

# **PROTEOMIC ANALYSIS OF CARDIAC EXTRACELLULAR MATRIX IN A PORCINE MODEL OF ISCHEMIA-REPERFUSION INJURY**

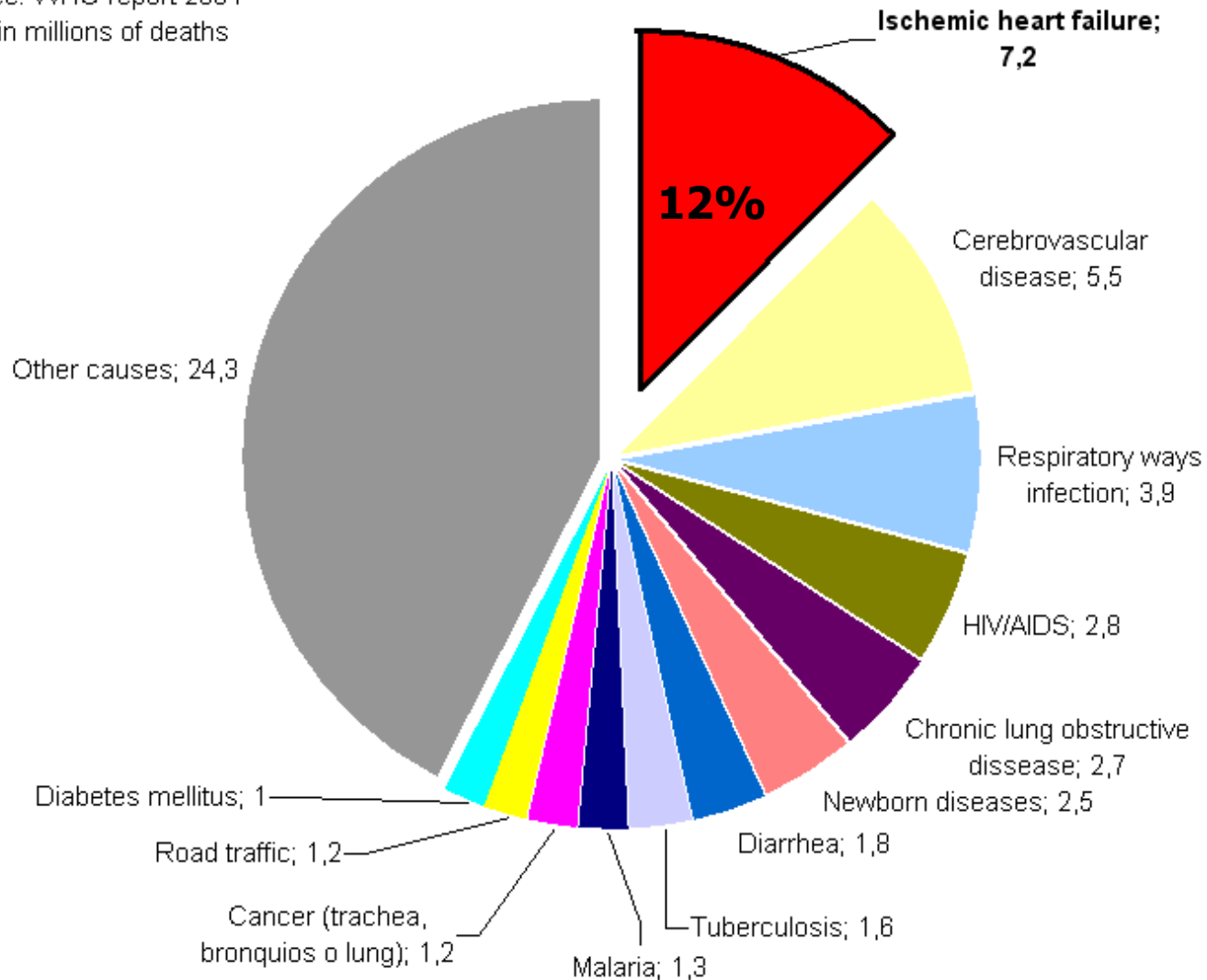
New roles for known proteins?

Javier Barallobre-Barreiro

**Major death causes in 2004**

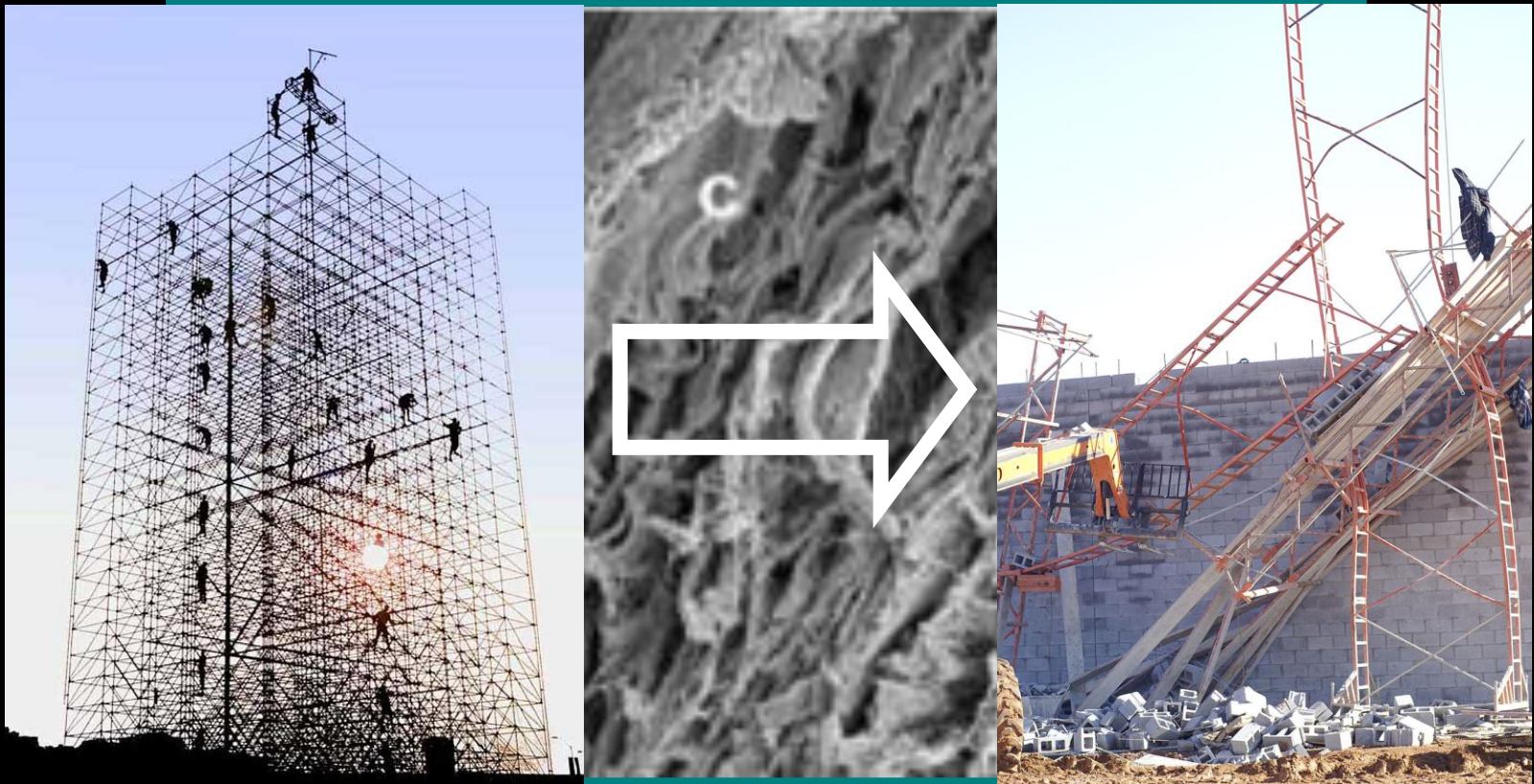
Source: WHO report 2004

Data in millions of deaths



Heart is composed of **70% non-myocytes** and only 30% myocytes  
but

most of the **studies have focused on myocytes**  
with little emphasis on the other cell types and structures.



- **Scaffold** for the myocyte and nonmyocyte cells
- Surrounds and **interconnects** cellular structures
- **Distributes mechanical forces**
- **Transmits mechanical signals** to cells via surface ECM receptors
- **Fluid movement** in the extracellular environment

## Proteoglycans & glycoproteins

Signaling and turnover of the ECM itself.  
Can bind factors that contribute to the concentration of inflammatory components forming chronic inflammation.

## Interstitial collagens

The density of the ECM affects compliance, movement of cells and fluid within, availability of cell receptors and substrates and retention of ECM components, such as proteoglycans.

## Proteases

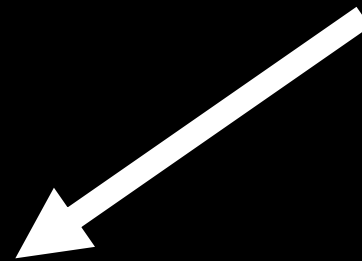
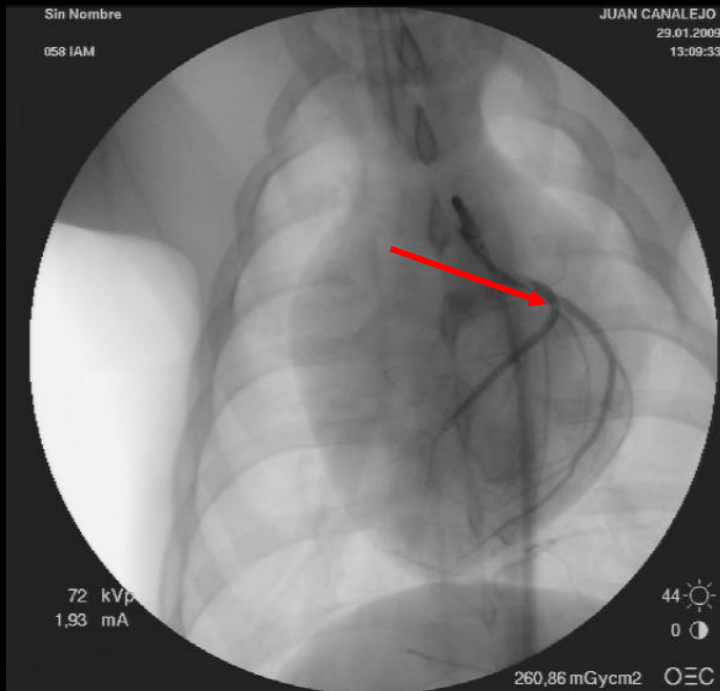
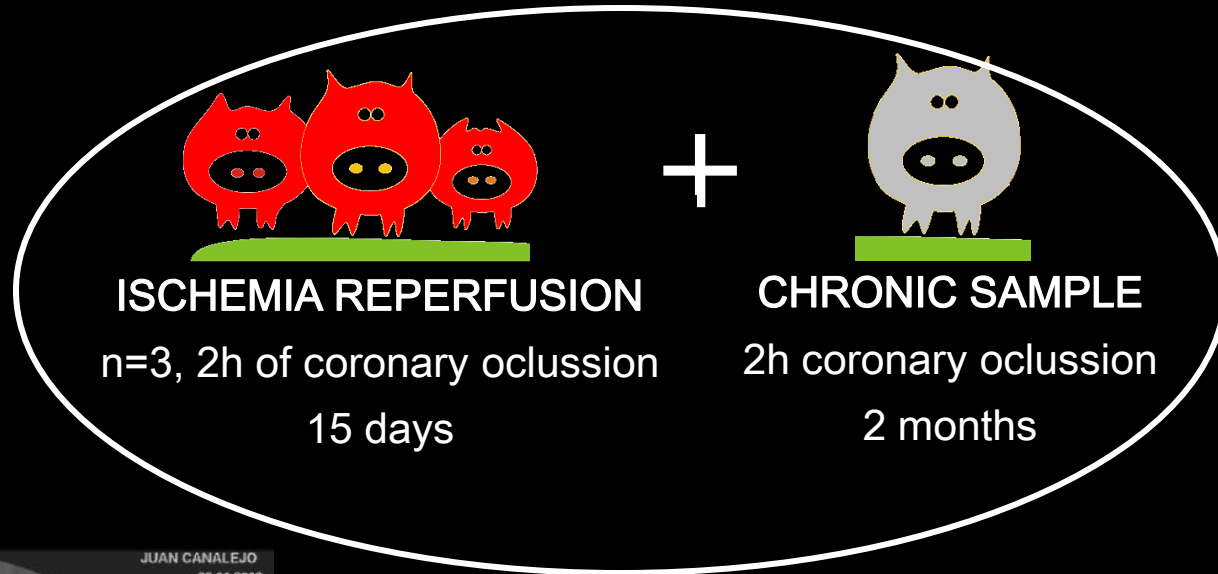
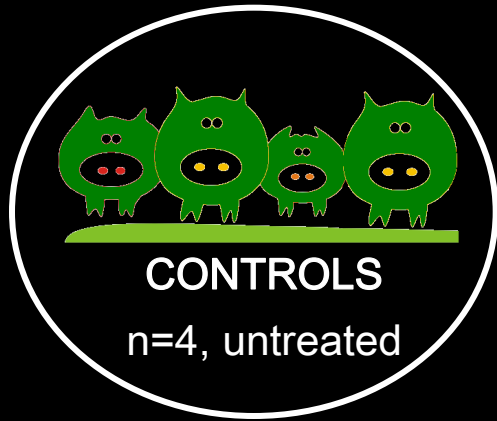
Part of a biochemical cascade within the ECM. Essential for turnover of ECM components, activation of latent factors, and remodeling.

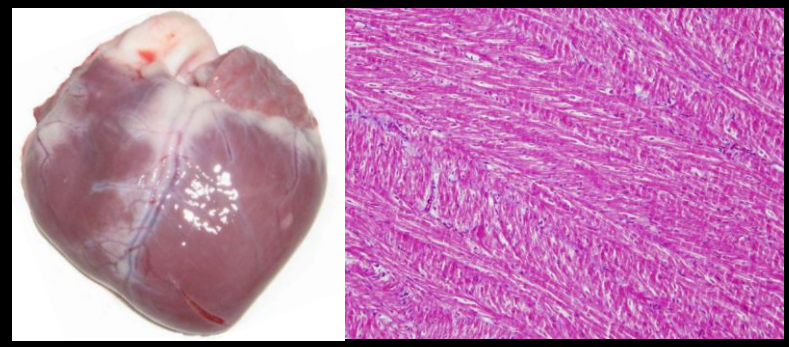
## Cytokines

TGF-beta. Regulation of cell proliferation, migration, differentiation, apoptosis, and ECM production. Central role in fibrosis. Stimulates production of collagen while inhibiting its degradation.

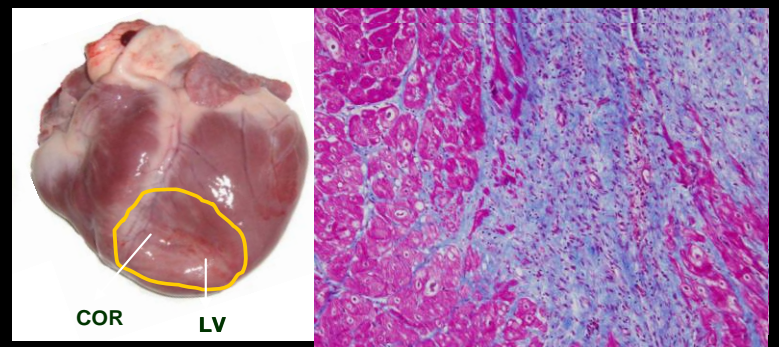
## Growth factors

Role in normal and pathological growth and so, in ECM changes



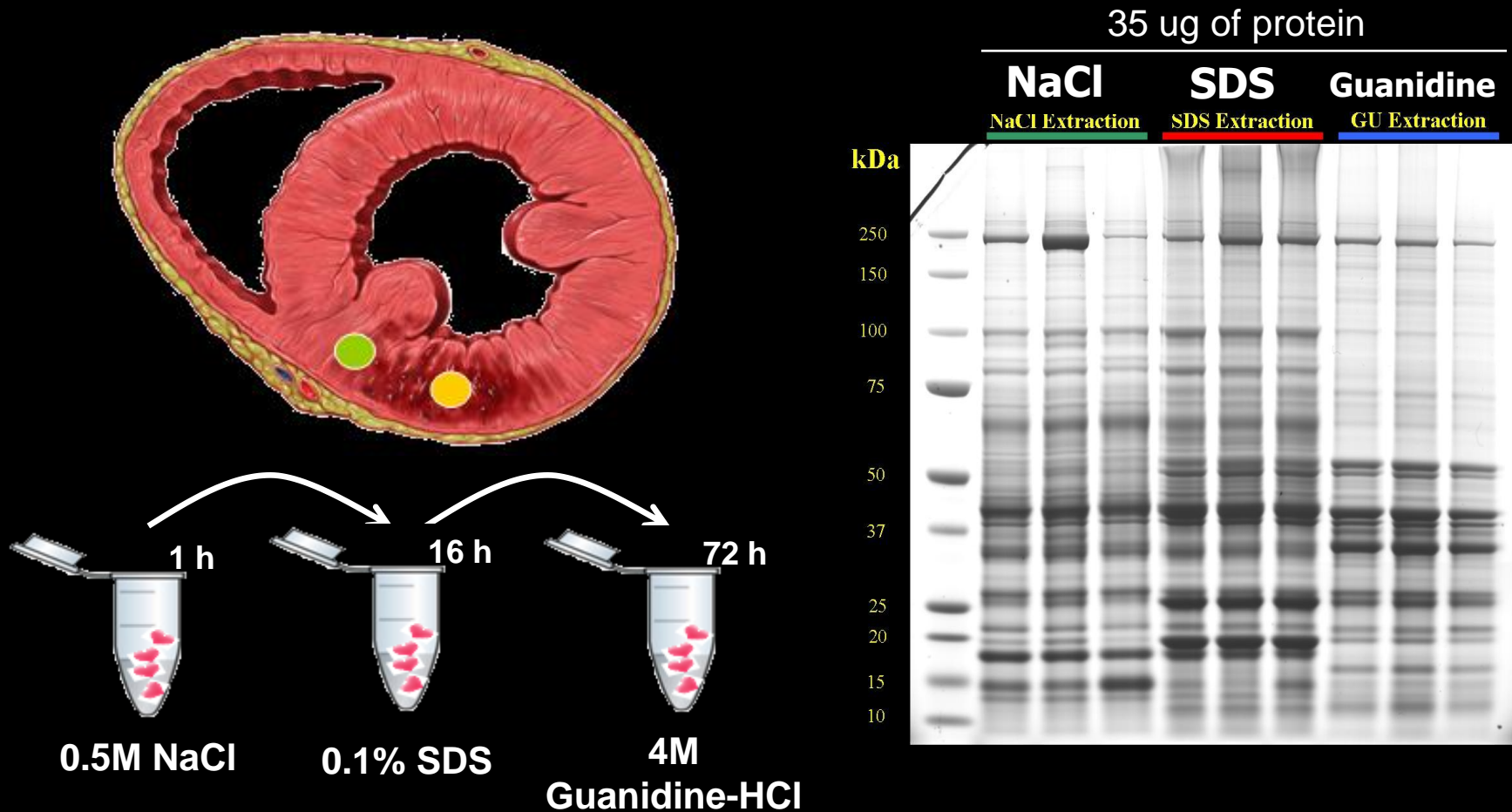


Control

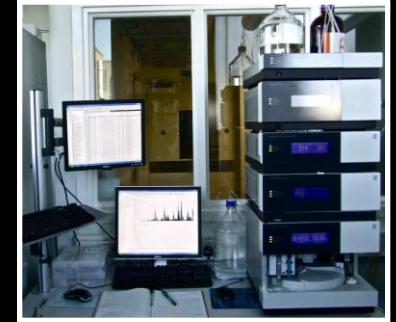


15 days after ischemia-reperfusion

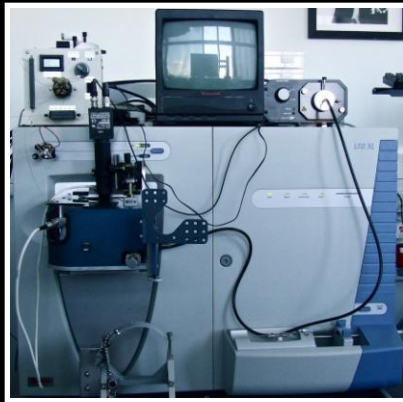
Didangelos A, Yin X, Mandal K, Baumert M, Jahangiri M, Mayr M. *Proteomic characterization of extracellular space components in the human aorta.* MCP in Press. June 15, 2010.



Silver stain → Digestion (trypsin) → Peptide separation



Dionex Ultimate 3000 HPLC



LQT Orbitrap XL

Hybrid  
Pig / Human  
DB

→ X! Tandem

→ SeQuest



Rank	Protein Name	Probability	Score	Length	Charge	Mass	Modifications	Peptide Count	Protein Count
1	Protein A	100%	100	100	100	100	100	100	100
2	Protein B	95%	95	95	95	95	95	95	95
3	Protein C	90%	90	90	90	90	90	90	90
4	Protein D	85%	85	85	85	85	85	85	85
5	Protein E	80%	80	80	80	80	80	80	80

[ Spectral count ]



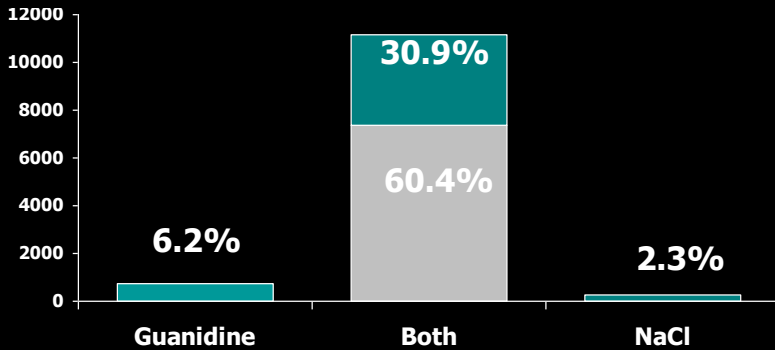
## Proteoglycans (60)



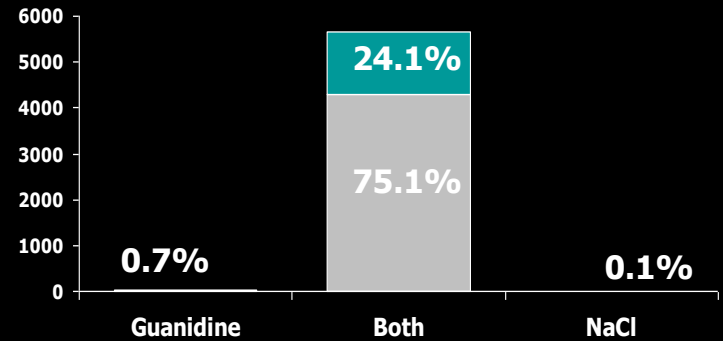
## Collagens (28)



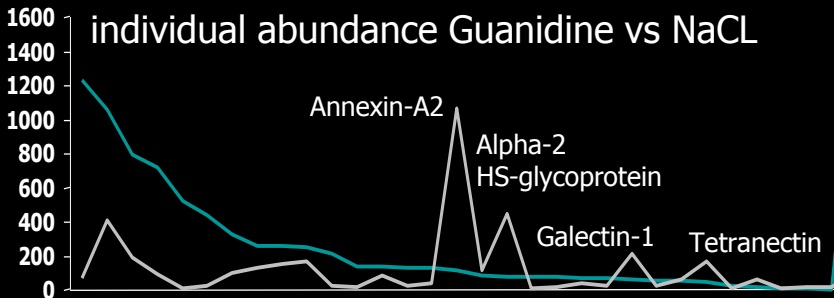
### Proteoglycans: spectra distribution



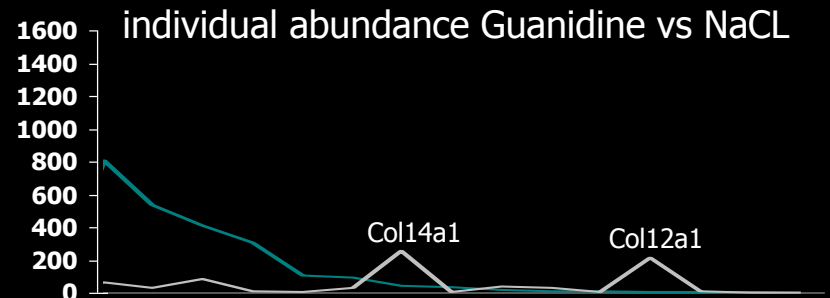
### Collagens: spectra distribution



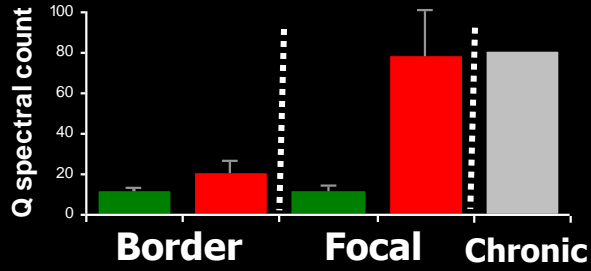
### Proteoglycans:



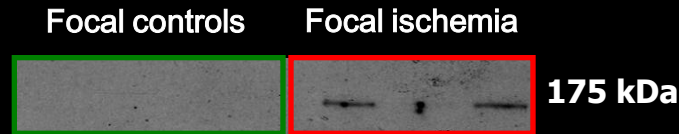
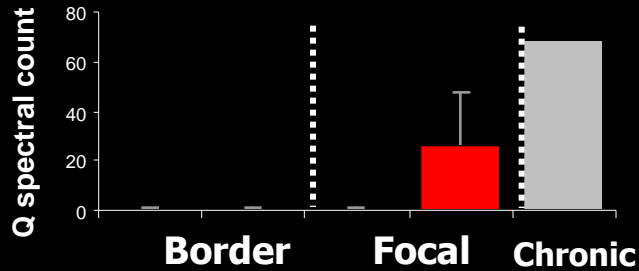
### Collagens:



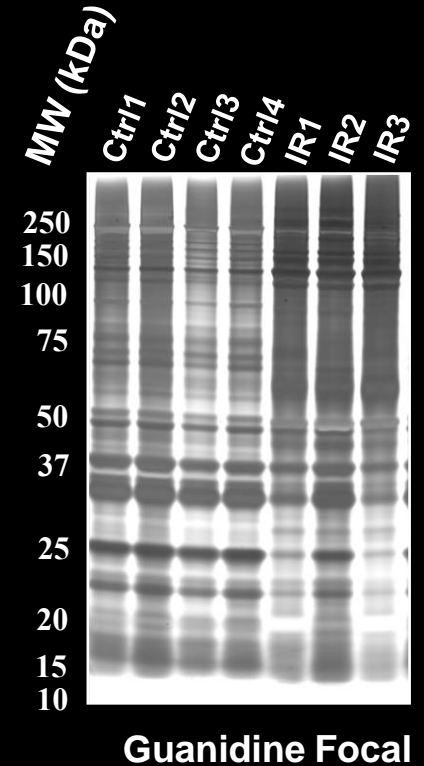
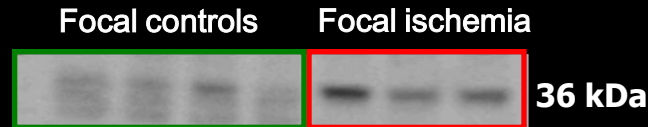
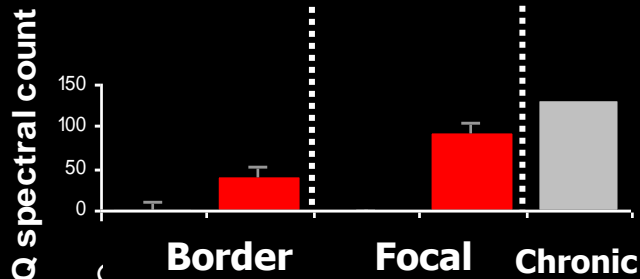
## DERMATOPONTIN

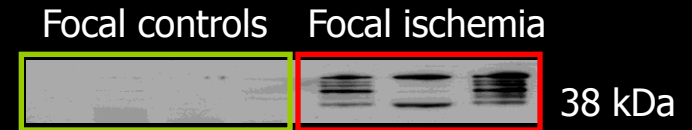
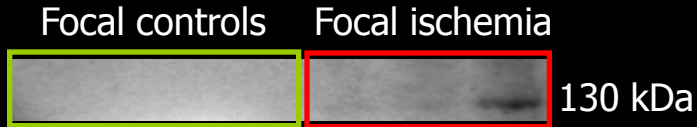
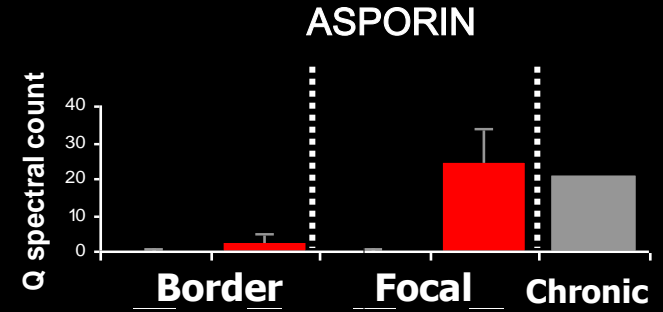
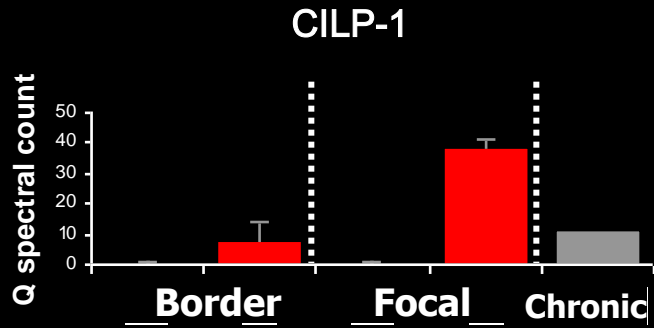


## ACLP

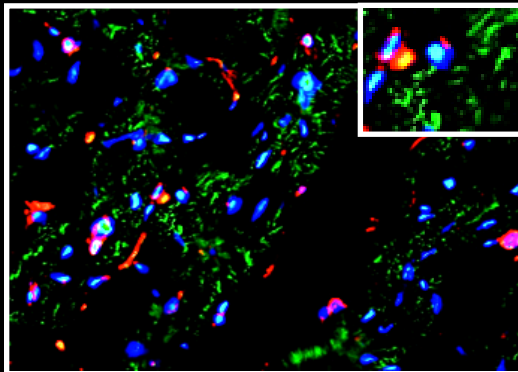


## BIGLYCAN

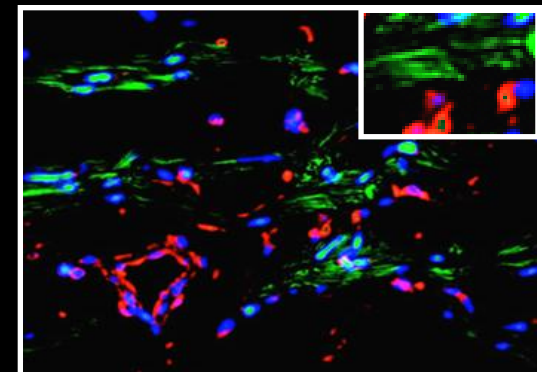




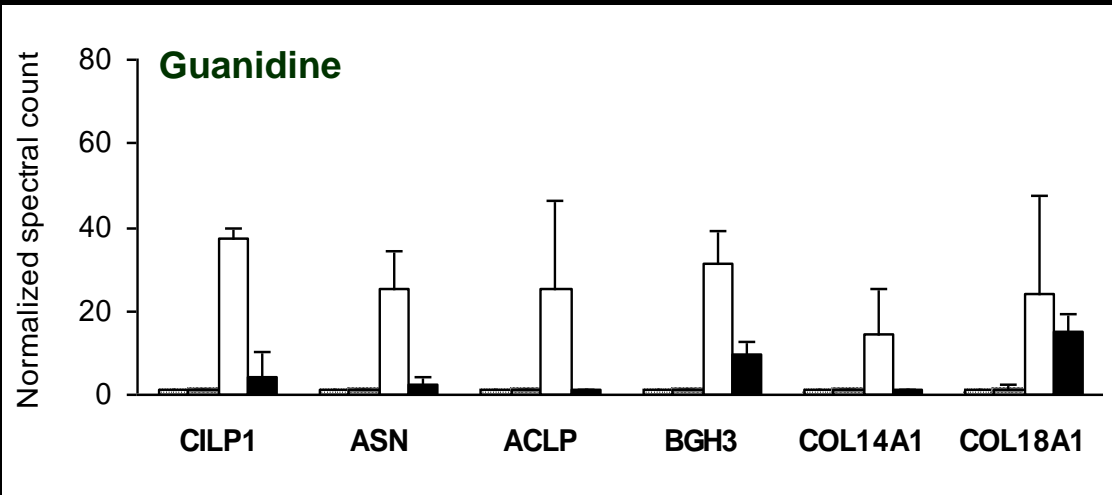
## CILP-1 + Vimentin + DAPI



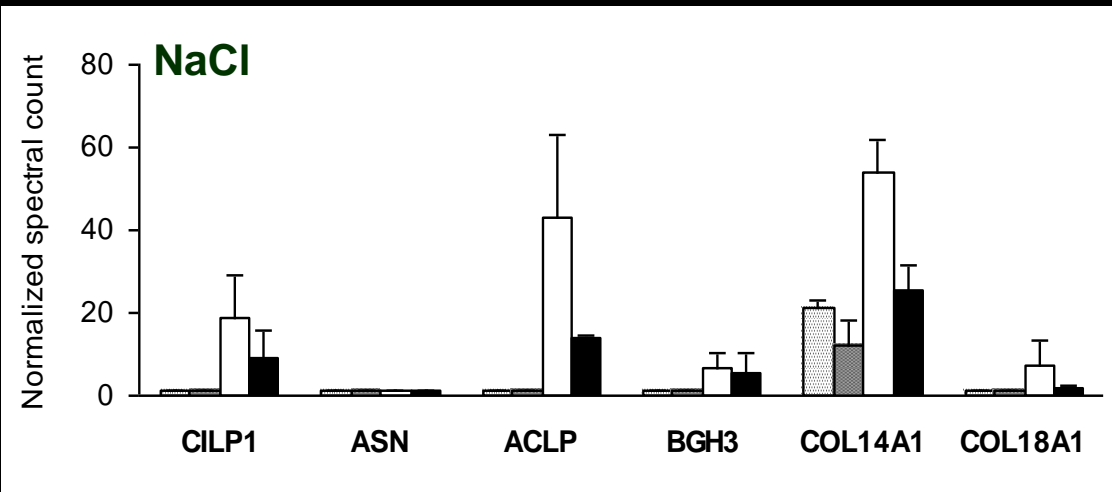
## Asporin + Vimentin + DAPI



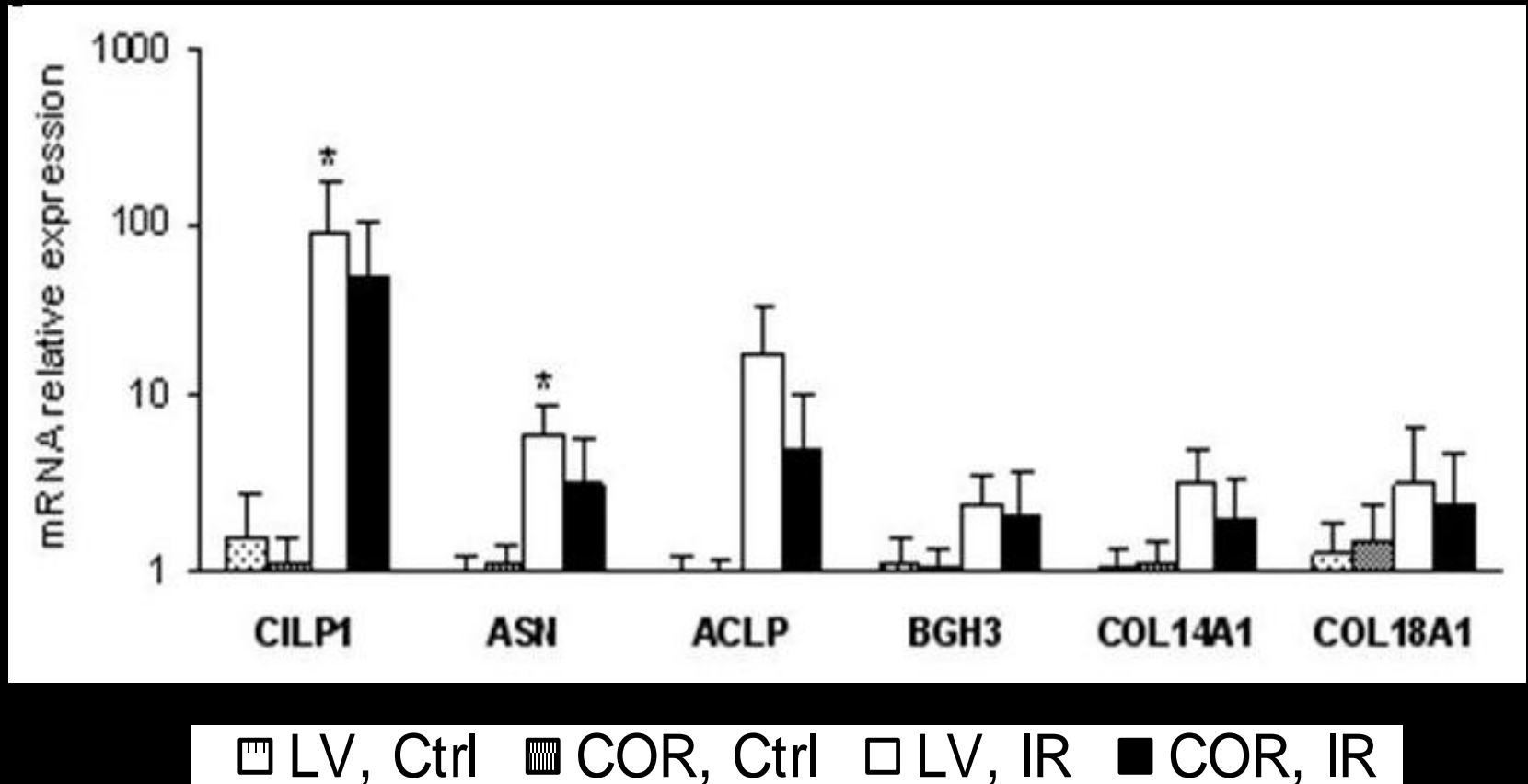
## Differences on spectral count



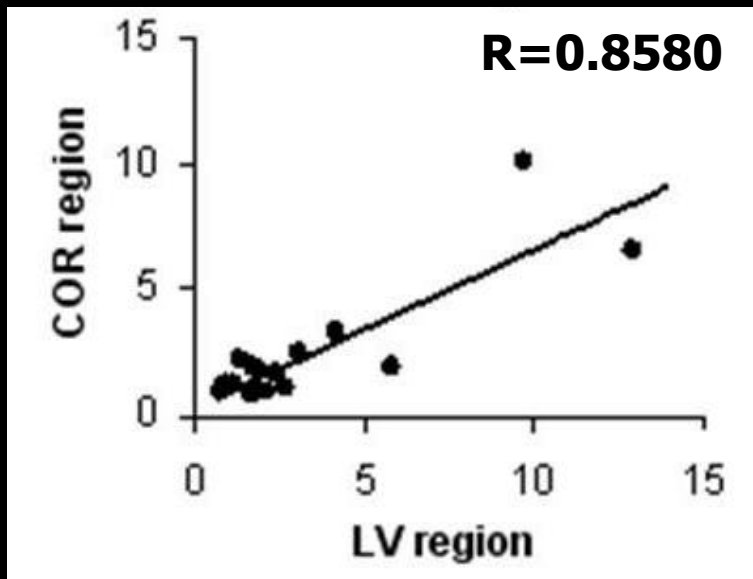
□ LV, Ctrl    ▨ COR, Ctrl  
 □ LV, IR    ■ COR, IR



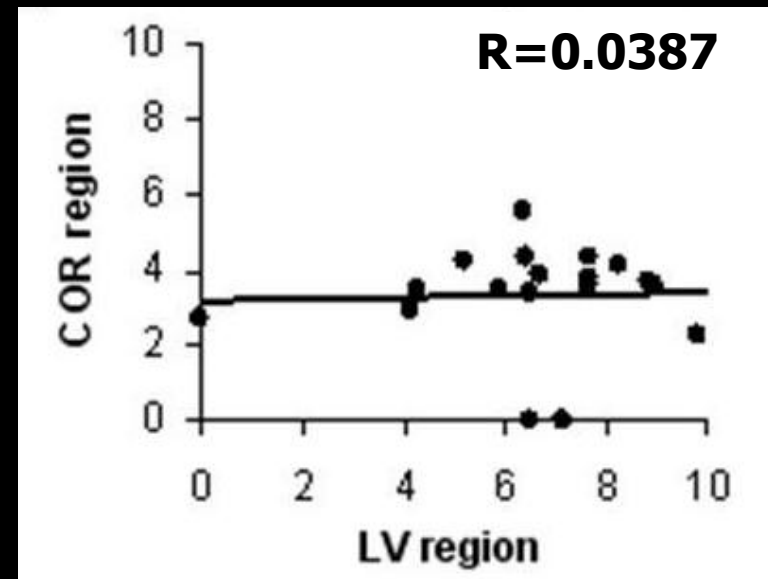
## Differences on mRNA expression



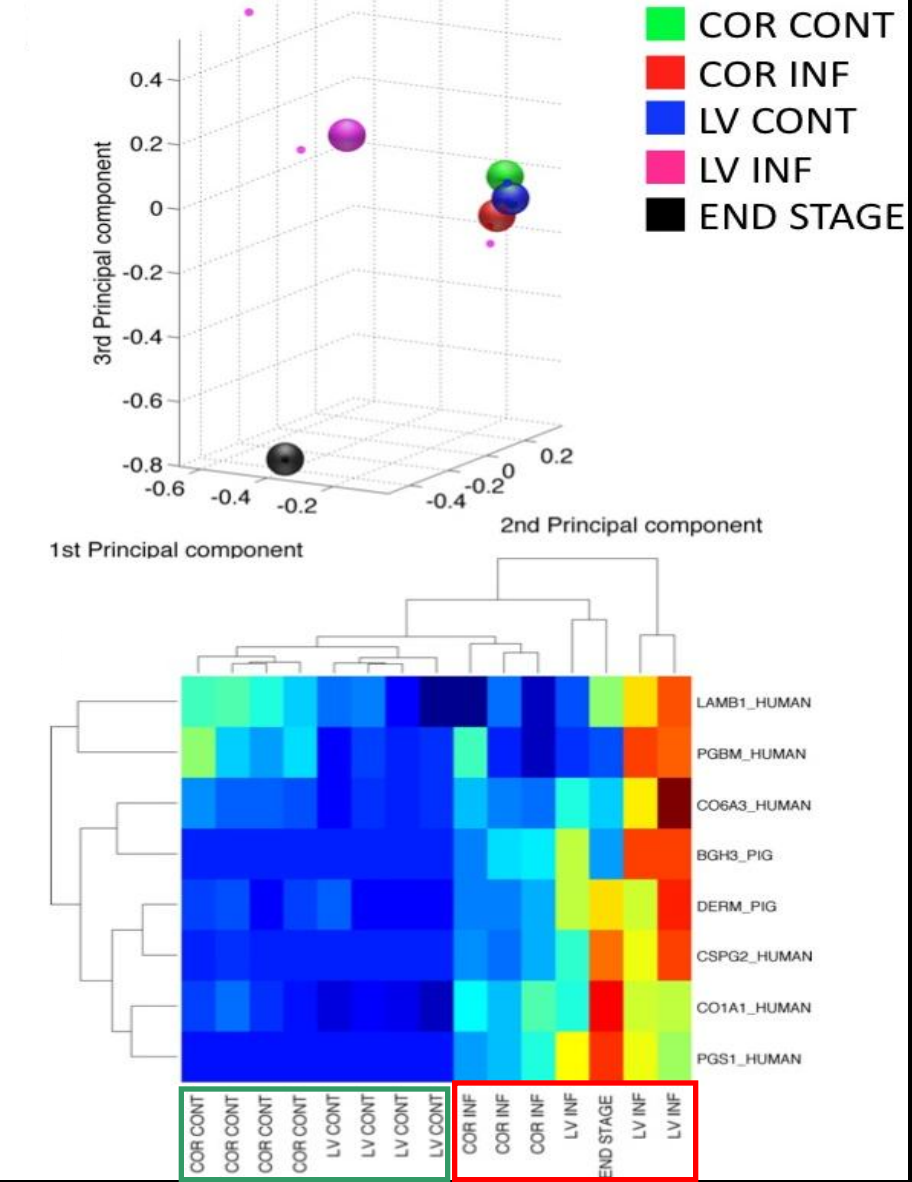
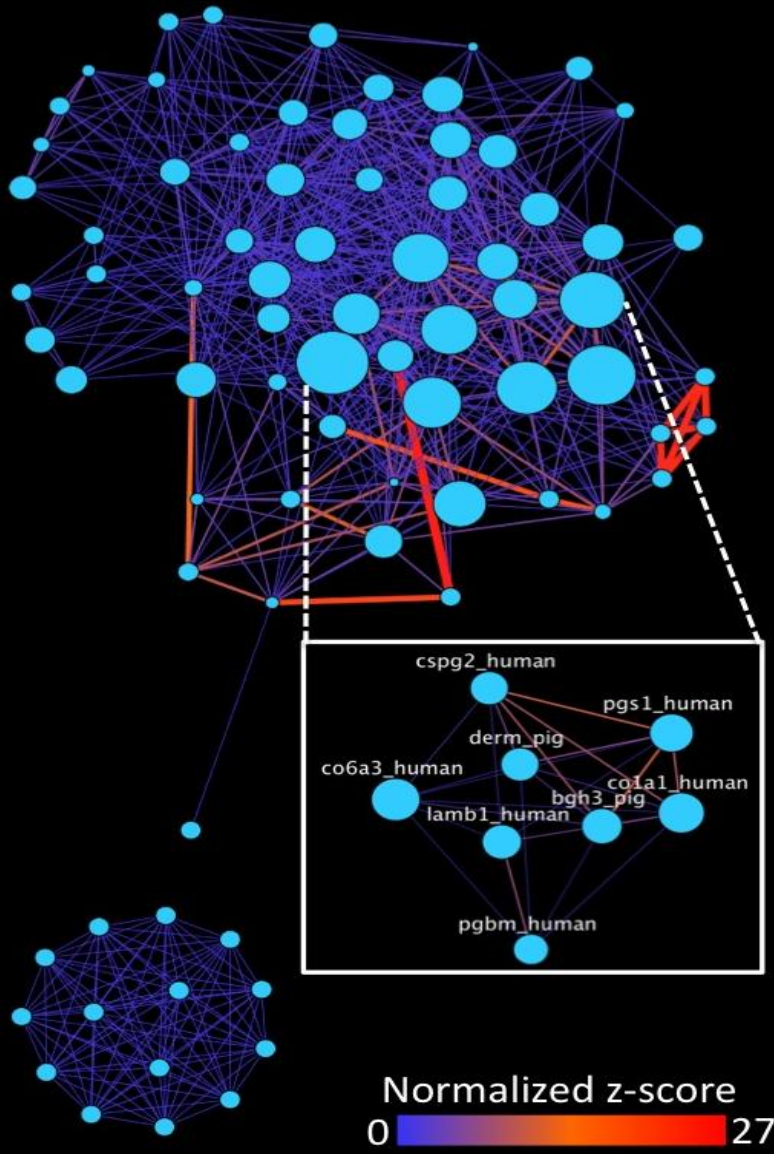
qRT-PCR



Spectral count



mRNA picks the current trend on both regions, but do not discriminate actual differences due to ECM accumulation.



	Total entries	+ Matrix	+ Heart/Cardiac	+ Heart Remodelling
<b>CILP (1)</b>	<b>26 (1)</b>	<b>19</b>	<b>0</b>	<b>0</b>
<b>Asporin</b>	<b>40</b>	<b>36</b>	<b>0</b>	<b>0</b>
<b>Dermatopontin</b>	<b>30</b>	<b>27</b>	<b>1</b>	<b>0</b>
<b>ACLP</b>	<b>35</b>	<b>8</b>	<b>1*</b>	<b>0</b>
<b>Mimecan</b>	<b>39</b>	<b>14</b>	<b>2</b>	<b>0</b>
<b>Nidogen 2</b>	<b>38</b>	<b>25</b>	<b>2</b>	<b>0</b>
<b>Versican</b>	<b>822</b>	<b>574</b>	<b>&lt;15</b>	<b>3</b>
<b>Vitronectin</b>	<b>4226</b>	<b>1728</b>	<b>&lt;30</b>	<b>6</b>
<b>Perlecan</b>	<b>760</b>	<b>398</b>	<b>4**</b>	<b>0</b>
<b>Decorin</b>	<b>1680</b>	<b>113</b>	<b>58</b>	<b>14</b>
<b>Agrin</b>	<b>773</b>	<b>173</b>	<b>5</b>	<b>0</b>
<b>Collagen I</b>	<b>3053</b>	<b>1580</b>	<b>191</b>	<b>52</b>
<b>Collagen III</b>	<b>721</b>	<b>309</b>	<b>95</b>	<b>27</b>
<b>Collagen XIV</b>	<b>31</b>	<b>21</b>	<b>0</b>	<b>0</b>

HEART REMODELING: "X" AND heart AND remodeling NOT arterial NOT aorta NOT valve NOT aortic  
 HEART/CARDIAC : "X" AND heart OR cardiac NOT arterial NOT aorta NOT valve NOT aortic

\*Identification  
 \*\*Very specific papers



## Mimecan

Bone specific protein. Induces **bone** formation in conjunction with **TGF-beta-1** or TGF-beta-2.

## Asporin

2001. "Identification and characterization of asporin. A novel member of the **SLRPs** closely related to decorin and biglycan."

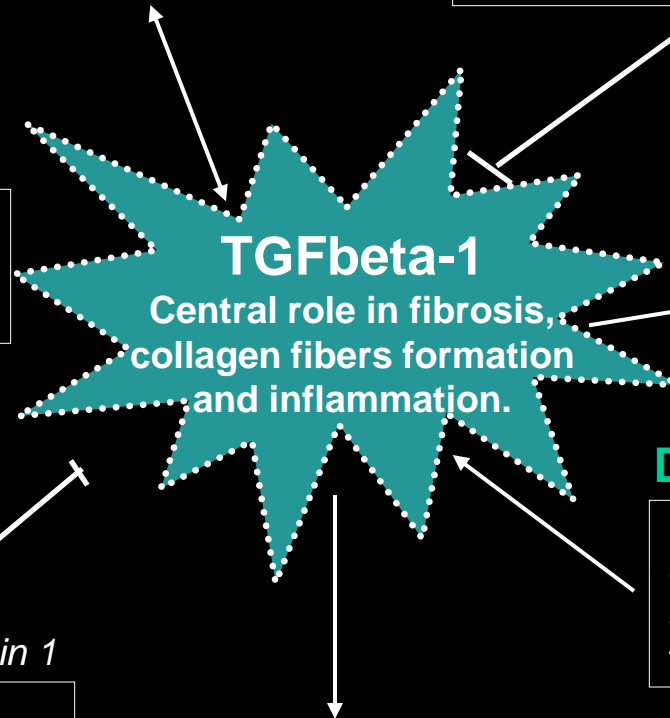
## Matrilin-4

Major component of the **ECM of cartilage**. Present in embryonic kidney, lung and placenta.

## BGH3

*TGFbeta-induced protein g-h3*

Binds to type I, II, and IV collagens. **Induced by TGFbeta.**



**TGFbeta-1**  
Central role in fibrosis,  
collagen fibers formation  
and inflammation.

## Dermatopontin

**Enhances TGFbeta1** activity. Accelerates **collagen fibril formation**, and stabilizes collagen fibrils against low-temperature dissociation.

## ACLP *Aortic Carboxipeptidase*

Promotes macrophage **inflammatory responsiveness** by up-regulating NF-kappaB via I kappa-B-alpha negative regulation.

## CILP-1

*Cartilage Intermediate Layer Protein 1*

**Cartilage specific.** Role in cartilage scaffolding. May act by antagonizing TGFbeta1 and IGF1. Suppresses sulfated proteoglycan synthesis. May **inhibit TGFbeta1-mediated induction of cartilage matrix genes.**

?

- This is the first **comparative** proteomic study focusing on **cardiac ECM** after ischemia.
- qRT-PCR correlation experiments showed proteomics to pick **differences not measurable** by other techniques.
- We have discovered a **set of ECM proteins** that might have **critical roles** on wound healing and scar formation after ischemic heart failure, so this may offer invaluable clues leading to new therapeutic approaches
- The actual role of highlighted proteins here should be figure of **further study**.
- **Quantitative proteomics** in tissues will be essential for the application of proteomics in **clinical research**.

## In **A Coruña**, SPAIN

Nieves Doménech

Mariana Fernández-Caggiano

Oskar M. de Ilárduya

María Fraga Mariño

Patricia Añón

Marta García

Guillermo Aldama

Ramón Calviño

Eduardo López

Alberto Centeno

## In **London**, UK

Manuel Mayr

Thanos Didangelos

Xiaoke Yin

Marianna Prokopi

Angelika Sage

Antonios Kourliouros

Christin Stegemann

Anna Zampetaki

Ursula Mayr

Salil Srivastava



**Thank you!**