

Analysis of RNA stability in pig *post mortem* skeletal muscle with Affymetrix GeneChip® Genome Arrays: implications for gene expression studies

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POST MORTEM DELAY AND RNA QUALITY



SAMPLING



STORAGE IN
LIQUID
NITROGEN

**CAN WE CONSIDER POST
MORTEM SKELETAL
MUSCLE (MEAT) AN
USEFUL TISSUE FOR
GENE EXPRESSION
STUDIES ?**

AIM

**TO EVALUATE THE RNA
STABILITY in *POST*
MORTEM SKELETAL MUSCLE
FROM PIGS and USE IT IN
TRANSCRIPTOMIC
ANALYSIS**

PILOT STUDY

Materials and Methods

SAMPLING/1

- *Semimembranosus* muscle was sampled from 4 legs of different commercial heavy pigs
- The first sampling was carried out at 20 min *post mortem*
- Following the cold chain of the slaughterhouse other 4 samples, from the same legs, were collected at 2, 6, 24, 48 and 72 hours *post mortem*.



Material and Methods

RNA EXTRACTION AND QUALITY CONTROLS

Samples were stored at -80 °C

Total RNA was extracted using the RNeasy Midi kit (Qiagen)

Quality controls by:

- 1. Agarose gel**
- 2. Agilent Bioanalyzer and RIN**
- 3. 28S/18S**
- 4. GAPDH amplification**

Materials and Methods

Microarray analysis

GENE CHIP® PORCINE GENOME ARRAYS were hybridized with RNA obtained from:

3 pigs

at 20 min, 2, 6 and 24 h *post mortem*

using the Affymetrix recommended protocol



Material and Methods

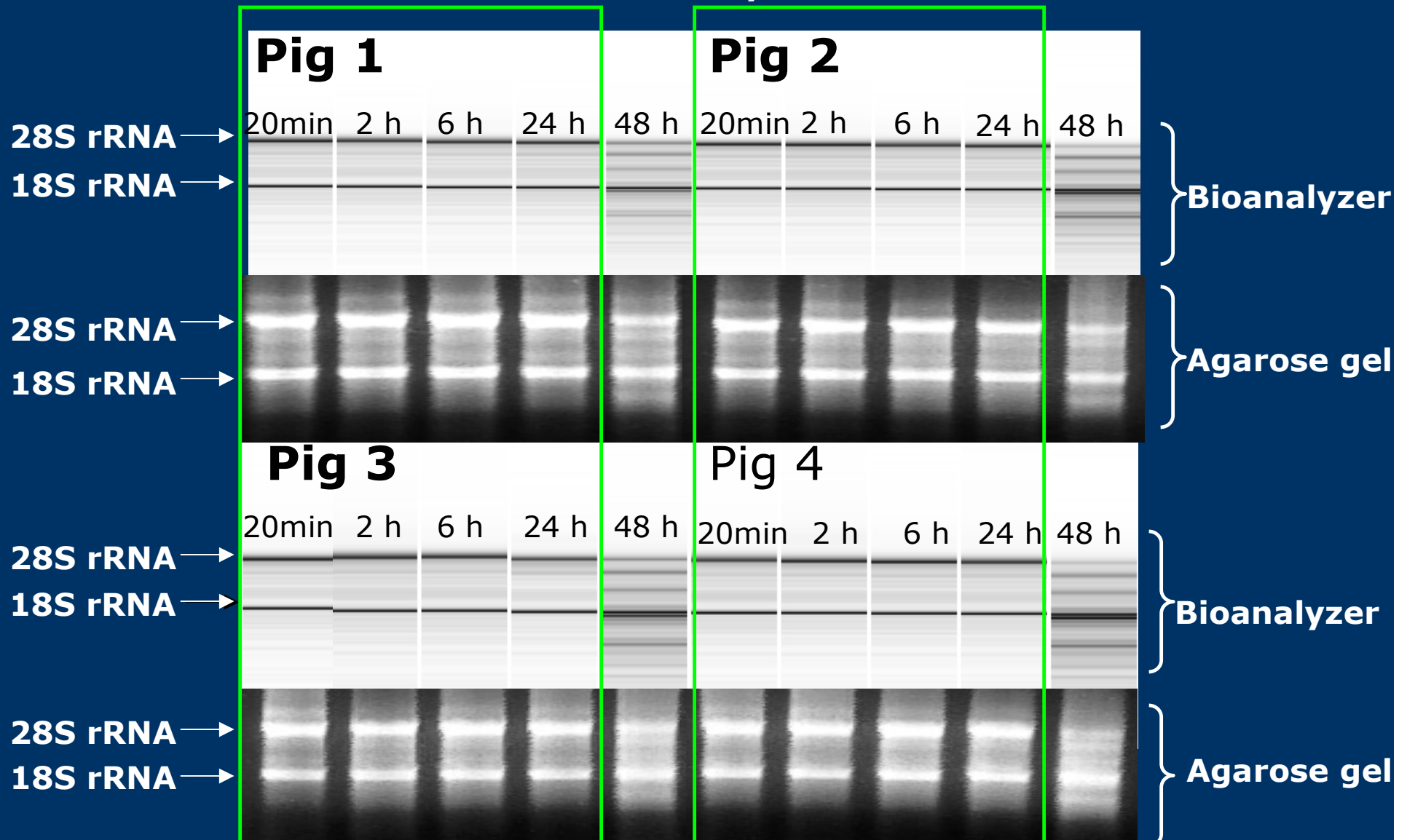
DATA ANALYSIS

- 1. *affy* package was used to normalize expression values (RMA) in R**
- 2. Application of non-specific filtering**
- 3. EDGE software (Storey et al., 2005) was used for significance analysis of time course variation**
- 4. Additional RNA quality controls were calculated with R using hybridization data**

RESULTS

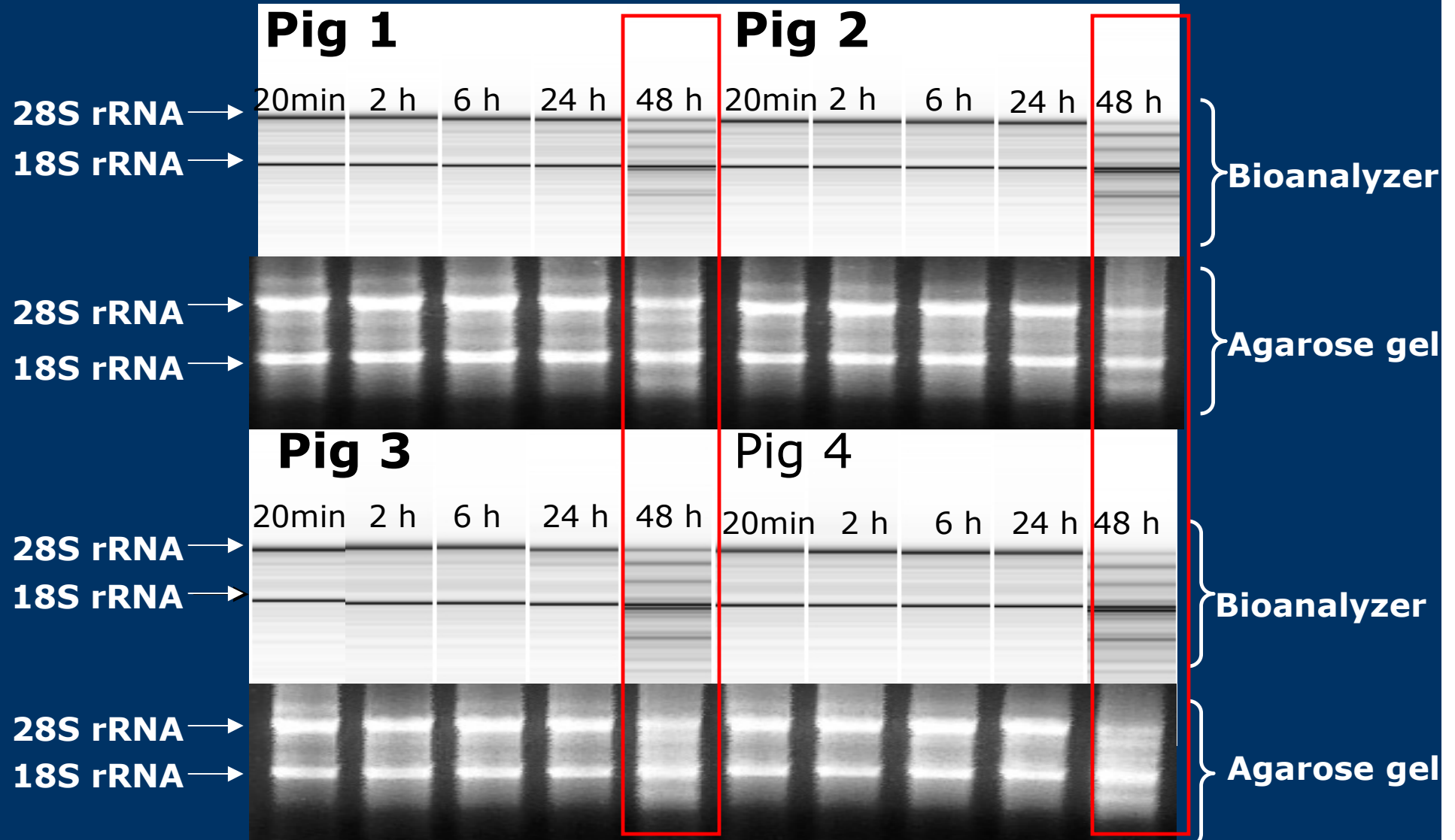
RESULTS/1

RNA quality control/Agarose gel and Bioanalyzer



RESULTS/1

RNA quality control/Agarose gel and Bioanalyzer



RESULTS/2

RNA quality control/RIN and

28S/18S

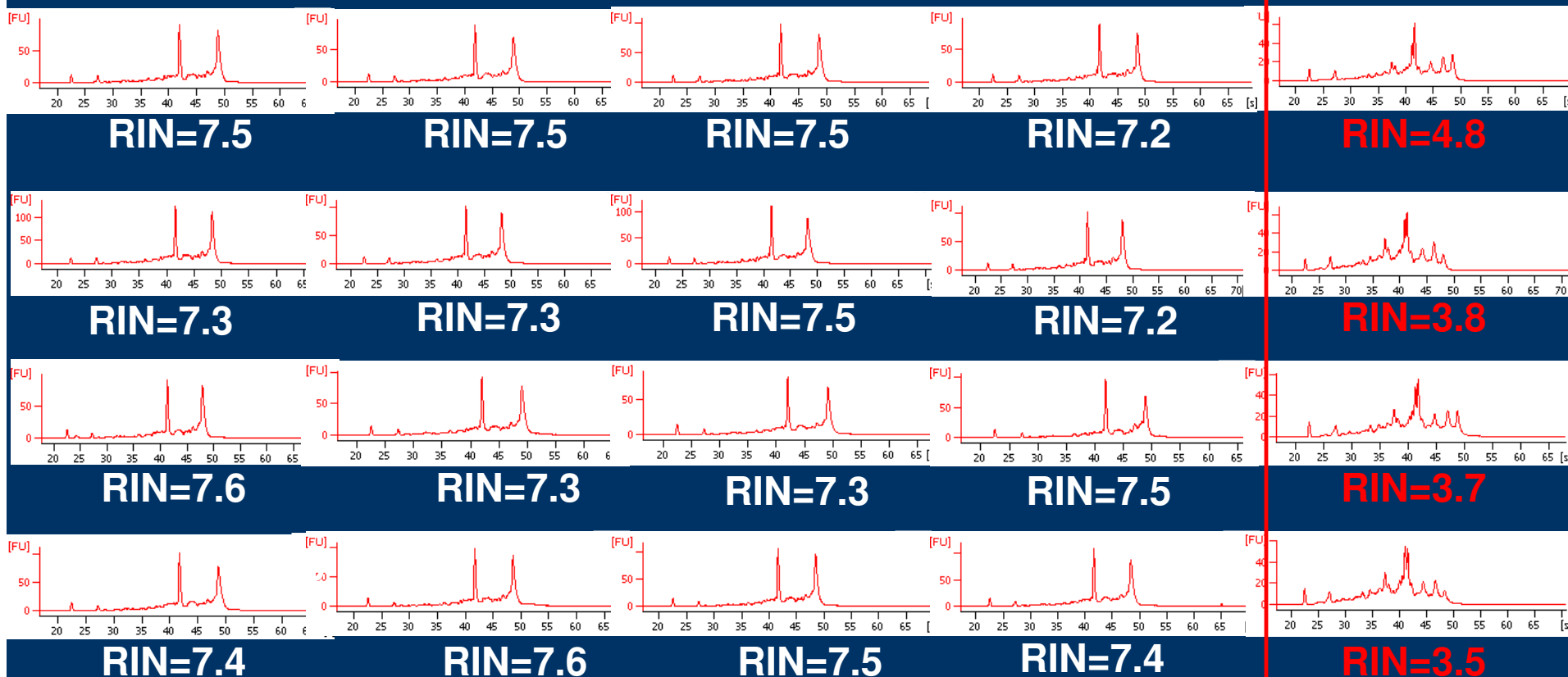
20 min

2 h

6 h

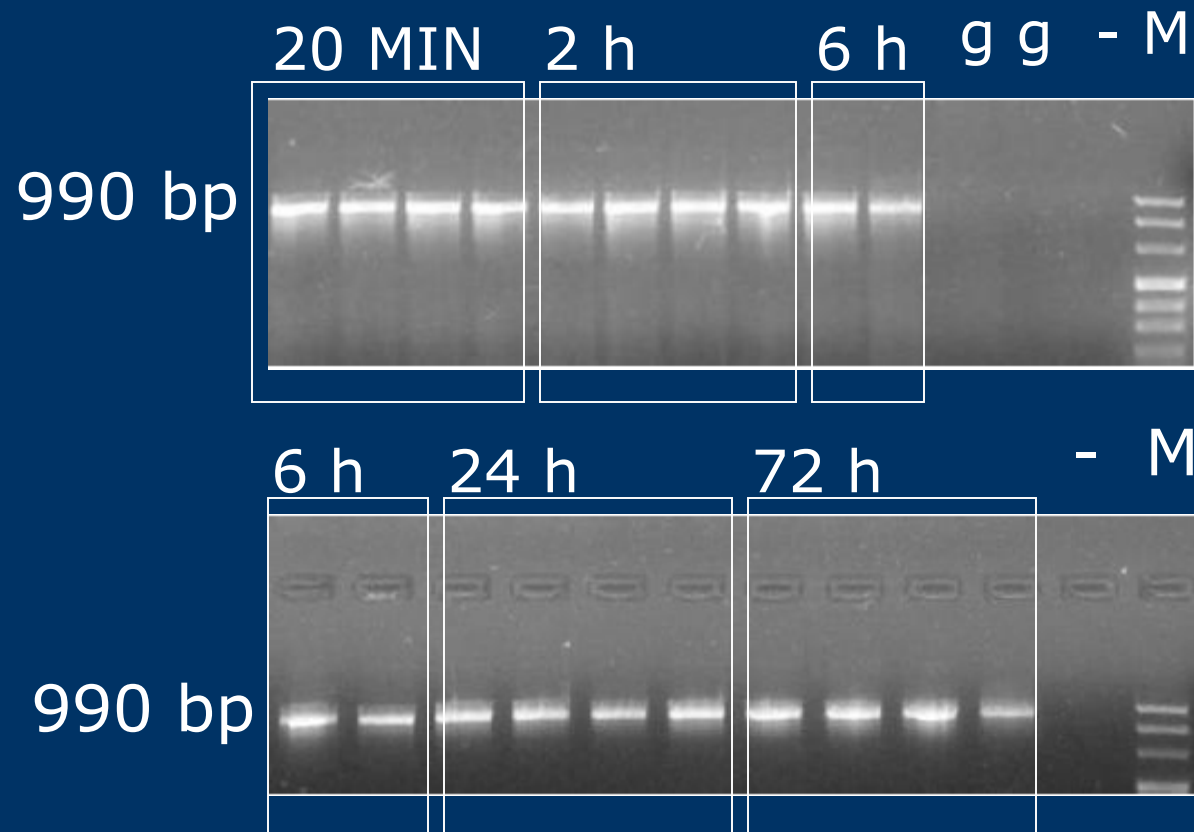
24 h

48 h



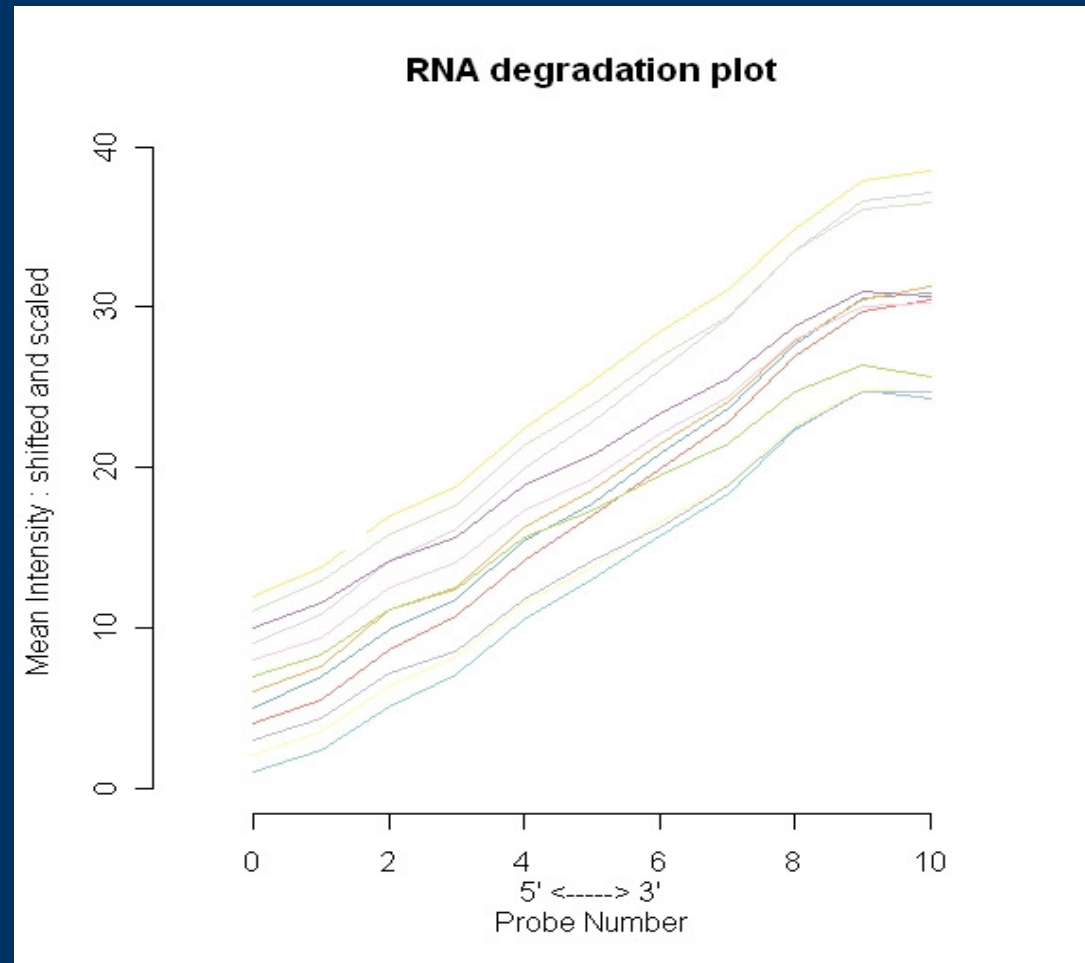
RESULTS/3

RNA quality control/GAPDH amplification



RESULTS/4

RNA DEGRADATION PLOT



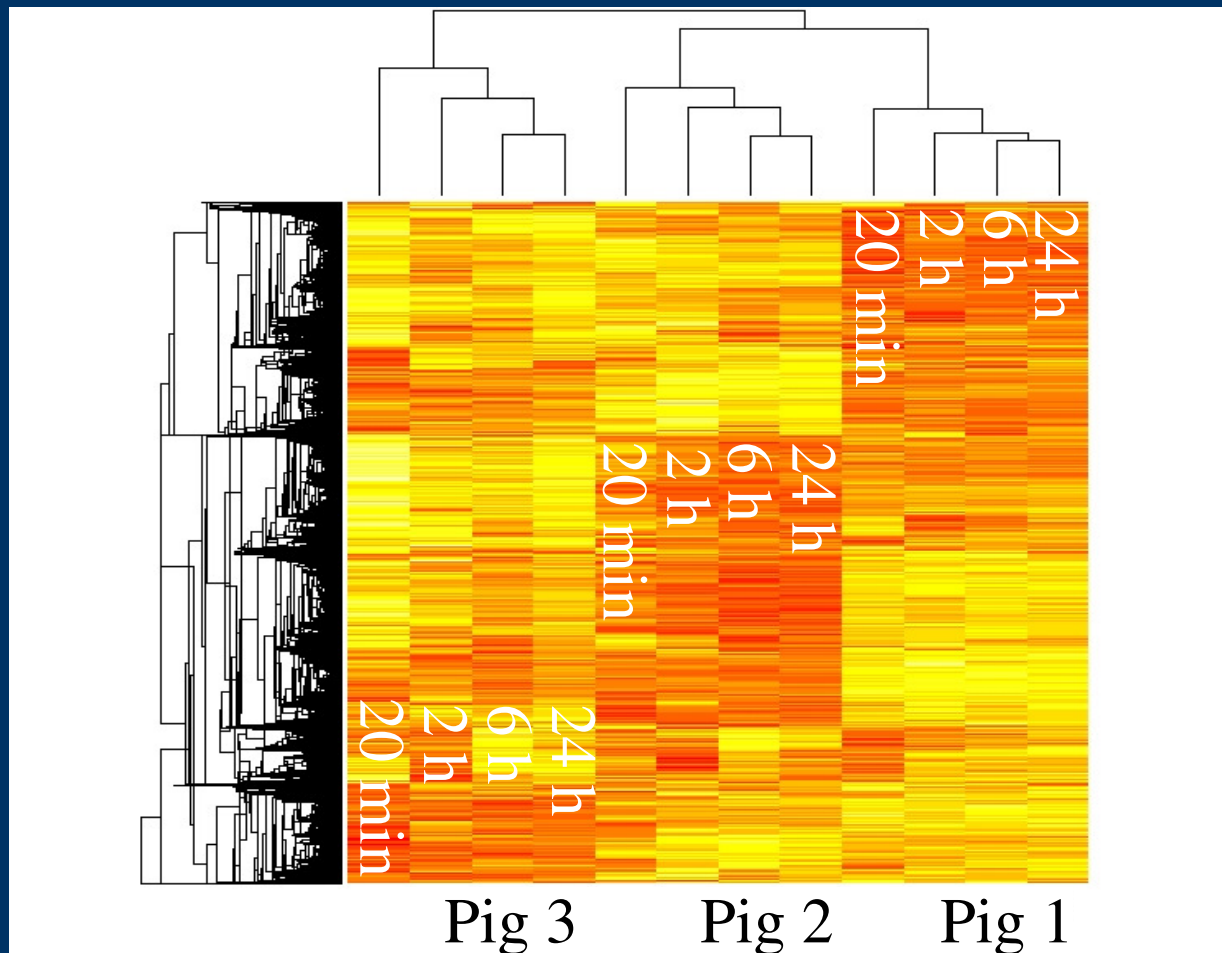
RESULTS/5

CHIP QUALITY CONTROL

CHIP/PM interval	% Present Call	Average background	Scaling Factor
1A/20 min	53.88	54.81	0.66
1B/2 h	54.39	66.69	0.50
1C/6 h	54.69	61.21	0.54
1D/24 h	54.22	56.55	0.56
2A/20 min	53.64	49.1	0.69
2B/2 h	53.07	52.5	0.67
2C/6 h	53.04	64.77	0.56
2D/24 h	53.08	58.32	0.65
3A/20 min	55.99	46.14	0.66
3B/6 h	54.95	60.26	0.51
3C/6 h	55.18	53.0	0.59
3D/24 h	53.31	46.94	0.69

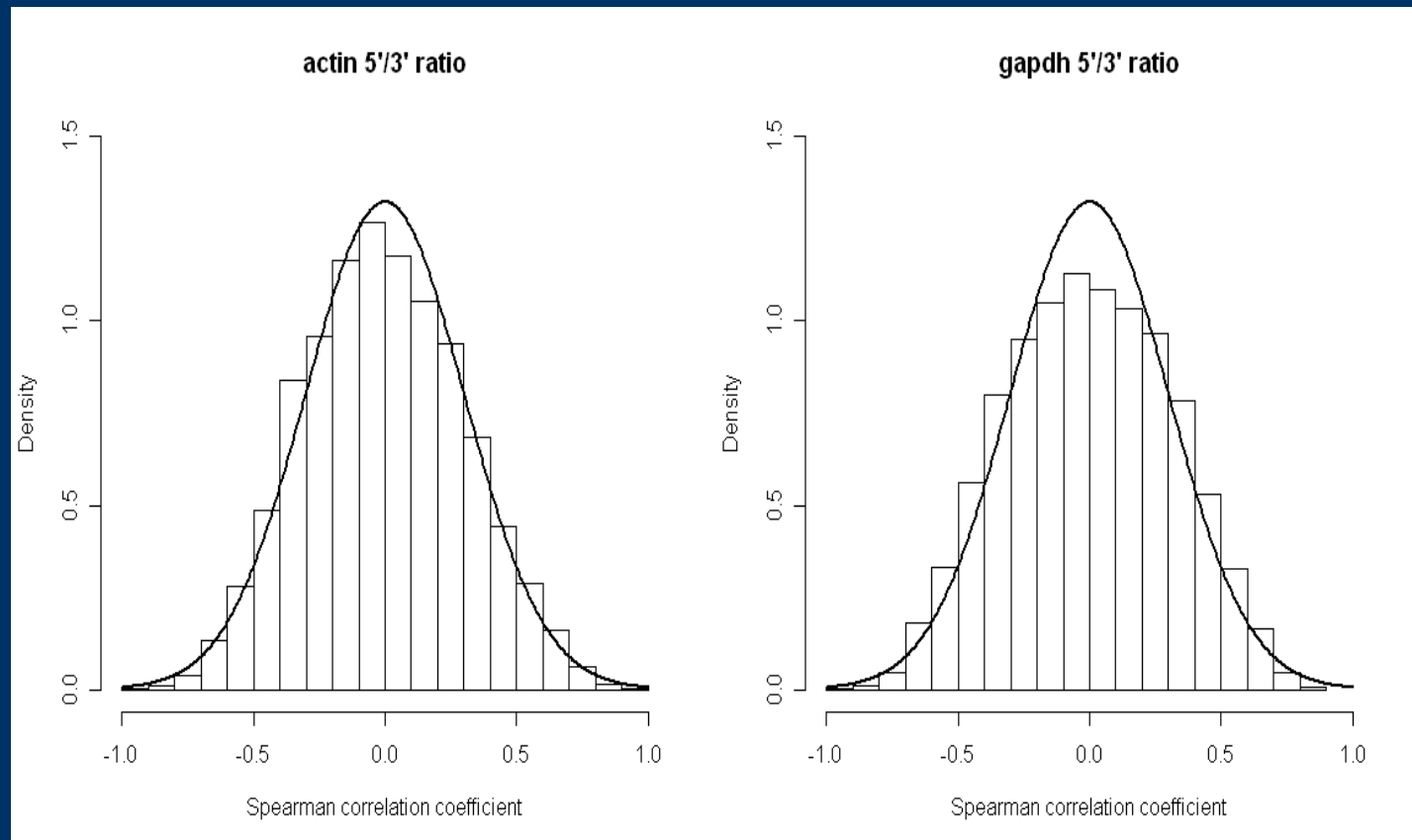
RESULTS/6

Cluster analysis of 5203 genes retained after filtering

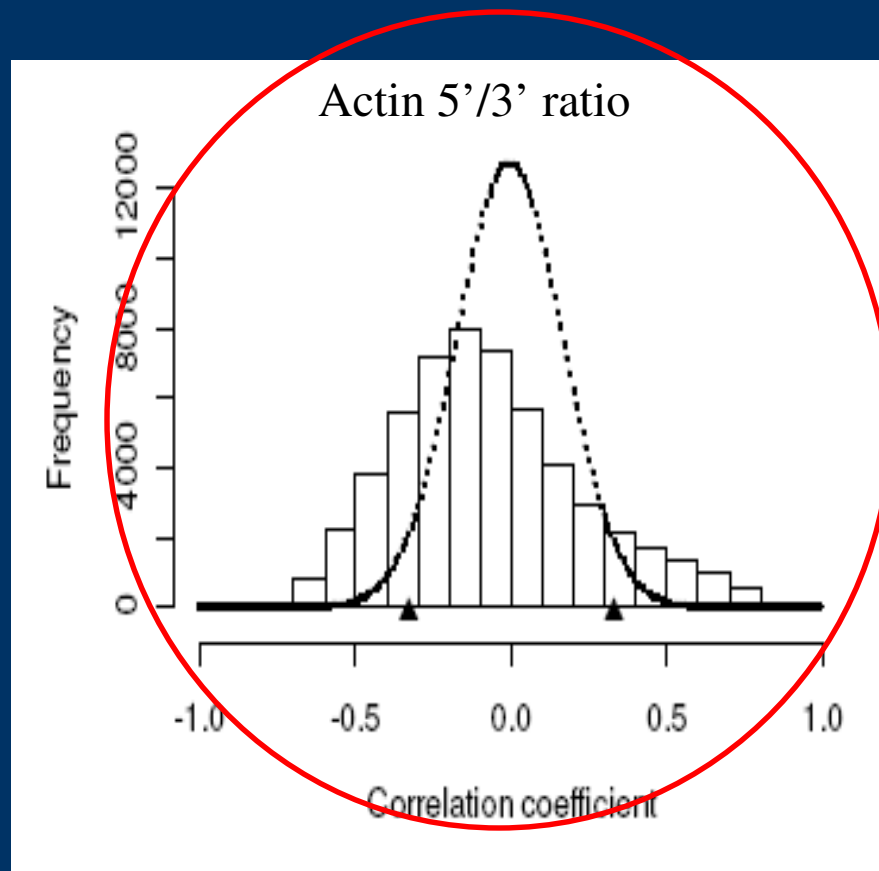


RESULTS/7

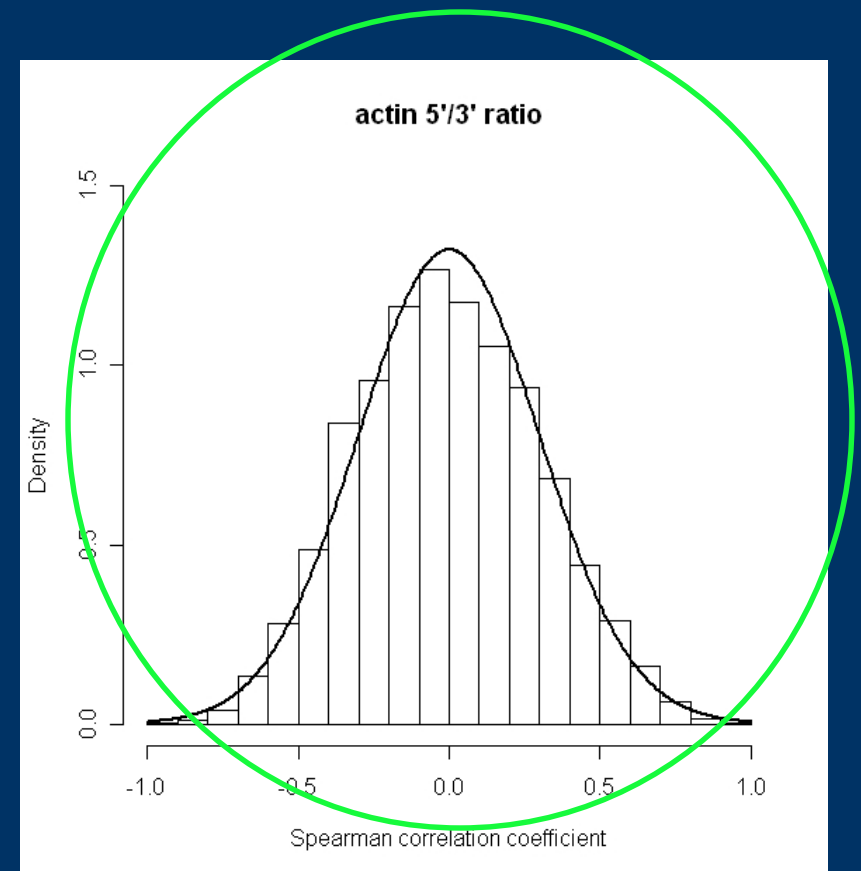
Correlation structure caused by RNA quality for actin and GAPDH



NO CORRELATION (POPOVA ET AL. 2008)

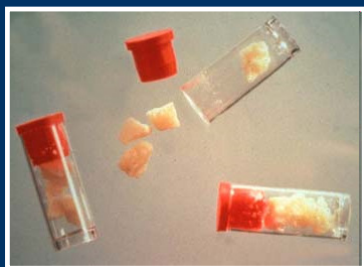


our data

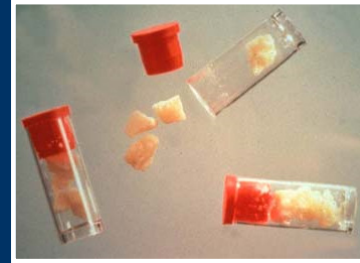


Number of RNA quality dependent transcripts

	Pvalue <0.05 (Expected 5%)	Pvalue <0.01 (Expected 1%)
ACTIN	4.93	0.93
GAPDH	5.3	0.73



IN MUSCLE PIG



CONCLUSION/1

- IT IS POSSIBLE TO OBTAIN RNA OF GOOD QUALITY TILL 24 HOURS POST MORTEM
- THIS RNA CAN BE USED FOR GENE EXPRESSION ANALYSIS
- TISSUE SAMPLING CAN BE SIMPLER

CONCLUSION/2

NEW PERSPECTIVES OF APPLICATION
OF GENE EXPRESSION ANALYSIS FOR

- AUTHENTICATION AND
TRACEABILITY OF MEAT PRODUCTS
- IDENTIFICATION OF BIOMARKERS
FOR MEAT QUALITY AND PRE-
SLAUGHTERING CONDITIONS

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**THANKS FOR
YOUR
ATTENTION**