

Osteoarthritis a complex disease with high social economic burden

Osteoarthritis (OA)

- Degenerative joint disease
- Prevalent
- No effective treatment



Major cause of disability among elderly affecting mobility and hampering daily life activities

Impediments OA disease management

- **Complex heterogeneous disease**
- **Little insight in disease etiology**
- **Difficult diagnosis**

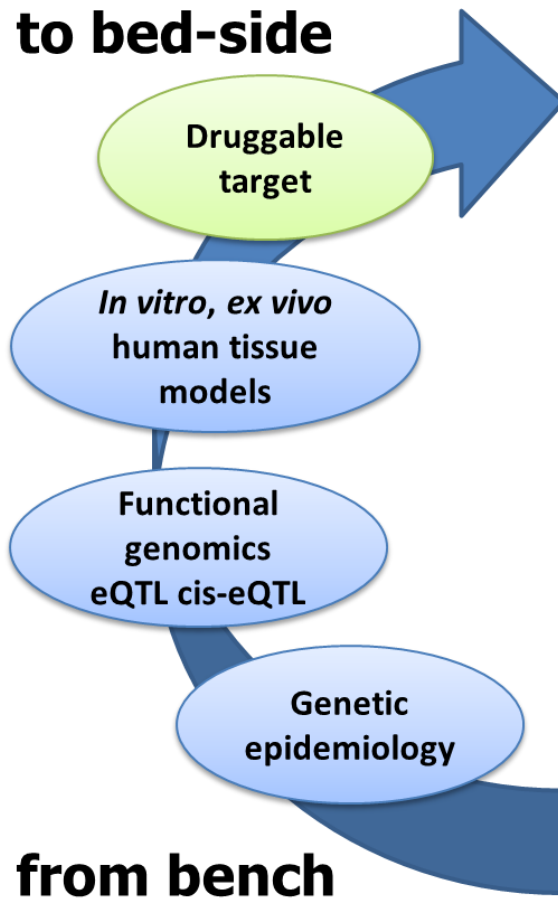


Severe backlog in development of effective disease modifying OA therapies

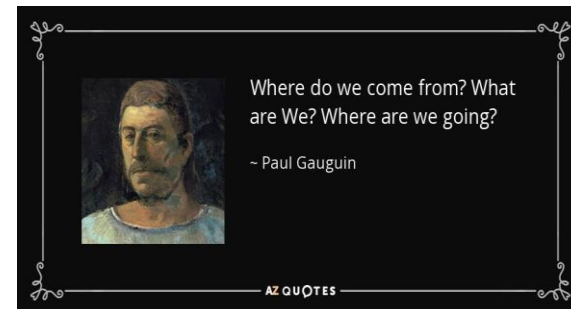
Which step in the Freedman et al strategy?

1. Which type of study is powerful in identifying underlying disease mechanisms?

Overview

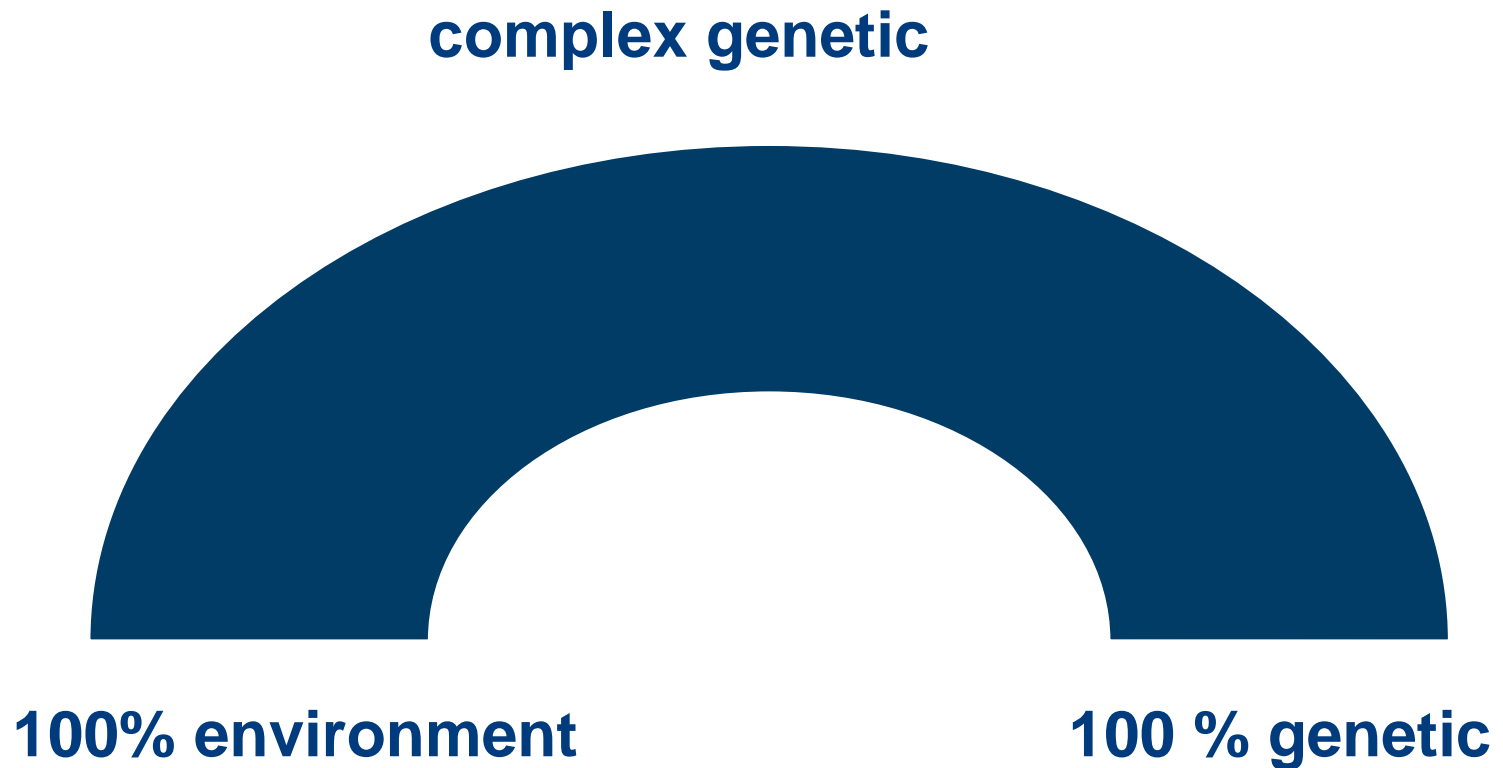


- Novel underlying disease pathways
- Novel druggable targets



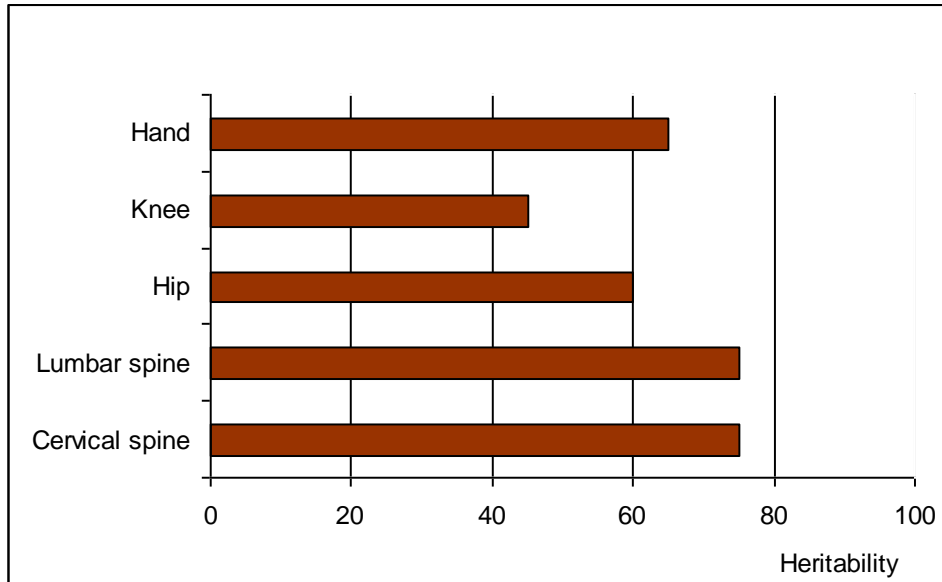
Heritability and the genetic study design

Balance between heritability and environment

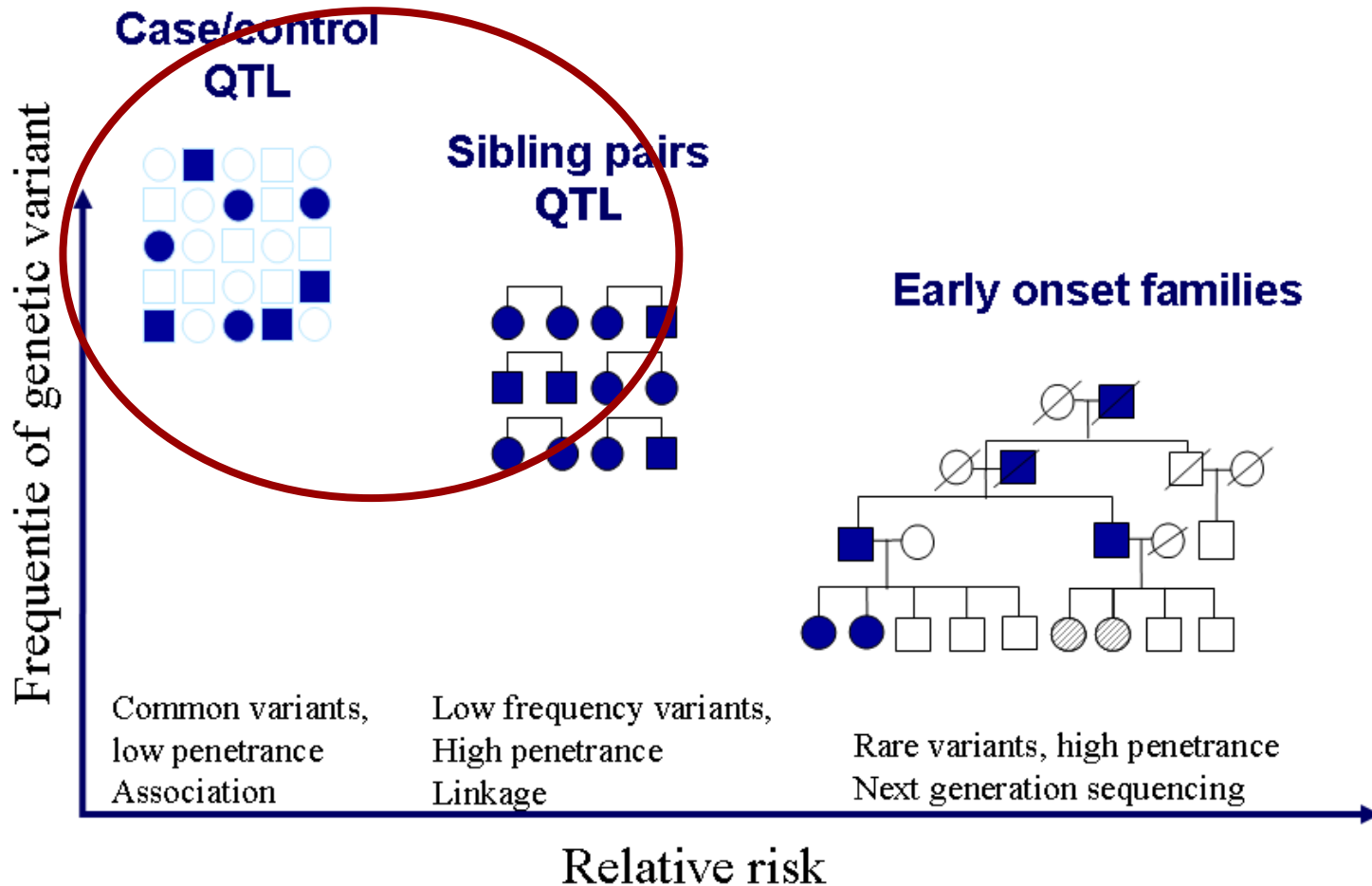


Determines genetic study design

Osteoarthritis - Heritability

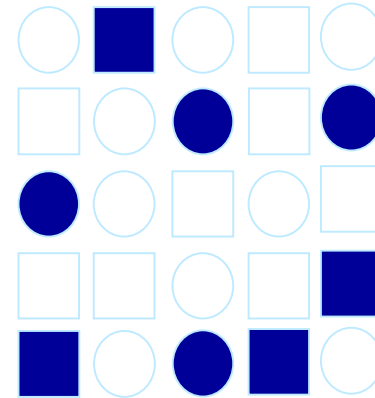


Study design depends on inheritance pattern



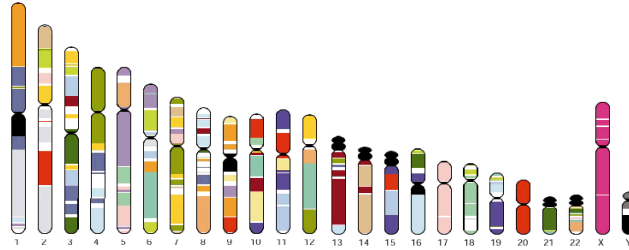
Association analyses case/controls

- Cases and controls
- Complex phenotype (common)
- Model free
- Sharing of alleles between cases versus controls
- Use SNPs close together



Finding association is about finding genes / pathways changing your risk to develop disease

Possible genetic approaches



Candidate genes

**Hypothesis driven -
Educated guess**

Genome wide scan

**Discovery driven -
Acknowledged lack of
knowledge**

Identification of *DIO2* as OA susceptibility locus

The GARP study

GARP study

- 188 sibling pairs + 4 trios
- OA; ACR criteria and radiographs
- Age: 60 yrs (range 43-79)
- Female: 82%

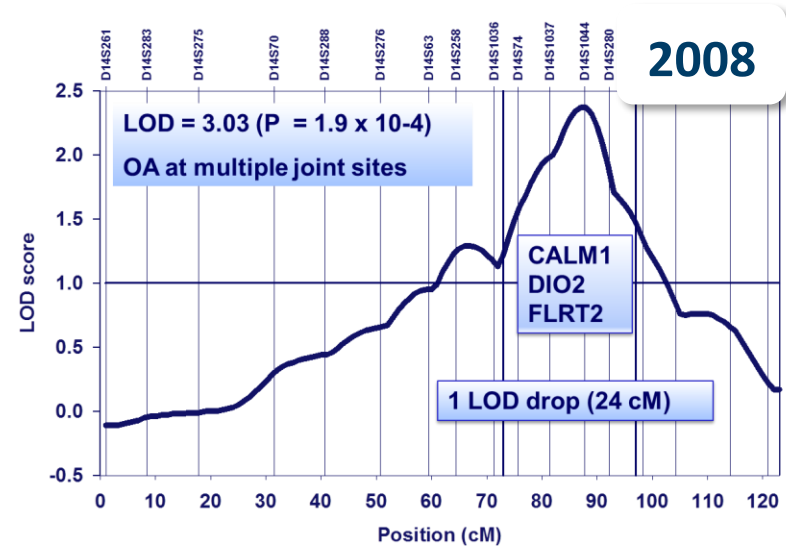
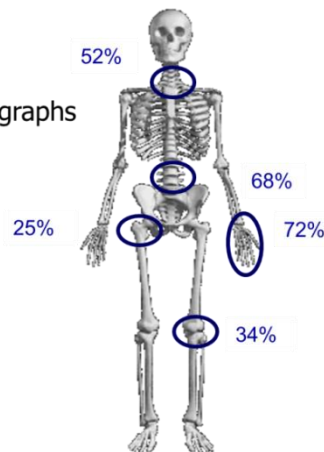
Inclusion:

≥ 2 joints OA

Progression:

2 jr: 100 pairs

5 jr: 200 pairs



Initial study to indicate thyroid signaling conferring risk to osteoarthritis

How to delineate the risk locus?

Which step in the Freedman et al strategy?

1. Using linkage disequilibrium (LD structure) to find candidate gene

BOX 1 STRATEGIES TO PROGRESS FROM TAG SNP TO MECHANISM

1) Target resequencing efforts using linkage disequilibrium (LD) structure.

may be limited by functional methods in rat are promising association studies

DIO2, OA susceptibility gene

The Garp study, combined linkage association

<i>Gene</i>	<i>SNP reference</i>	<i>allele</i>	<i>alias</i>	<i>MAF</i>	<i>P-value</i>
<i>DIO2</i>	rs12885300	C>T	ORFaGly3Asp	0.36	0.04
	rs2267872	G>A		0.09	0.30
	rs225011	T>C		0.43	0.14
	rs225014	T>C	Thr92Ala	0.36	0.006
	rs10136454	C>T		0.02	0.60

Are we convinced of this locus being a strong risk gene?

Which step in the Freedman et al strategy?

2. Used other populations to refine LD regions / association to pinpoint a strong OA risk candidate gene

BOX 1 STRATEGIES TO PROGRESS FROM TAG SNP TO MECHANISM

- 1) Target resequencing efforts using linkage disequilibrium (LD) structure. may be limited by functional methods in rat are promising expression analysis.
- 2) Use other populations to refine LD regions (for example African ancestry with shorter LD and more heterogeneity). ii) Use chromatin association regulatory regions to determine

Initial replication, OA susceptibility gene

DIO2 haplotype rs12885300-rs225014 C-c

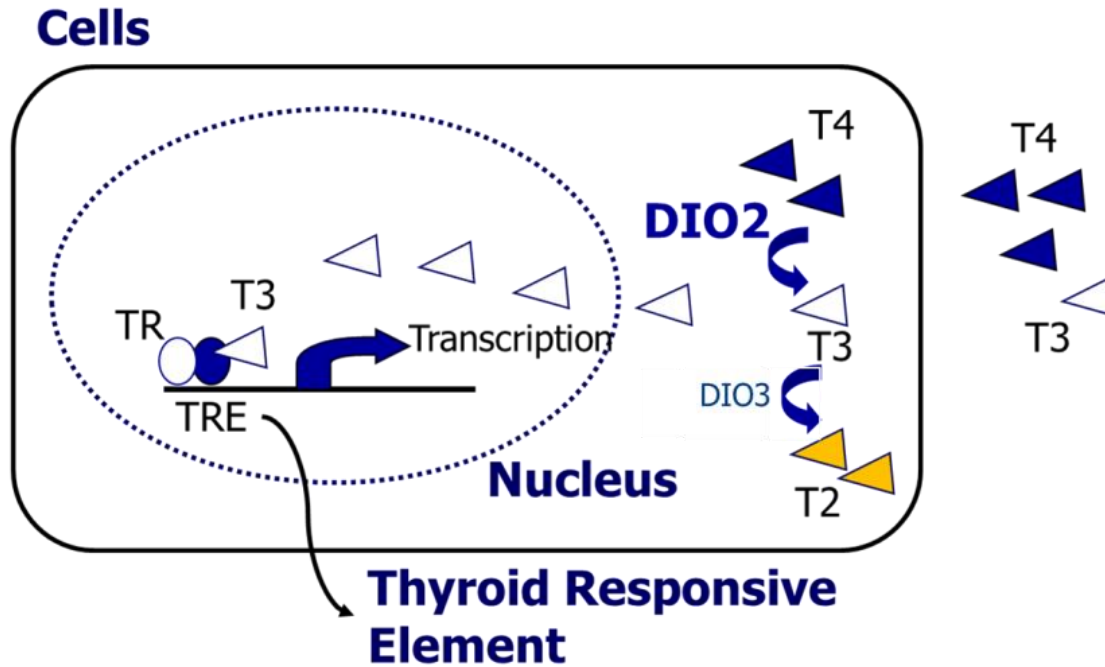
Female cases severe hip OA

<i>Gene</i>	<i>OR Recessive model</i>	<i>P of OR</i>	<i>P value heterogeneity test</i>
<i>All*</i>	1.8 (1.4-2.3)	2x10⁻⁵	0.6
UK (Oxford)	2.1 (1.4-3.2)	0.001	
NL (R'dam)	1.9 (1.0-3.5)	0.040	
Japan (Riken)	1.5 (1.0-2.3)	0.047	

*Random effect meta-analyses

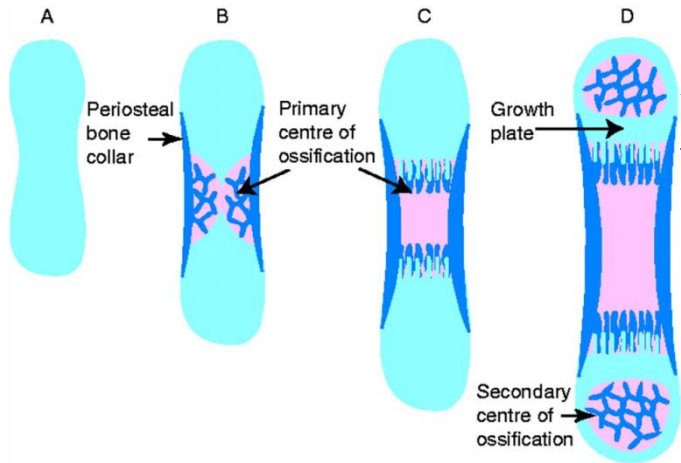
Identification of *DIO2* as OA susceptibility locus

The GARP study



Initial study to indicate thyroid signaling conferring risk to osteoarthritis

Growth plate; elongation of long bones via endochondral ossification



- Cartilage
- Bone
- Bone marrow (including blood vessels)

E J Mackie et al. J Endocrinol 2011;211:109-121

Stem cells

Growth plate chondrocytes

Proliferation

Hypertrophic

Mineralization

Bone

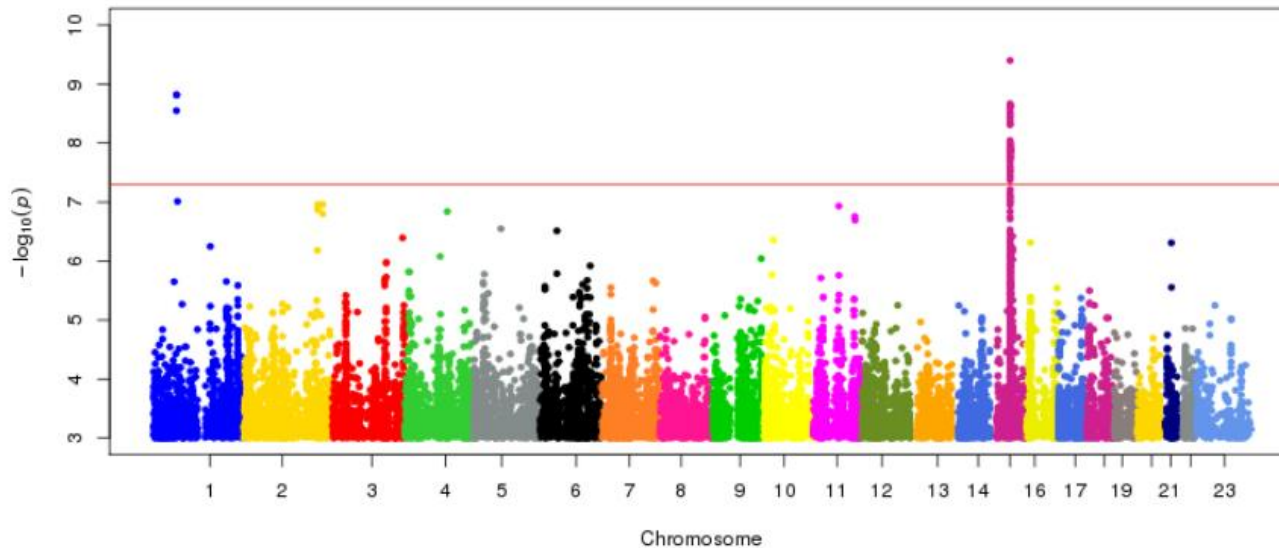


Active intracellular thyroid (T3) triggers terminal maturation of growth plate chondrocytes to allow transition to bone

Wang et al. 2007 J bone and Min Res. 22; 1988-95

Additional OA genes in thyroid pathway

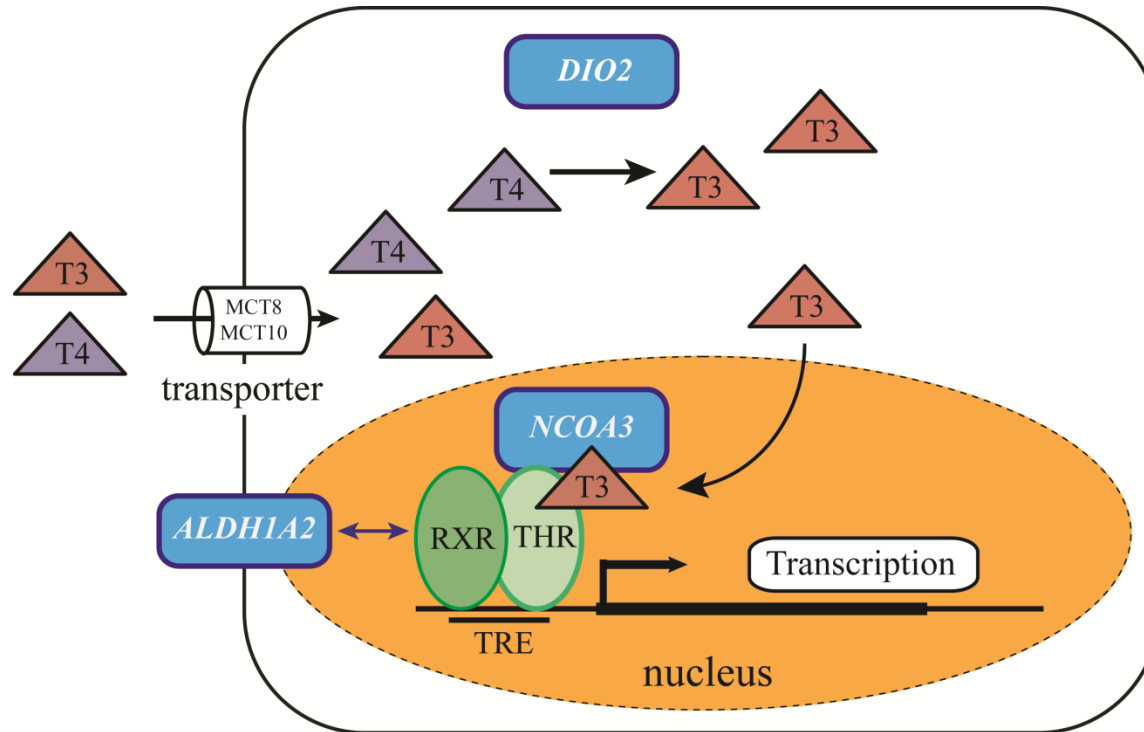
- Large scale genome wide meta analyses of osteoarthritis;
ALDH1A2, *NCOA3*



Styrkarsdottir et al. 2014 Nat Genet 46: 498-502

Evangelou et al. 2014 Ann Rheum Dis 73:2130-6

Intracellular levels of active thyroid



Intracellular thyroid signaling may be a common underlying osteoarthritis pathway

Formulate hypothesis

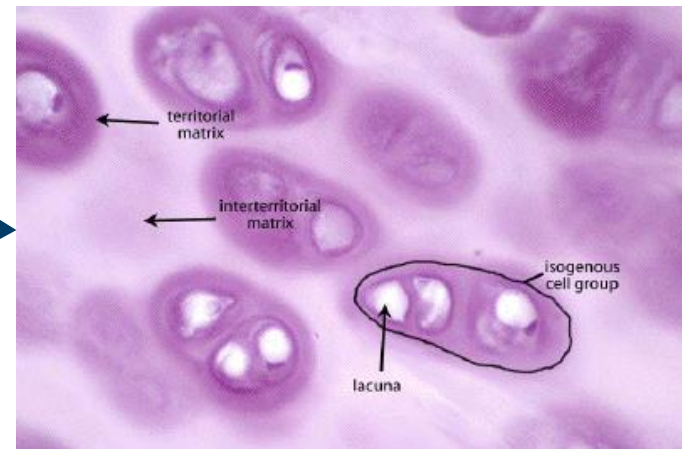
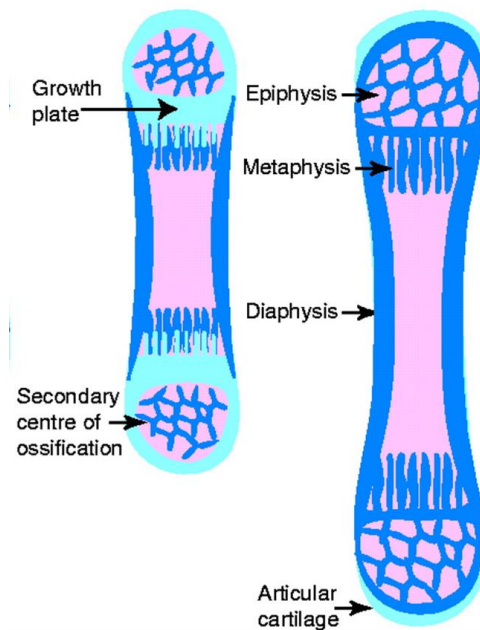
Developmental process of endochondral ossification

Late cause of a late life disease?



Articular chondrocytes

- **Highly specialized, post-mitotic cell**
- **Maturation arrested**
- **Require phenotypic plasticity and shift between active metabolic and maturational arrested states to respond to environmental challenges.**



Healthy articular cartilage

Endochondral ossification and Osteoarthritis

Late life effect of *DIO2*

Late life
disruption of epigenetic silencing of thyroid
signaling in articular cartilage



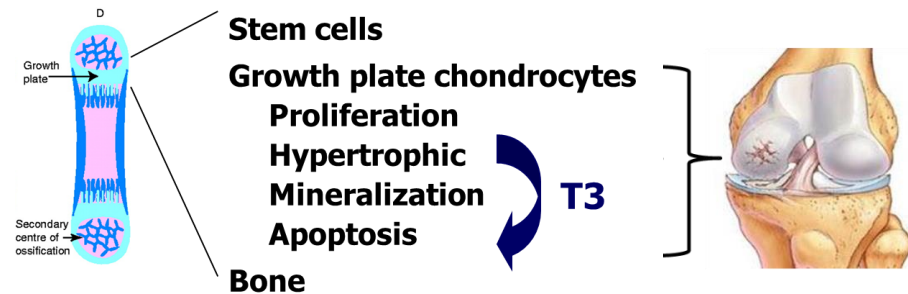
Loosening of maturational arrested state



Debilitating cartilage signaling

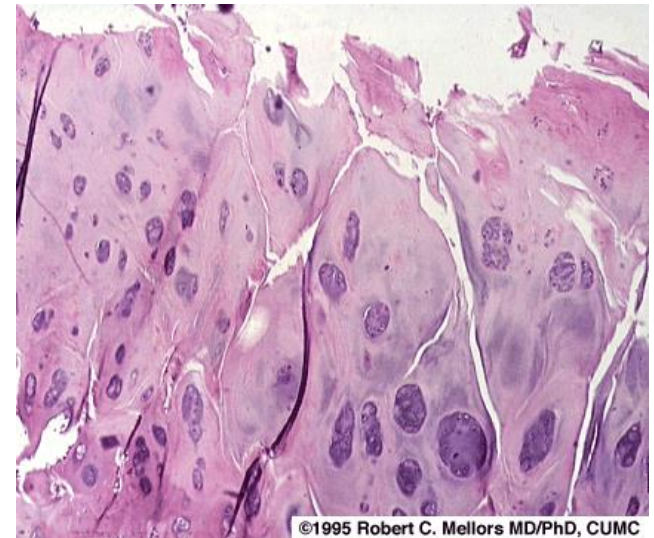
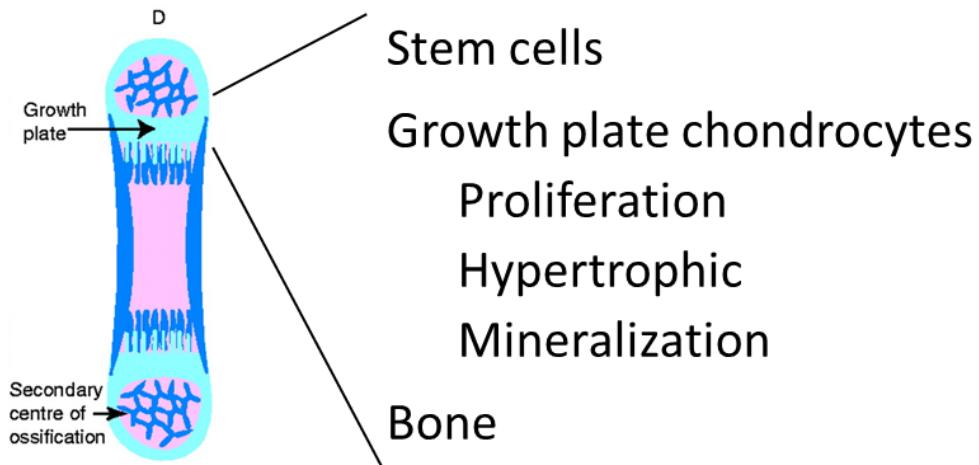


Osteoarthritis
susceptibility



Chondrocytes in OA pathophysiology

- Loss of maturational arrested state and recuperation of growth plate morphology
- Proliferation, while degrading and calcifying the articular cartilage matrix.



OA affected articular cartilage

OA phenotype in articular cartilage; developmental process of endochondral ossification

The recuperation of thyroid signaling in osteoarthritic cartilage?

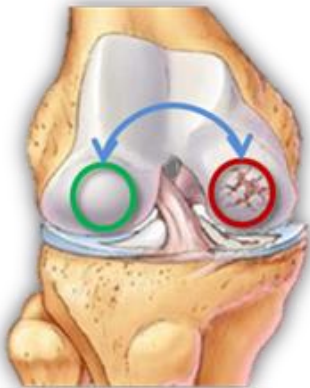
But to do functional studies disease tissue and in vitro cell models are necessary

Research Articular osteoArthritis Cartilage

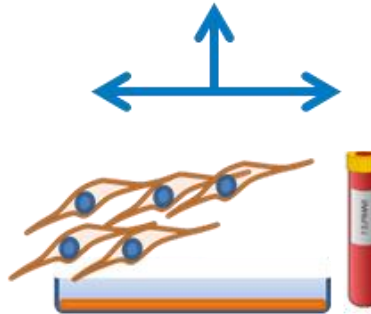
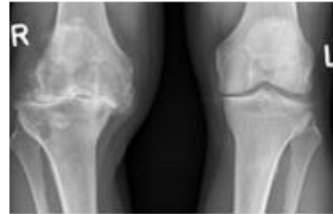
RAAK study (collaboration with Orthopaedics, RGHH Nelissen)

Biobank

N~400



Subtype 1



Subtype 2

Collection of joint tissues of OA patients: **preserved** and **lesioned** cartilage, DNA, RNA, blood and cells (MSCs and primary chondrocytes).

Functional characterization of the DIO2 risk locus

What would be your primary questions?

Gene:

Expression gene/protein is disease relevant tissue

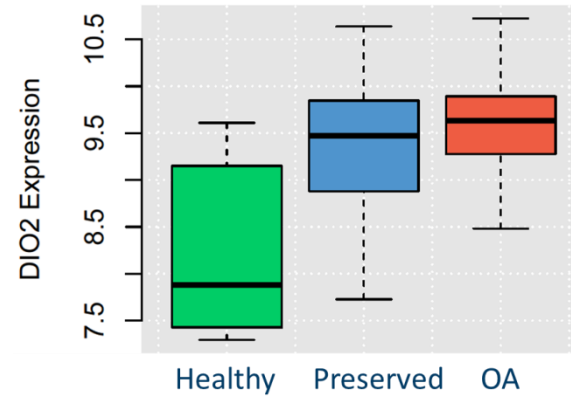
Is the gene responsive to disease process

DIO2 expression in articular cartilage

2010

DIO2 mRNA expression high in OA cartilage compared to healthy

Ijiri et al. 2010



DIO2 protein expression in articular cartilage

2010

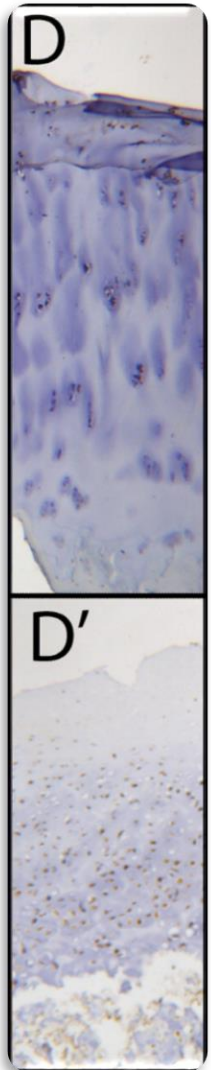
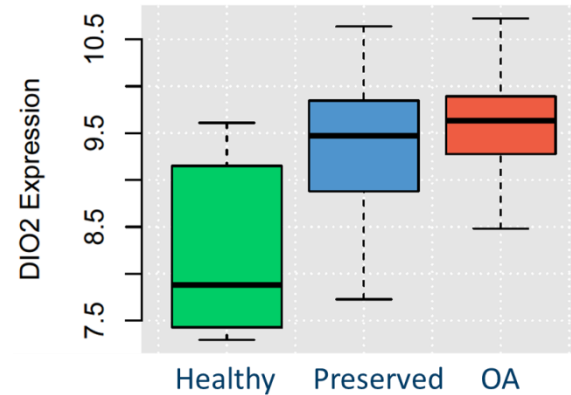
***DIO2 mRNA* expression high in OA cartilage compared to healthy**

Ijiri et al. 2010

2012

DIO2 protein expression up regulated in OA affected cartilage

Bos et al. 2012



What would be your next question?

3. Determined expression levels of nearby genes as a function of genotype at each locus (eQTL).

..in disease relevant tissue!

BOX 1 STRATEGIES TO PROGRESS FROM TAG SNP TO MECHANISM

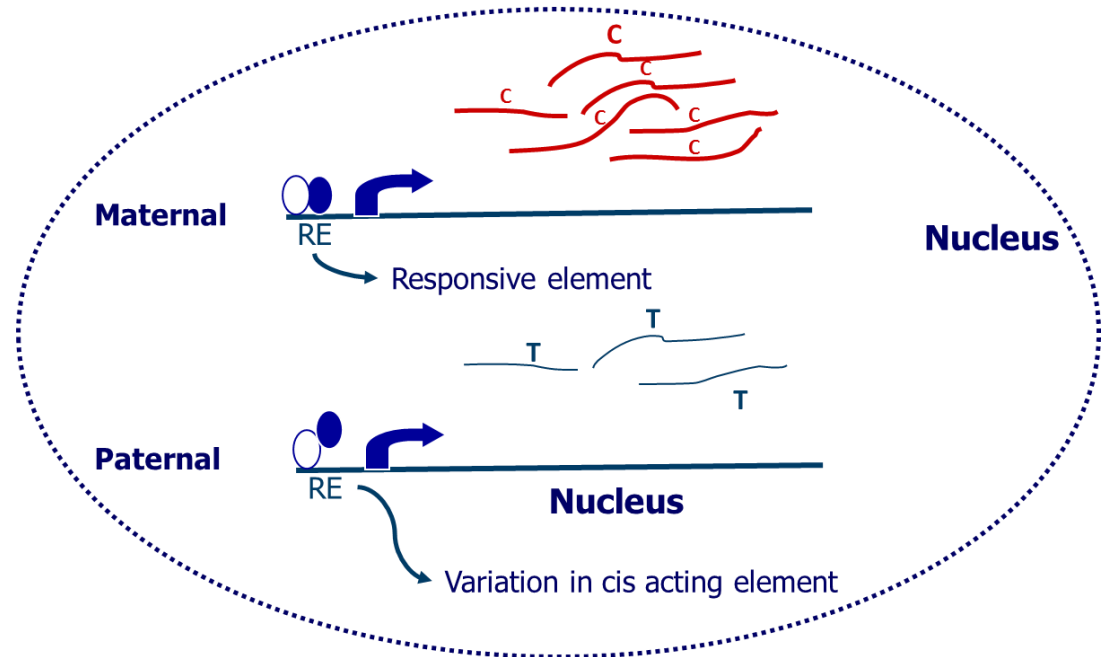
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may be limited by function
methods in rat are promisi
expression analysis.
ii) Use chromatin associat
regulatory regions to deter
(compare with eQTL data)
iii) Targeted gene perturba
iv) Explore fully genome u

Does the SNP affect expression of positional gene?

Test functional relevance of susceptibility SNPs:

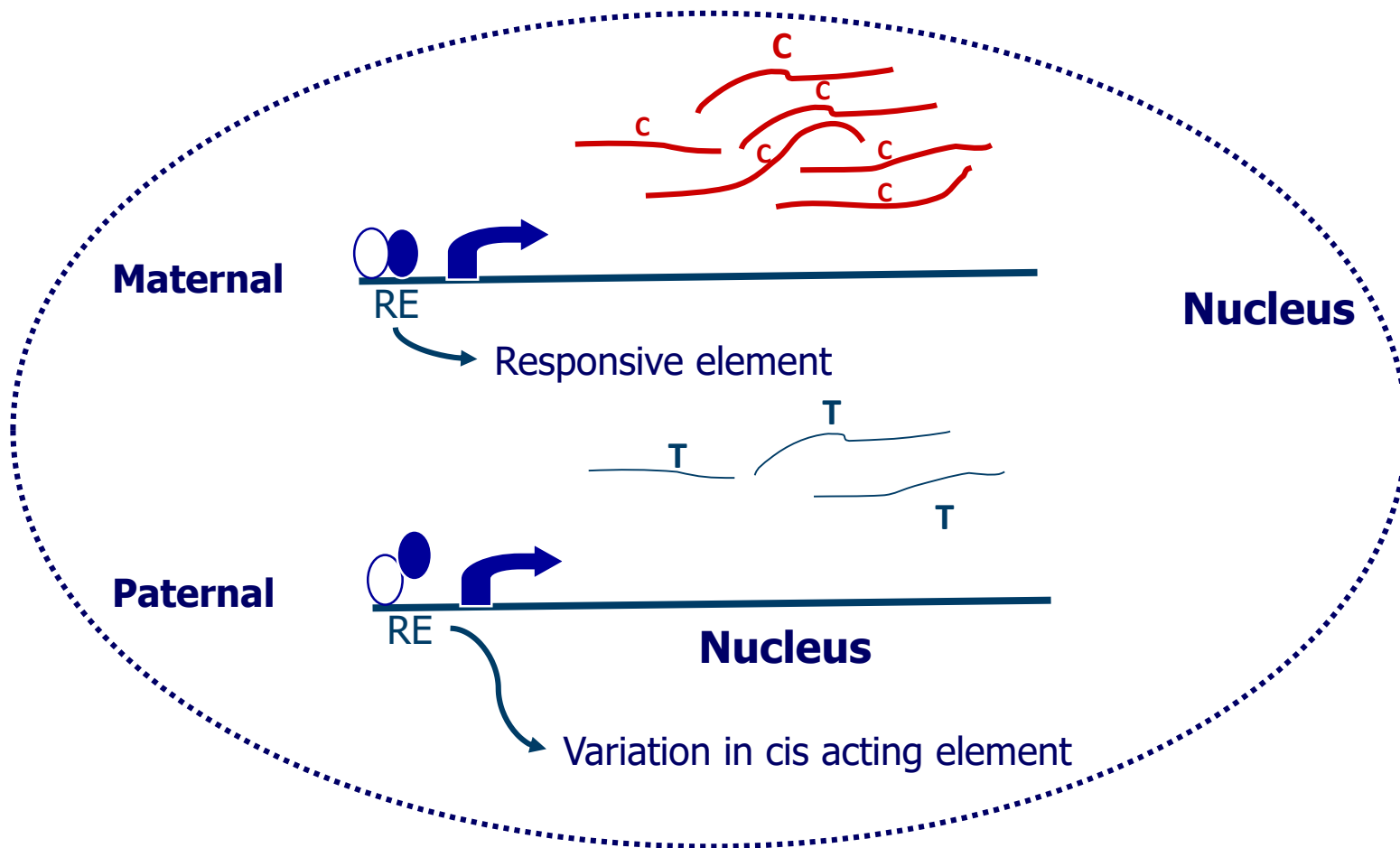
- SNPs in regulatory elements
- Differences in RNA stability
- Epigenetic mechanisms
- Tissues



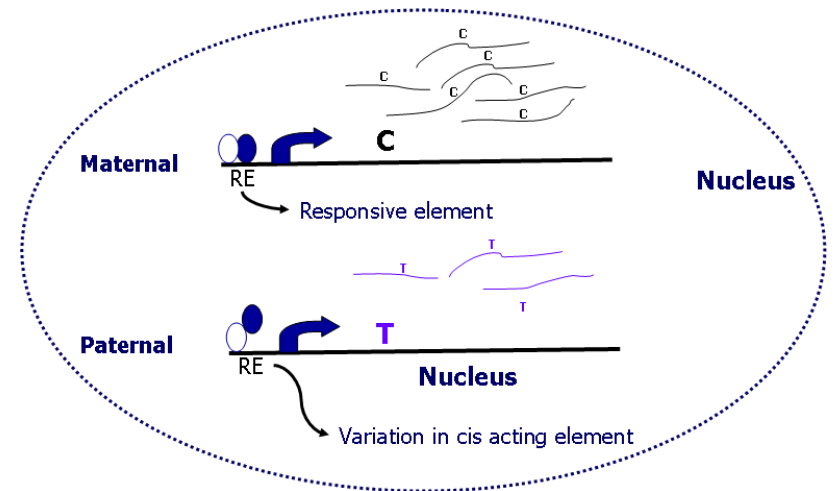
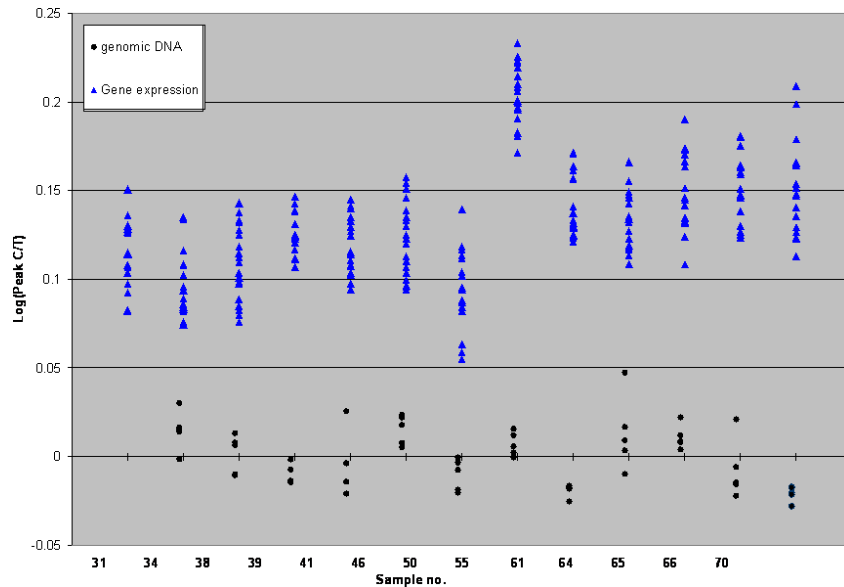
Subtle changes in expression regularly underlie complex diseases.

Differential allelic expression

Genetic variation at *cis*-acting regulator elements



Differential allelic expression DIO2



Significant increased expression of the DIO2 susceptibility allele in OA cartilage

DIO2 in articular cartilage

2010

DIO2 mRNA expression
absent in healthy and
high in OA cartilage

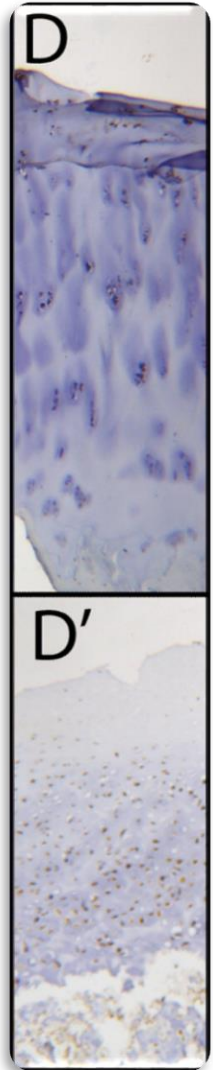
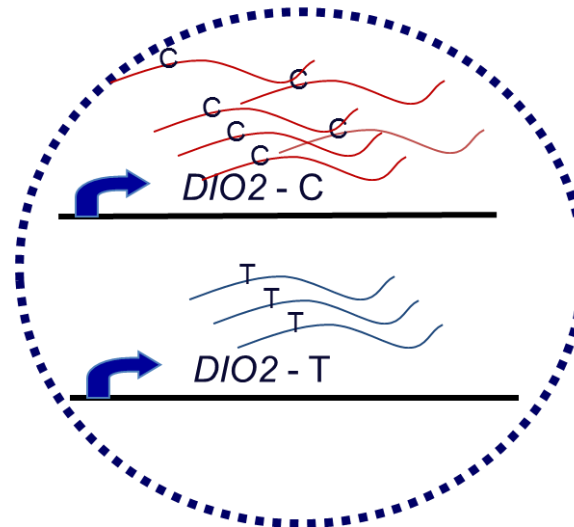
Ijiri et al. 2010

2012

Allelic imbalance &
protein up regulation

Bos et al. 2012

Rs225014 Allelic Imbalance



- Potential relevance DIO2 in OA pathology
- Cis-eQTL function & direction of effect of risk allele

4. Characterized gene regulatory regions by multiple techniques

..in disease relevant tissue!

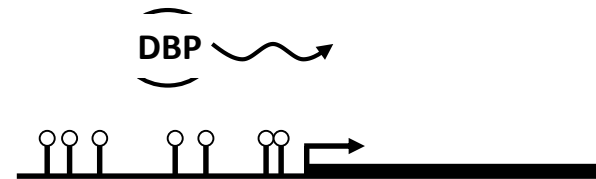
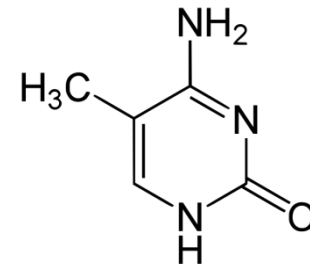
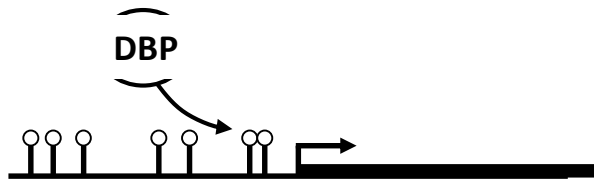
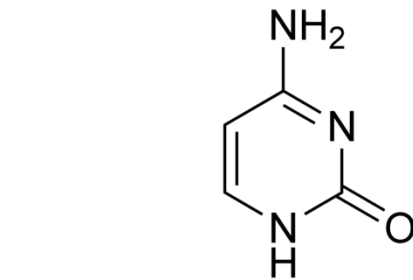
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Epigenetics – DNA methylation

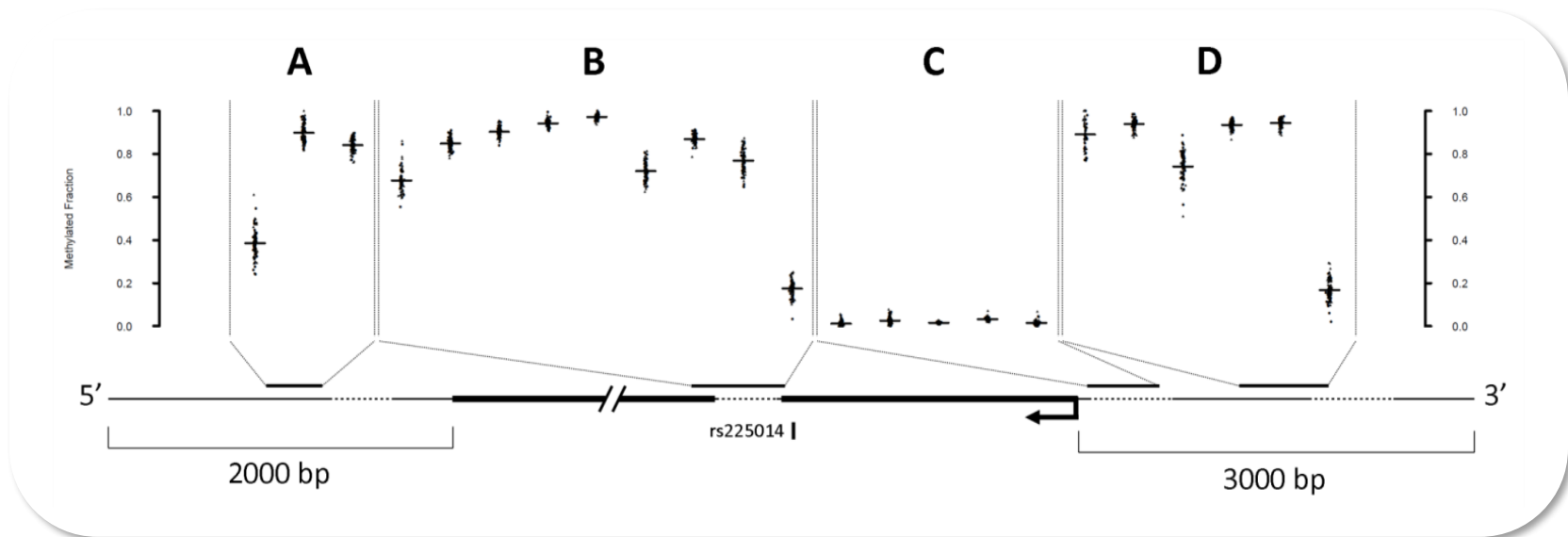
Mechanisms to adapt to environmental changes such as mechanical stress, disease and age.

- **miRNAs**
- **Histon modifications**
- **DNA methylation**
- ...



Regulation of *DIO2* expression

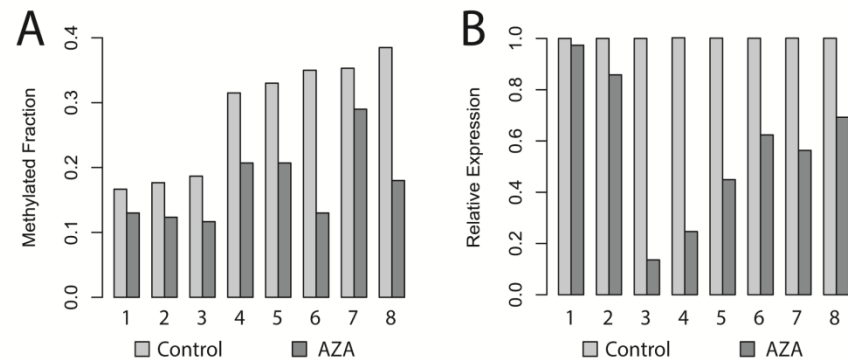
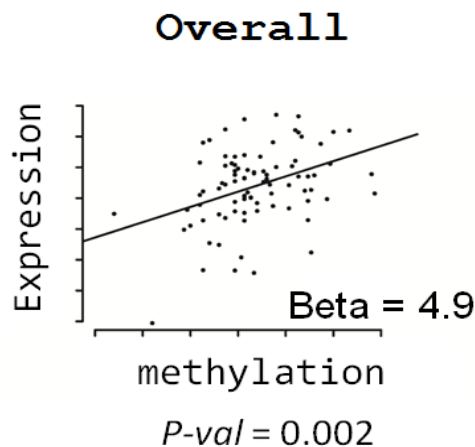
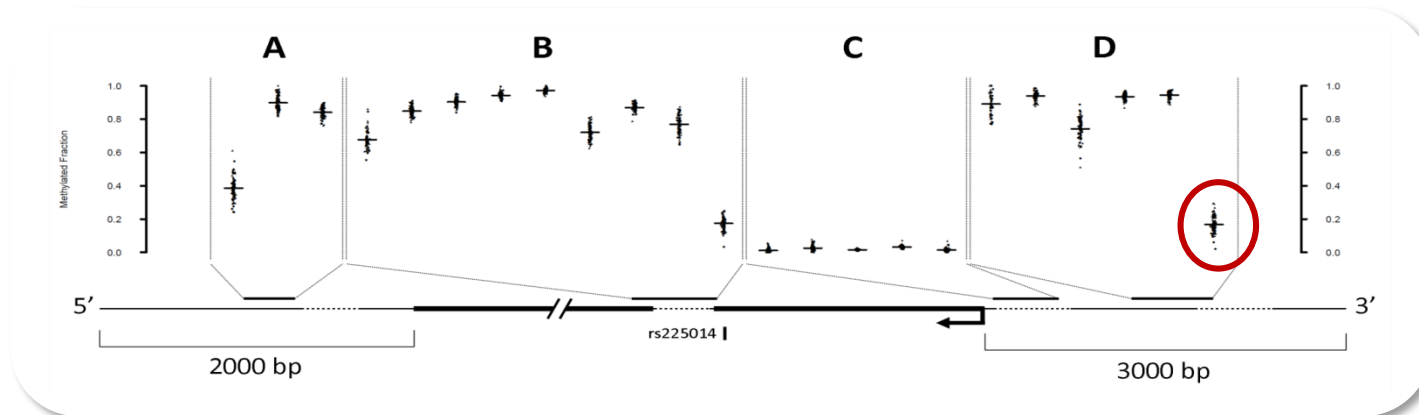
Gene targeted methylation at CpG sites (Epityper, Sequenom)



N. Bomer, W den Hollander and YFM Ramos et al. ARD 2015

Regulation of *DIO2* expression

Gene targeted methylation at CpG sites (Epityper, Sequenom)



***DIO2* expression in articular cartilage is modulated by methylation at CpG ~-2000 bp**

Which next step in the Freedman et al strategy?

- 4. Characterized gene regulatory regions by multiple techniques**
- 7. Explore epigenetic mechanisms in the context of genome wide genetic polymorphisms**

..in disease relevant tissue!

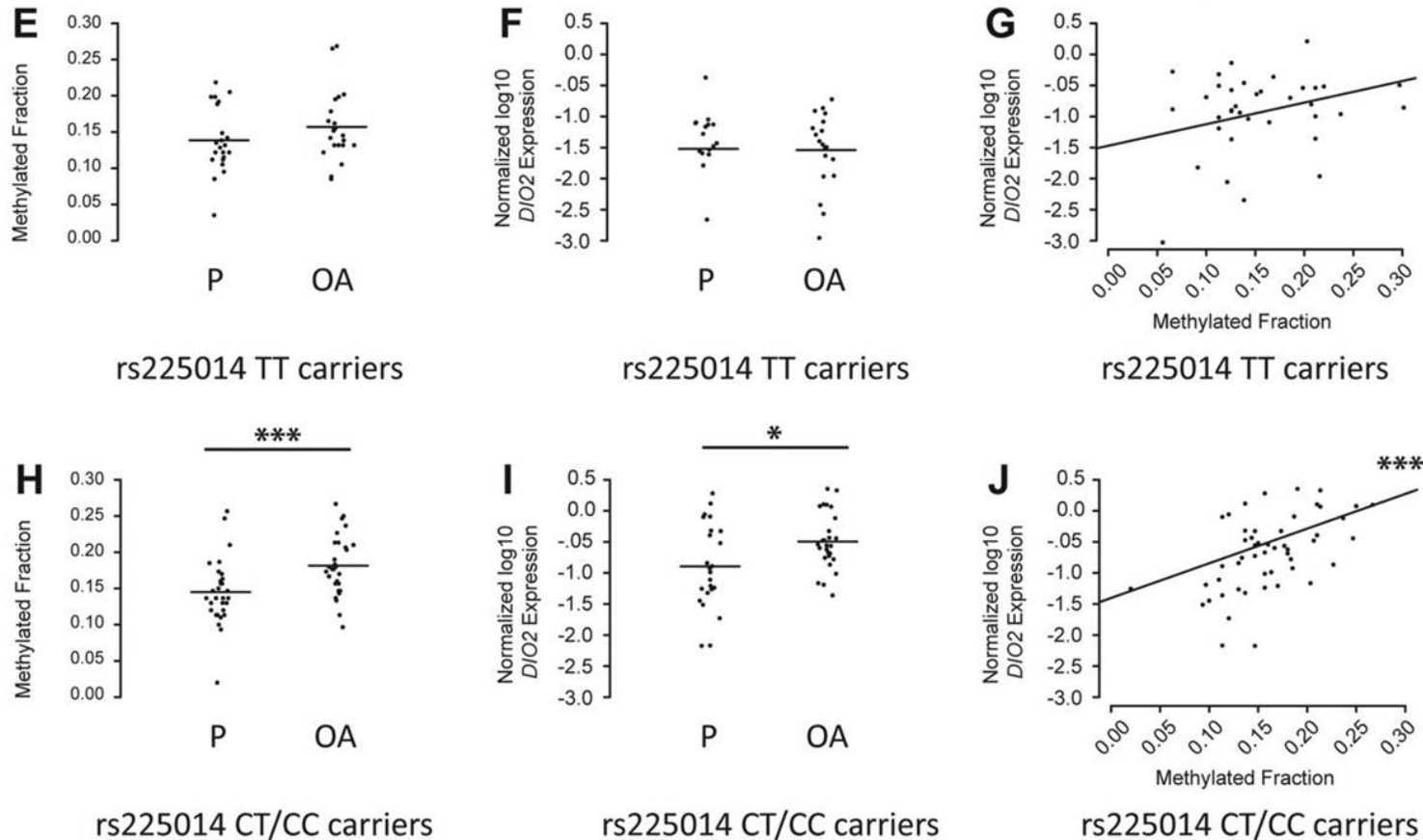
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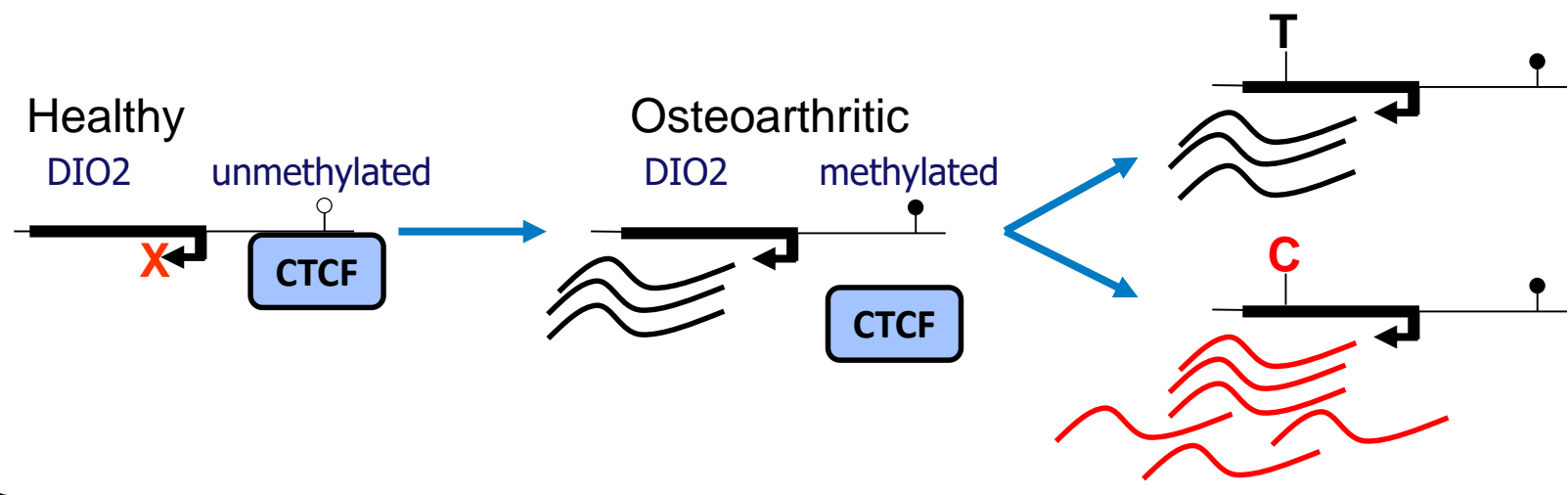
Does the *DIO2* rs255014 modulates the effect?

Regulation of *DIO2* expression

Gene targeted methylation at CpG sites (Epityper, Sequenom)



***DIO2* expression is more sensitive to methylation changes in rs225014 risk allele carriers.**



Which step in the Freedman et al strategy?

8. Employ (*in vitro*) cell models and tissue reconstructions to evaluate mechanisms using gene perturbations and polymorphic variants.

..in human tissue!

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- 5) Combine regulatory regions with risk loci using coordinates from multiple reference genomes to capture all variation within the shorter regulatory regions that correlates with the tag SNP at each locus.
- 6) Multiple experimental manipulations in model systems are needed to progressively implicate transcription units (genes) in mechanisms relevant to the associated loci:
 - i) Knockouts of regulatory regions in animal (difficult and may be limited by functional redundancy, but new targeting methods in rat are promising) models followed by genome-wide expression analysis.
 - ii) Use chromatin association methods (3C, CHIA-PET) of regulatory regions to determine the identity of target genes (compare with eQTL data).
 - iii) Targeted gene perturbations in somatic cell models.
 - iv) Explore fully genome-wide eQTL and miRNA quantitative variation correlation in relevant tissues and cells.
- 7) Explore epigenetic mechanisms in the context of genome-wide genetic polymorphism.
- 8) Employ cell models and tissue reconstructions to evaluate mechanisms using gene perturbations and polymorphic variants. The human cancer cell xenograft has re-emerged as a minimal *in vivo* validation of these models.
- 9) Above all, resist the temptation to equate any partial functional evidence as sufficient. Published claims of functional relevance should be fully evaluated using the steps detailed above.

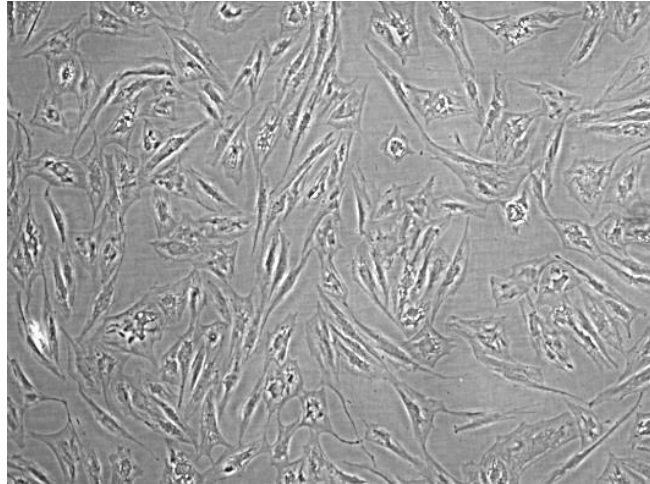
Human 3D *in vitro* model of cartilage

What is direct effect of DIO2 upregulation?

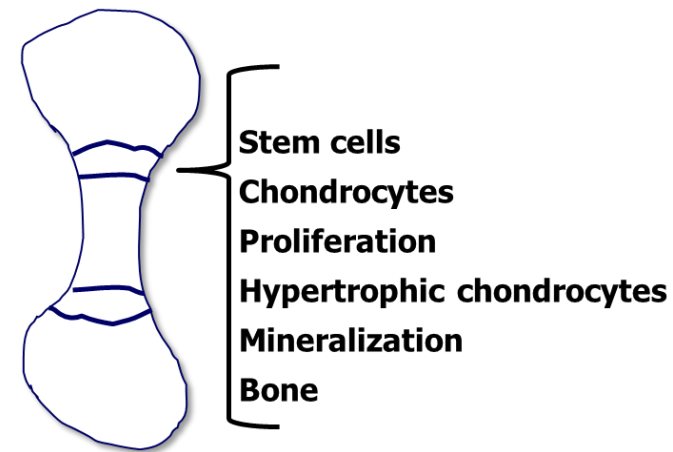
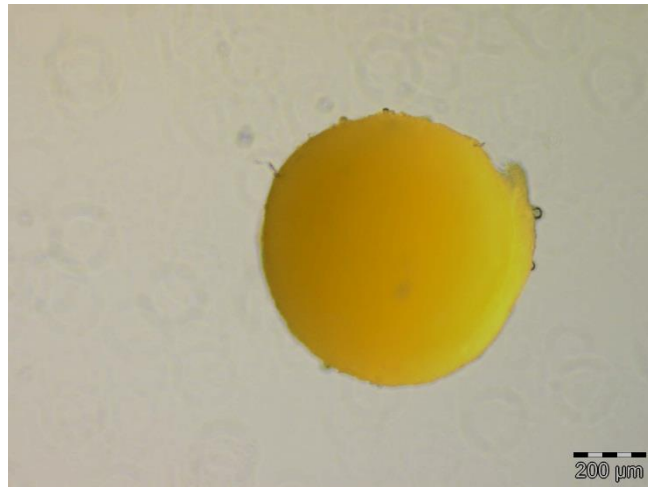
Human *in vitro* chondrogenesis model

Stemcells, primary chondrocytes

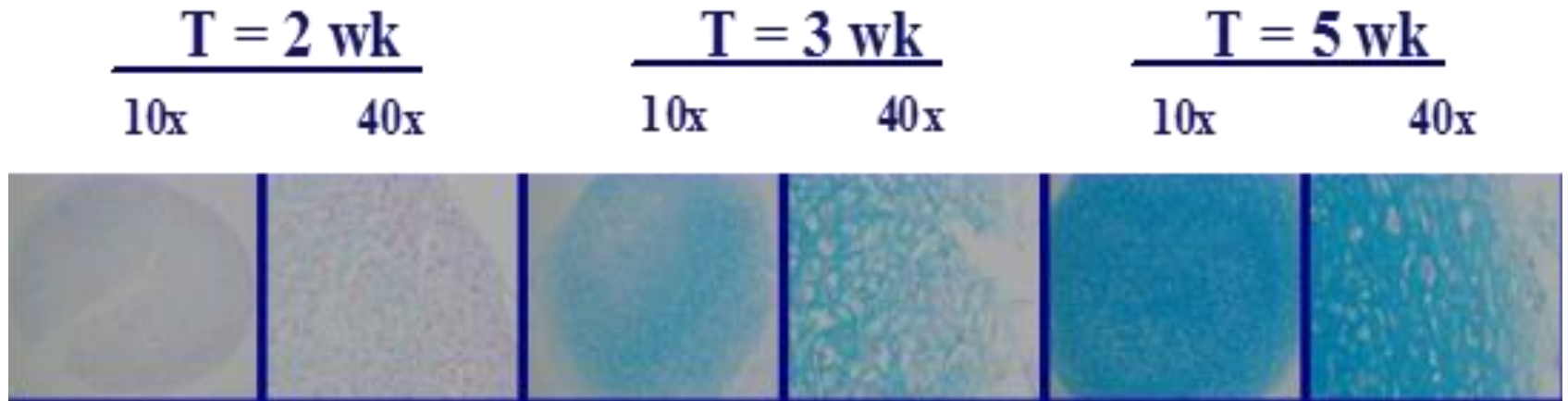
Growing cells
(monolayer)



Chondrocyte pellet
cartilage formation



In vitro chondrogenesis model Stemcells, primary chondrocytes

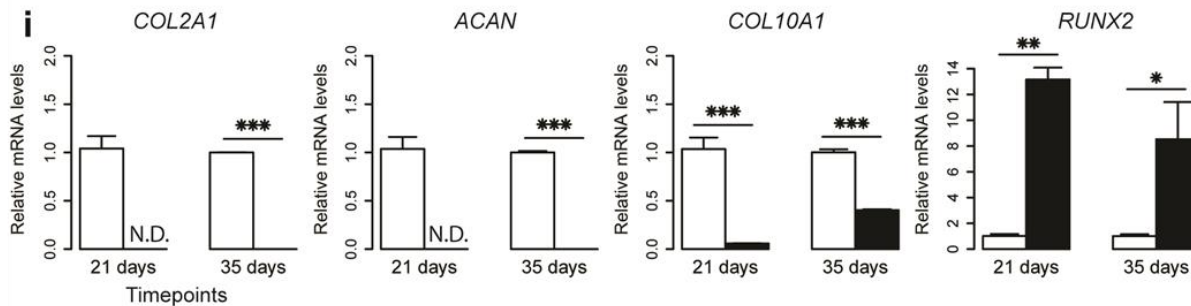
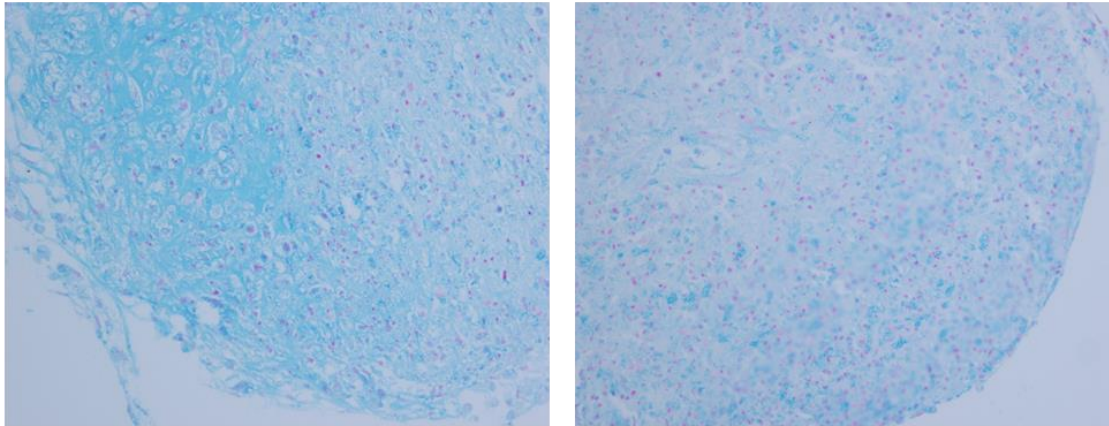


In vitro chondrogenesis model using human bone marrow derived mesenchymal stem cells. Alcian blue staining

What is direct effect of DIO2 upregulation on cartilage integrity?

BM-MSC based *in vitro* chondrogenesis model

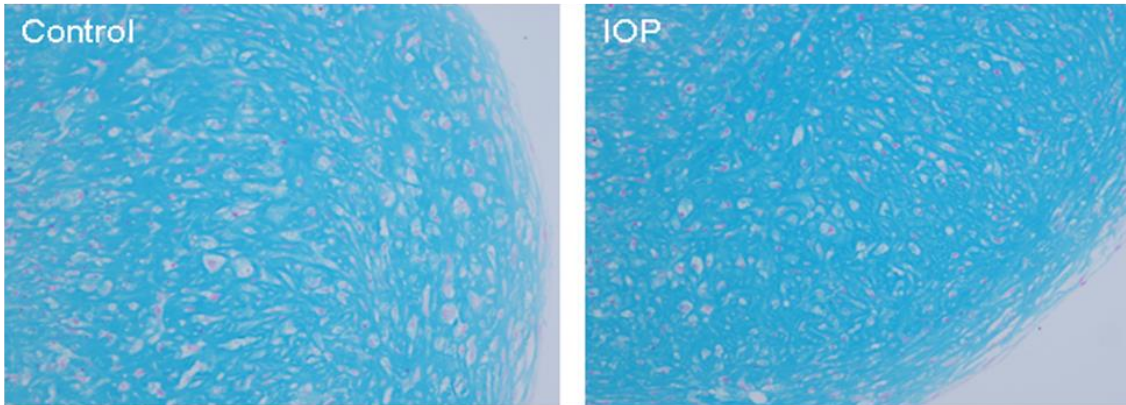
Overexpression of DIO2



Direct detrimental effect of DIO2 on cartilage matrix deposition
Destruction without early hypertrophy (COLX)

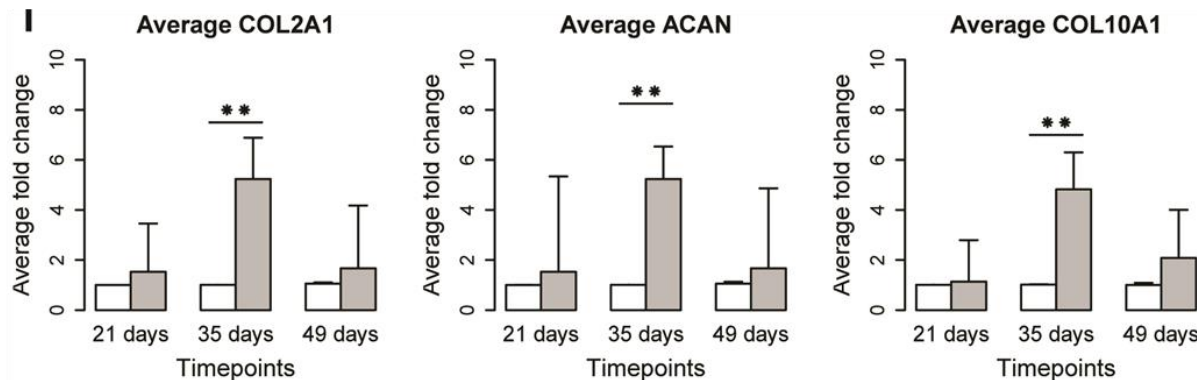
BM-MSK based *in vitro* chondrogenesis model

Inhibition of DIO2 function



IOP = Iopanoic acid, an oral cholecystographic agent, an effective inhibitor of iodothyronine deiodinase and medication for thyrotoxicosis.

Tyer et al. Endocr Pract. 2014 20 (10):1084-1092



Beneficial effect of DIO2 on cartilage matrix deposition
Early hypertrophy (COLX), no destruction

N. Bomer, W den Hollander and YFM Ramos et al. ARD 2015

Conclusions human *in vitro* studies DIO2

Direct detrimental effect of DIO2 on cartilage matrix deposition .

Beneficial effect of DIO2 on cartilage matrix deposition

What about *in vivo* studies?

6. Multiple experimental manipulations in model systems are needed to progressively implicate transcription units (genes) in mechanisms relevant to the associated loci

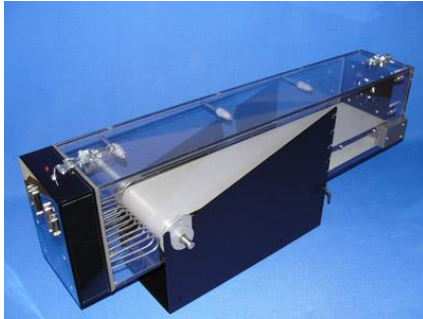
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DIO2 Knock-Out model

Collaboration KU Leuven, Leuven, Belgium

Design: Running induced mechanical stress



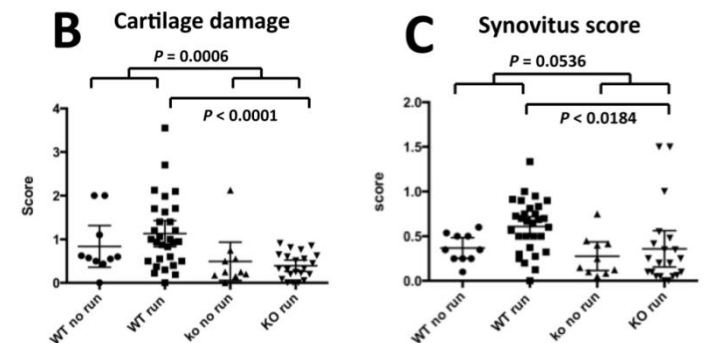
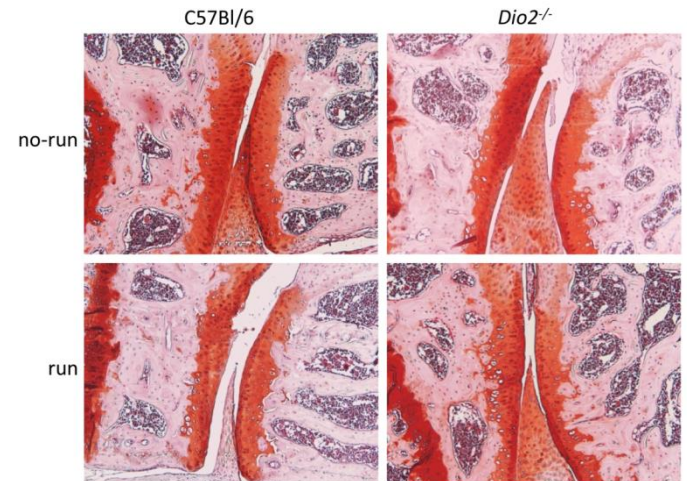
DIO2-KO & Control
(C57BL/6 males)



For 3 weeks -> 5 days/week -> 60 min/day
(60min at 11m/min, 5 incline)



Induce cartilage damage

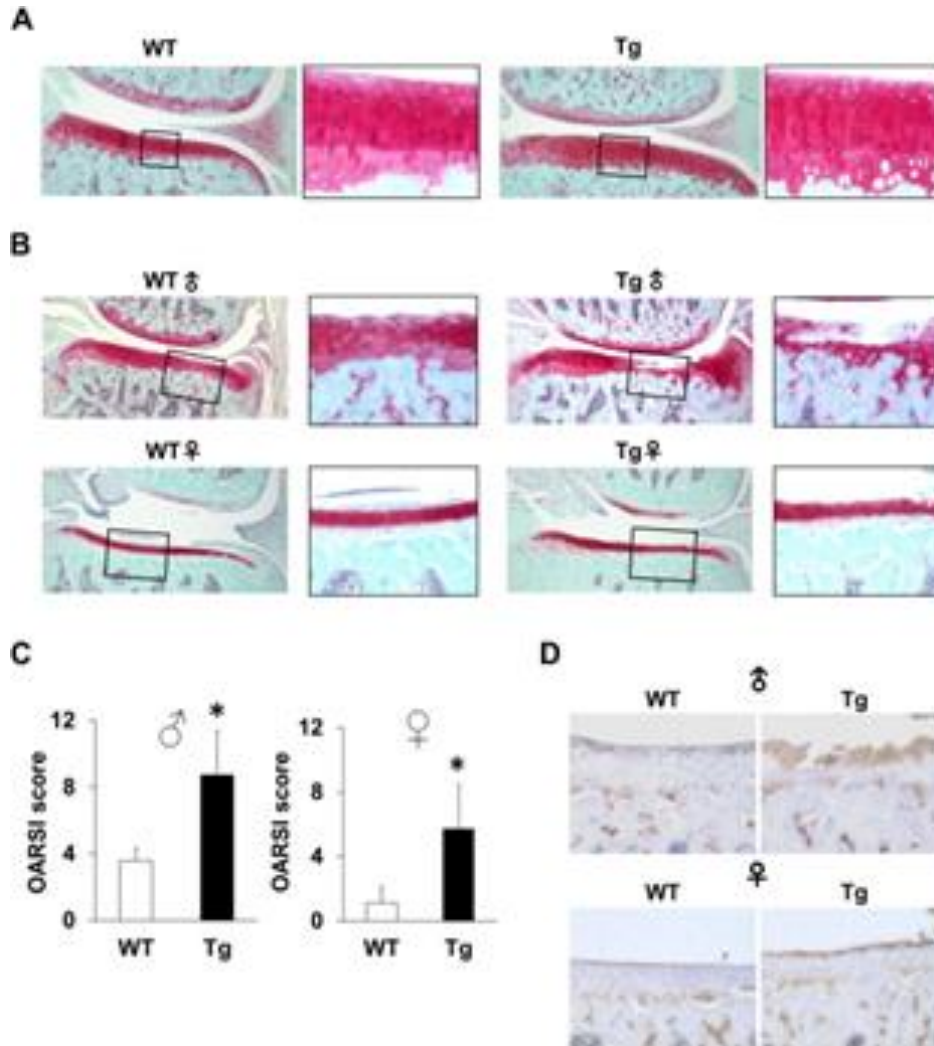


**Dio2-/- mice protected against cartilage damage
only upon exercise-induced OA**

Bomer et al. Ann Rheum Dis. (2015)

2015

Tissue specific induction *DIO2* in rats



**Destruction of cartilage only
upon applying OA model**

Nagase et al. Ann Rheum Dis 2013

2013

Conclusions *in vitro animal* studies DIO2

**Tissue specific upregulation of *DIO2* in rat cartilage
Prone to OA after applying OA model**

**DIO2 knock out mice protected against cartilage damage
only upon exercise-induced OA**

BOX 1 STRATEGIES TO PROGRESS FROM TAG SNP TO MECHANISM

- 1) Target resequencing efforts using linkage disequilibrium (LD) structure.
- 2) Use other populations to refine LD regions (for example African ancestry with shorter LD and more heterogeneity).
- 3) Determine expression levels of nearby genes as a function of genotype at each locus (eQTL).
- 4) Characterize gene regulatory regions by multiple empirical techniques bearing in mind that these are tissue and context specific.
- 5) Combine regulatory regions with risk loci using coordinates from multiple reference genomes to capture all variation within the shorter regulatory regions that correlates with the tag SNP at each locus.
- 6) Multiple experimental manipulations in model systems are needed to progressively implicate transcription units (genes) in mechanisms relevant to the associated loci:
 - i) Knockouts of regulatory regions in animal (difficult and may be limited by functional redundancy, but new targeting methods in rat are promising) models followed by genome-wide expression analysis.
 - ii) Use chromatin association methods (3C, CHIA-PET) of regulatory regions to determine the identity of target genes (compare with eQTL data).
 - iii) Targeted gene perturbations in somatic cell models.
 - iv) Explore fully genome-wide eQTL and miRNA quantitative variation correlation in relevant tissues and cells.
- 7) Explore epigenetic mechanisms in the context of genome-wide genetic polymorphism.
- 8) Employ cell models and tissue reconstructions to evaluate mechanisms using gene perturbations and polymorphic variants. The human cancer cell xenograft has re-emerged as a minimal *in vivo* validation of these models.
- 9) Above all, resist the temptation to equate any partial functional evidence as sufficient. Published claims of functional relevance should be fully evaluated using the steps detailed above.

Pharmacological attenuation of thyroid hormone signaling; An evidence-based treatment option for Osteoarthritis



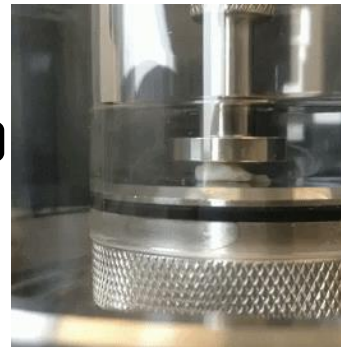
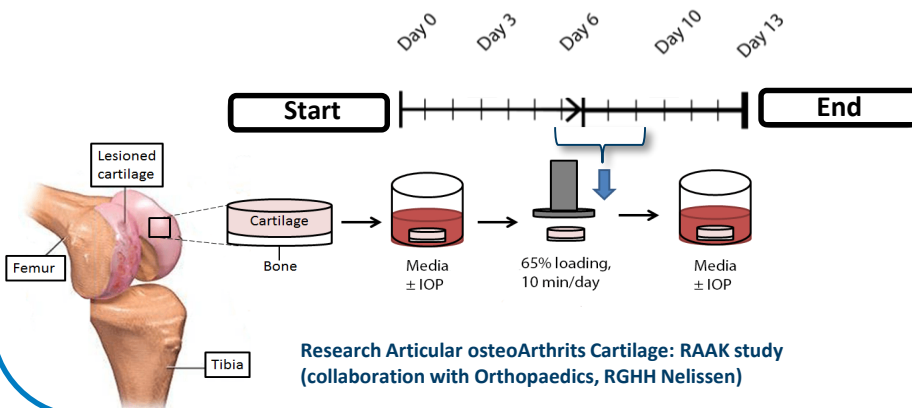
The human explant model



DutchArthritisSociety
ReumaNederland



Pre-clinical human *ex vivo* osteochondral explant model



Readout of model:

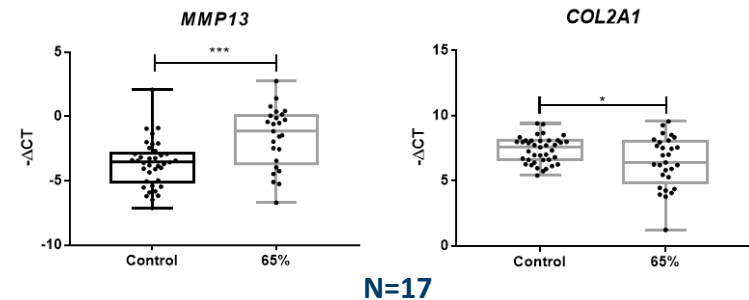
- Gene expression
- Sulphated GAG loss
- Cartilage structure
- Mechanical properties

Model optimization – mechanical loading

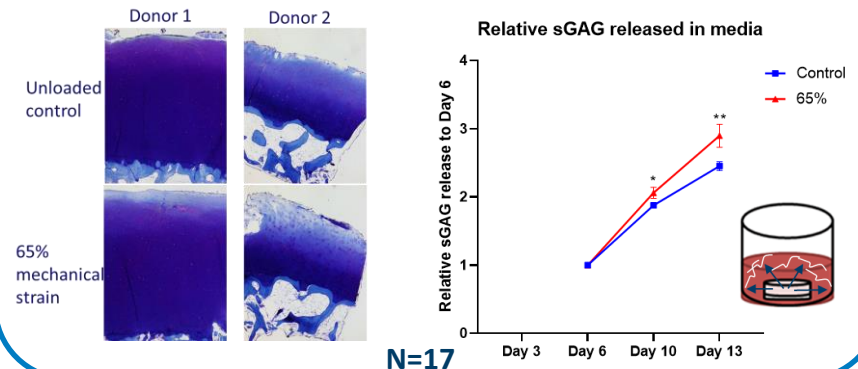
Mechanical stress induces detrimental changes to the cartilage:

- Increased detrimental gene expression (*MMP13*)
- Reduced matrix producing gene expression (*COL2A1*)
- Increased loss of matrix (sGAG) from cartilage

Gene expression

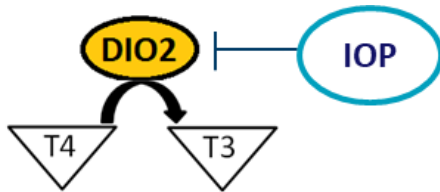


Matrix loss

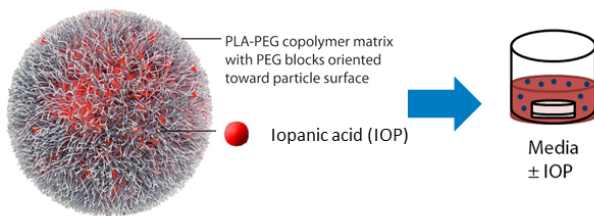


Model optimization – drug delivery

Inhibition of DIO2



Nanoparticles for delivery of IOP



(In collaboration with
Radiology (TNI), dr. L. Cruz)

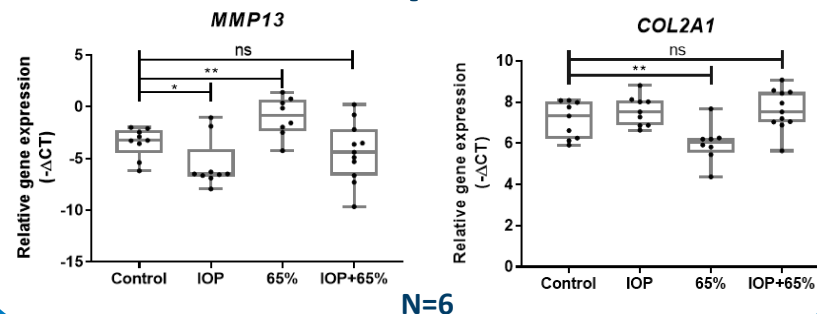
Does inhibition of thyroid signaling
prevent mechanical induced
detrimental changes?

Can IOP inhibit mechanical induced damage?

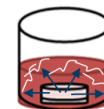
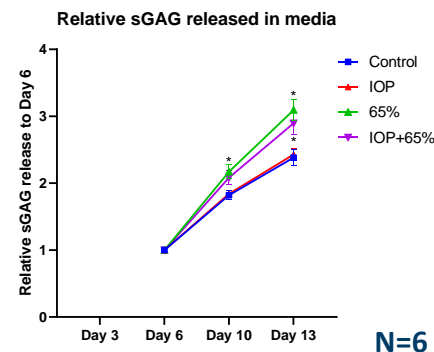
Inhibition of thyroid signaling (IOP) alleviated these detrimental changes to the cartilage

Nanoparticles containing IOP show similar results on gene expression

Gene expression

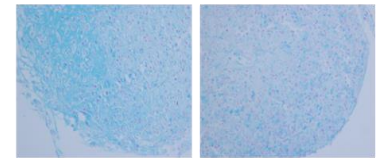
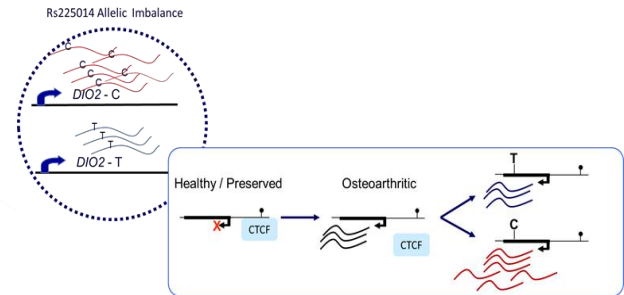


Matrix loss

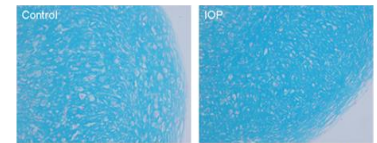


In summary

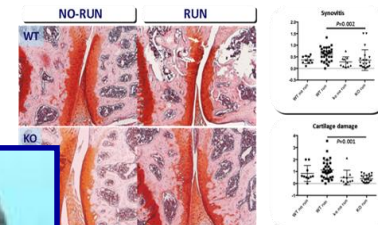
- Risk allele modulates epigenetically regulated transcription of *DIO2* in articular cartilage
- *DIO2* up-regulation affects propensity of chondrocytes to undergo terminal maturation.
- Attenuating thyroid signaling may be a key factor in securing joint tissue homeostasis and a likely druggable target



Direct detrimental effect of *DIO2* on cartilage matrix deposition & maintenance



Direct beneficial effect of *DIO2* on cartilage matrix deposition and maintenance





Osteoarthritis research group