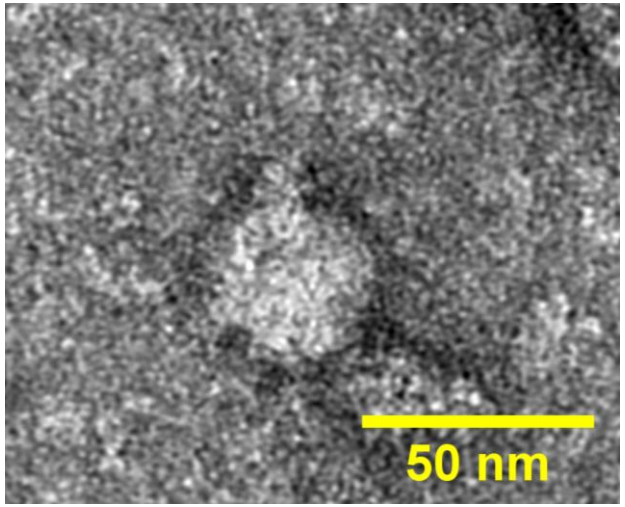
SERUM PROTEOMICS OF CMS FIELD OUTBREAK SAMPLES

Moore, L.; Thompson, K.; Costa, J.; Sourd, P.; Bordeianu, A.;
Chadwick, C.; Moghadam, M.; Brady, N.; Eckersall, D.; del-Pozo, J.

TALK OUTLINE

- Why biomarkers? / Previous work
- Study design
- Results
- Conclusions and further study



PMCV

WHY BIOMARKERS?

Mortality Timing

Frequently: 2y at sea (pre-harvest)

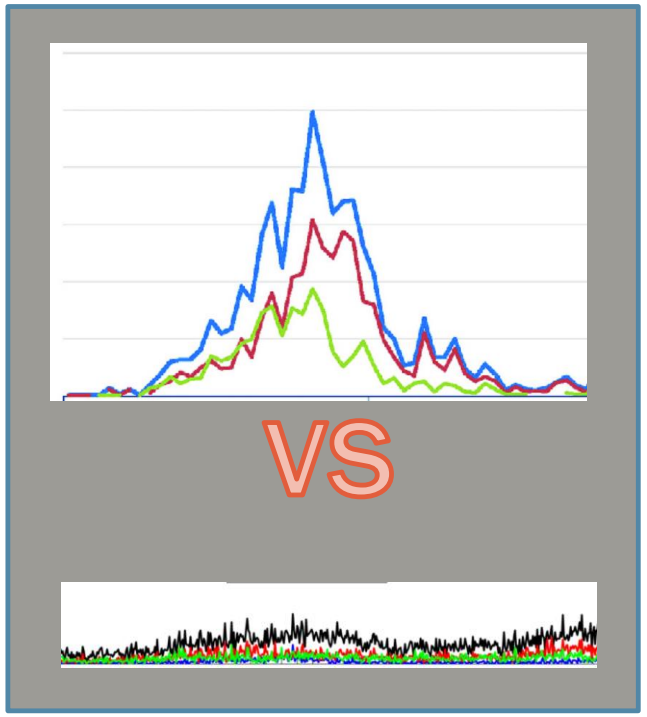
Recently: 1-7m post-transfer!

Mortality pattern

Protracted/mild mortalities

Sudden outbreaks/severe mortality

Mortality Pattern



CLINICAL, EPIDEMIOLOGICAL, PATHOLOGICAL DATA SUGGESTS SUBCLINICAL CMS IS COMMON IN AFFECTED SITES

(i.e. a clinically healthy cage/site with subclinical cases)

"chronic cardiac patients"

WHY BIOMARKERS?

Clinical signs detection

Ancillary testing

Histology &/or rtPCR

CMS diagnosis

(+ or -)

ISSUES

Sampling of clinically ill fish
Late diagnosis > more impact?
Destructive > smaller sample

SERUM BIOMARKERS

DESIRABLE

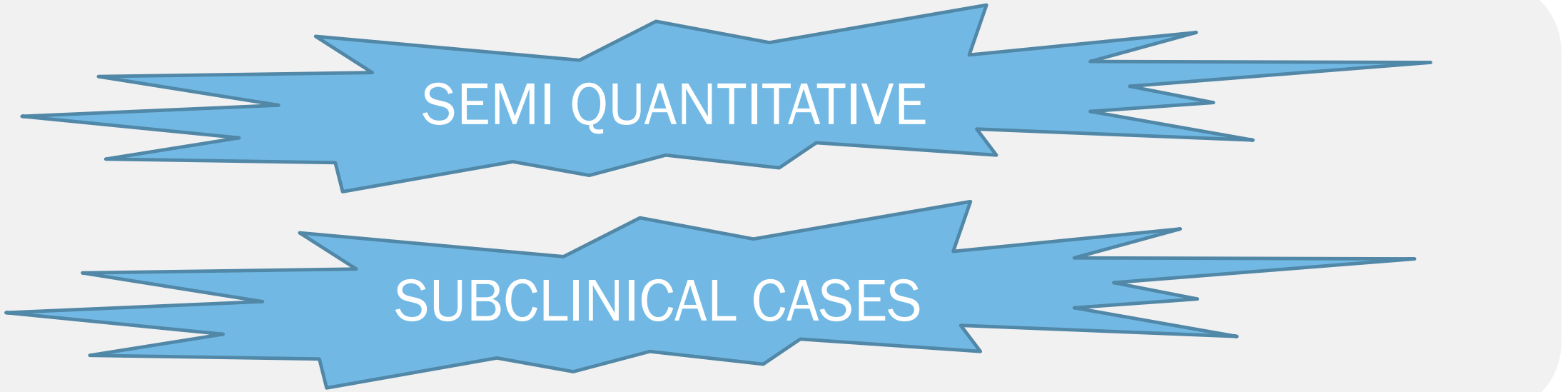
- Random subclinical testing
- Early diagnosis, prognostic
- Non destructive > larger sample >↑ sample power

Proteomic characterization of serum proteins from Atlantic salmon (*Salmo salar* L.) from an outbreak with cardiomyopathy syndrome

Janina Z. Costa[1] | Jorge del Pozo[2] | Kevin McLean[3] | Neil Inglis[3] | Philippe Sourd[4] | Andrei Bordeianu[4] | Kim D. Thompson[1]

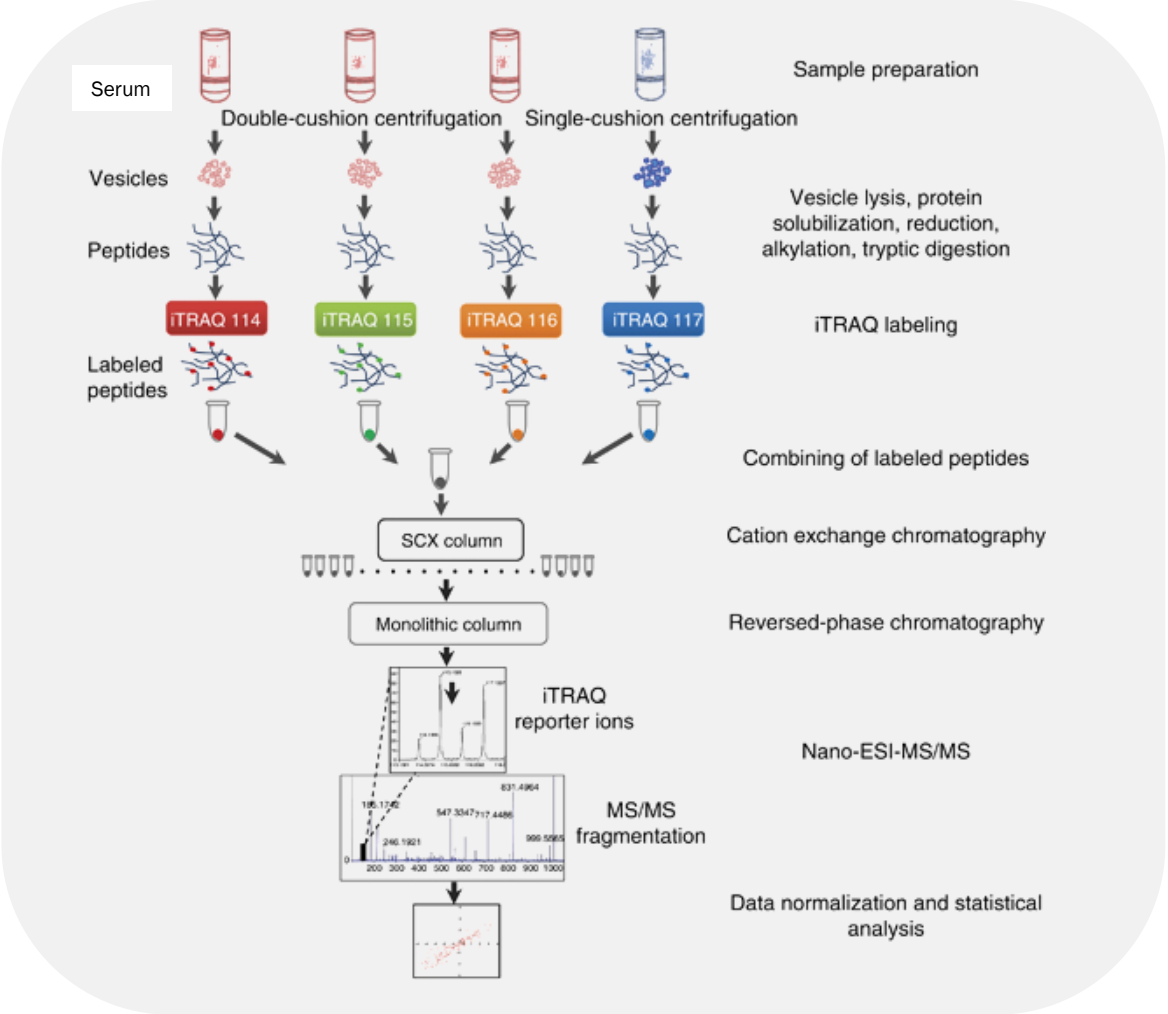
Leakage Enzymes	Host Reaction	Regeneration / Remodeling
Creatine kinase	Haptoglobin*	Fibronectin
Lactate dehydrogenase	Fibrinogen*	Lumican
Glycogen phosphorylase	Kininogen*	Retinol-binding*
Carbonic anhydrase	α_2-macroglobulin*	Lipocalin
	Ceruloplasmin*	
	Complement factor B*	
	Serine protease-like	
* = acute phase protein		

STUDY DESCRIPTION



SEMI-QUANTITATIVE PROTEOMICS (ITRAQ)

- Isobaric tags for relative absolute quantitation of proteins (iTraQ)



STUDY DESCRIPTION

Cases and Controls Biobank

- **28 Samples** arranged in 7 iTraQ experiments
- Randomly chosen (large sample set)
- Each experiment

  - Negative control
  - Low PCMV load
  - Medium PCMV load
  - High PCMV load

  Subclinical CMS

iTraQ – Relative Quantification

- Evaluation of common patterns across experiments
- *Relative ratio data*

1- Candidate biomarkers

Subclinical CMS

(n=21)

VS

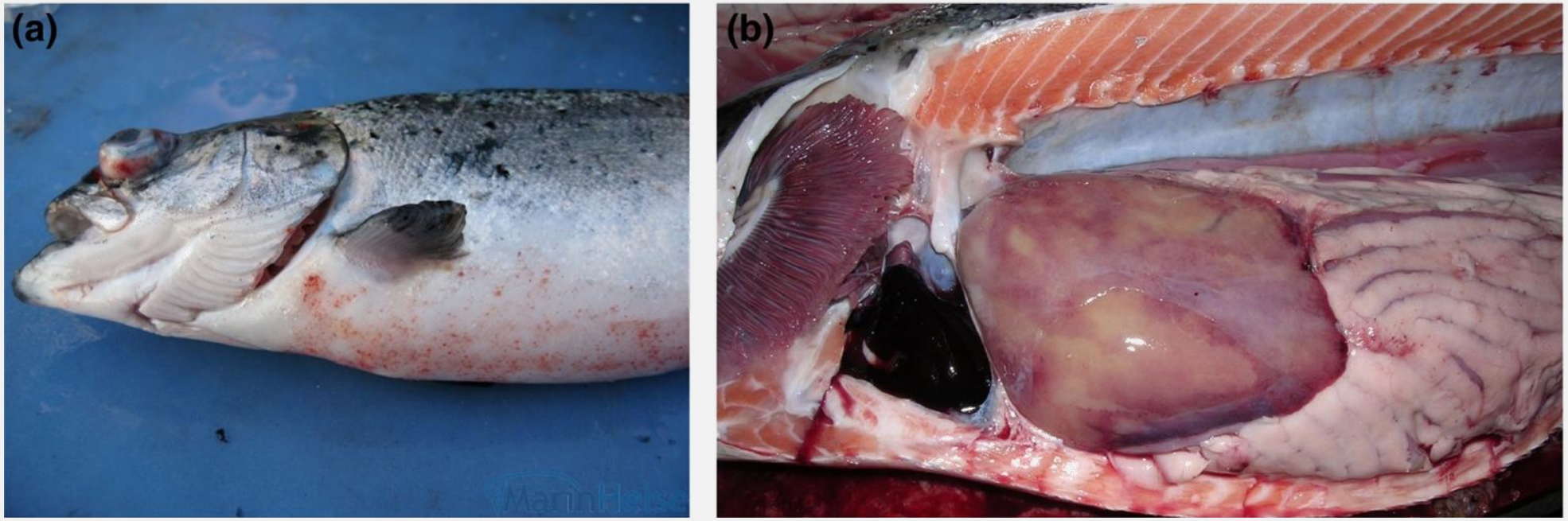
Healthy

(n=7)

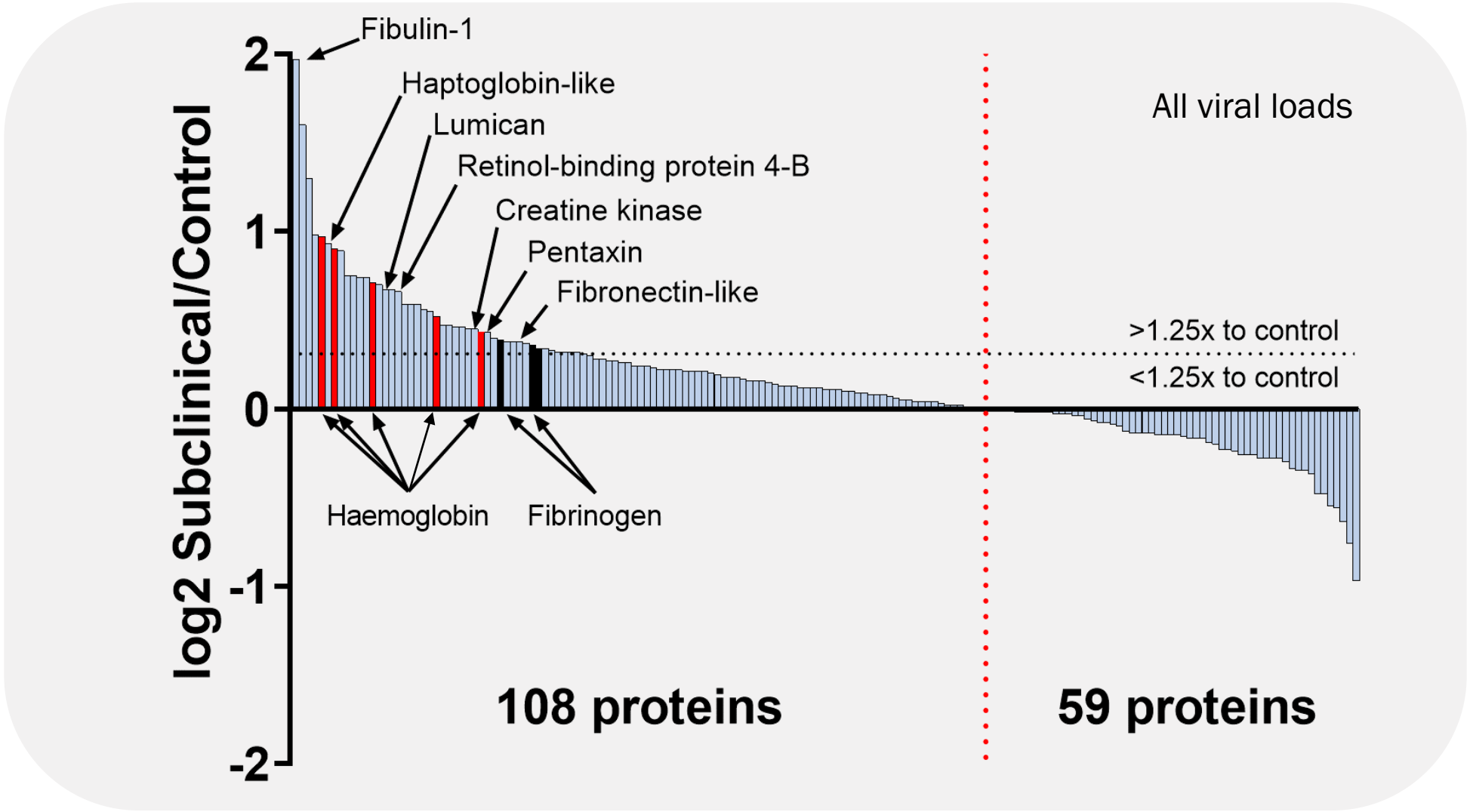
2-Candidate biomarkers

PMCV viral load

RESULTS



Garseth et al. J Fish Dis **41:** 11-26, 2018


Fibulin-1
Haptoglobin-like
Lumican
Retinol-binding protein 4-B
Creatine kinase
Pentaxin
Fibronectin-like
All viral loads
>1.25x to control
<1.25x to control
log2 Subclinical/Control
2
1
0
-1
-2
Haemoglobin
Fibrinogen
108 proteins
59 proteins

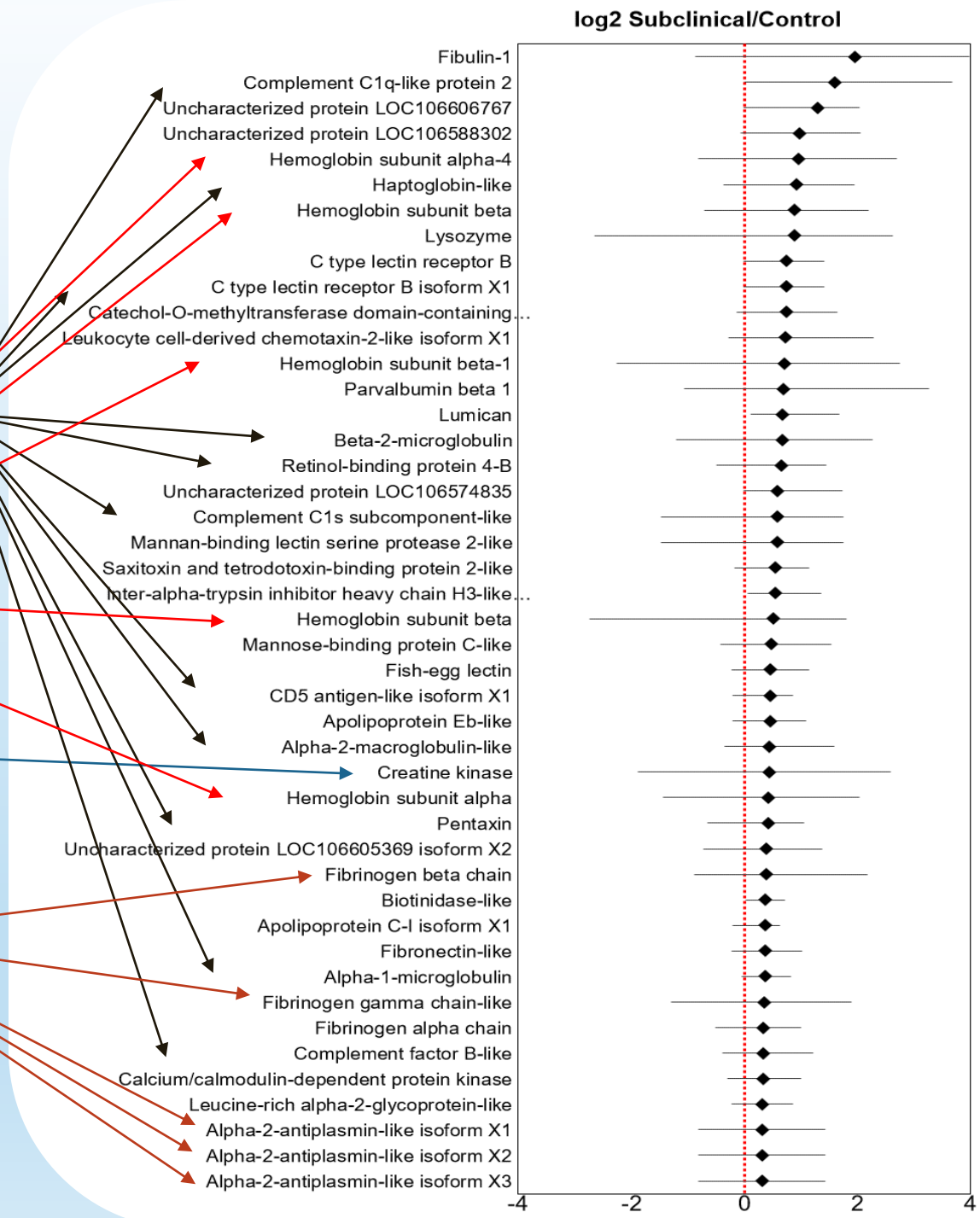
Others

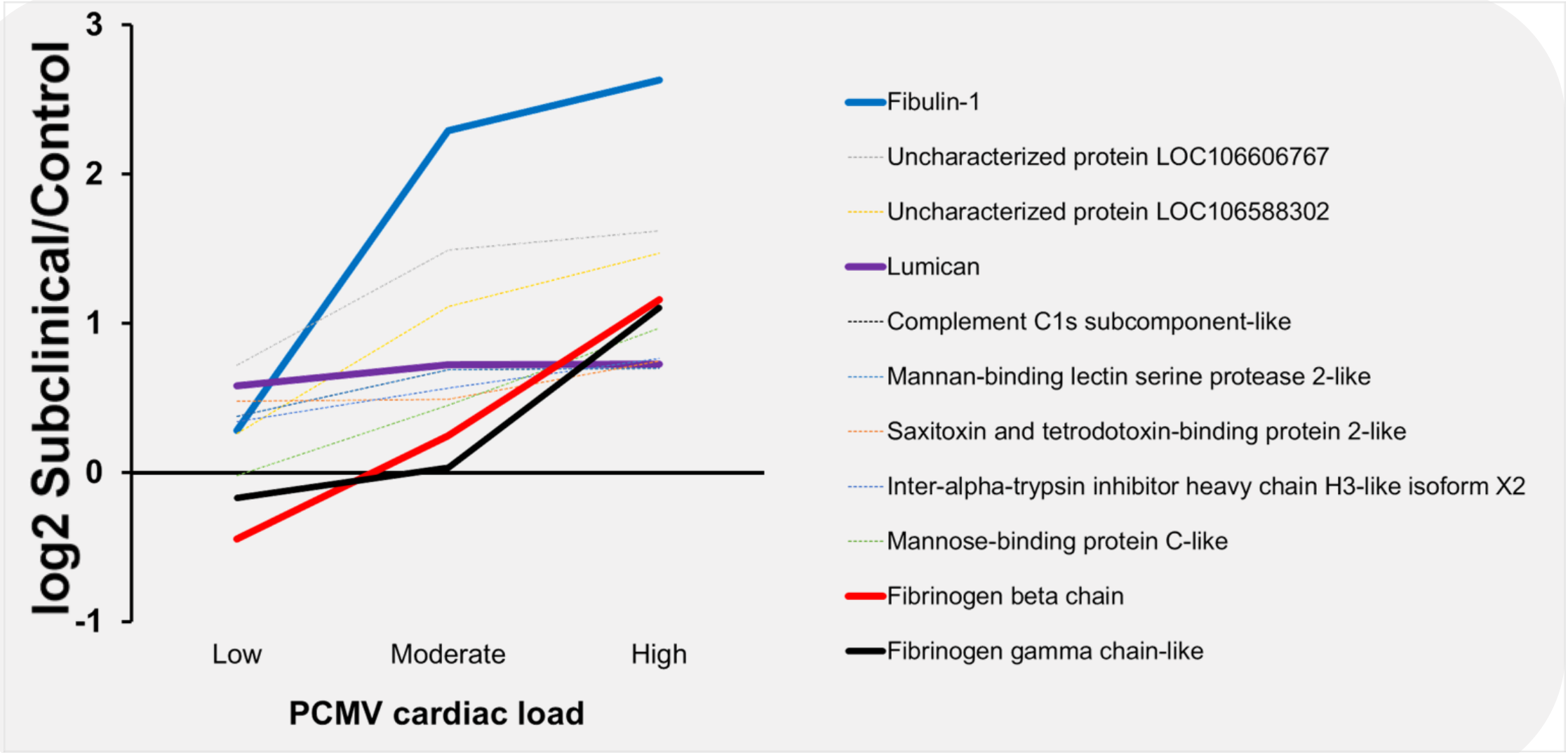
Acute phase proteins (11)

Haemolysis (5)

Leakage proteins (1)

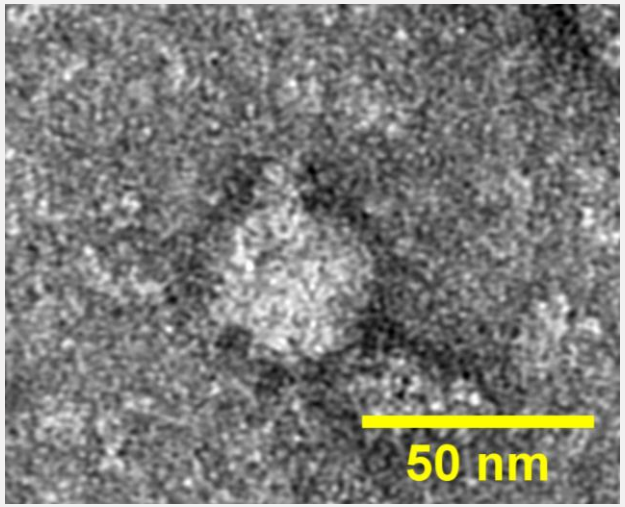
Hypercoagulability




log2 Subclinical/Control
3
2
1
0
-1
Low
Moderate
High
PCMV cardiac load
Fibulin-1
Uncharacterized protein LOC106606767
Uncharacterized protein LOC106588302
Lumican
Complement C1s subcomponent-like
Mannan-binding lectin serine protease 2-like
Saxitoxin and tetrodotoxin-binding protein 2-like
Inter-alpha-trypsin inhibitor heavy chain H3-like isoform X2
Mannose-binding protein C-like
Fibrinogen beta chain
Fibrinogen gamma chain-like

CONCLUSIONS

- Candidate biomarkers identified
  - Acute phase proteins
  - Hypercoagulability/Haemolysis
  - Leakage biomarkers
  - Other
- Further characterisation required
  - Immunoassay development and diagnostic validation



PMCV

THANK YOU, ANY QUESTIONS?

Moredun Research Institute

Kim Thompson

Janina Costa

Cooke Aquaculture Scotland

Philippe Sourd

Andrei Bordeianu

The University of Edinburgh
The Royal (Dick) School of Veterinary Studies

Roslin

Jorge del Pozo

University of Glasgow

David Eckersall

Nicola Brady

Life Diagnostics, Ltd.

Chris Chadwick

Benchmark Genetics

Hooman Moghadam