



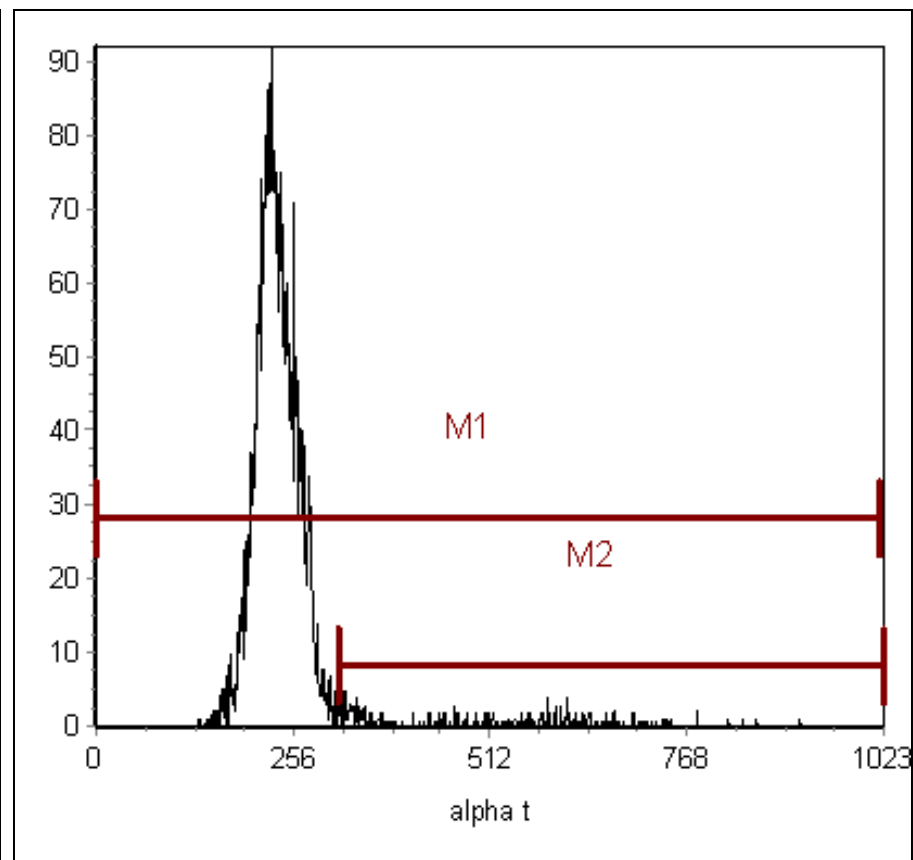
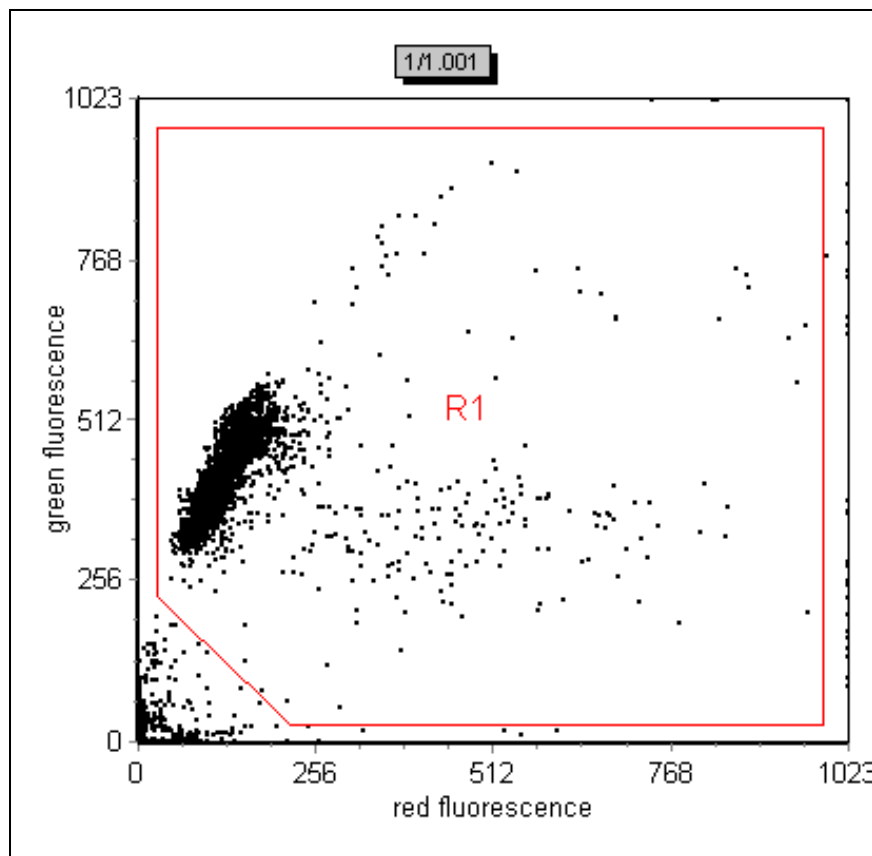
## *Application of next generation cytomics in AI semen quality control*

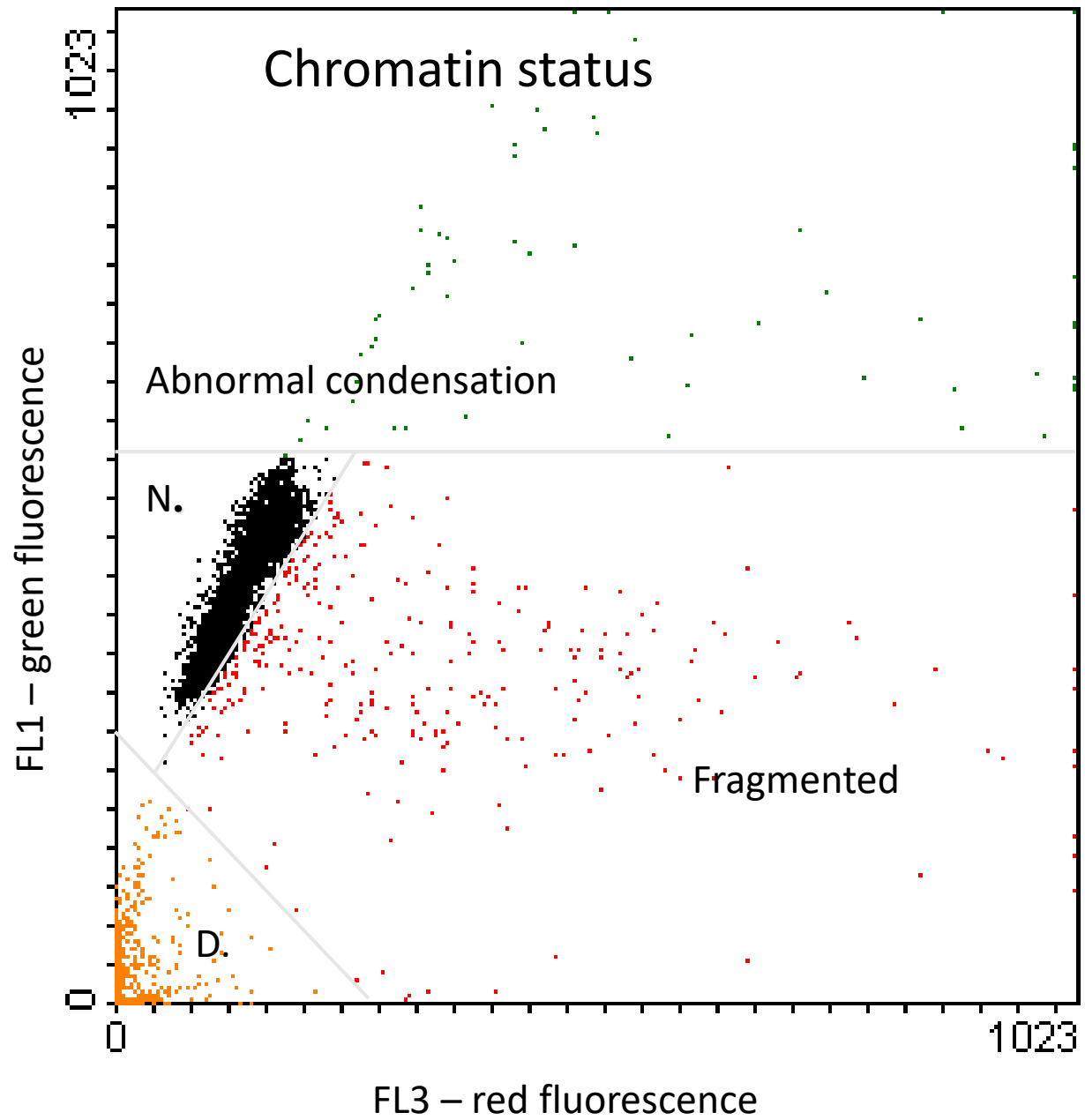
Dr. Szabolcs T. Nagy

Hungarian University of Agriculture and Life Sciences  
Institute of Animal Sciences  
Department of Precision Livestock Farming and Animal  
Biotechnics  
Keszthely, Hungary



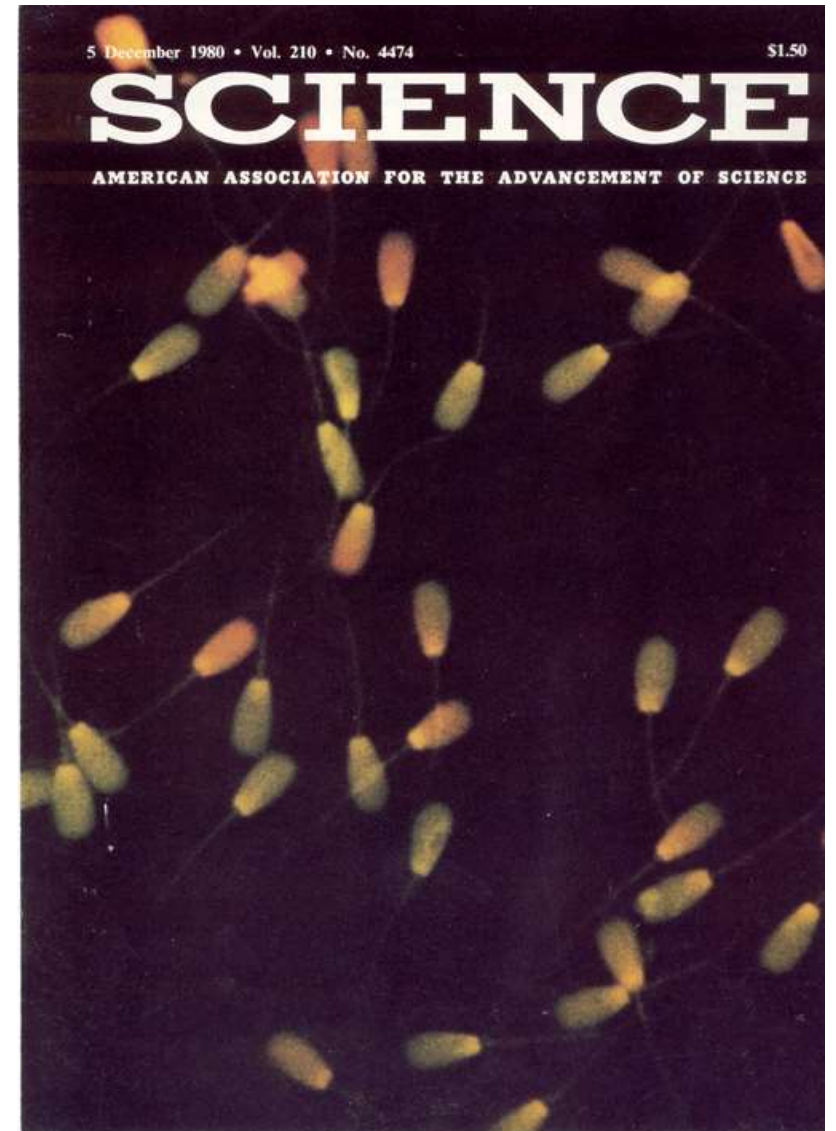
# SPERM CHROMATIN STRUCTURE ASSAY™





## QUANTAL vs. QUANTITATIVE

- Yes-or-no (quantal): viability
- Quantitative: mitochondria, DNA-fragmentation, etc.





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Theriogenology

Theriogenology 63 (2005) 1752–1763

[www.journals.elsevierhealth.com/periodicals/the](http://www.journals.elsevierhealth.com/periodicals/the)

## Sperm chromatin stability in frozen-thawed semen is maintained over age in AI bulls

Triin Hallap<sup>a,c,\*</sup>, Szabolcs Nagy<sup>a,b,d</sup>, Margareta Håård<sup>e</sup>,  
Ülle Jaakma<sup>c</sup>, Anders Johannisson<sup>b</sup>,  
Heriberto Rodriguez-Martinez<sup>a</sup>





Contents lists available at SciVerse ScienceDirect

Theriogenology

journal homepage: [www.theriojournal.com](http://www.theriojournal.com)



## Sperm chromatin structure and sperm morphology: Their association with fertility in AI-dairy Ayrshire sires

S. Nagy<sup>a,\*</sup>, A. Johannisson<sup>b</sup>, T. Wahlsten<sup>c</sup>, R. Ijäs<sup>d</sup>, M. Andersson<sup>e</sup>, H. Rodriguez-Martinez<sup>f</sup>

<sup>a</sup>Georgikon Faculty, Department of Animal Sciences and Animal Husbandry, University of Pannonia, Keszthely, Hungary

<sup>b</sup>Department of Anatomy, Physiology and Biochemistry, Swedish University of Agricultural Sciences (SLU), Ultuna, Uppsala, Sweden

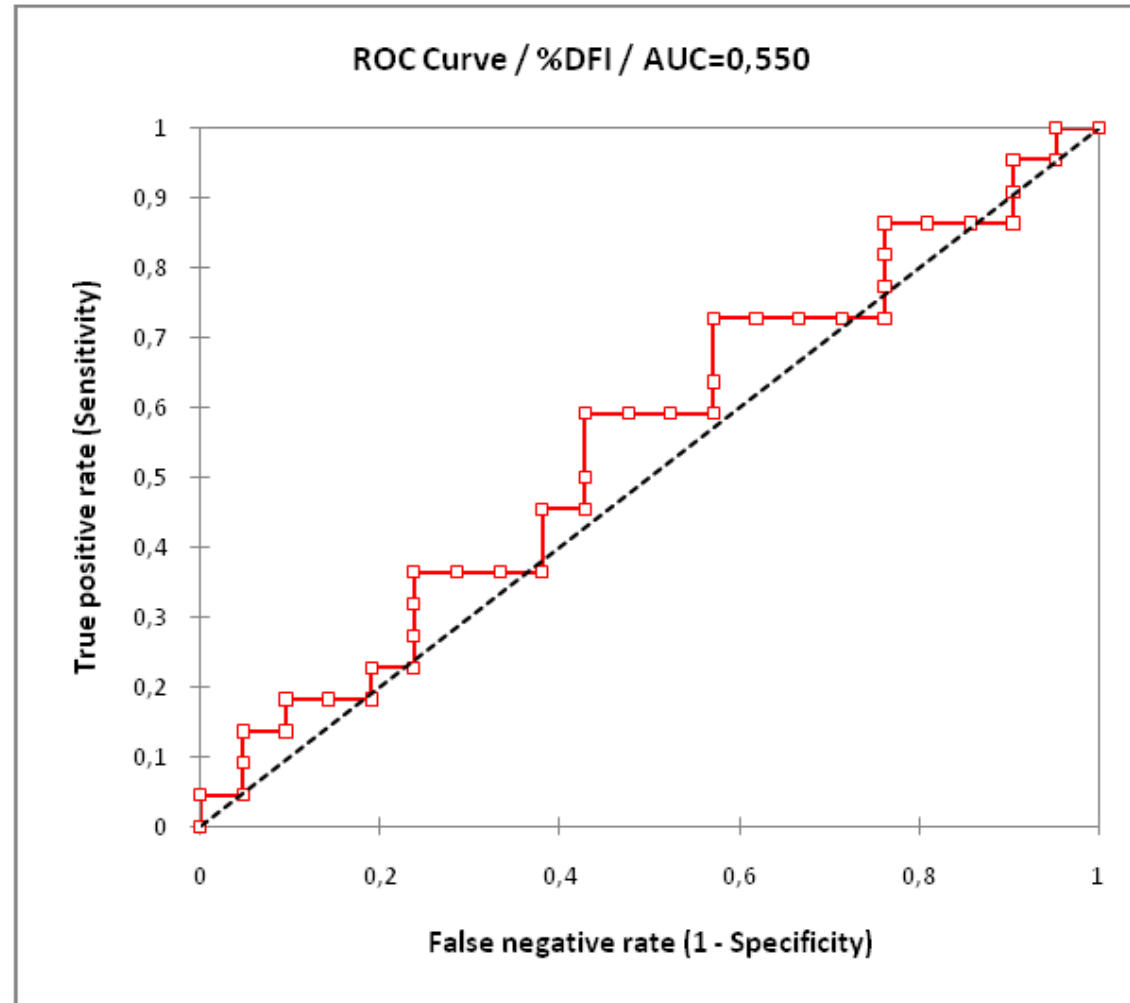
<sup>c</sup>Faba co-op Vantaa, Finland

<sup>d</sup>Viking Genetics Finland, Hollola, Finland

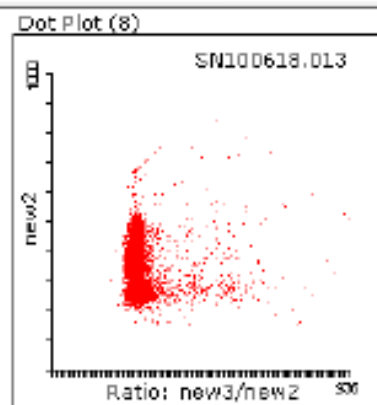
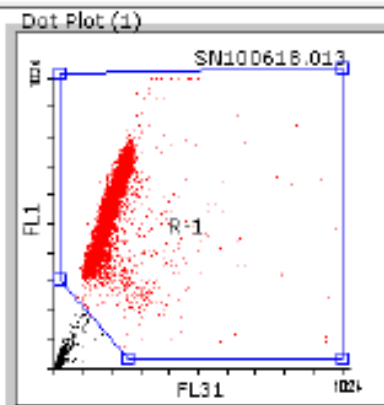
<sup>e</sup>Faculty of Veterinary Medicine, Department of Production Animal Medicine, University of Helsinki, Saarentaus, Finland

<sup>f</sup>Department of Clinical and Experimental Medicine, Linköping University, Linköping, Sweden

# SCSA diagnostic value...







Cell Calculator (2)

File Name SN100618.013  
 Parameter Name new1  
 Parameter Max 2000  
 Visualization Lin  
 Row Formula  $\{FL1\} + \{FL31\}$   
 Formula  $\{FL1\} + \{FL31\}$

Cell Calculator (3)

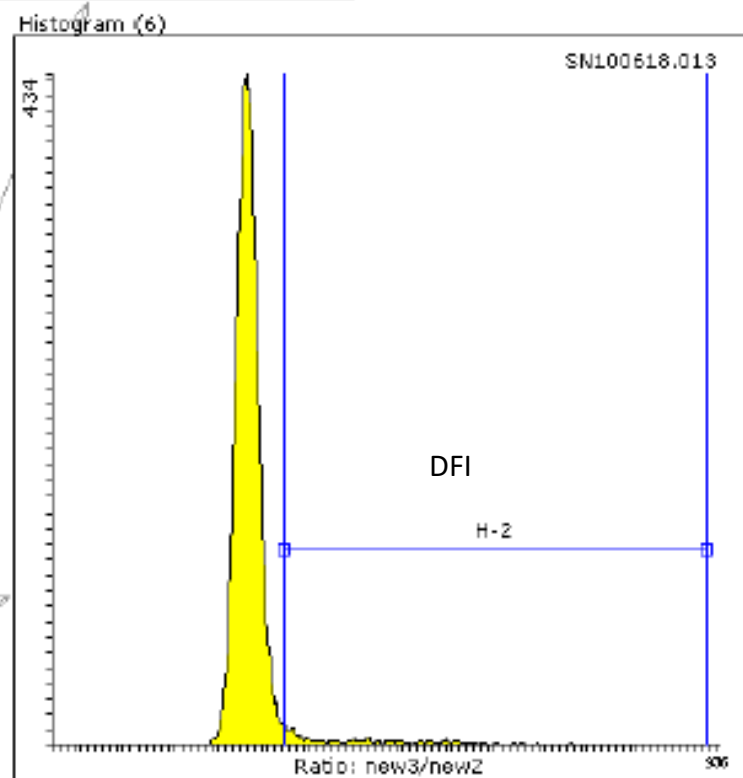
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 Parameter Name new2  
 Parameter Max 1000  
 Visualization Lin  
 Row Formula  $\{NEW1\} / 2$   
 Formula  $\{NEW1\} / 2$

Cell Calculator (4)

File Name SN100618.013  
 Parameter Name new3  
 Parameter Max 512000  
 Visualization Lin  
 Row Formula  $\{FL31\} * 512$   
 Formula  $\{FL31\} * 512$

Ratio Calculator (5)

File SN100618.013  
 Nominator new3  
 Denominator new2  
 Multiplier 1  
 Parameter max 936 (automatic)  
 Parameter name Ratio: new3/new2  
 Visualization Lin



Statistics (7)

	Events	% of Vis	Mean	GeoMean	Median	CU
All events	9 106	100,00	279,20	276,63	271,54	16,74
H-2	421	4,62	441,79	429,17	418,91	25,36







Contents lists available at [ScienceDirect](#)

## Applied Soil Ecology

journal homepage: [www.elsevier.com/locate/apsoil](http://www.elsevier.com/locate/apsoil)



Short communication

### Rapid analysis of photoautotroph microbial communities in soils by flow cytometric barcoding and fingerprinting

László Menyhárt<sup>a</sup>, Szabolcs Nagy<sup>b</sup>, Anita Lepossa<sup>c,\*</sup>

<sup>a</sup> University of Pannonia, Georgikon Faculty, Department of Economic Methodology, H8360 Keszthely, Deák F. u. 16., Hungary

<sup>b</sup> University of Pannonia, Georgikon Faculty, Department of Animal Sciences, H8360 Keszthely, Deák F. u. 16., Hungary

<sup>c</sup> University of Pannonia, Georgikon Faculty, Department of Crop Production and Land Use, H8360 Keszthely, Deák F. u. 16., Hungary



# R-environment



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▶ BiologicalQuestion (615)
▶ Infrastructure (341)
▶ ResearchField (469)
▶ StatisticalMethod (527)
▼ Technology (991)
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ddPCR (2)
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qPCR (11)
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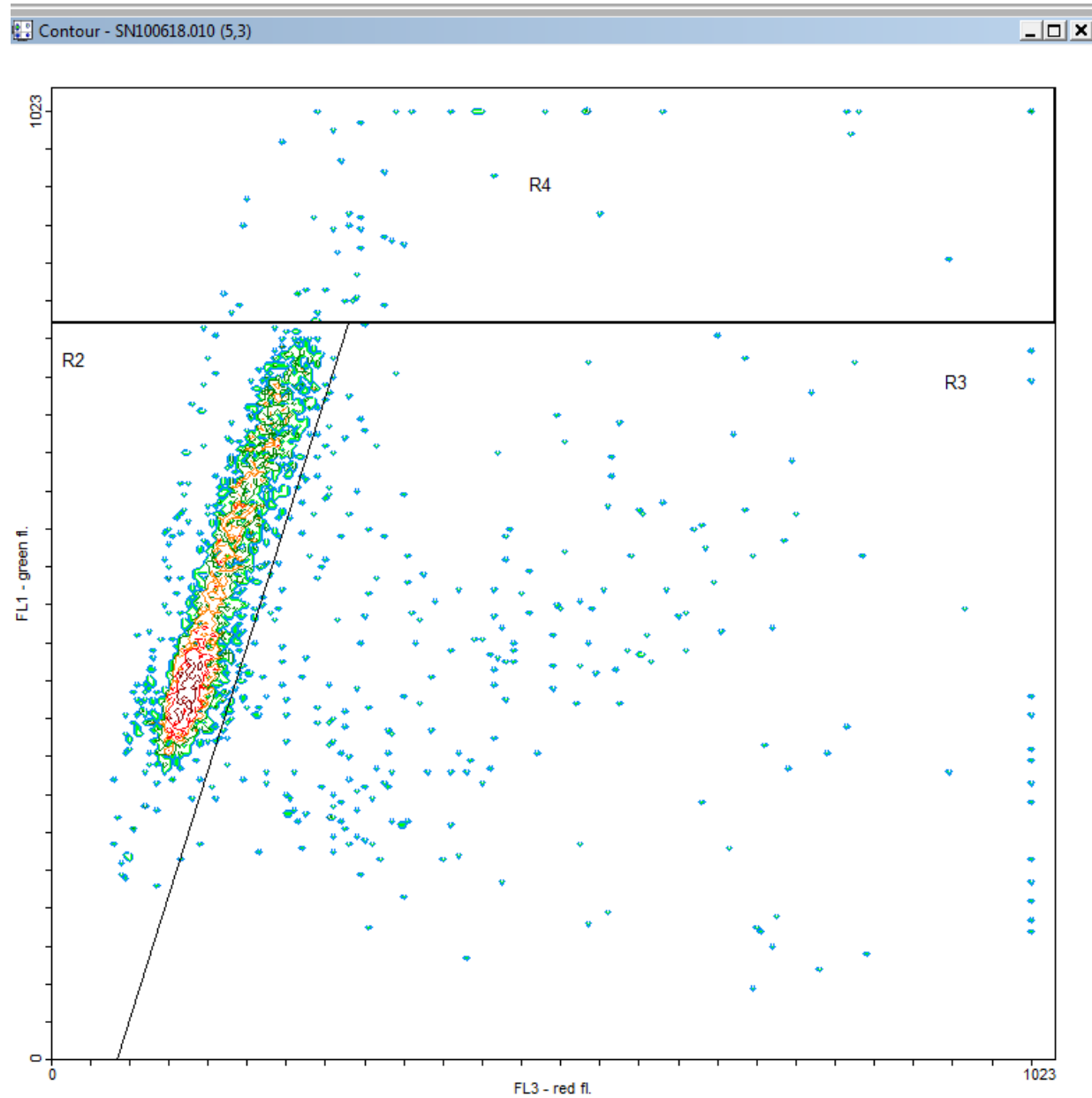
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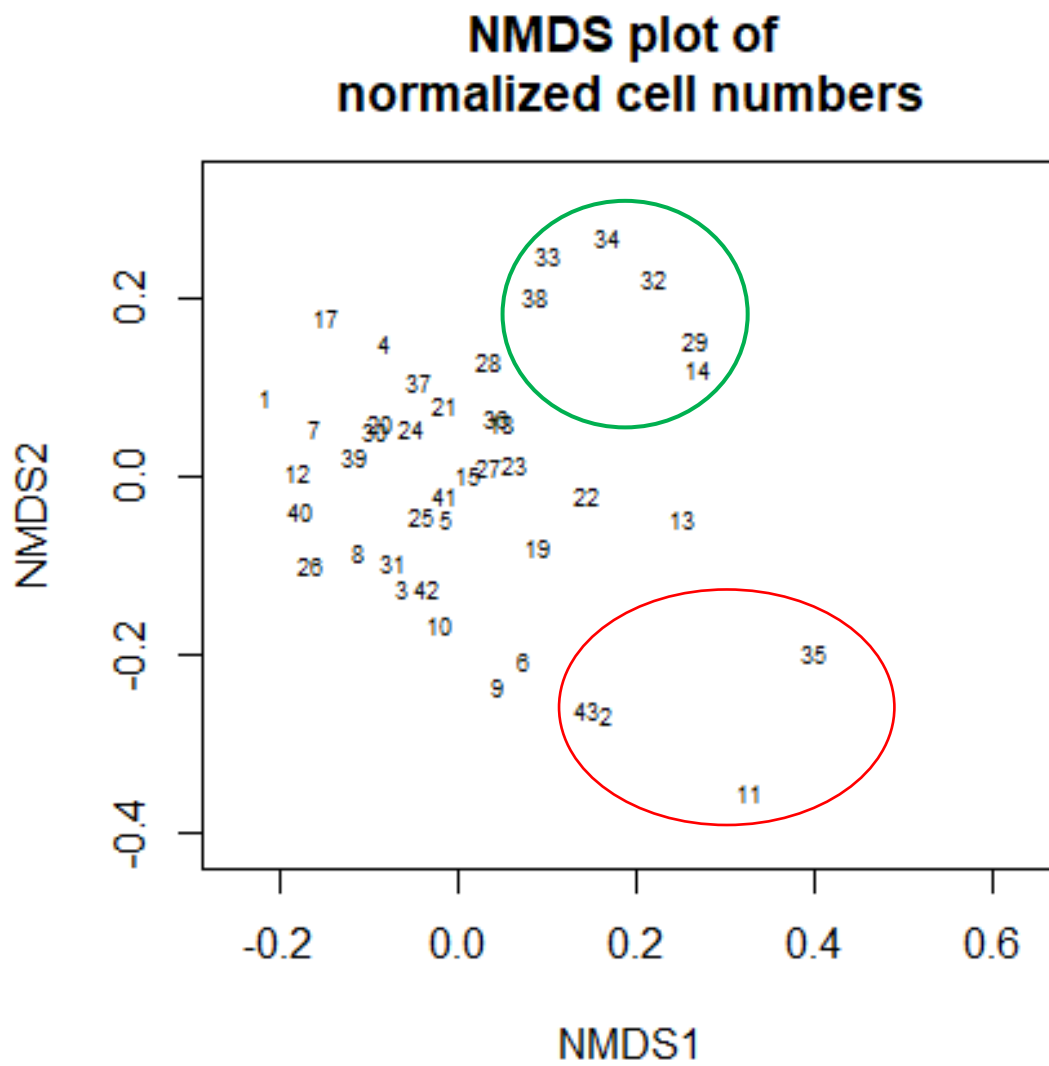
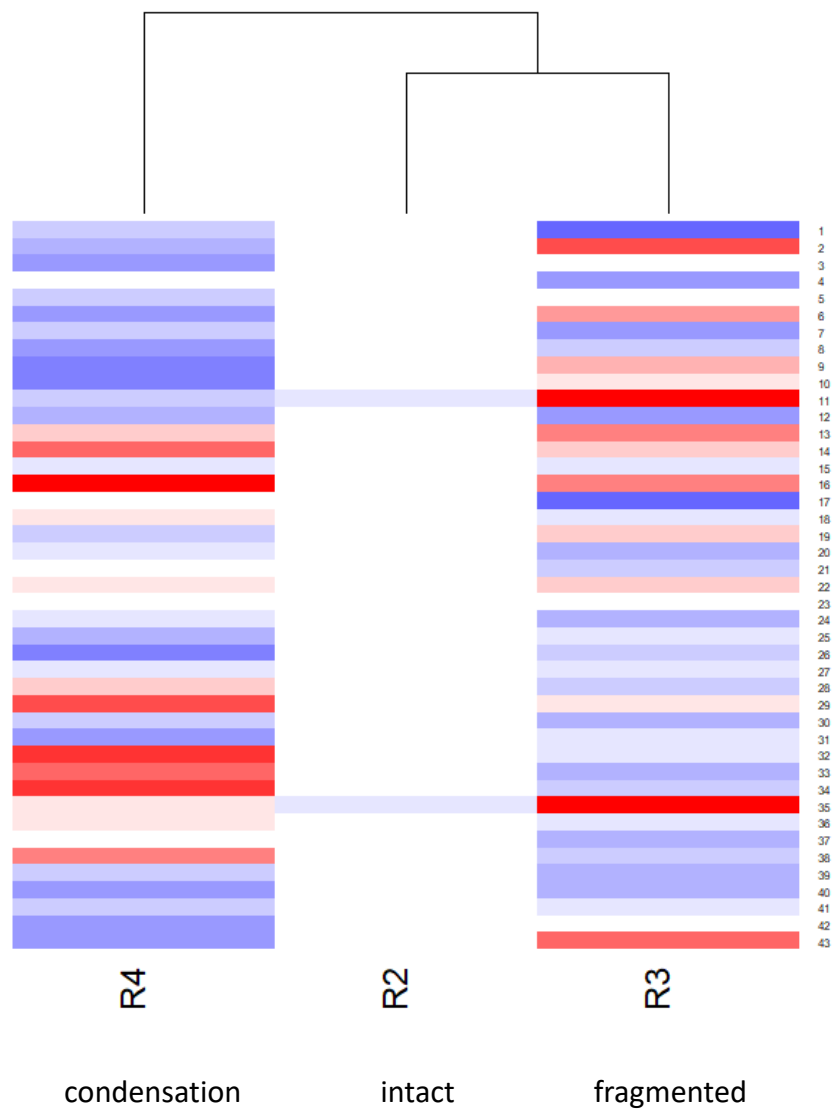
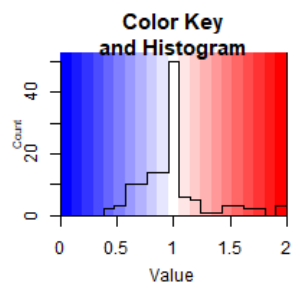
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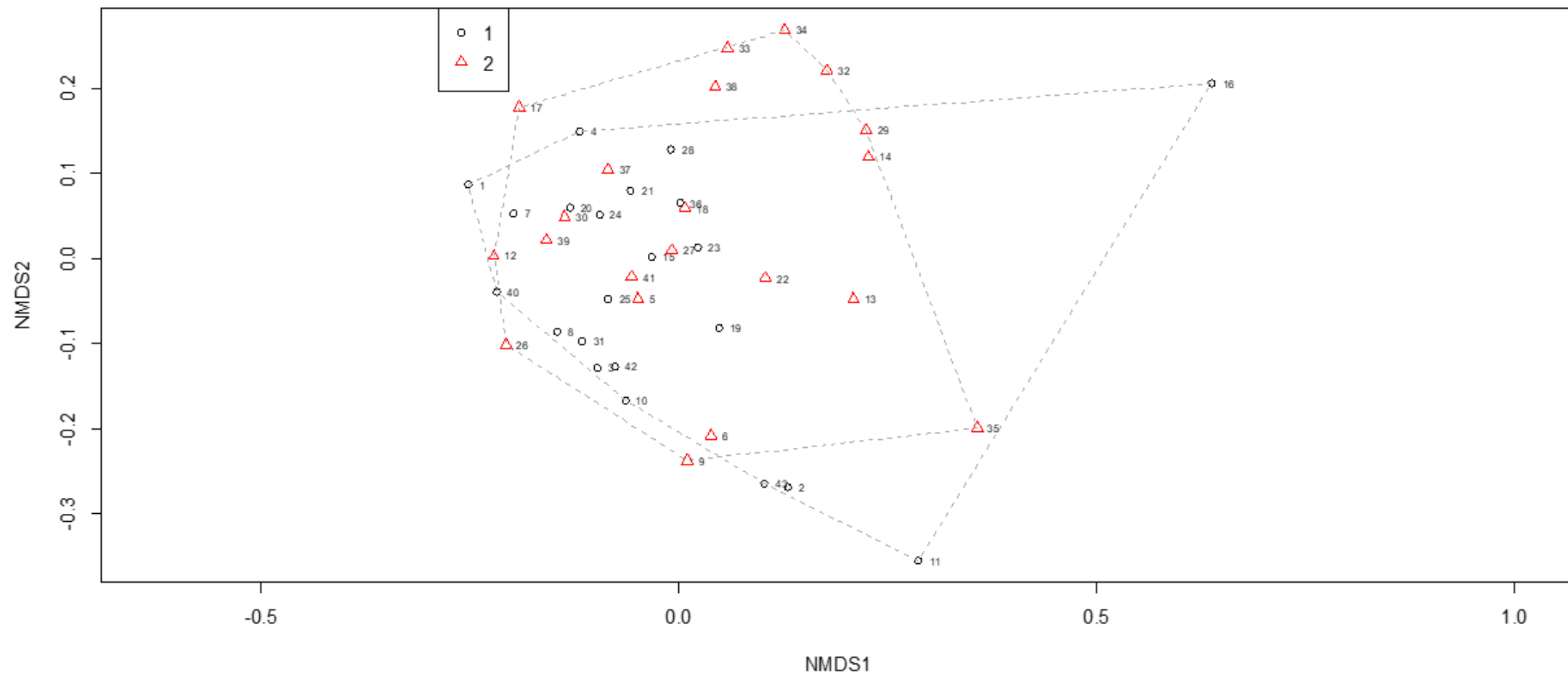
# Flow barcoding (CyBAR) - SCSA







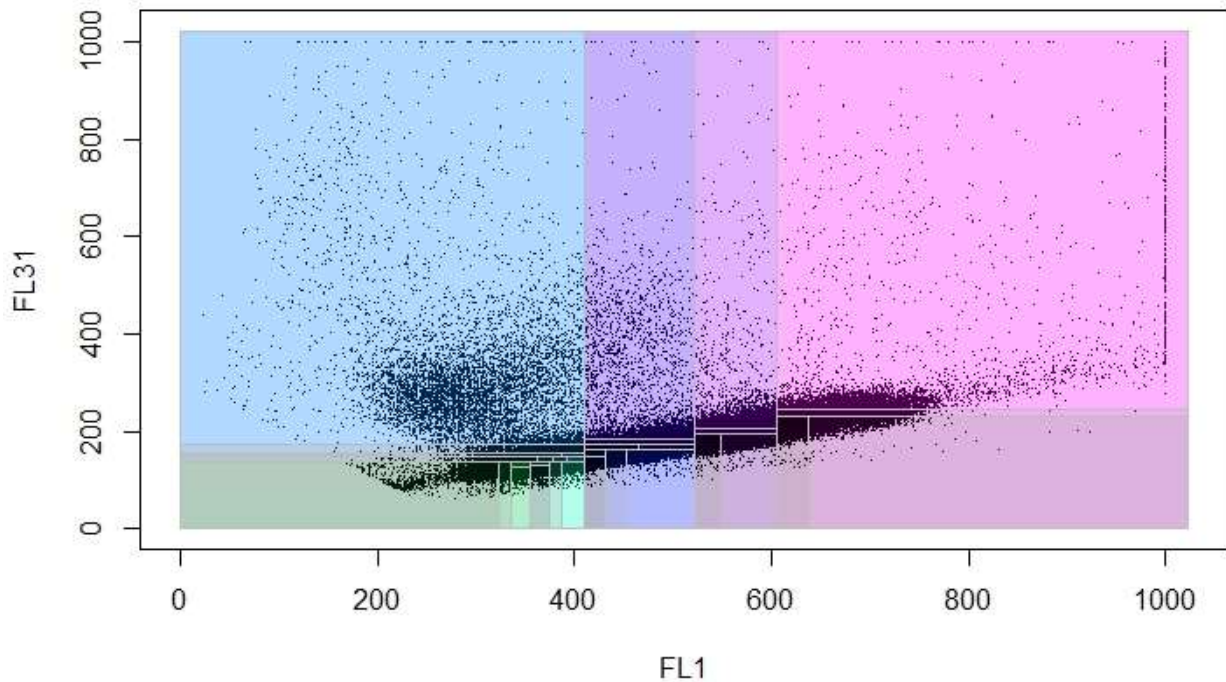
NMDS plot of  
SCSA\_CYBAR; NRR



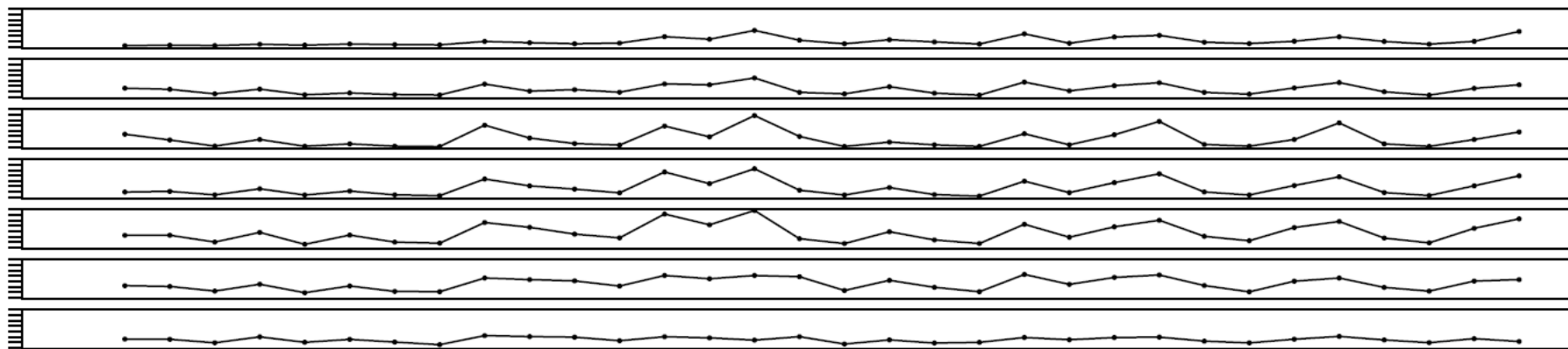
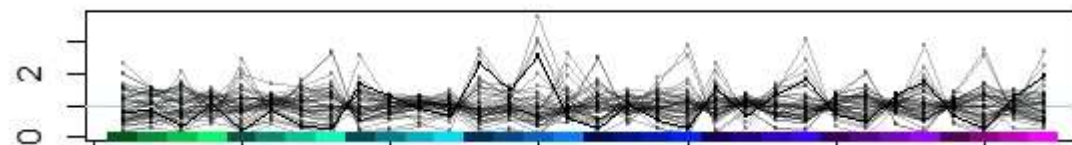
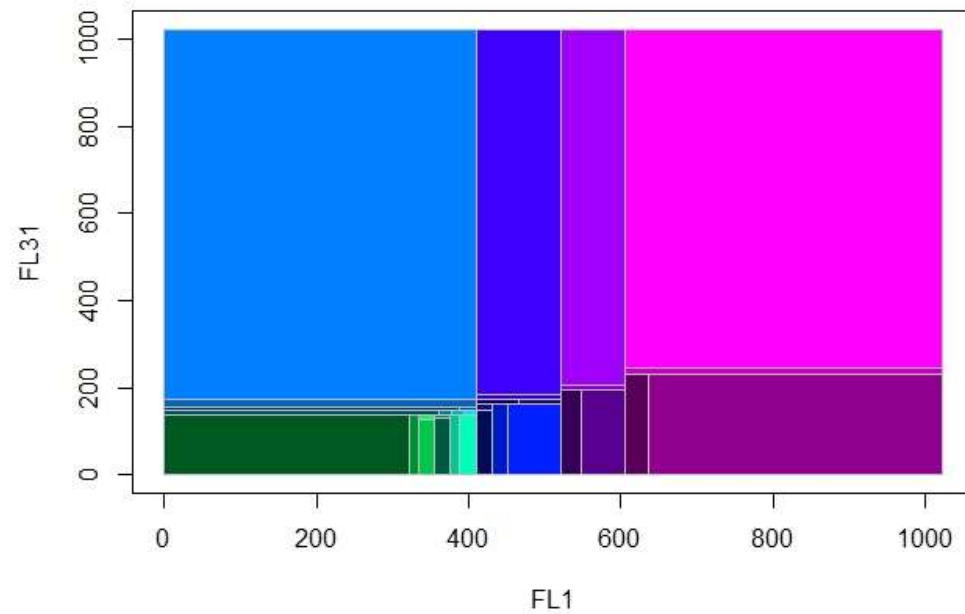
Legend: 1=low NRR; 2=normal NRR

# Flow fingerprinting (FlowFP) - SCSA

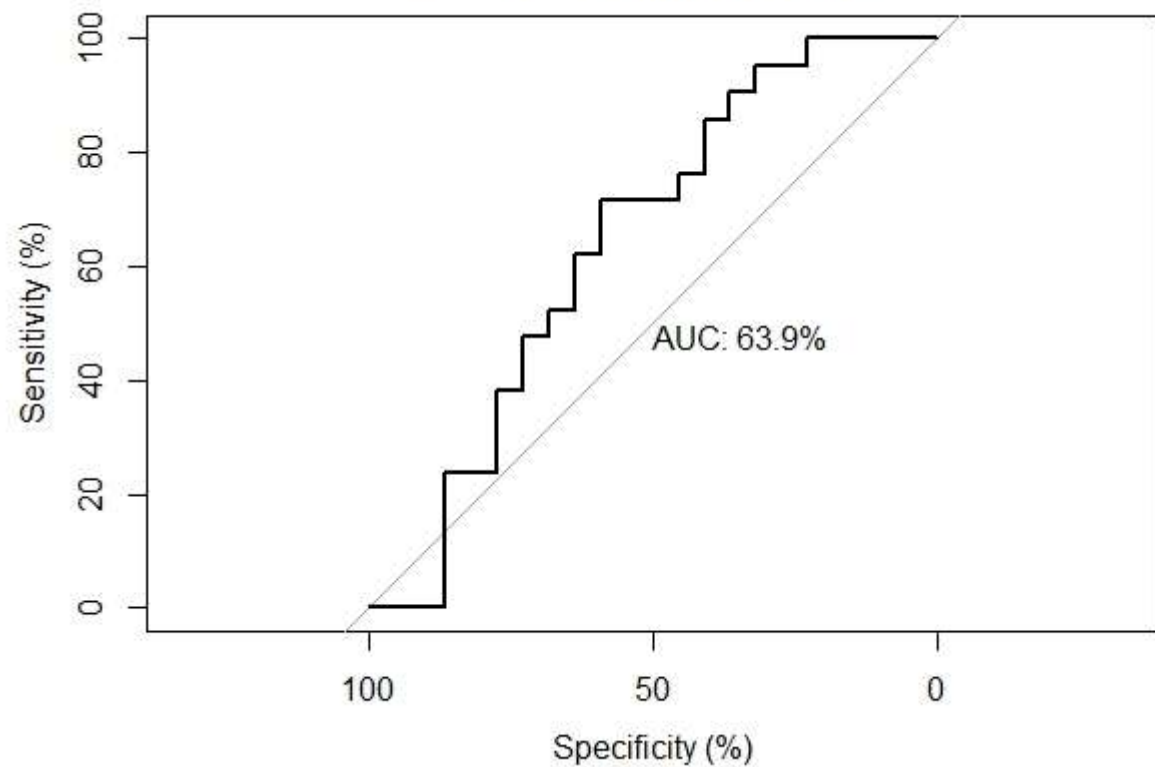
Model



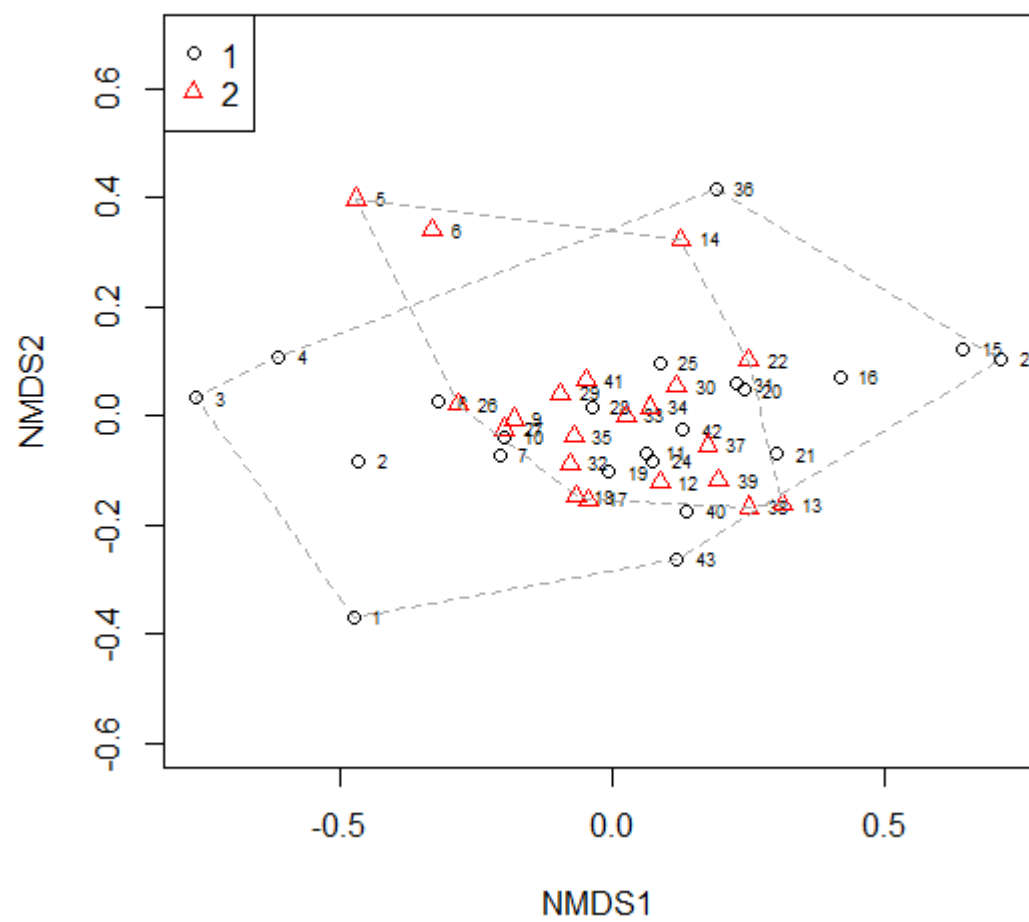
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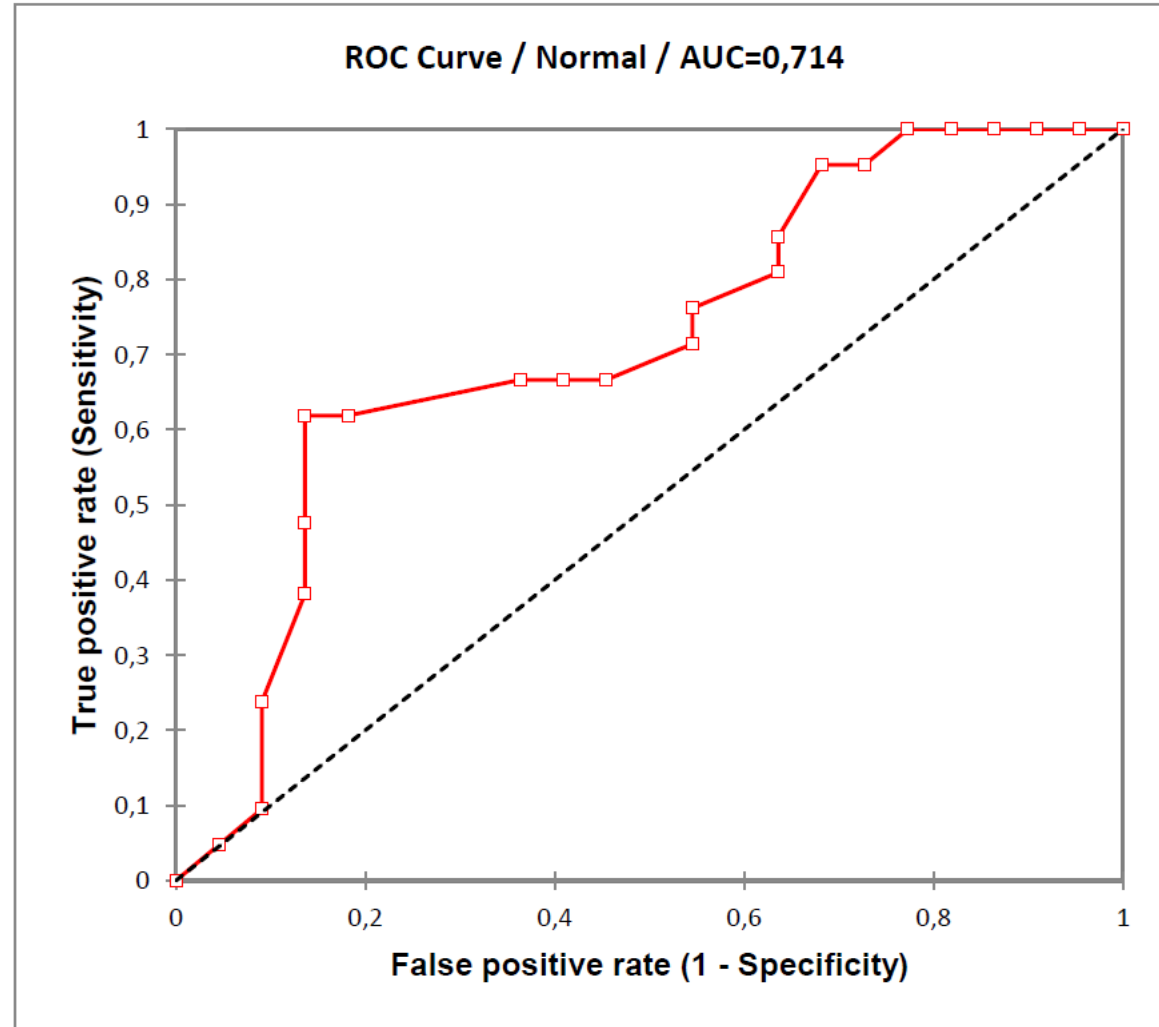
ROC SCSA fingerprint %



NMDS plot Fingerprint



# Normal morphology!

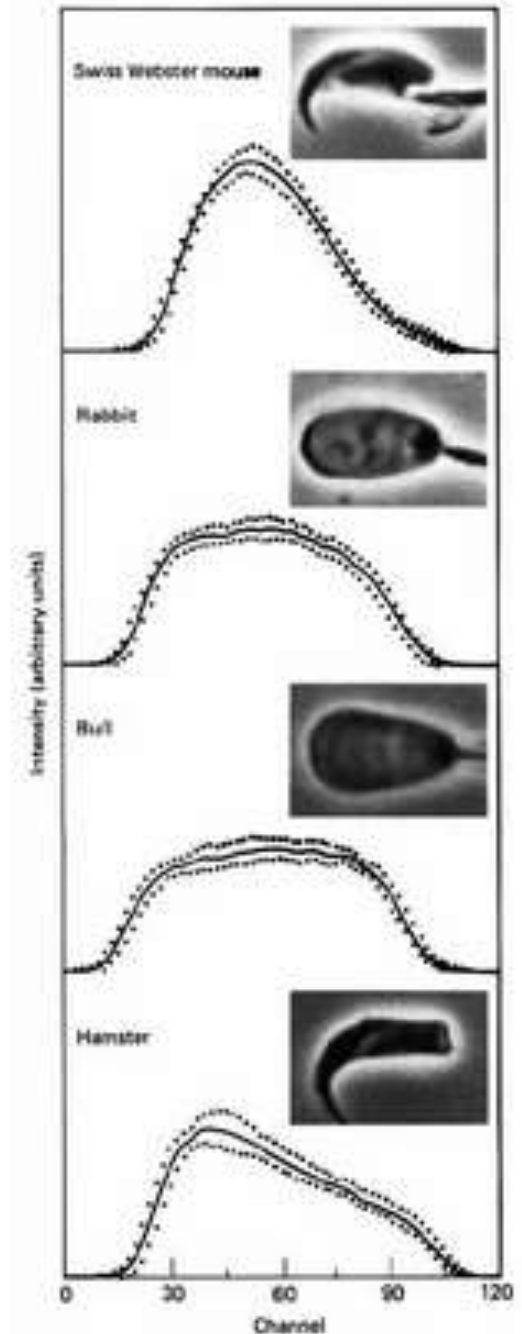


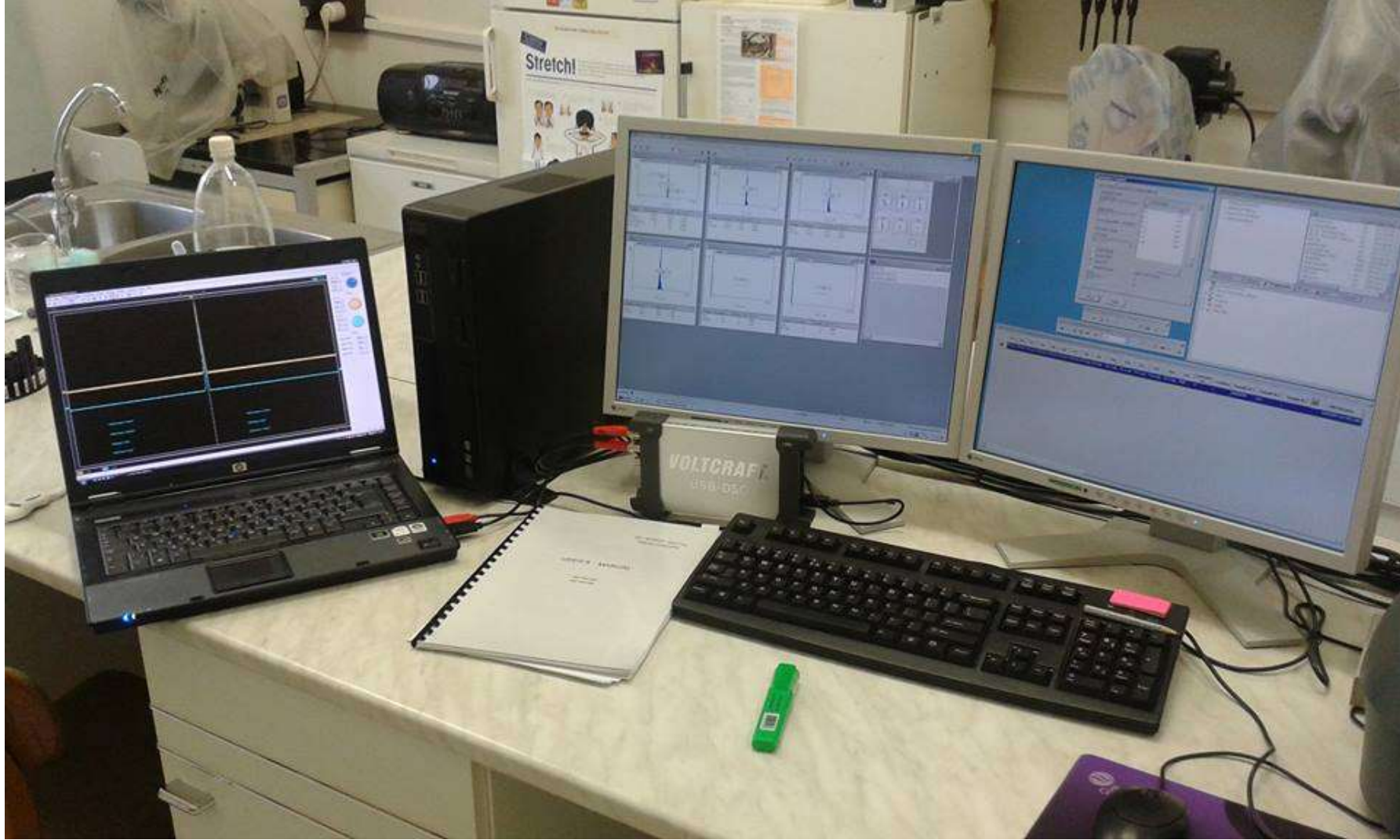
# Quantification of Mammalian Sperm Morphology by Slit-Scan Flow Cytometry<sup>1</sup>

David A. Benaron, Joe W. Gray,<sup>2</sup> Barton L. Gledhill, Suzanne Lake, Andrew J. Wyrobek, and Ian T. Young

Lawrence Livermore National Laboratory, Biomedical Sciences Division, L-452, University of California, Livermore, California 94550

Received for publication August 18, 1981; accepted November 19, 1981







# PulSA approach

## Pulse Width for Particle Sizing

Robert A. Hoffman<sup>1</sup>

<sup>1</sup>BD Biosciences, San Jose, California

### ABSTRACT

The widths of optical pulses in flow cytometry contain information about the size of particles. This size information is independent of many of the factors that affect light scatter as a measure of particle size, and any light scatter or fluorescence signal can be used to measure pulse width. For fluorescence signals, the pulse width can be predicted theoretically for many particle shapes, and quantitative size calibration is possible. To be a meaningful independent parameter, the pulse-width measurement must be independent of the pulse amplitude. This unit provides protocols for determining the signal range over which amplitude independent pulse-width measurements can be made and methods for calibrating the pulse-width measurements to particle diameter. Calibration and application examples are provided and briefly discussed. *Curr. Protoc. Cytom.* 50:1.23.1-1.23.17.

© 2009 by John Wiley & Sons, Inc.

Keywords: pulse width • flow cytometry • size • fluorescence • light scatter

Published: 18 March 2012

## Tracking protein aggregation and mislocalization in cells with flow cytometry

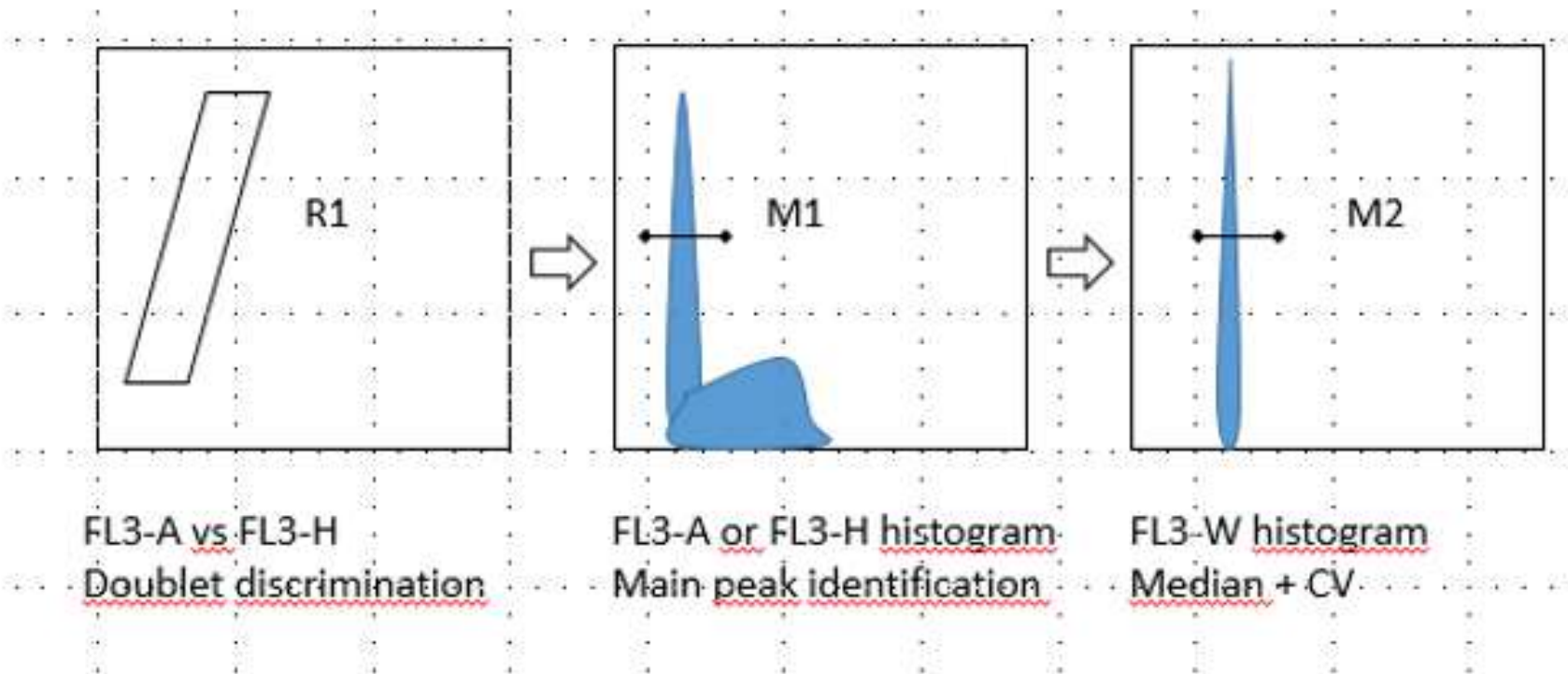
[Yasmin M Ramdzan](#), [Saskia Polling](#), [Cheryl P Z Chia](#), [Ivan H W Ng](#), [Angelique R Ormsby](#), [Nathan P Croft](#), [Anthony W Purcell](#), [Marie A Bogoyevitch](#), [Dominic C H Ng](#), [Paul A Gleeson](#) & [Danny M Hatters](#) 

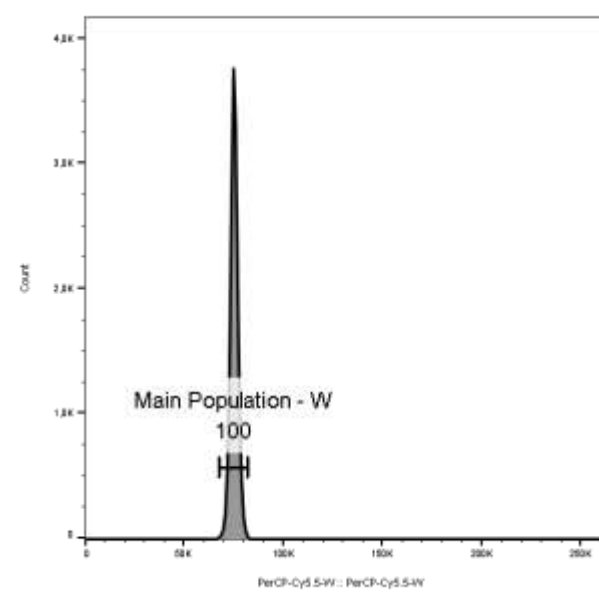
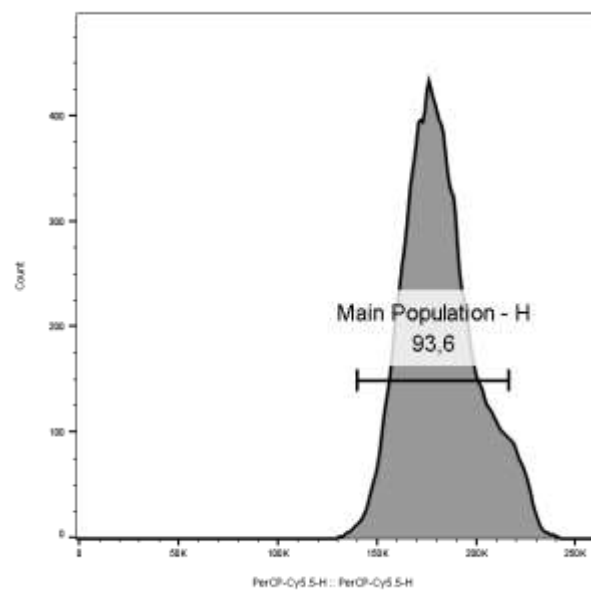
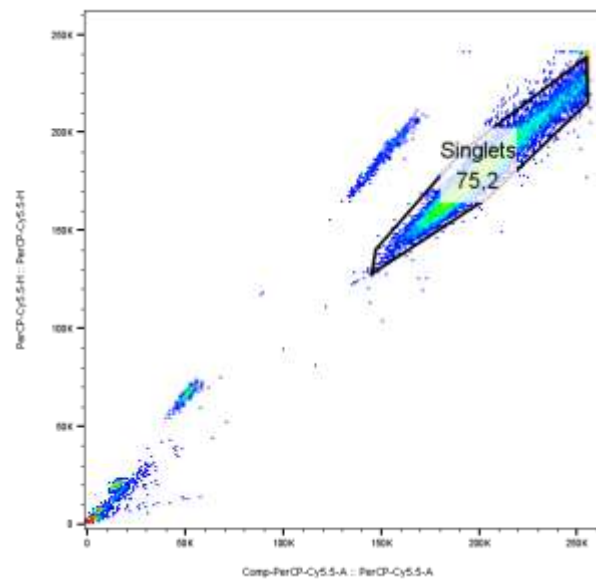
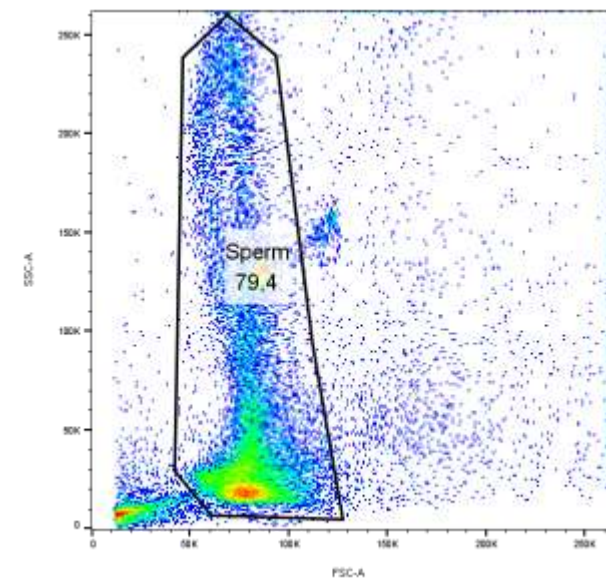
*Nature Methods* 9, 467–470 (2012) | [Cite this article](#)

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# PulSA approach – gating plan

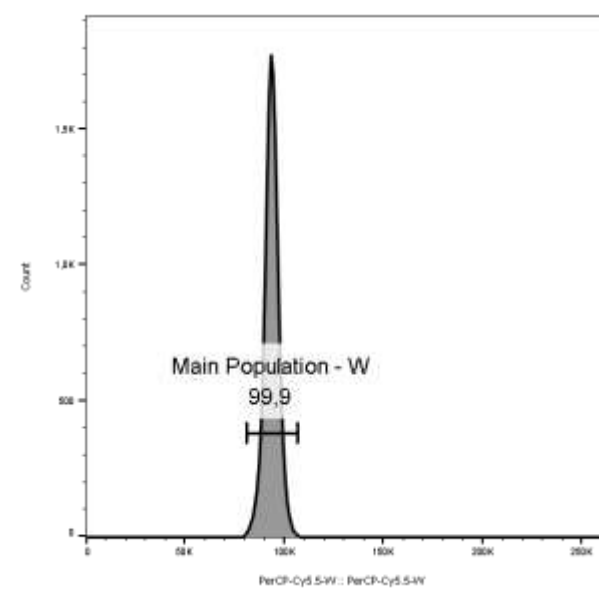
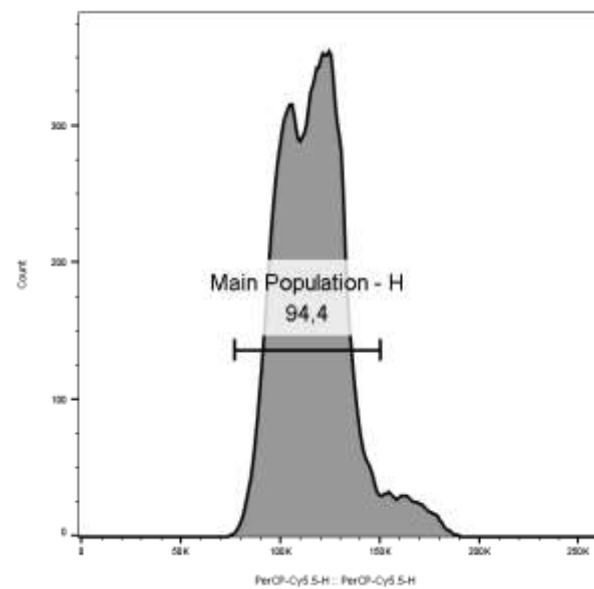
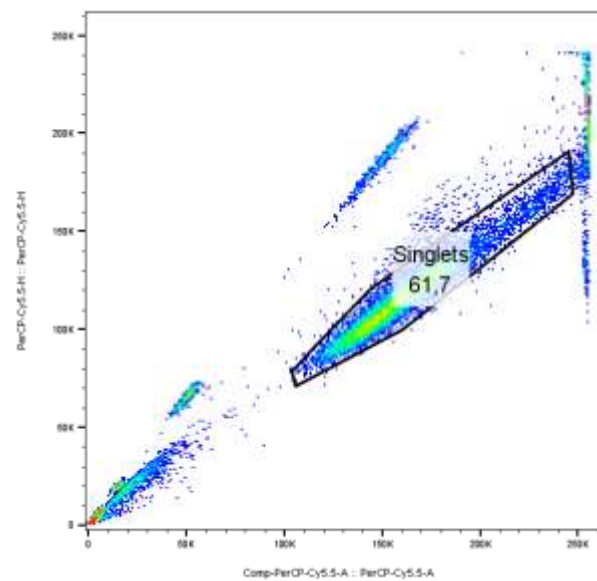
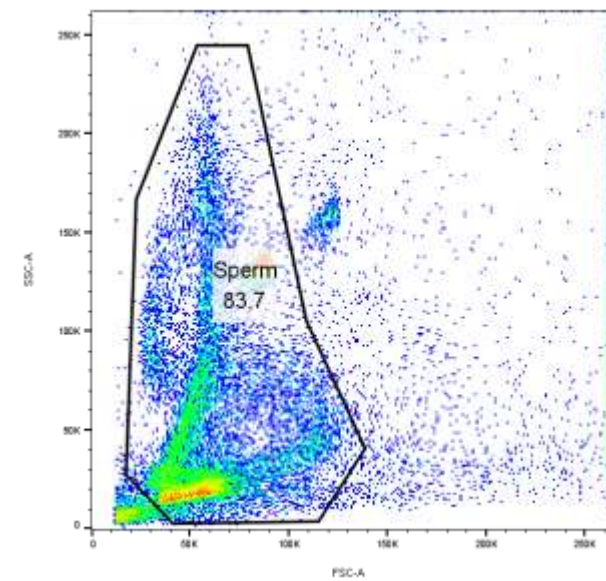
A two-step logical gating would be applied to do pulse shape analyses: doublet discrimination (R1), main peak identification (M2), then using R1 AND M1 logical gating, the FL3 Width histogram values (median or mean, CV) would be recorded.





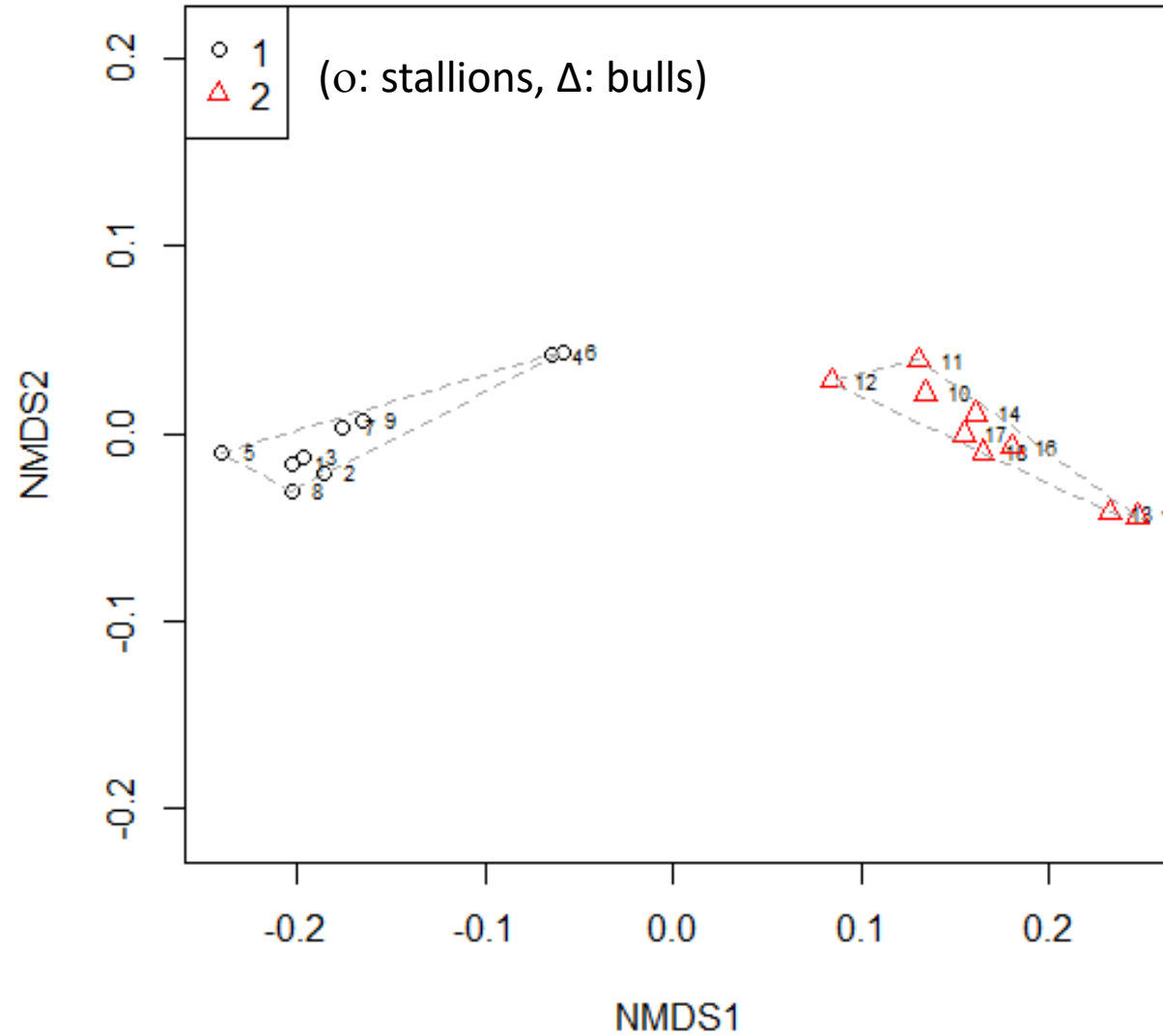
Stallion

Bull

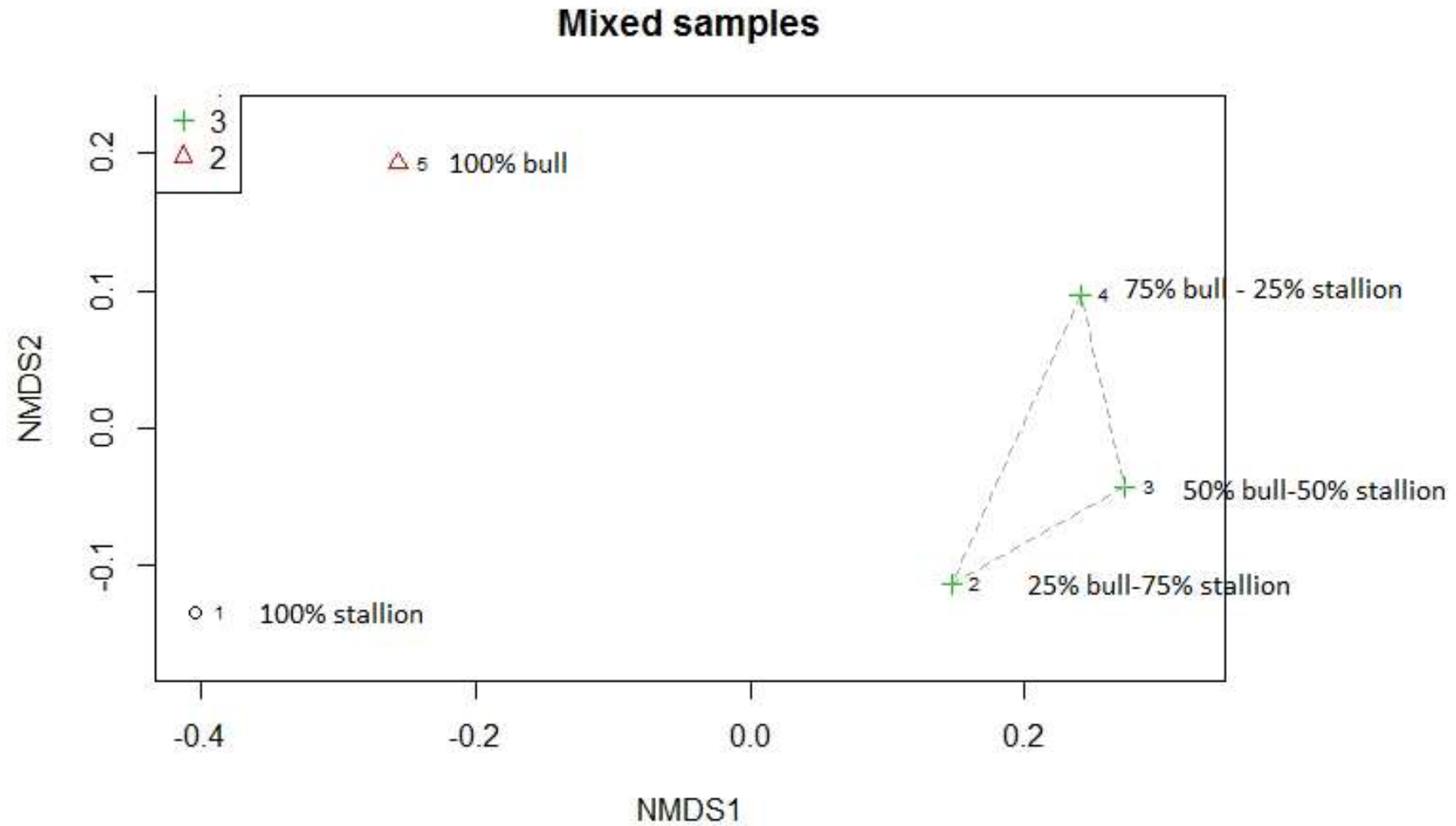


Bulls vs stallions

NMDS plot of Fxcycle with beads adjusted



# Bulls vs stallions – mixed samples („abnormals”)





**QUICK CYTOGENETIC SCREENING OF BREEDING BULLS  
USING FLOW CYTOMETRIC SPERM DNA HISTOGRAM  
ANALYSIS**

Szabolcs NAGY<sup>1\*</sup>, Péter J. POLGÁR<sup>1</sup>, Magnus ANDERSSON<sup>2</sup> and András KOVÁCS<sup>3</sup>

<sup>1</sup>Department of Animal Sciences and Animal Husbandry, Georgikon Faculty, University of Pannonia, Deák F. u. 16, H-8360 Keszthely, Hungary; <sup>2</sup>Department of Production Animal Medicine, Faculty of Veterinary Medicine, University of Helsinki, Saari Unit, Saarentaus, Finland; <sup>3</sup>Institute of Animal Science, Biotechnology and Nature Conservation, Faculty of Agricultural and Food Sciences and Environmental Management, University of Debrecen, Debrecen, Hungary

(Received 7 December 2015; accepted 4 May 2016)

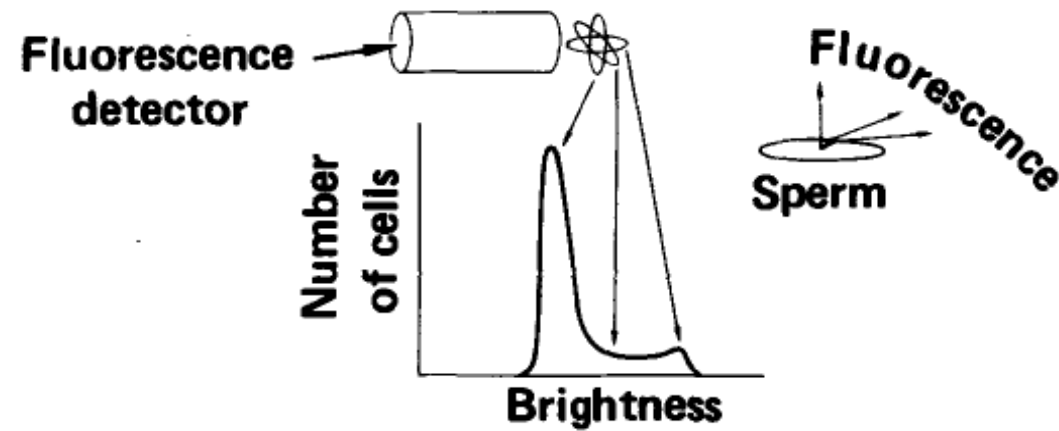
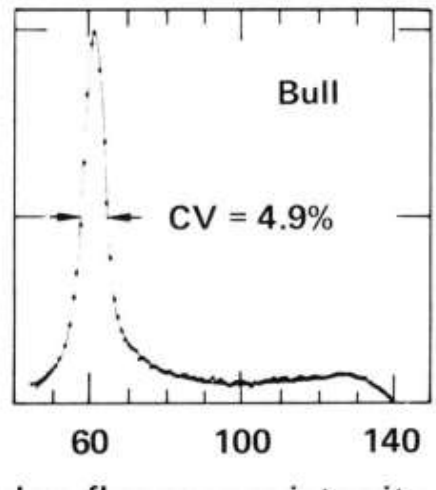


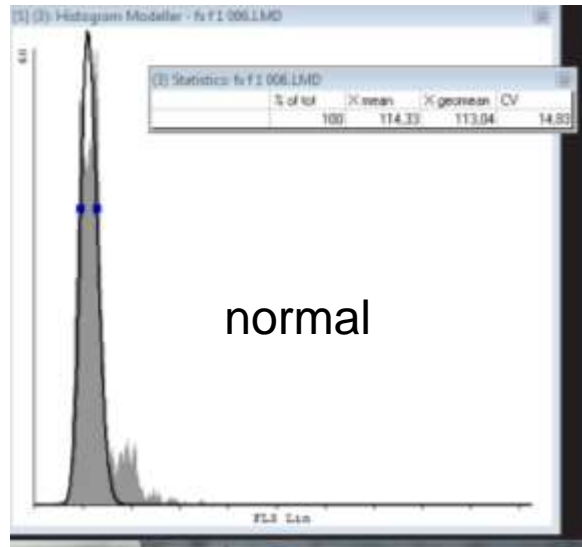
**Cytometry of Deoxyribonucleic Acid Content  
and Morphology of Mammalian Sperm<sup>1,2</sup>**

1983 J Dairy Sci 66:2623-2634

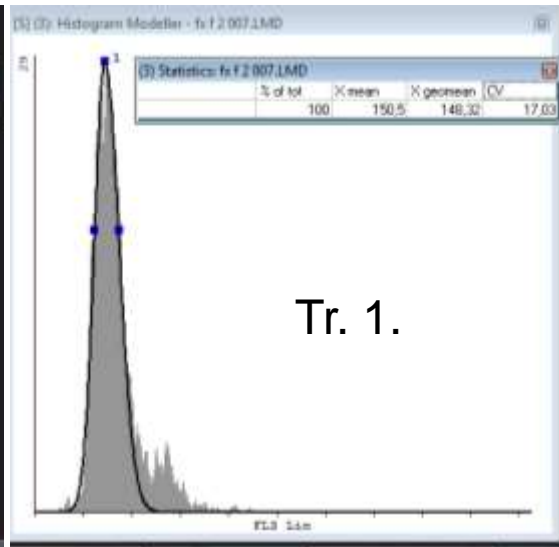
**BARTON L. GLEDHILL**  
Lawrence Livermore National Laboratory  
Biomedical Sciences Division  
University of California  
P. O. Box 5507 L-452  
Livermore 94550

Effect of random sperm head orientation on the DNA-histogram shape

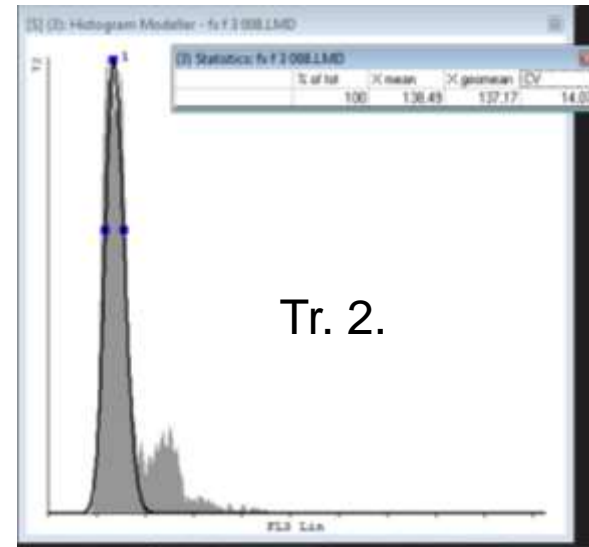




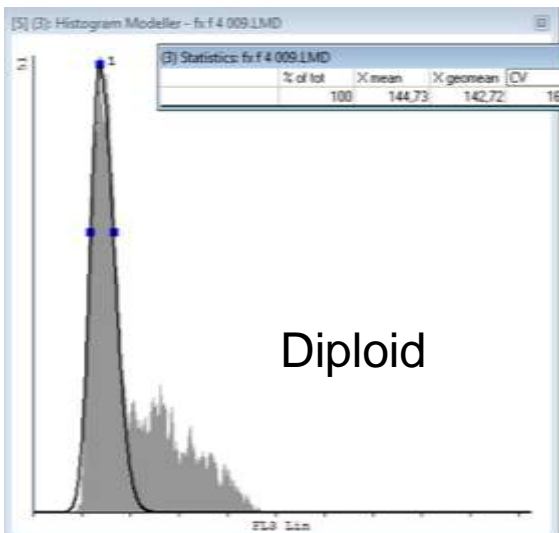
normal



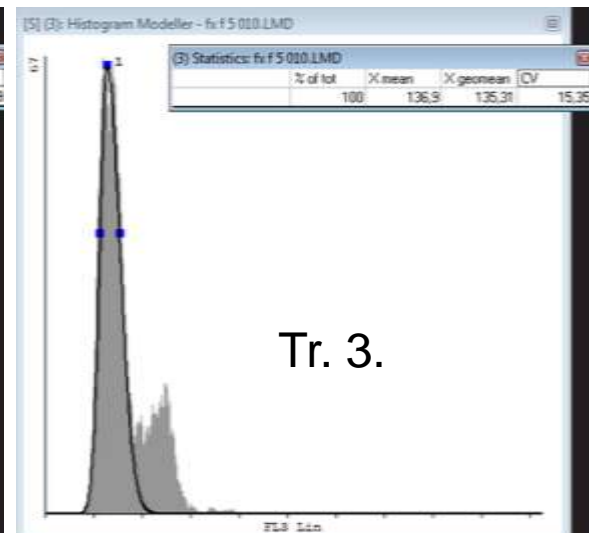
Tr. 1.



Tr. 2.



Diploid

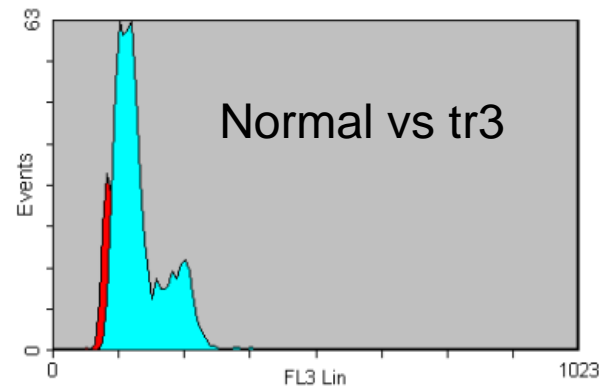
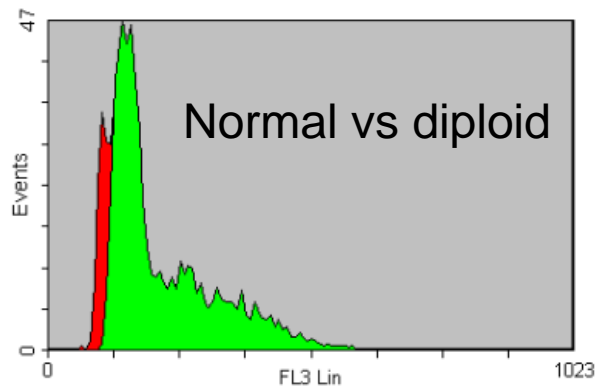
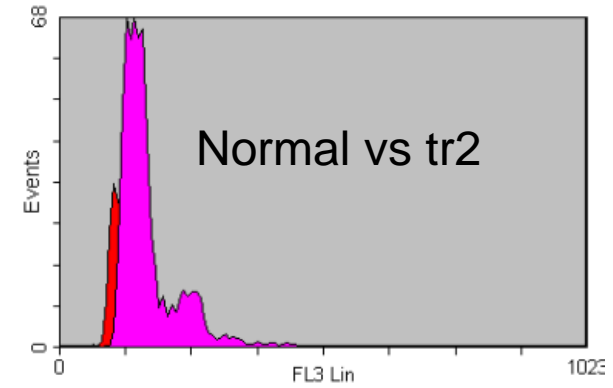
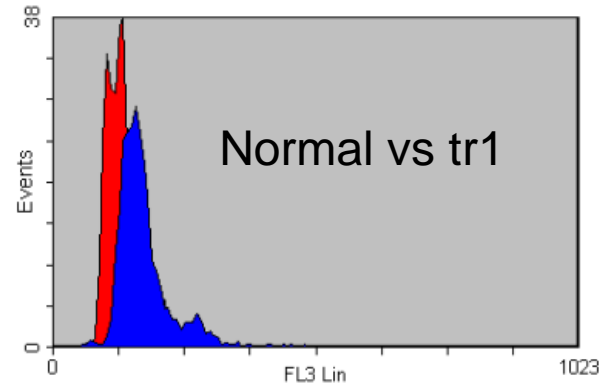
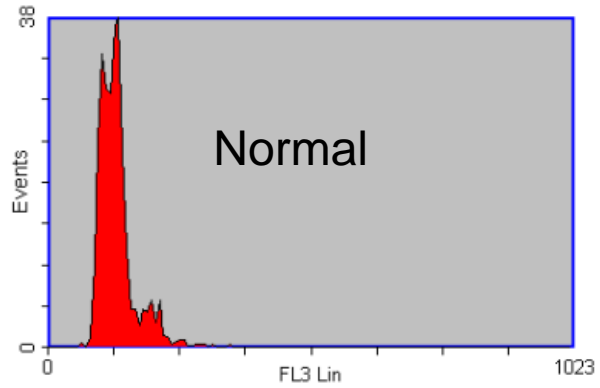


Tr. 3.

Histogram modelling:

Assuming normal distribution and adding a gaussian curve to the main peak

# Histogram overlapping for Kolmogorov-Smirnov analysis



## Cellular Symphony Flow Cytometry Software

Visit the website

### The Cellular Symphony

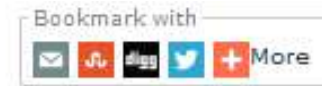
The Cellular Symphony is an audio representation of flow cytometric data. Each cell is represented by musical notes of timbre, pitch and volume dependent on its FCM parameters.

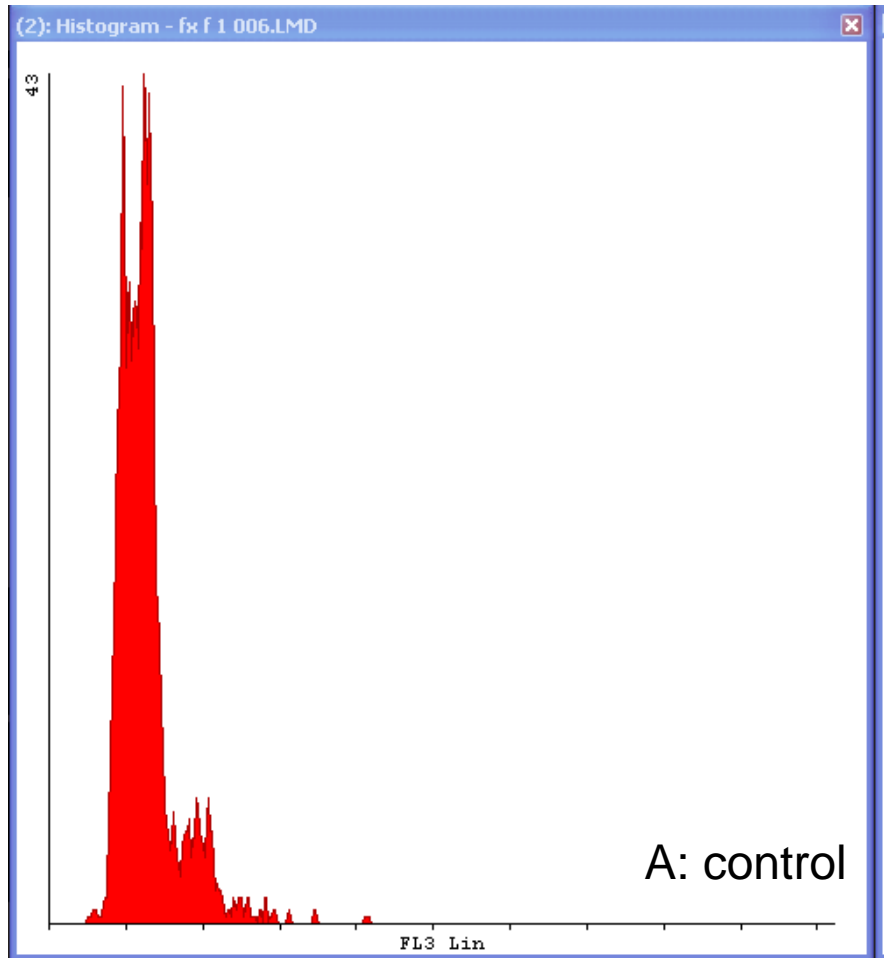
The program correlates the audio output with 2D and 3D graphical display. It may be that only a musical savant can detect the intricacies in a 3-instrument cellular symphony or it may be that the average cytometrist also can do so with practice. Your comments are invited.

This software has been developed and used at The Walter and Eliza Institute and is provided in a spirit of collegiality for testing by interested parties. It is provided without warranty of any kind and no claims are made regarding its suitability for any task. All are Java programs and will run on systems with Java 1.4.2 or later installed. Unpack the downloaded file to extract the application and launch by double-clicking.

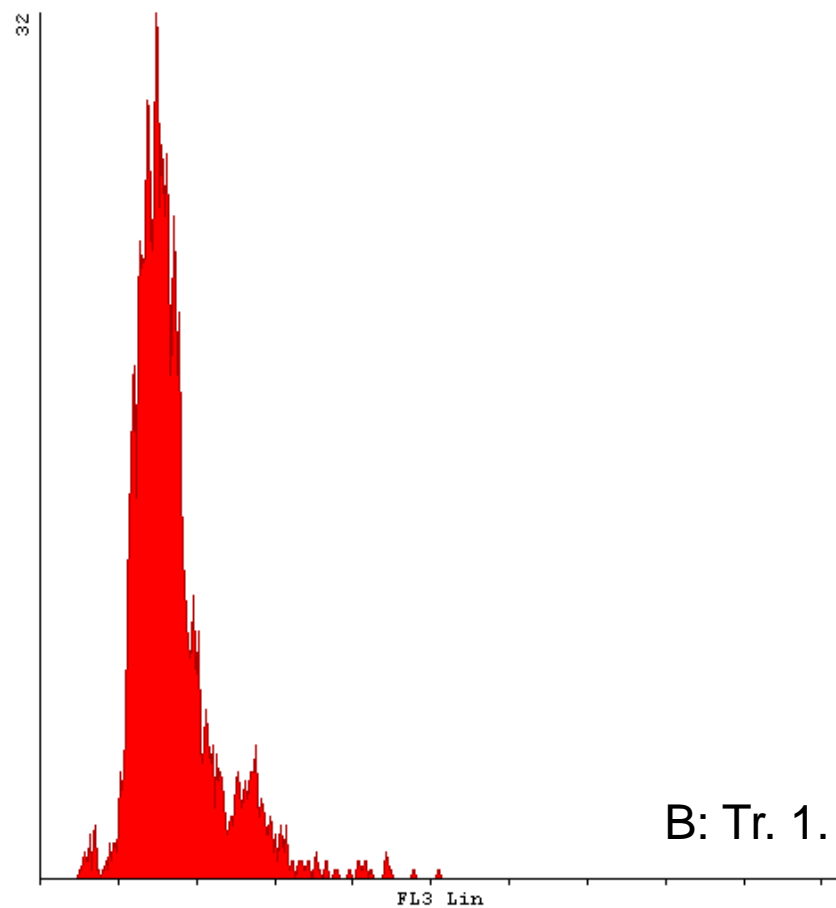
**WARNING: Do not subject primary data to any of these programs. All files should be backed up prior to processing.**

- [Download Cellular Symphony for Macintosh \[114,173 bytes\]](#).
- [Download Cellular Symphony for other systems \[429,226 bytes\]](#).





(2): Histogram - fx f 2 007.LMD



Cytogenet Genome Res 121:245–248 (2008)  
(DOI:10.1159/000138891)

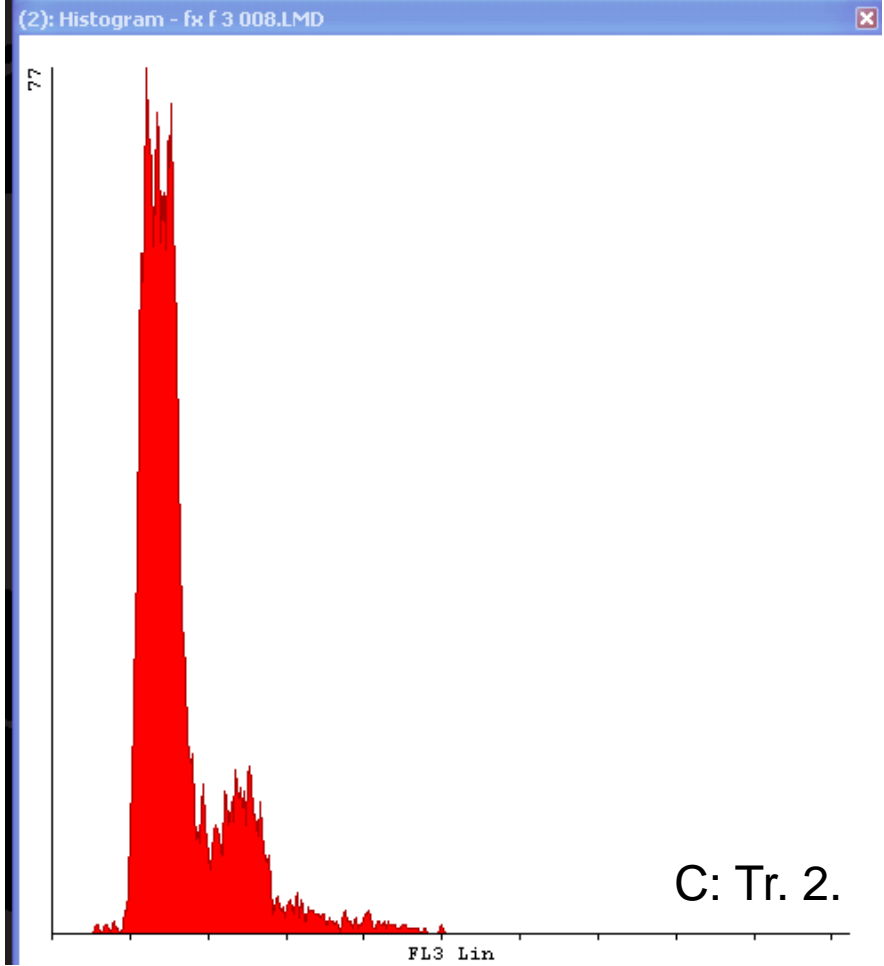
## Identification of a new reciprocal translocation in an AI bull by synaptonemal complex analysis, followed by chromosome painting

Switonski M.<sup>a</sup> · Andersson M.<sup>b</sup> · Nowacka-Woszek J.<sup>a</sup> · Szczerbal I.<sup>a</sup> · Sosnowski J.<sup>a</sup> · Kopp C.<sup>b</sup> · Cernohorska H.<sup>c</sup> · Rubes J.<sup>c</sup>

<sup>a</sup>University of Life Sciences, Poznan (Poland); <sup>b</sup>University of Helsinki, Helsinki (Finland); <sup>c</sup>Veterinary Research Institute, Brno (Czech Republic)







### Embryo quality and andrological study of two subfertile bulls versus five control bulls with normal fertility

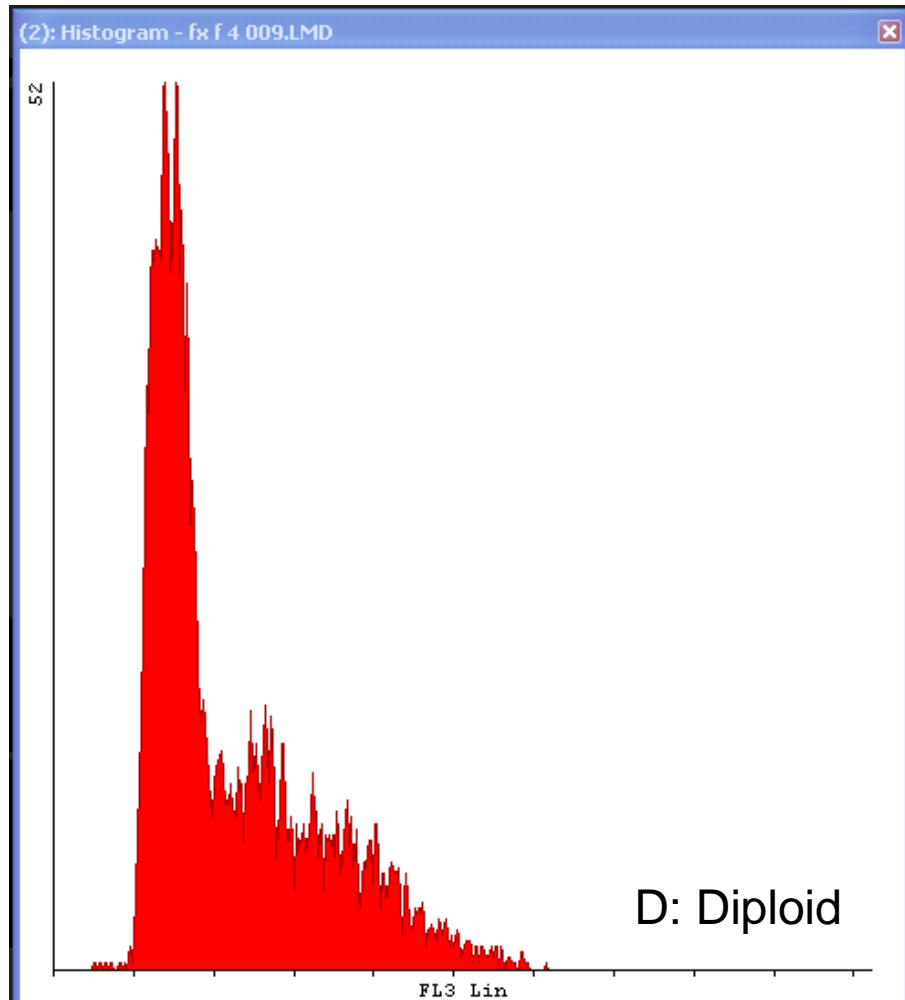
M. Andersson<sup>1</sup>, J. Aalto<sup>2</sup>, I. Gustavsson<sup>3</sup>

<sup>1</sup> Department of Obstetrics and Gynaecology College of Veterinary Medicine, Hautjärvi 04840, Finland

<sup>2</sup> Osuuskunta Itäjalostus, Pieksämäki 76101, Finland

<sup>3</sup> Swedish University of Agricultural Sciences Department of Animal Breeding and Genetics S-75007 Uppsala, Sweden





## Diploid spermatozoa caused by failure of the second meiotic division in a bull

T. Revay<sup>a</sup>, C. Kopp<sup>b</sup>, A. Flyckt<sup>b</sup>, J. Taponen<sup>b</sup>, R. Ijäs<sup>c</sup>, S. Nagy<sup>d</sup>, A. Kovacs<sup>e</sup>, W. Rensf, D. Rath<sup>g</sup>, A. Hidas<sup>a</sup>, J.F. Taylor<sup>h</sup>, M. Andersson<sup>b</sup>  

<sup>a</sup> Research Institute for Animal Breeding and Nutrition, Gödöllő, Hungary

<sup>b</sup> Department of Production Animal Medicine, University of Helsinki, Saarentaus, Finland

<sup>c</sup> Breeding Service Cooperative, Pieksämäki, Finland

<sup>d</sup> Institute of Analytics, Environmental Sciences and Limnology, University of Pannonia, Veszprem, Hungary

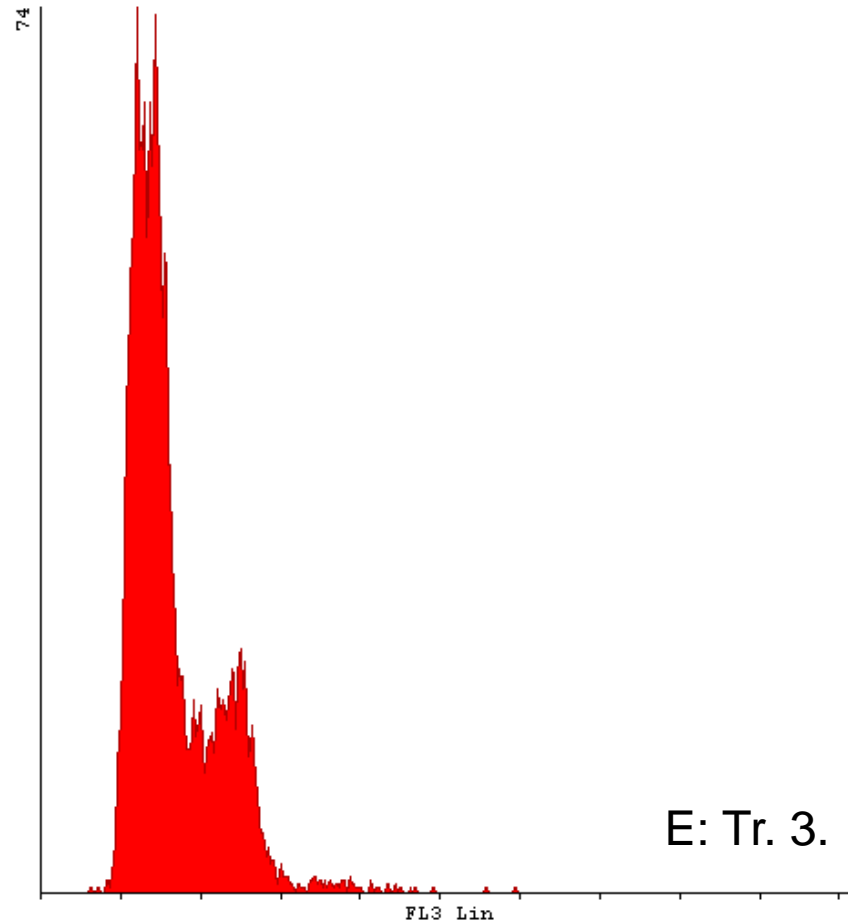
<sup>e</sup> Centre for Agricultural Sciences and Engineering, Institute of Animal Breeding Sciences, University of Debrecen, Debrecen, Hungary

<sup>f</sup> Department of Veterinary Medicine, University of Cambridge, Cambridge, United Kingdom

<sup>g</sup> Federal Agricultural Research Centre, Institute for Animal Breeding, Neustadt, Germany

<sup>h</sup> Division of Animal Sciences, University of Missouri, Columbia, Missouri, USA





PLoS One. 2013; 8(9): e75659.

PMCID: PMC3784456

Published online 2013 Sep 26. doi: [10.1371/journal.pone.0075659](https://doi.org/10.1371/journal.pone.0075659)

## Ectopic *KIT* Copy Number Variation Underlies Impaired Migration of Primordial Germ Cells Associated with Gonadal Hypoplasia in Cattle (*Bos taurus*)

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**Competing Interests:** The authors have declared that no competing interests exist.



# Acknowledgements

- National Scientific Research Fund, Hungary (NKFI OTKA K139145 )
- Anders Johannisson (SWE)
- Magnus Andersson (FIN)
- Andy Kovacs + (HUN)

**THANKS!**

