLOGIES GENETIQUES

ORIGINAL ARTICLE

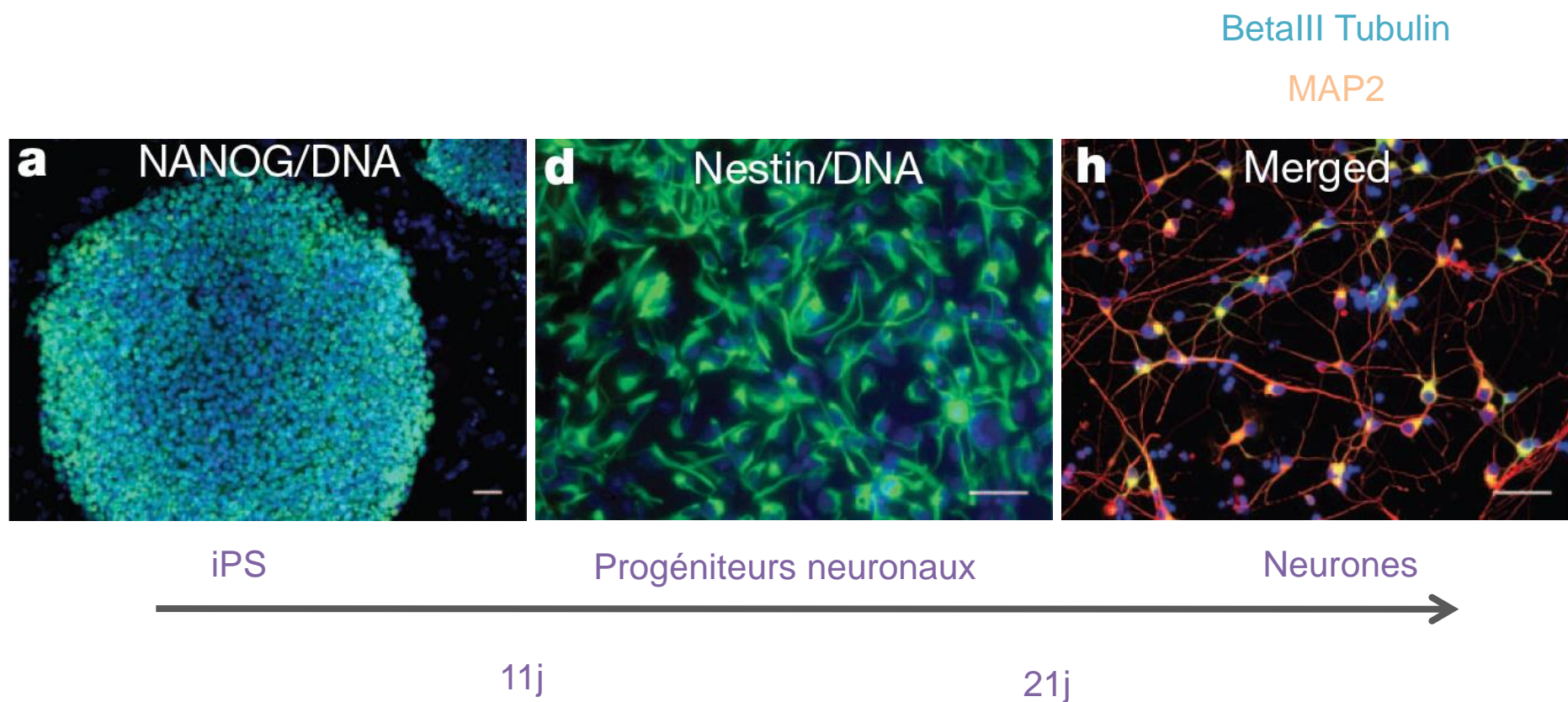
Patient-Specific Induced Pluripotent Stem-Cell Models for Long-QT Syndrome

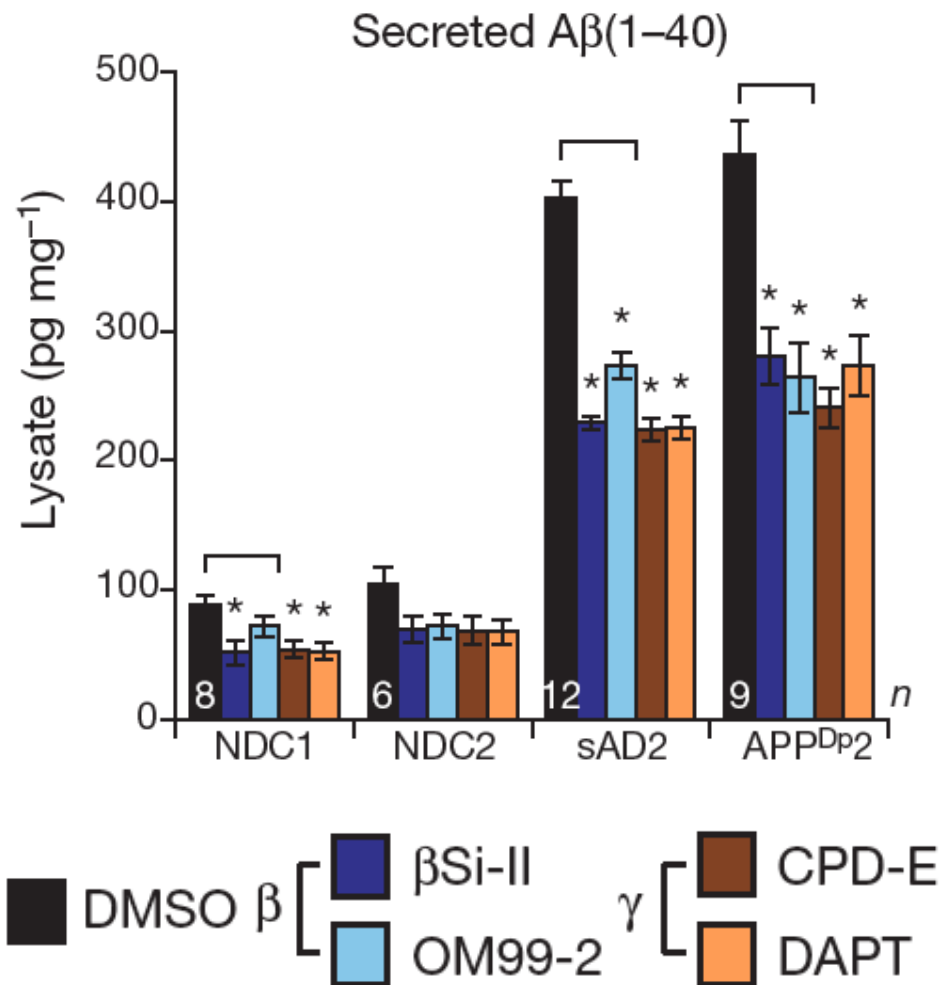
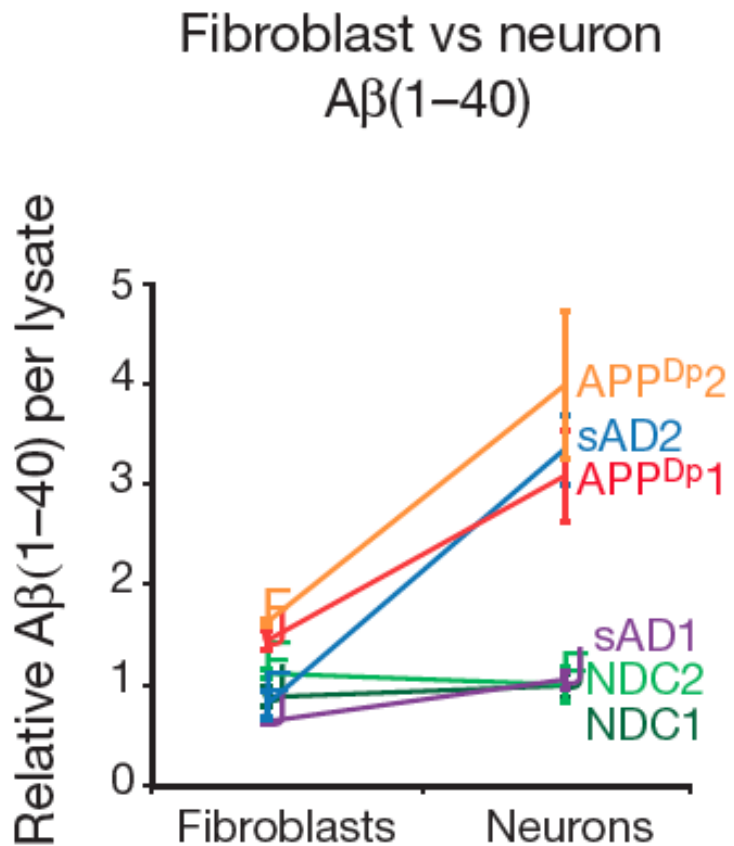
Alessandra Moretti, Ph.D., Milena Bellin, Ph.D., Andrea Welling, Ph.D., Christian Billy Jung, M.Sc., Jason T. Lam, Ph.D., Lorenz Bott-Flügel, M.D., Tatjana Dorn, Ph.D., Alexander Goedel, M.D., Christian Höhnke, M.D., Franz Hofmann, M.D., Melchior Seyfarth, M.D., Daniel Sinnecker, M.D., Albert Schömig, M.D., and Karl-Ludwig Laugwitz, M.D.



Probing sporadic and familial Alzheimer's disease using induced pluripotent stem cells

Mason A. Israel^{1,2}, Shauna H. Yuan^{1,3}, Cedric Bardy⁴, Sol M. Reyna^{1,2}, Yangling Mu⁴, Cheryl Herrera¹, Michael P. Hefferan⁵, Sebastiaan Van Gorp⁶, Kristopher L. Nazor⁷, Francesca S. Boscolo⁸, Christian T. Carson⁹, Louise C. Laurent⁸, Martin Marsala^{5,10}, Fred H. Gage⁴, Anne M. Remes¹¹, Edward H. Koo³ & Lawrence S. B. Goldstein^{1,3}



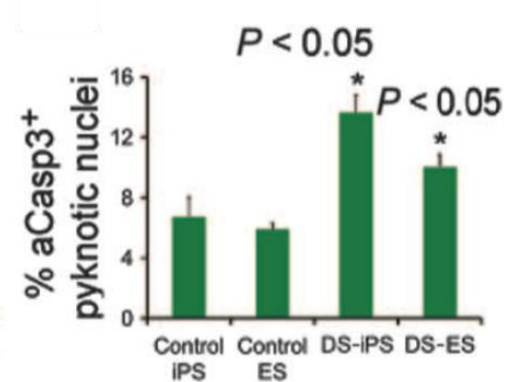
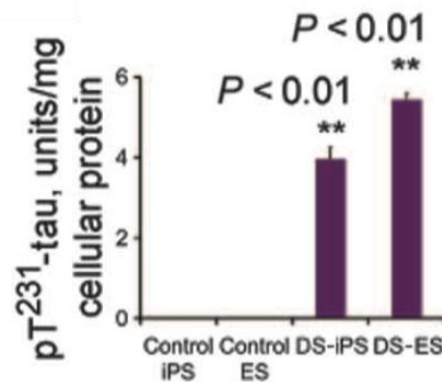
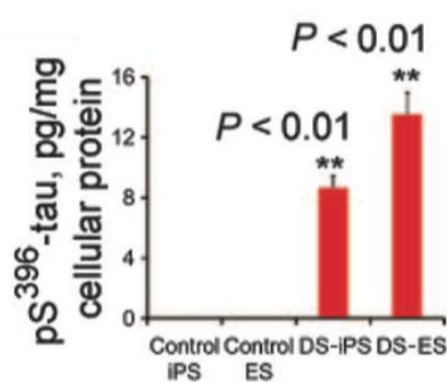
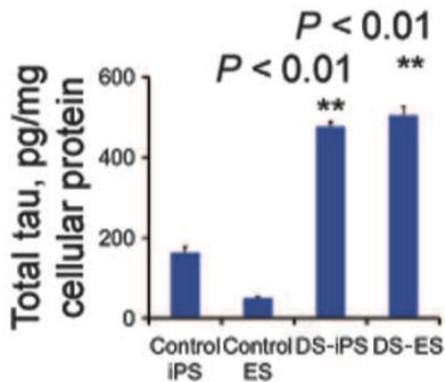


A Human Stem Cell Model of Early Alzheimer's Disease Pathology in Down Syndrome

Yichen Shi, *et al.*

Sci Transl Med 4, 124ra29 (2012);

DOI: 10.1126/scitranslmed.3003771



ESSAIS CLINIQUES

Table 1 | **hESC and iPSC-based products in clinical trials**

Cell type (product name)	Company or group	Trial location	Disease	Stage of trial	Cell delivery	Status of trial
hESC-derived RPE (MA09-hRPE)	Ocata Therapeutics	United States	Dry AMD	Phase I/II	Cell suspension	Active, not recruiting
hESC-derived RPE (MA09-hRPE)	Ocata Therapeutics	United States	Stargardt	Phase I/II	Cell suspension	Active, not recruiting
hESC-derived RPE (MA09-hRPE)	Ocata Therapeutics	United Kingdom	Stargardt	Phase I/II	Cell suspension	Recruiting
hESC-derived RPE (MA09-hRPE)	CHABiotech (licensed from Ocata)	Korea	Dry AMD	Phase I/II	Cell suspension	Recruiting
hESC-derived RPE (MA09-hRPE)	CHABiotech (licensed from Ocata)	Korea	Stargardt	Phase I	Cell suspension	Active, not recruiting
hESC-derived RPE (MA09-hRPE)	University of California, Los Angeles (with Ocata's cells)	United States	MMD	Phase I/II	Cell suspension	Not yet recruiting
iPSC-derived RPE (autologous)	Rikagaku Kenkyūsho (RIKEN) Institute	Japan	Wet AMD	Phase I	Monolayer sheet (no membrane)	On hold
hESC-derived RPE (PF-05206388)	Pfizer	United Kingdom	Wet AMD	Phase I	Membrane-immobilized monolayer sheet	Recruiting
hESC-derived RPE (Opregen)	Cell Cure Neuroscience	Israel	Dry AMD	Phase I/II	Cell suspension	Recruiting
hESC-derived CD15 ⁺ ISL-1 ⁺ cardiac progenitors	Assistance publique, Hôpitaux de Paris	France	Severe heart failure	Phase I	Cells embedded in fibrin patch	Recruiting
hESC-derived pancreatic endoderm (VC-01)	Viacyte	United States	Type I diabetes	Phase I/II	PEC-01 cells encapsulated in a medical device	Recruiting
hESC-derived oligodendrocyte progenitors (AST-OPC1)	Asterias Biotherapeutics	United States	Spinal cord injury	Phase I	Cell suspension	Completed (took over from Geron)
hESC-derived oligodendrocyte progenitors (AST-OPC1)	Asterias Biotherapeutics	United States	Spinal cord injury	Phase I/II	Cell suspension	Recruiting

AMD, age-related macular degeneration; hESC, human embryonic stem cell; iPSC, induced pluripotent stem cell; MMD, myopic macular degeneration; RPE, retinal pigment epithelium.
 Kimbrel EA et al. *Nature Reviews Drug Discovery*, 2015 14: 681–692.



Human embryonic stem cell-derived cardiac progenitors for severe heart failure treatment: first clinical case report

Philippe Menasché^{1,2,3*}, Valérie Vanneaux^{4,5}, Albert Hagège^{2,3,6}, Alain Bel¹, Bernard Cholley^{2,7}, Isabelle Cacciapuoti^{4,5}, Alexandre Parouchev^{4,5}, Nadine Benhamouda⁸, Gérard Tachdjian⁹, Lucie Tosca⁹, Jean-Hugues Trouvin^{10,11}, Jean-Roch Fabreguettes¹², Valérie Bellamy³, Romain Guillemain⁸, Caroline Suberbielle Boissel¹³, Eric Tartour^{2,3,8}, Michel Desnos^{2,3,6}, and Jérôme Larghero^{4,5,14}

Menasche P et al. *European Heart Journal*, 2015 36: 2011–2017

LIMITES

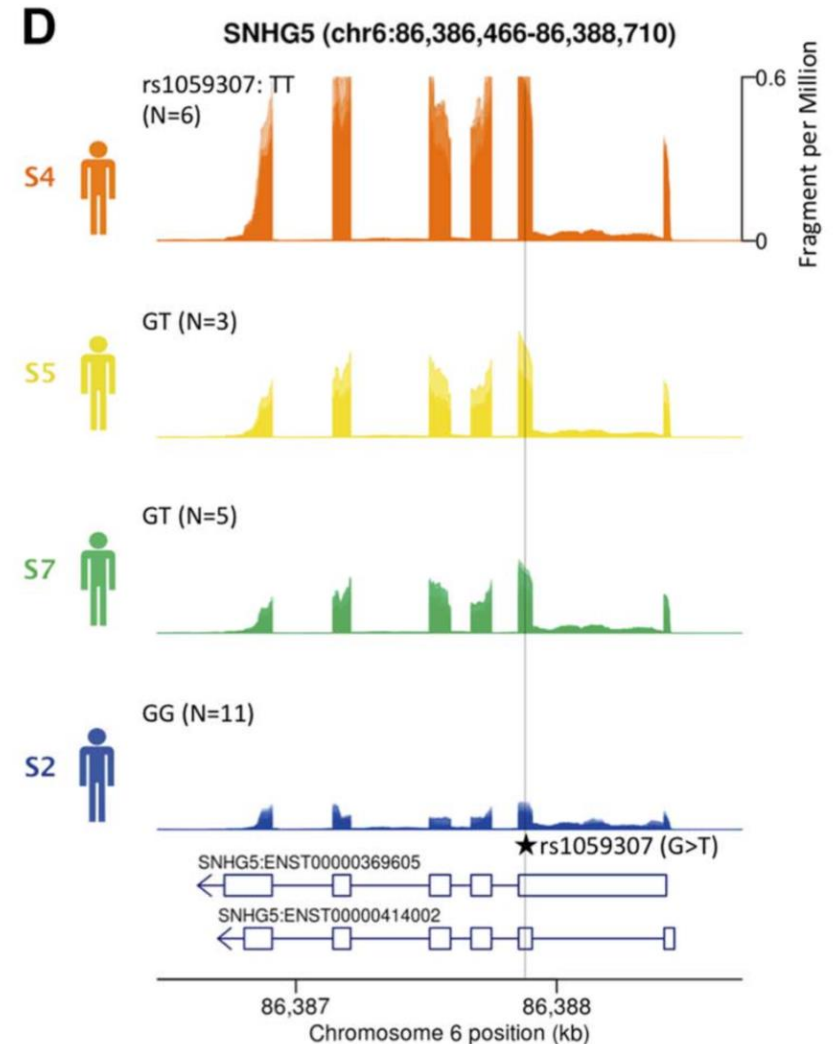
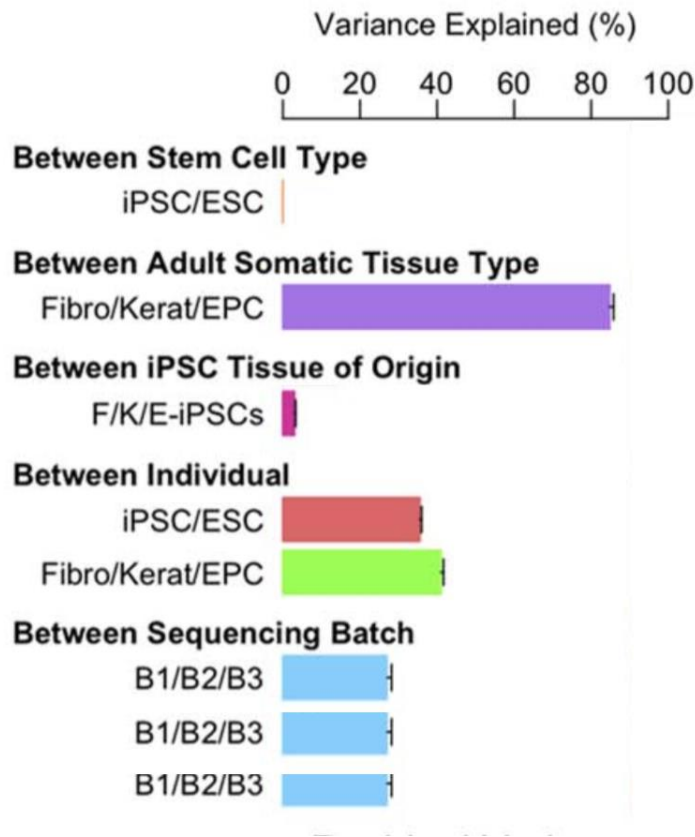
iPS = ES ?

- Anomalies épigénétiques
- Anomalies génétiques secondaires à la reprogrammation

- N'est pas retrouvé par tous (sauf mutagénèse insertionnelle!): dépend du protocole de reprogrammation?



L'essentiel de la variabilité vient du fond génétique



- [1] F. Rouhani, et al., "Genetic background drives transcriptional variation in human induced pluripotent stem cells," PLoS Genet, vol. 10, Montpellier ACLF 2016 p. e1004432, Jun. 2014.



iPS = ES !

ARTICLES

**nature
biotechnology**

A comparison of genetically matched cell lines reveals the equivalence of human iPSCs and ESCs

Jiho Choi^{1-3,10}, Soohyun Lee^{4,10}, William Mallard^{5,6}, Kendell Clement^{2,5,6}, Guidantonio Malagoli Tagliazucchi^{4,7}, Hotae Lim⁸, In Young Choi⁸, Francesco Ferrari⁴, Alexander M Tsankov^{2,5,6}, Ramona Pop^{2,5,6}, Gabsang Lee⁸, John L Rinn^{5,6,9}, Alexander Meissner^{2,5,6}, Peter J Park⁴ & Konrad Hochedlinger¹⁻³

NATURE BIOTECHNOLOGY VOLUME 33 NUMBER 11 NOVEMBER 2015

ANOMALIES GENETIQUES INDUITES PAR LA CULTURE

Recurrent gain of chromosomes 17q and 12 in cultured human embryonic stem cells

Jonathan S Draper^{1,6}, Kath Smith^{2,6}, Paul Gokhale¹, Harry D Moore³, Edna Maltby², Julie Johnson⁴, Lorraine Meisner⁴, Thomas P Zwaka⁵, James A Thomson⁵ & Peter W Andrews¹

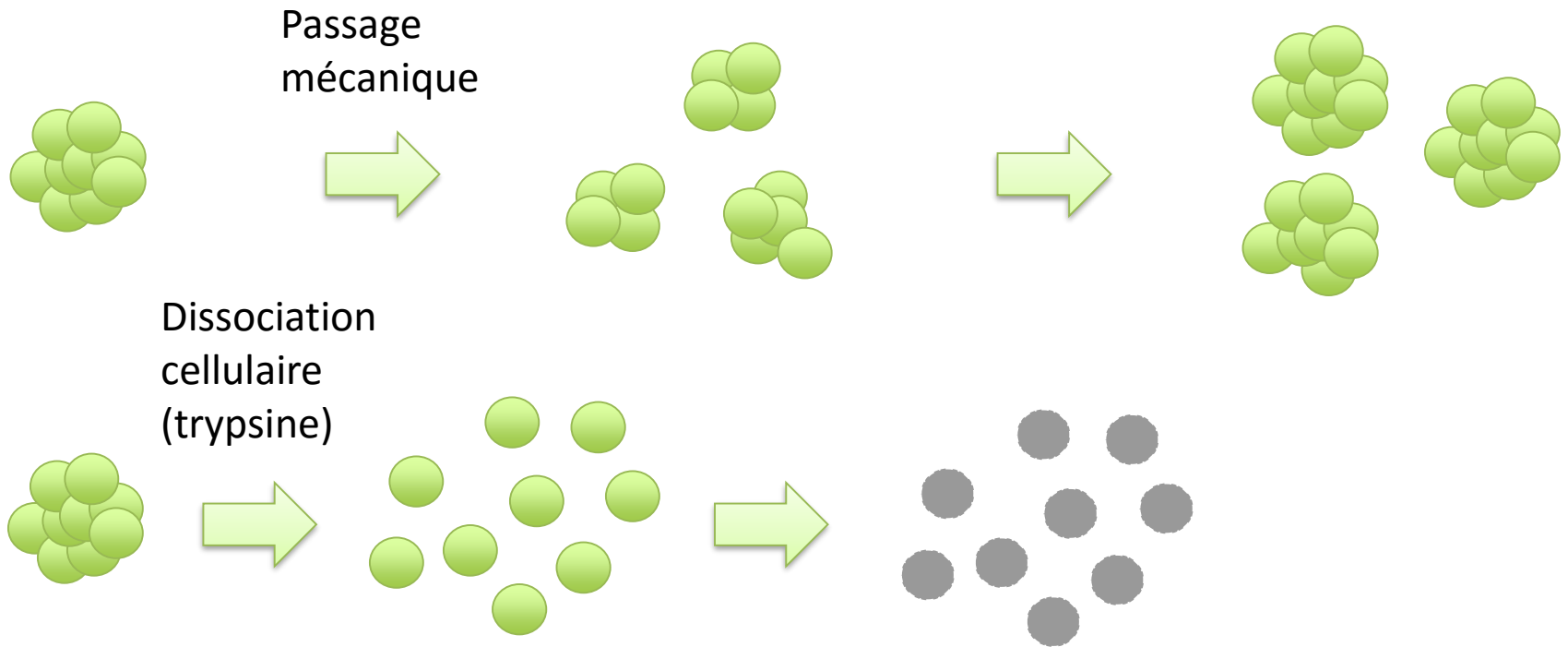
We have observed karyotypic changes involving the gain of chromosome 17q in three independent human embryonic stem (hES) cell lines on five independent occasions. A gain of chromosome 12 was seen occasionally. This implies that increased dosage of chromosome 17q and 12 gene(s) provides a selective advantage for the propagation of undifferentiated hES cells. These observations are instructive for the future application of hES cells in transplantation therapies in which the use of aneuploid cells could be detrimental.

NATURE BIOTECHNOLOGY VOLUME 22 NUMBER 1 JANUARY 2004

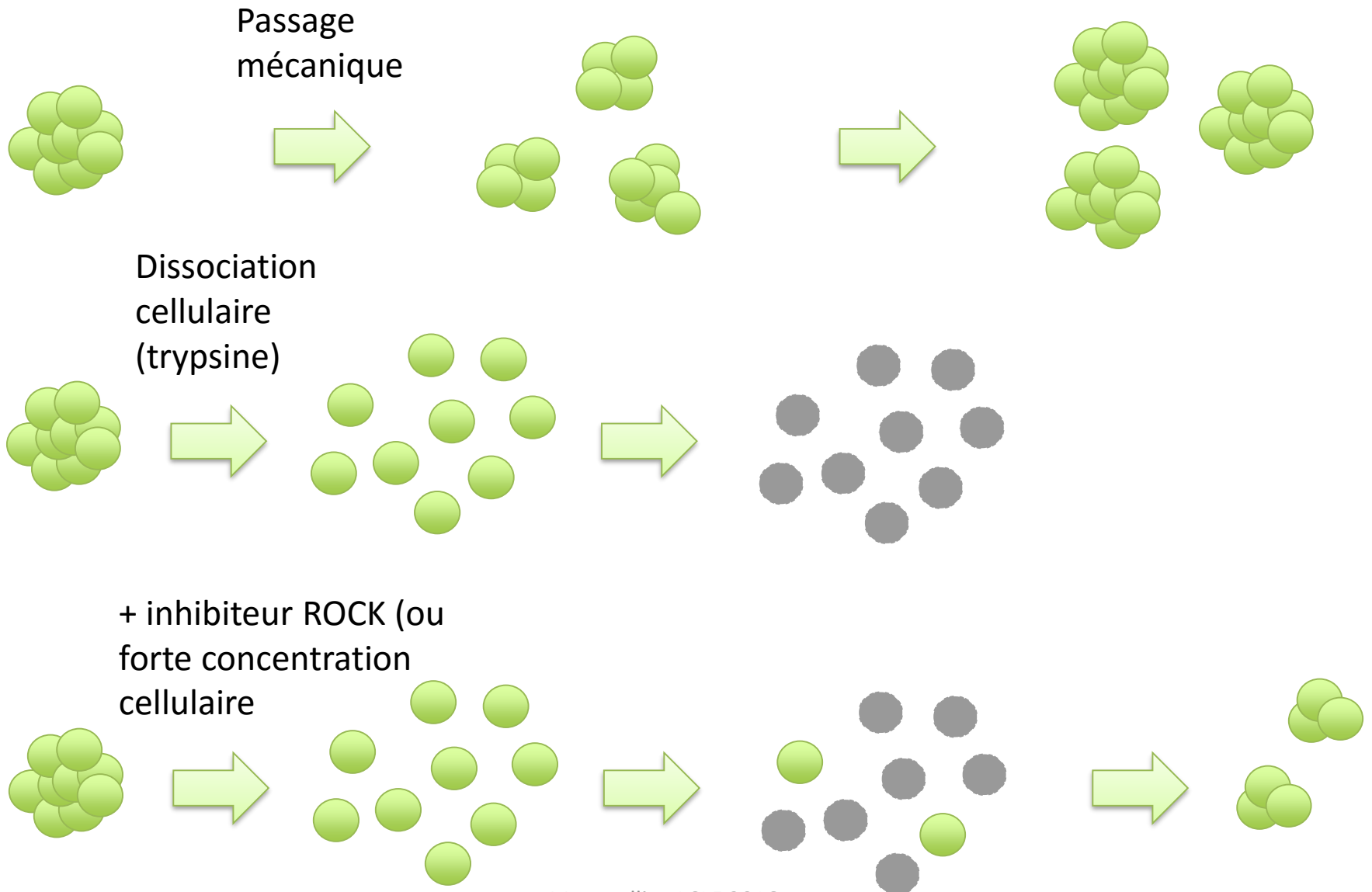
1. Chronologie et déterminants de cette instabilité
 1. A quelle vitesse les anomalies apparaissent-elles?
 2. Impact des conditions de culture (passage)
 3. Anomalies de caryotype vs infra-caryotypique?
2. Quelles anomalies génétiques?
3. Conséquences?

CHRONOLOGIE ET DETERMINANTS

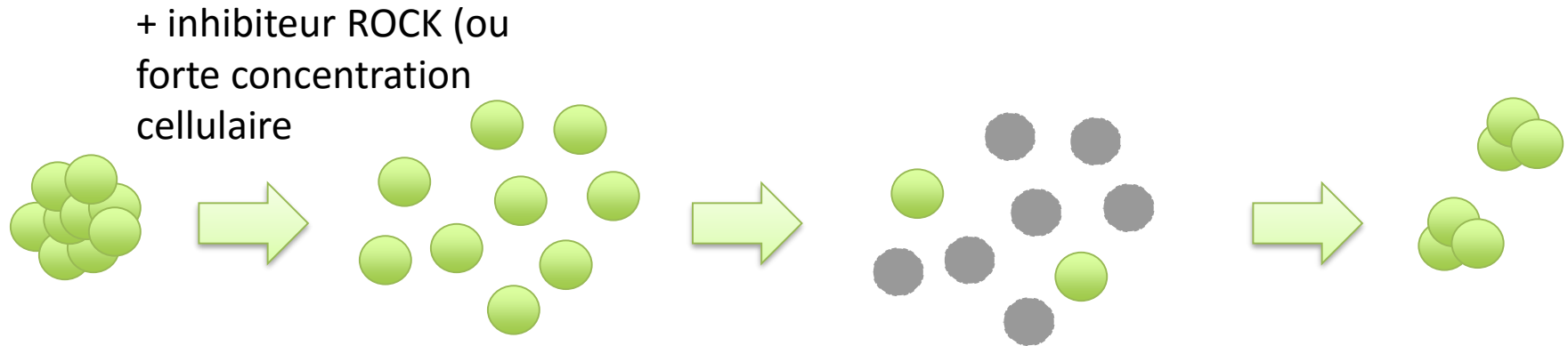
Impact de la dissociation cellulaire : “adaptation”



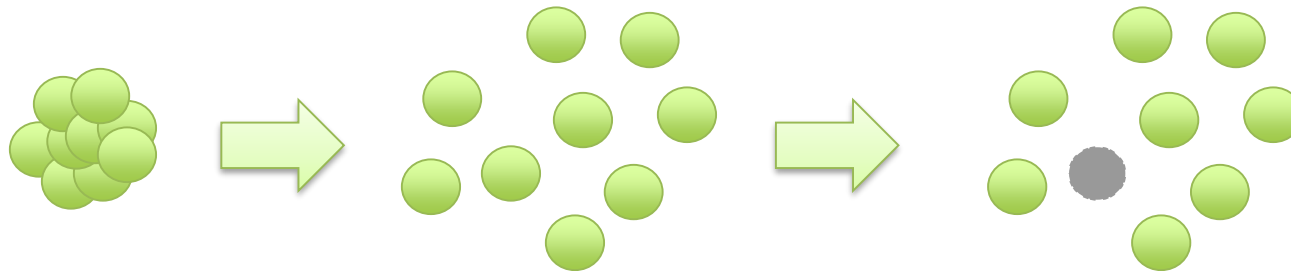
Impact de la dissociation cellulaire : “adaptation”



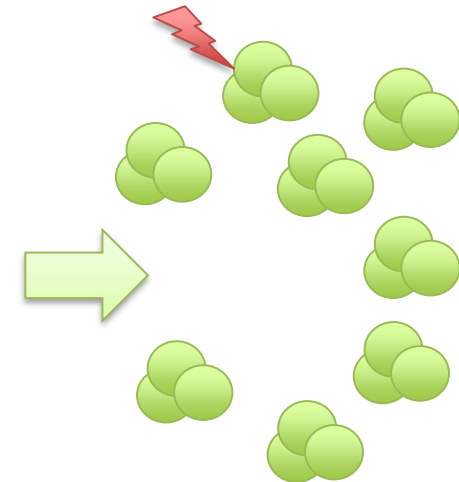
“Adaptation” à la dissociation cellulaire



Après 5 à 10 passages :
adaptation

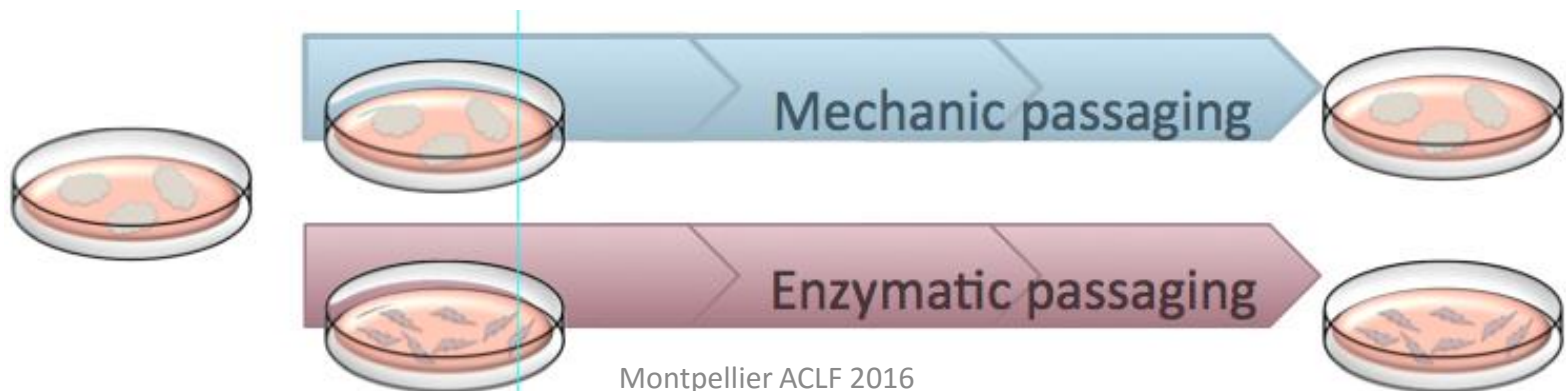


Anomalies
génétiques



ETUDE DES ANOMALIES GENETIQUES INDUITES PAR LE STRESS DE LA DISSOCIATION CELLULAIRE

- Comparaison d'un passage mécanique vs. enzymatique
- 3 lignées ES humaines à passage précoce:
 - HD129: p16 et HD291: p13; HS306: p25
- Trois techniques d'analyse génétique:
 - Caryotype
 - Puces à AND SNP 6.0 (Affymetrix)
 - NGS



Anomalies caryotypiques

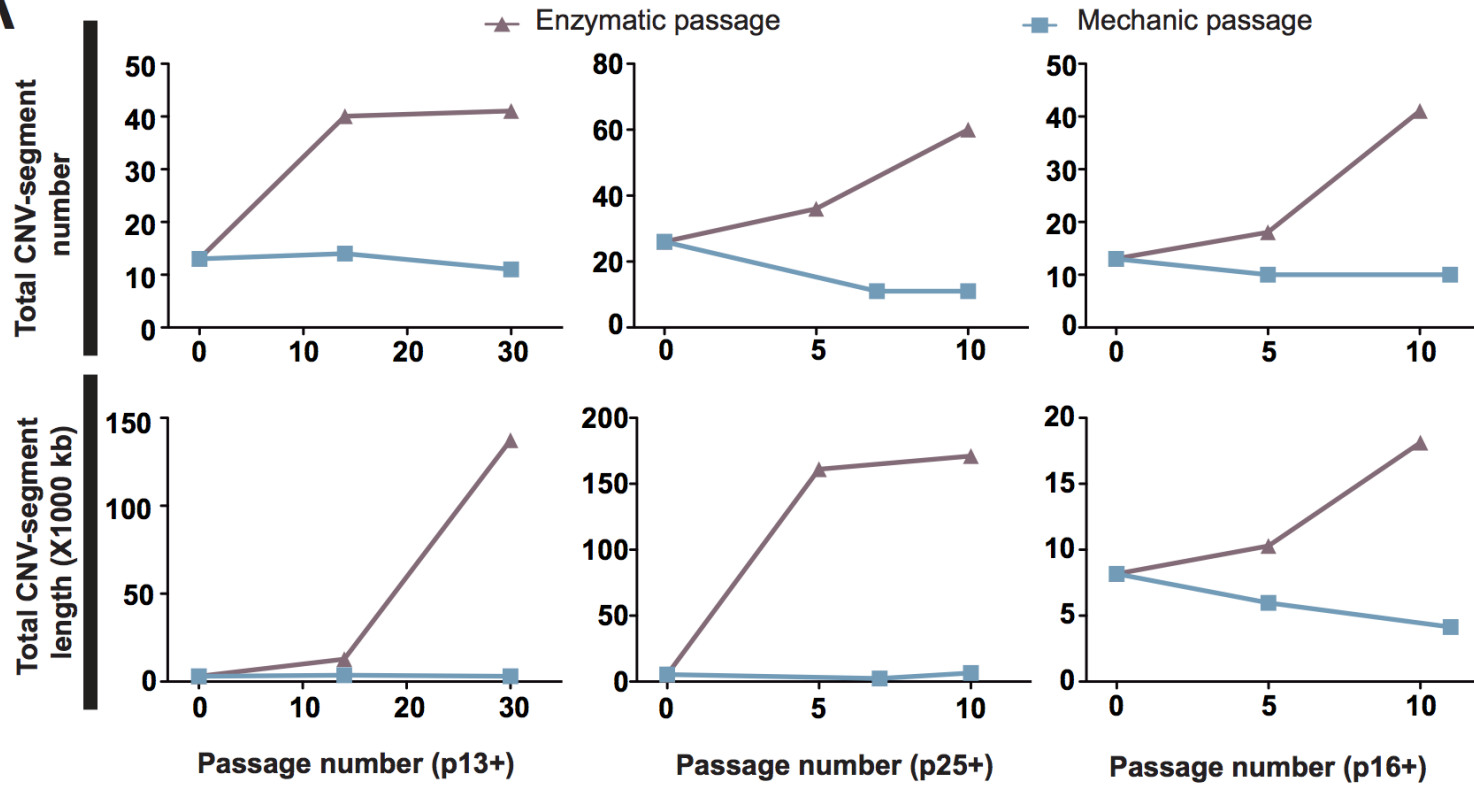
Cell line	Passage	Karyotype [Number of metaphases]
HD129	p16+MP5	46, XY [13]
HD129	p16+MP9	46, XY [14]
HD291	p13+MP15	46, XY [11]
HD291	p13+MP30	46, XY [15]
HD291	p13+MP44	46, XY [20]
HS306	p25+MP10	46, XX [17]

Anomalies caryotypiques

Cell line	Passage	Karyotype [Number of metaphases]
HD129	p16+MP5	46, XY [13]
HD129	p16+MP9	46, XY [14]
HD129	p16+EP9	mos 47, XY, +20 [8]/46, XY, -13, +20 [1]/ 46, XY [47]
HD291	p13+MP15	46, XY [11]
HD291	p13+MP30	46, XY [15]
HD291	p13+MP44	46, XY [20]
HD291	p13+EP34	47, XY, +12 [14]
HD291	p13+EP30MP17	47, XY, +12 [15]
HS306	p25+MP10	46, XX [17]
HS306	p25+EP5	mos 46, XX, i(7)(q10) [12]/ 47, XX, i(7)(q10), +3q, del(10q)? [1]/47, XX, dble i(7)(q10), +7 [3]/46, XX, i(7)(q10), del(9q) [2]/46, XX, i(7)(q10), del(9ter), del(10q) [2]//47, XX, i(7)(q10), +20 [1]
HS306	p25+EP11	46, XX, i(7)(q10) [17]

Copy Number Variation (CNV)

A



■ Mechanic passage ▲ Enzymatic passage

NGS

- Analyse en cours
 - Peu de mutations
 - Hasard ou déterminisme de ces mutations de novo?

Conclusion 1

- Instabilité génétique des CSP:
 - Fortement dépendant du type de passage
 - Peut-être très rapide (5 passages)
 - Anomalies caryotypiques et CNV
- NB : anomalies de caryotype récurrent mais plutôt tardif, CNV non récurrent et précoce

QUELLES ANOMALIES GENETIQUES?



Nicolas Girault, Master 2

Said Assou, IR

Anthony Boureux, MCU

Thérèse Commes, PU

John De Vos, PUPH

Seadb.org (unpublished)



Welcome in SEA database

Pluripotent stem cells such as Induced pluripotent stem cells (iPSCs) or embryonic stem cells (ESCs), as well as other stem cell, hold great promise for biomedical research and medical applications. However, stem cells might harbor genetic aberrations. Therefore, there is a need of guidelines to define the acceptable level of genomic integrity of stem cells for biomedical applications. SEA database is designed to store and display genetic abnormalities that have been reported in stem cells. The collection and computing of such abnormalities are a necessary step to propose guidelines for acceptable genomic integrity of stem cells.

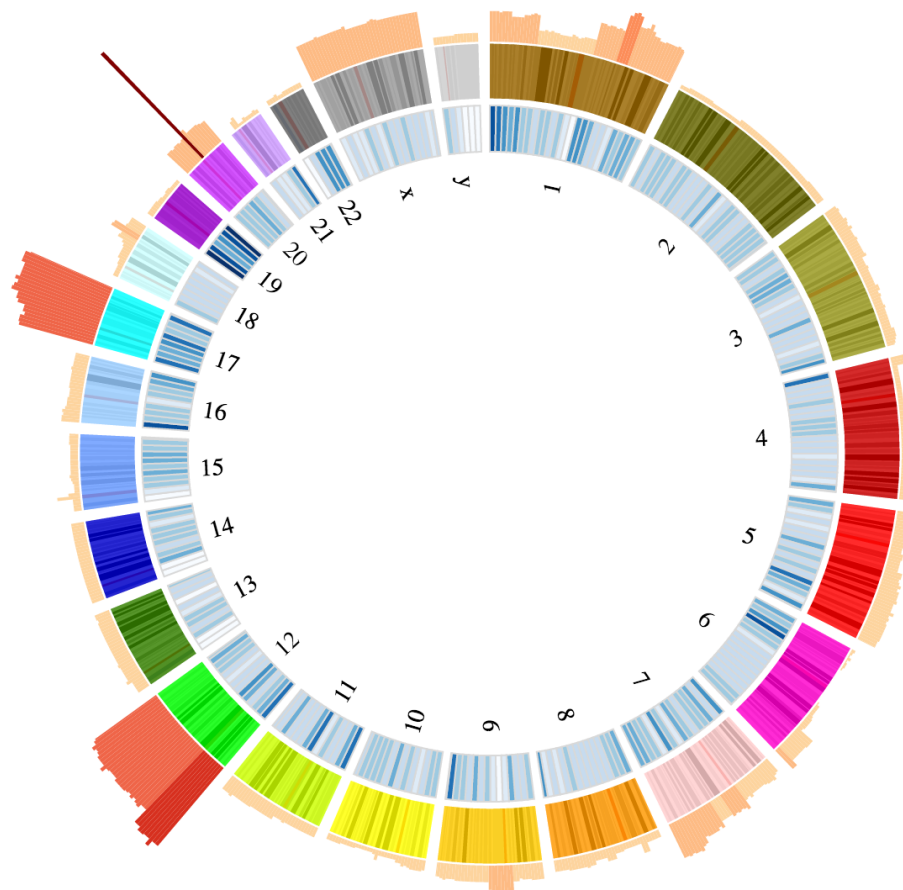
SEA database contains 101 [studies](#), 905 [samples](#) and **405735** [abnormalities and variants!](#)

Search SEA

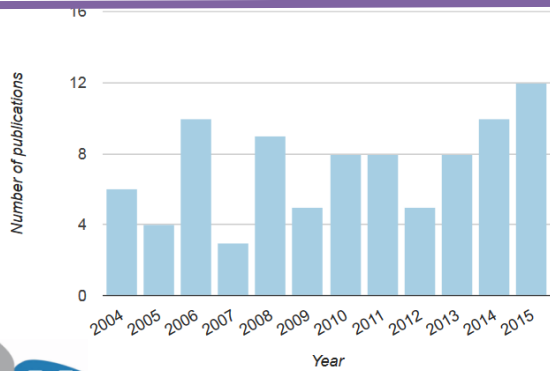
Search on genome browser. e.g. NANOG, 20:28400001..31500000

GO

Click and browse SEA abnormalities



SEAdb



Extraction

SEAdb



Inventaire de ces anomalies dans les CSP

101

Etudes

Auteur

PMID

Année

Journal

Equipe

905

Echantillons

Type d'échantillon

Paramètre de culture

Méthode de détection

405735

Variants

Trisomy

SNV

CNV

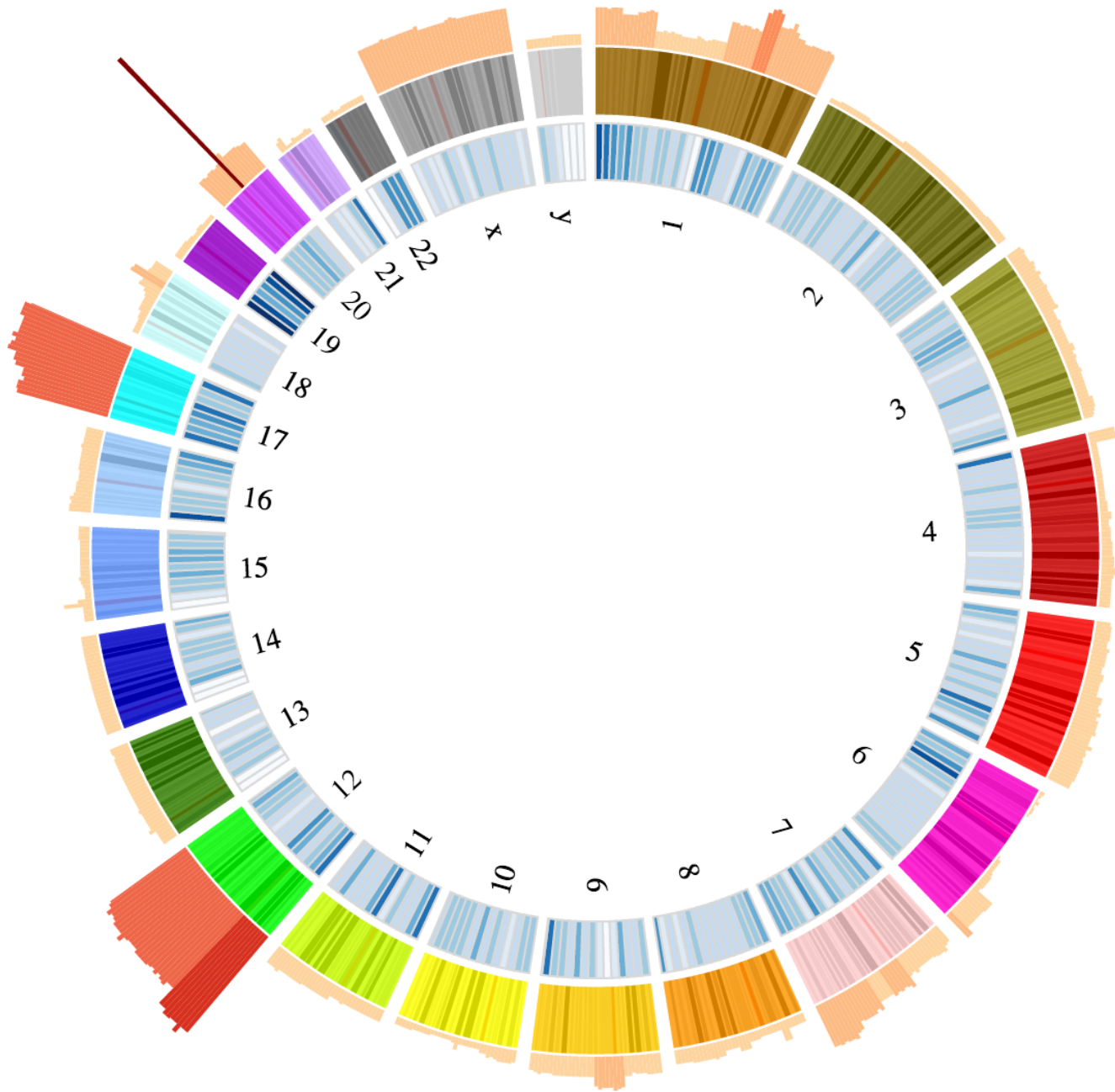
LOH

Deletion

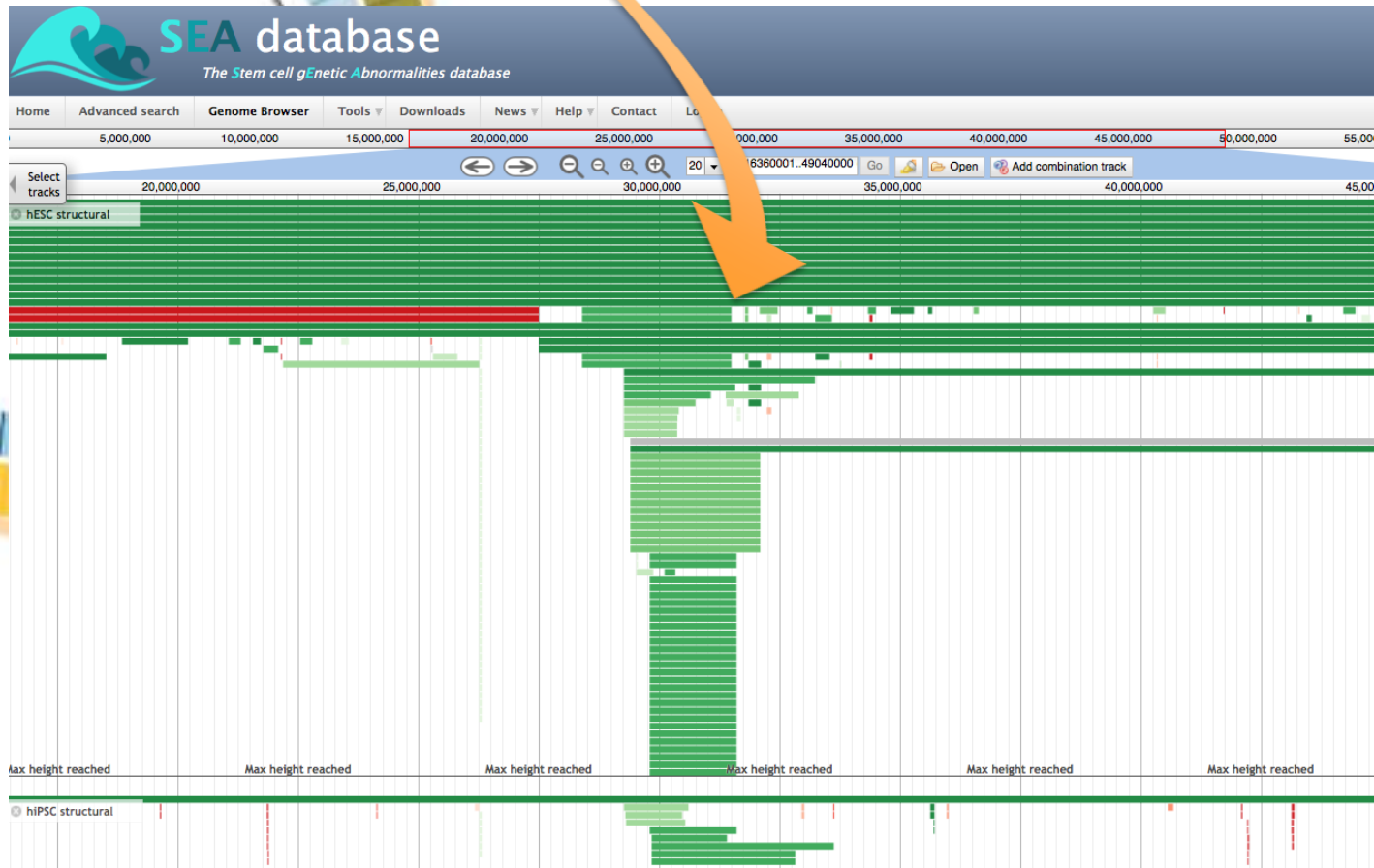
Translocation

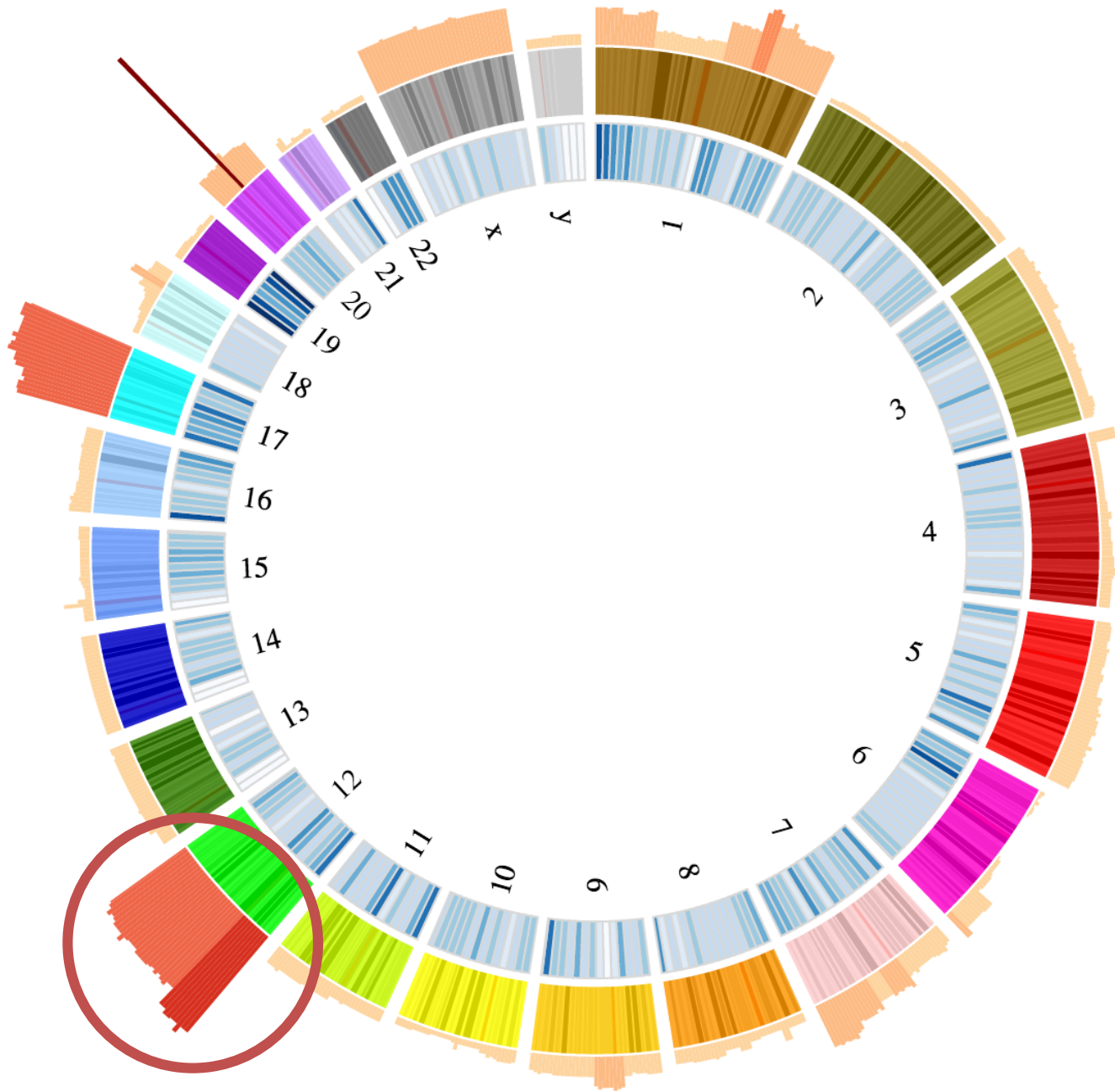
Duplication

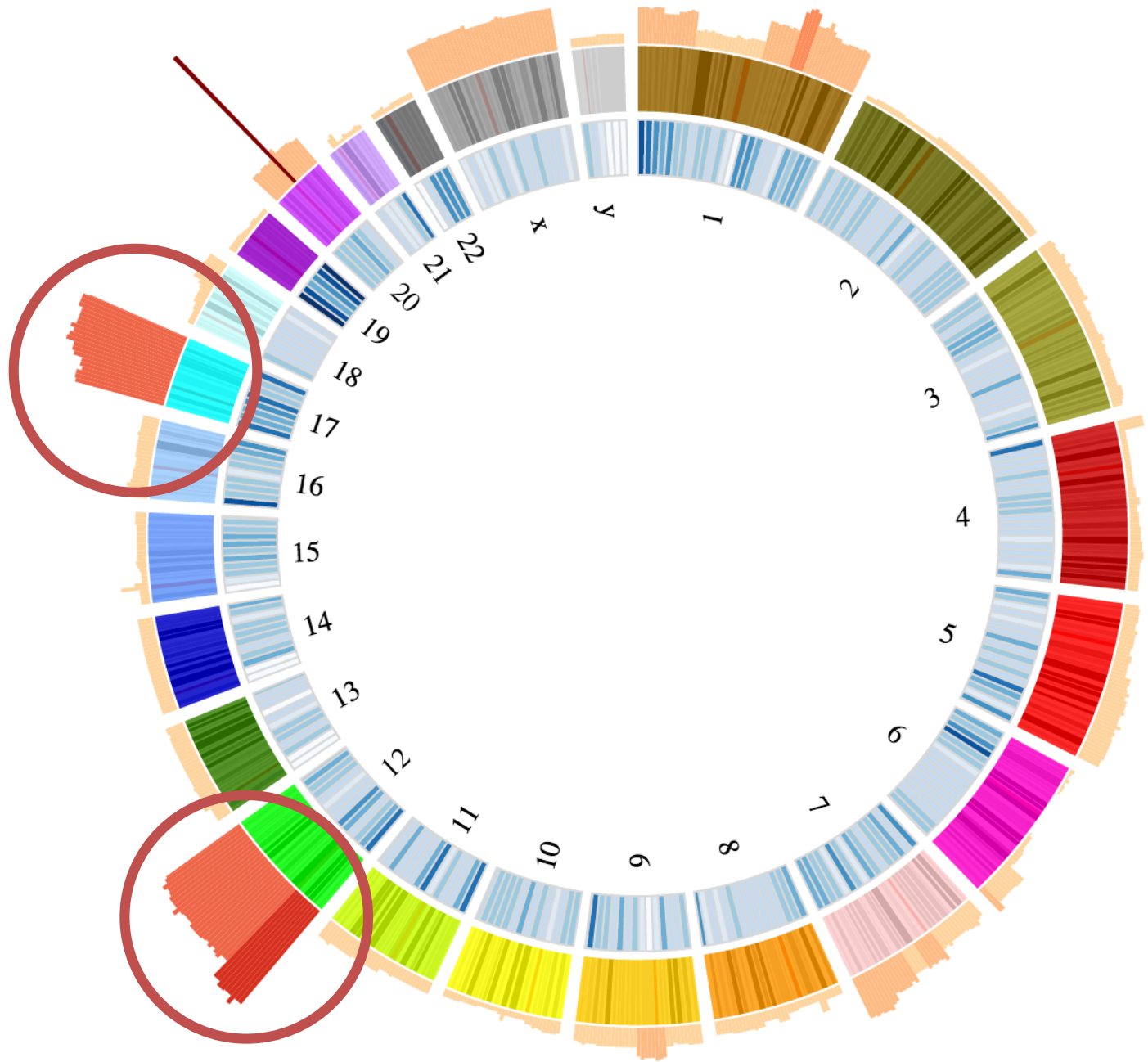
M. Helleier AD 2016

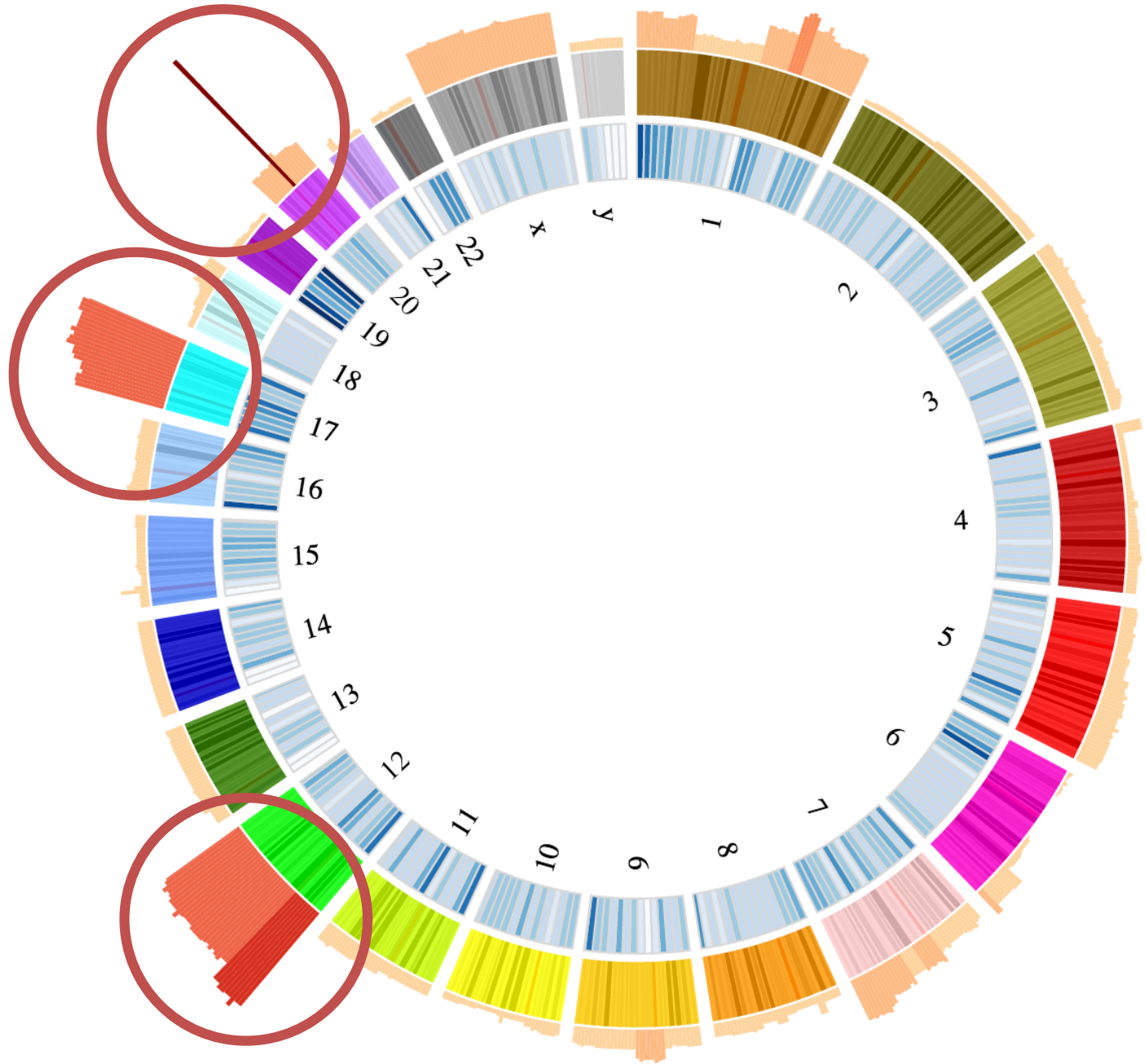


Zoom via a genome browser



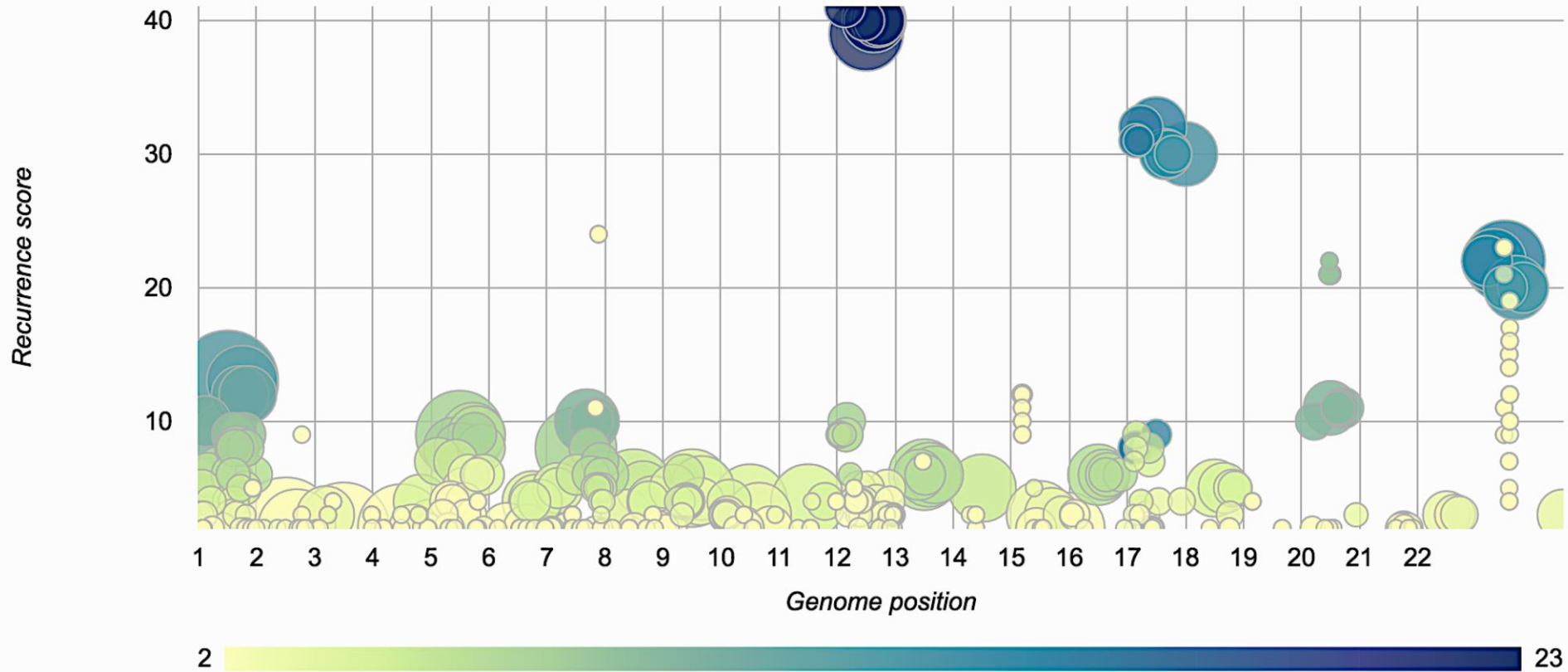






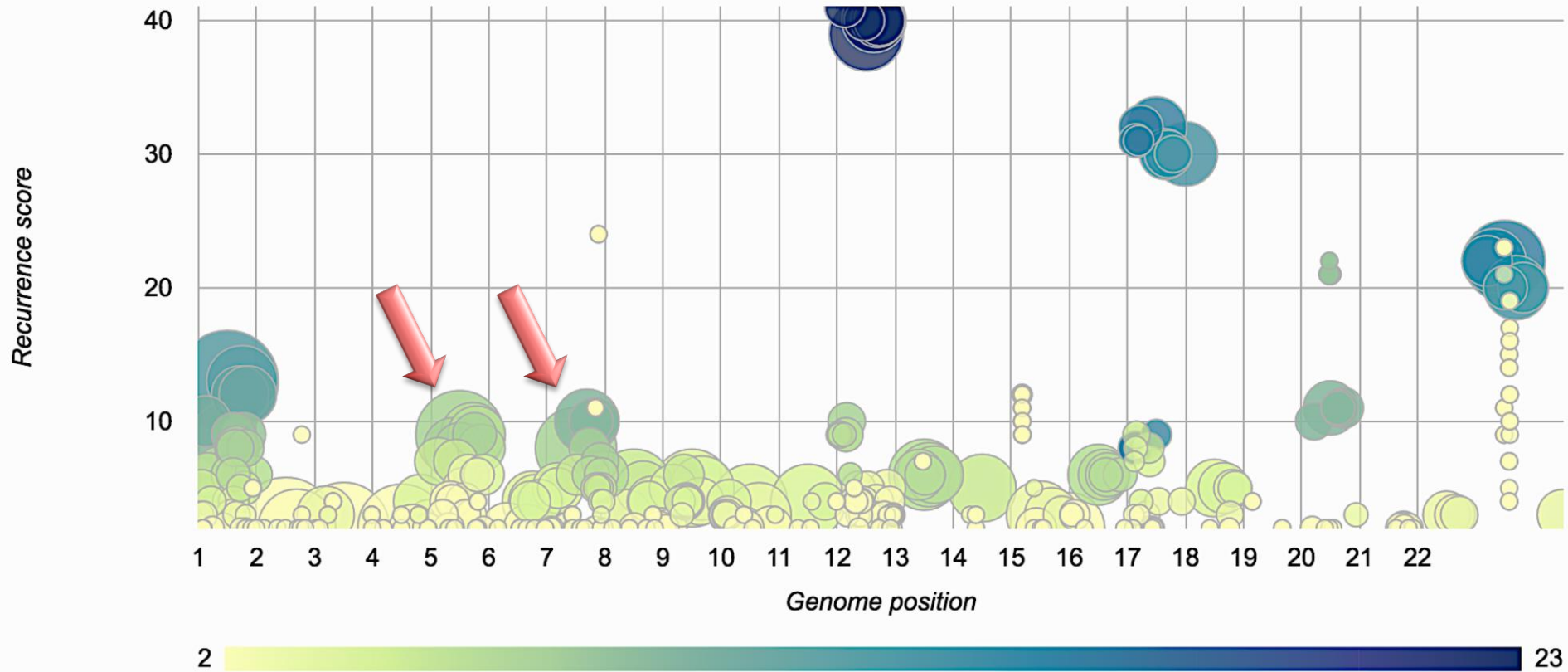
“HOTSPOT FINDER”

“HOTSPOT FINDER”



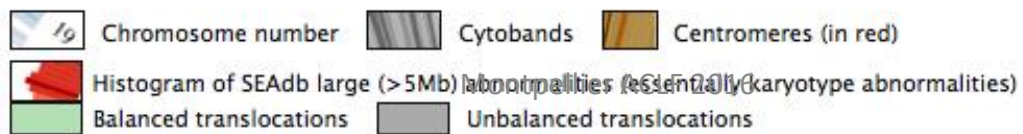
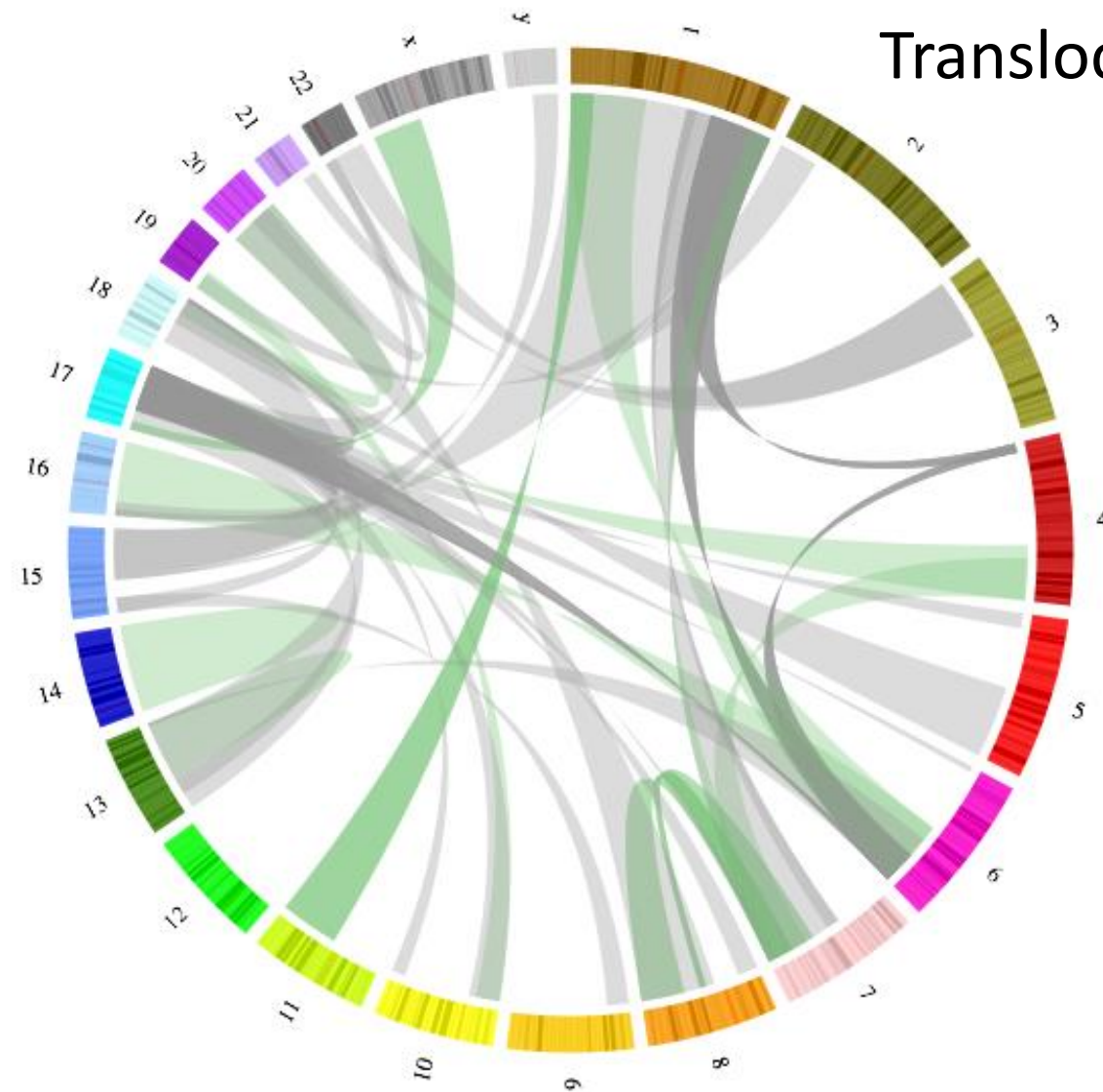
Color gradient: # studies - bubble size: length of the genomic region

“HOTSPOT FINDER”

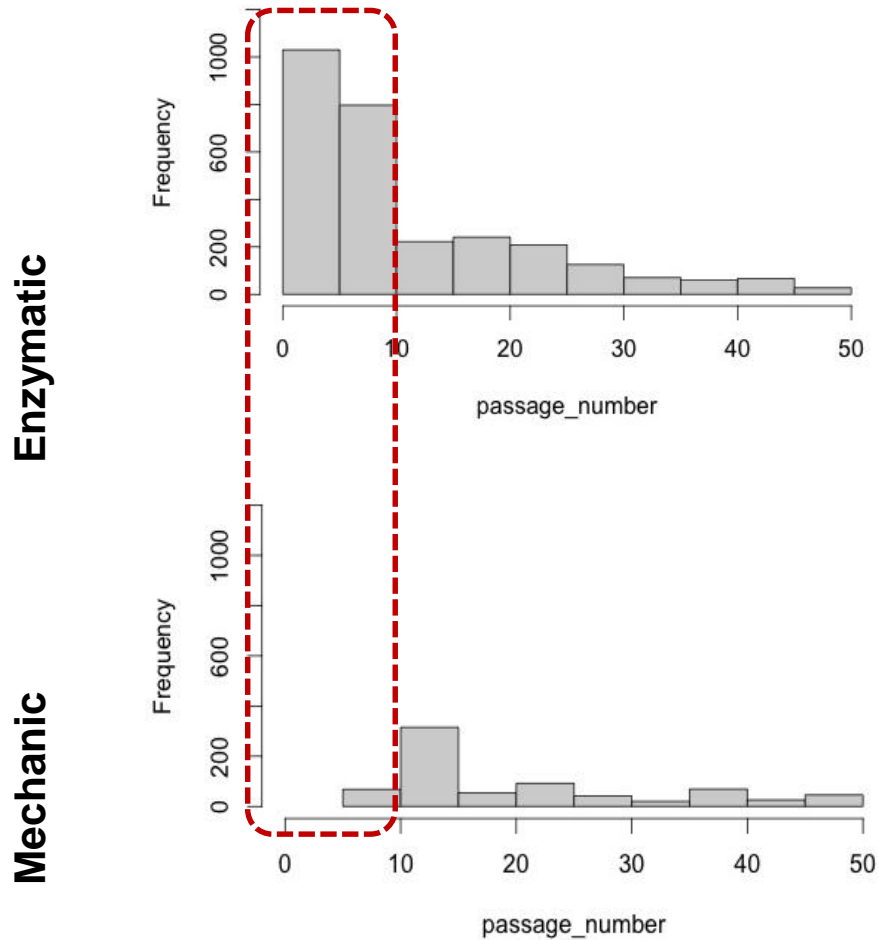


Color gradient: # studies – bubble size: length of the genomic region

Translocations



Impact de la méthode de passage sur la fréquence des variants

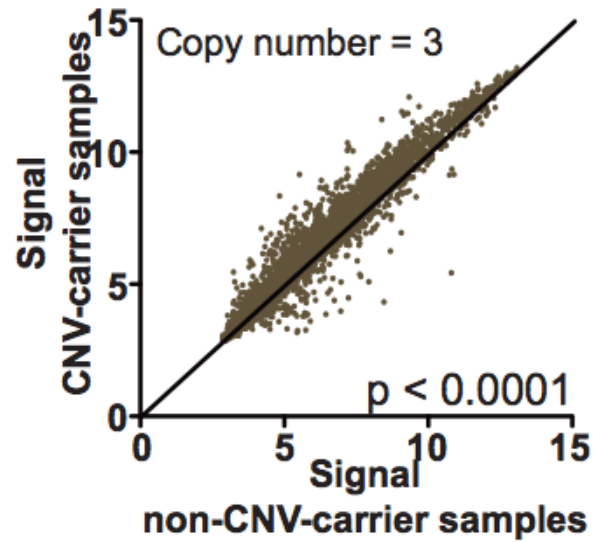
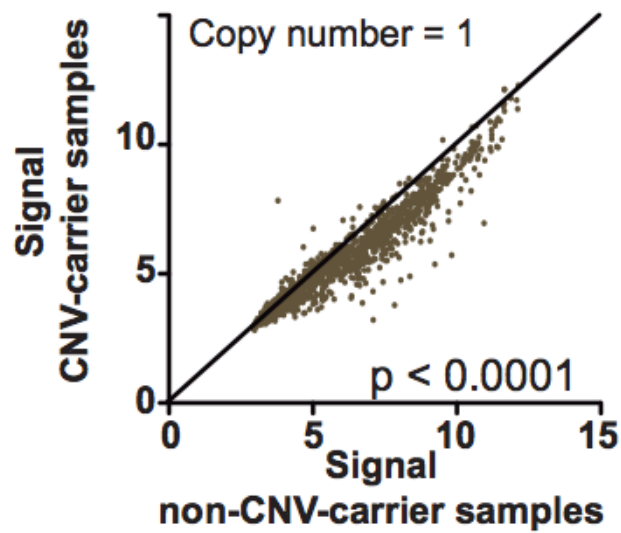


Conclusion 2

- Les principales anomalies génétiques récurrentes:
 - Aneuploïdies
 - Et des gains > 1Mb
 - Ce sont des anomalies « hyperrécurrentes »

ALTERATION DU TRANSCRIPTOME

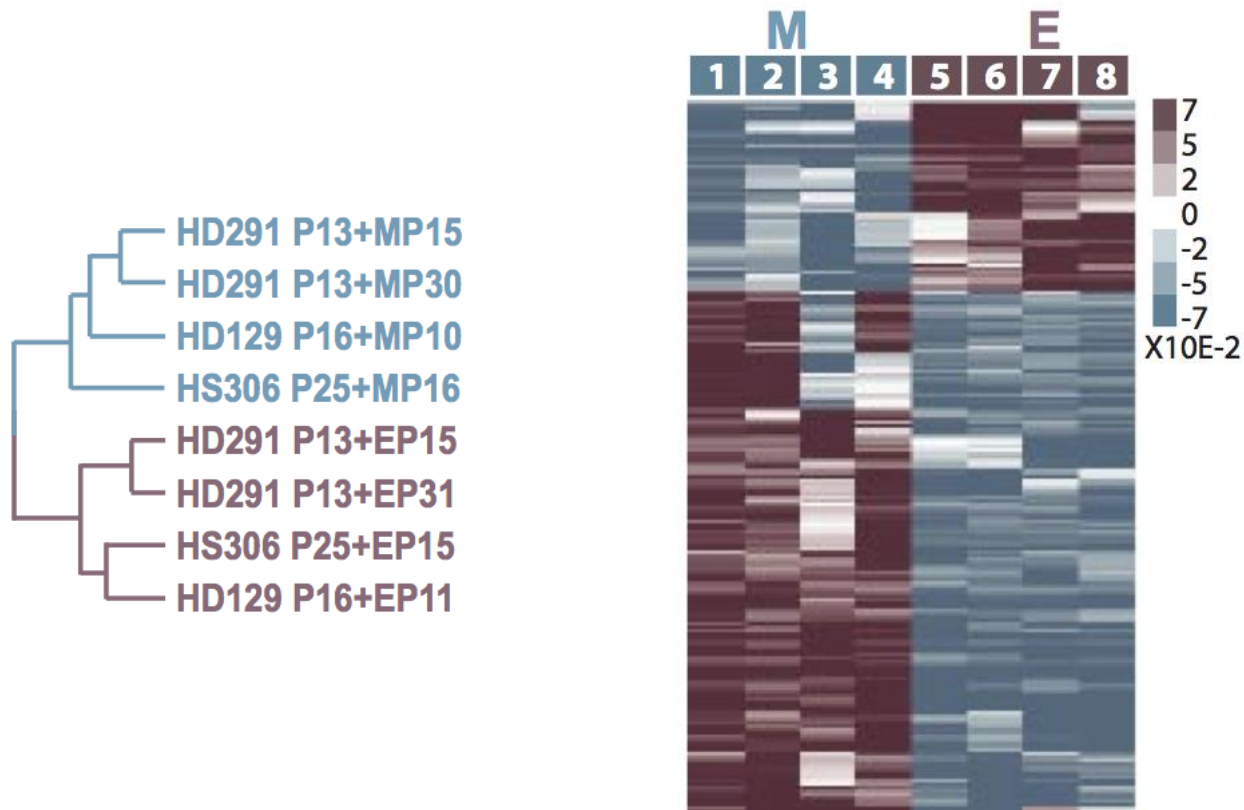
COPY NUMBER EFFECT



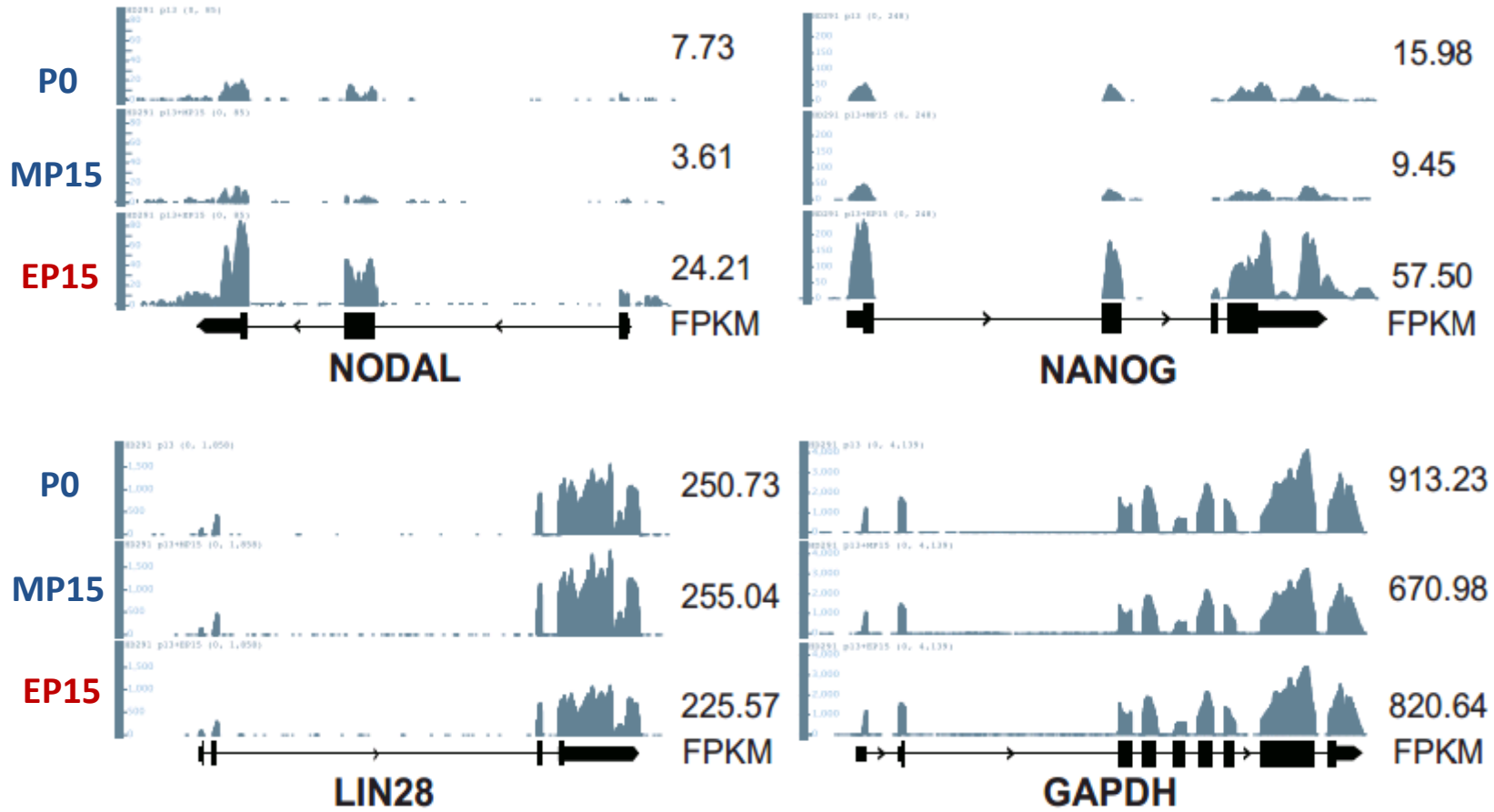
COPY NUMBER EFFECT?

- 320 probesets avec au moins un $FC > 4$ dans une lignée (max : 119,04)
- 22 probesets localisées sur un CNV (max : 7,8)

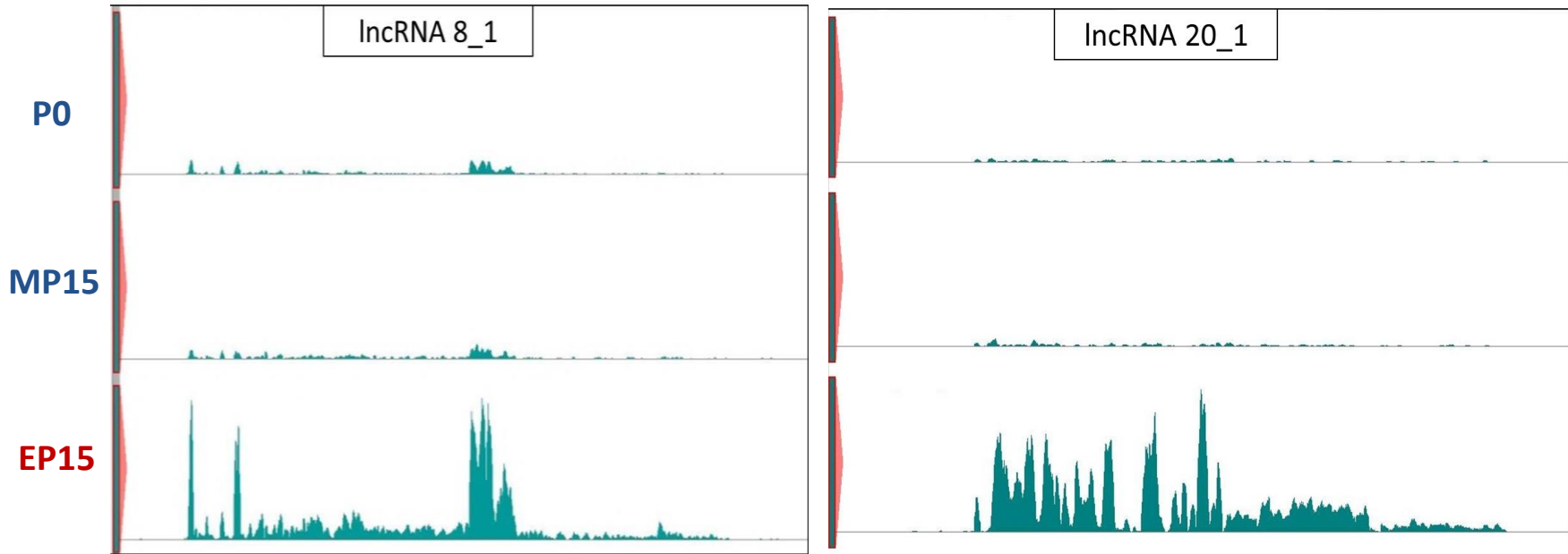
Signature transcriptionnelle caractéristique



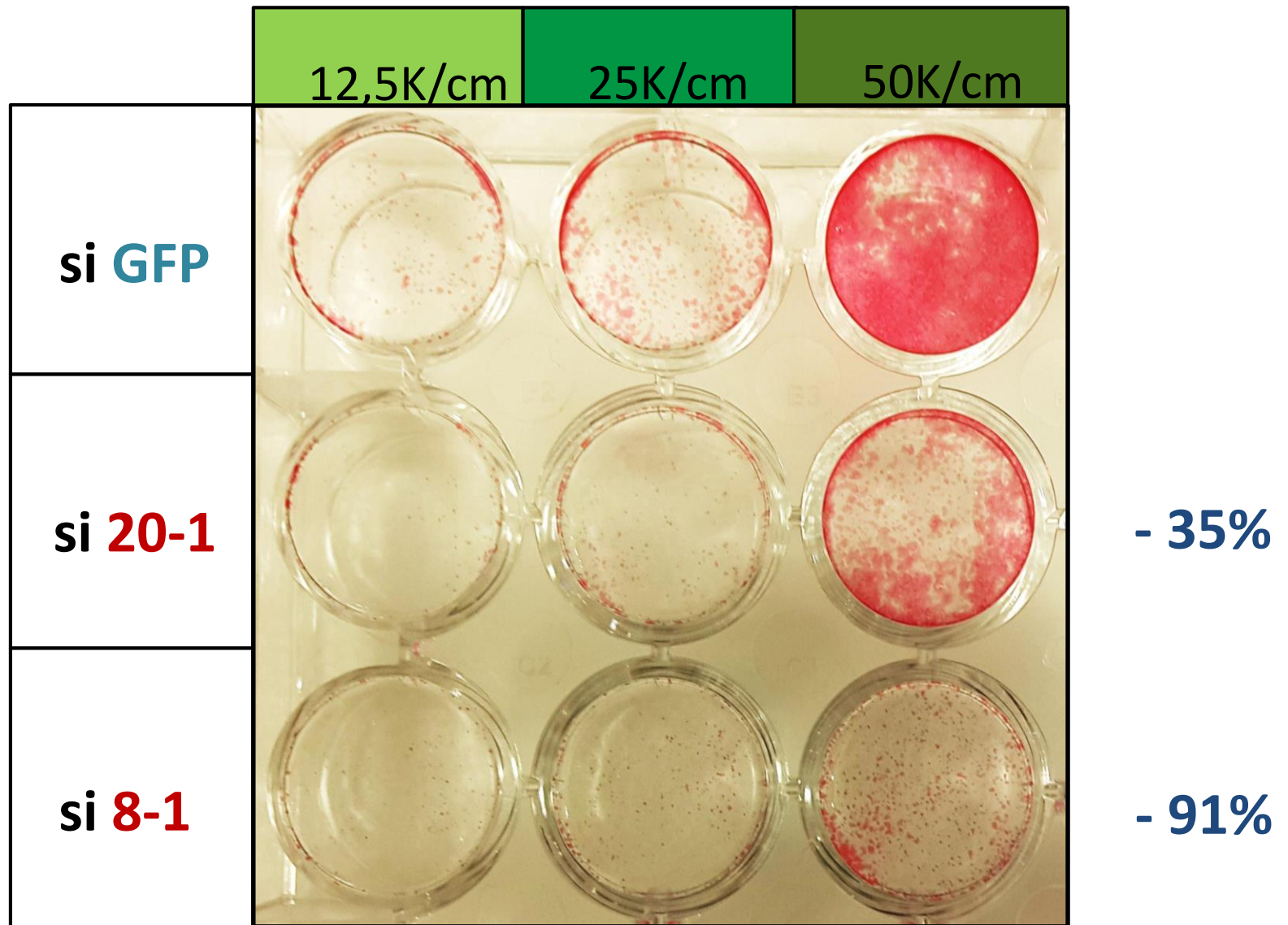
mRNAseq



Long non-coding RNA



- Certains lncRNA induits massivement ($> \times 50$)



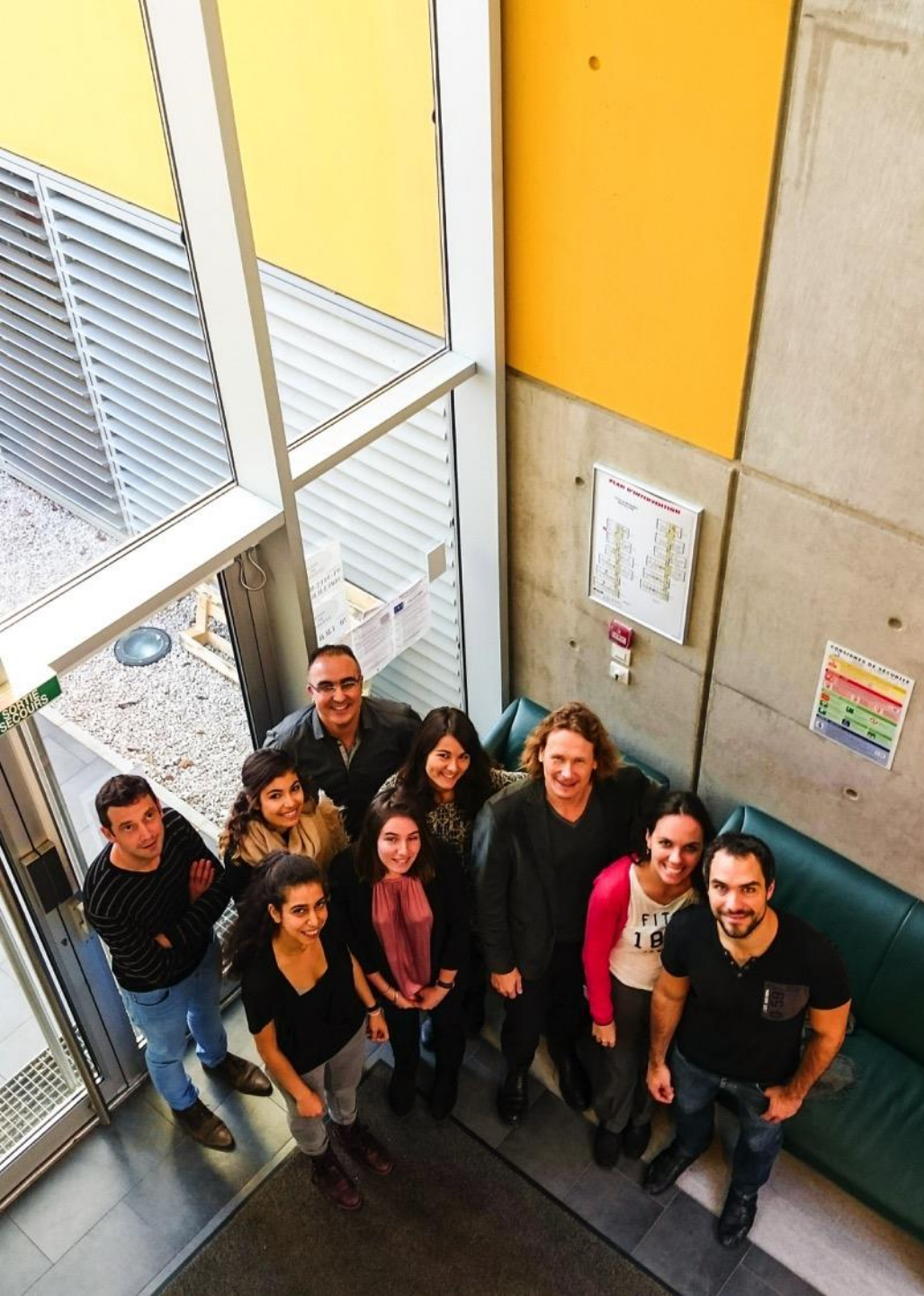
○ Knock-down par siRNA sur cellules adaptées

Conclusion 3

- Modifications transcriptome plus importantes que ne le voudraient les anomalies génétiques
- Modifications du phénotype précèdent le changement génétique?

Conclusion générale

- iPS : modèle prometteur d'étude des maladies génétiques
- Attention aux aneuploïdes induites par la culture
 - surveillance régulière de la culture (caryotype, FISH?, puces? séquençage?)
 - iPS « naïves »?



Present and past members :

Engi AHMED

Caroline SANSAC

Julien BOUCKENHEIMER

Jean-Marie RAMIREZ

Said ASSOU

Arnaud BOURDIN

John DE VOS

Mathilde PLINET

Nicolas AUSSEL

Nicolas GIRAULT

Qiang BAI

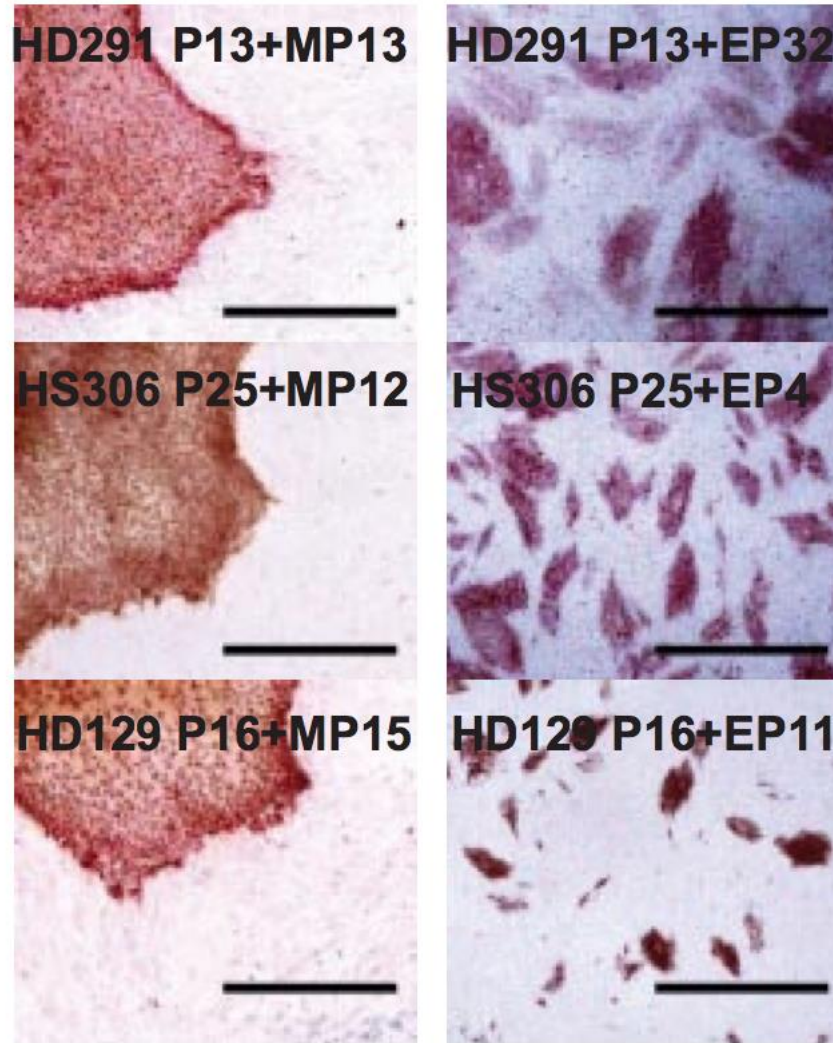
Doris CERECEDO

COLLABORATIONS

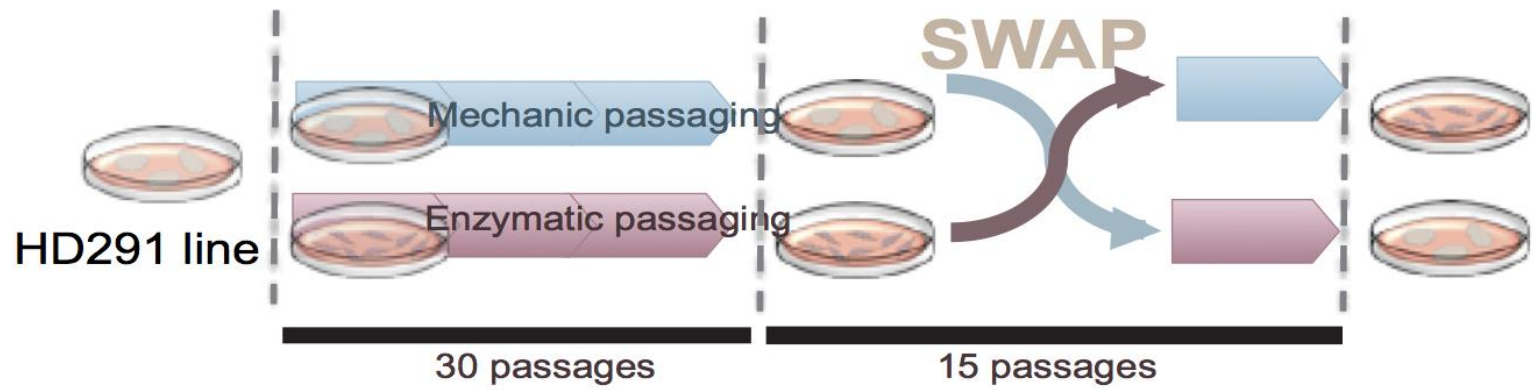
Franck PELLESTOR (CHROMOSTEM)

Jean-Marc LEMAITRE

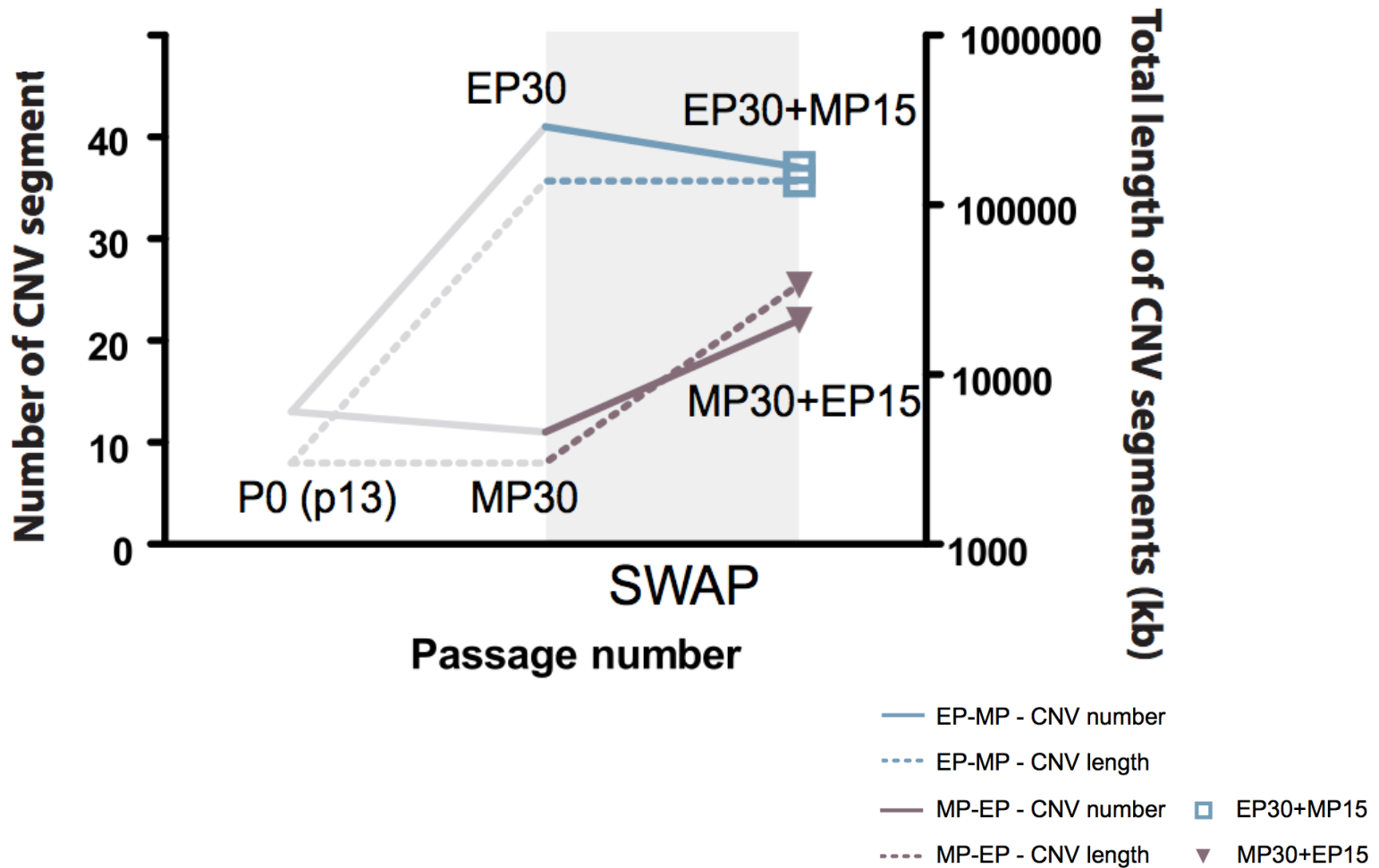
Outi HOVATTA



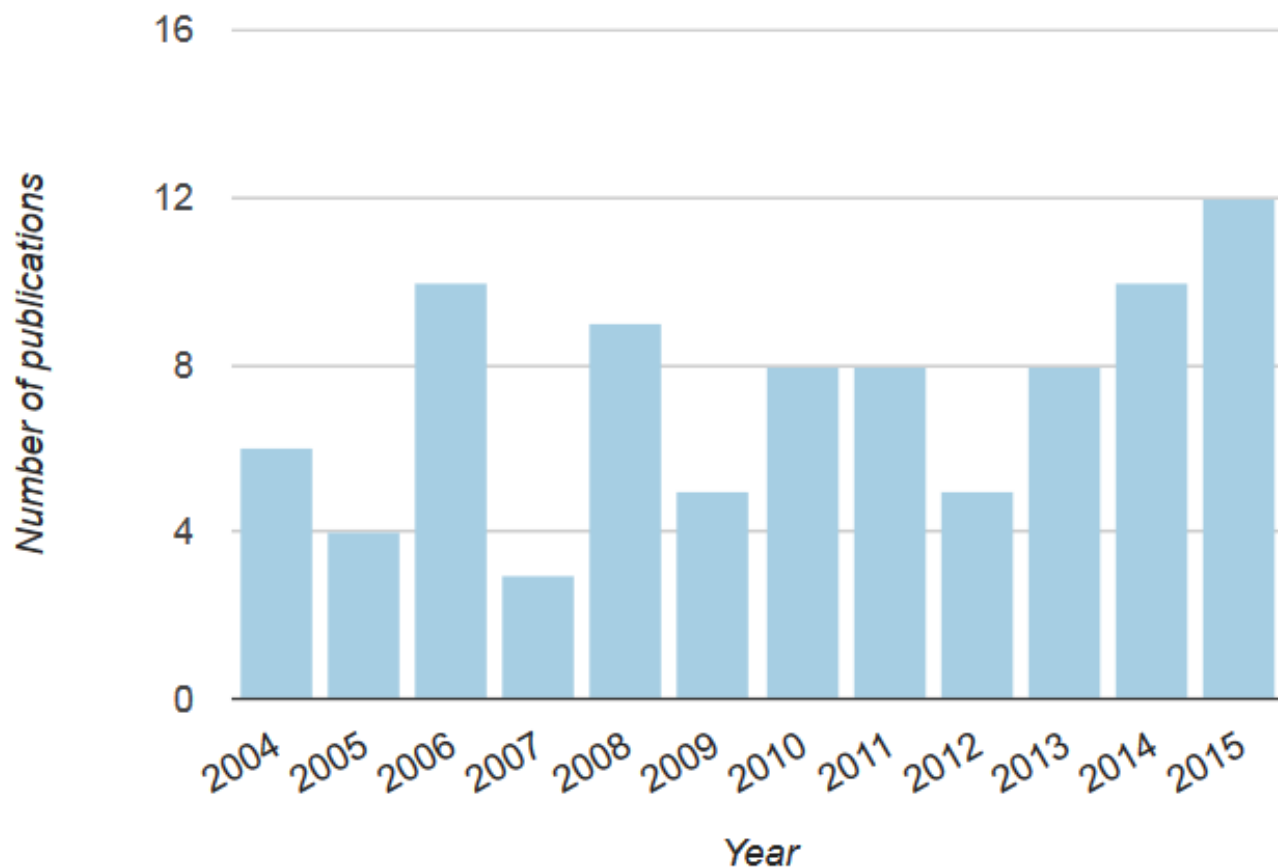
SWAP



SWAP



Nombre de publications par année



Where SEAdb studies come from

