



APLICACIONES

Revolucione el laboratorio con todas las posibilidades de su BioAnalizador ADN, ARN y proteínas

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Agenda

Introducción al BioAnalizador

Aplicaciones para DNA

- ☐ Analisis de productos de PCR
- ☐ Aplicaciones en alimentación
- ☐ Aplicaciones en estudios clínicos
- ☐ NGS

Aplicaciones para ARN

+Algoritmo RIN

+Small RNA

Aplicaciones para proteínas



WE MAKE IT. *You make it happen.*
OpenGenomics



Bioanalizador 2100

Una plataforma de posibilidades infinitas para el análisis de ADN, ARN, proteínas y células

Disfrute ya de nuestras promociones especiales*:

25% por la compra de un BioAnalizador 2100

25% en cualquier tipo de chips o reactivos para el análisis de ADN, ARN y proteínas

El Bioanalizador 2100 permite realizar automáticamente separaciones electroforéticas y análisis por fluorescencia de células mediante citometría de flujo.

Sus ventajas principales son:

- Kits de chips y reactivos listos para su utilización
- Consumo mínimo de muestra (1 a 4 μ L) y resultados en 30 minutos
- Mejora de la exactitud y fidelidad en las mediciones.
- Resultados comparables entre experimentos y laboratorios
- Datos digitales para la facilidad del análisis, presentación y archivo de datos



Para beneficiarse de estas ofertas, por favor, contacte con su representante local de Agilent y proporcione el código promocional **S_1103_BIOA**.

*hasta el 31 de marzo de 2011 en Agilent Technologies



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Electrophoresis Product Portfolio

CE – Capillary Electrophoresis

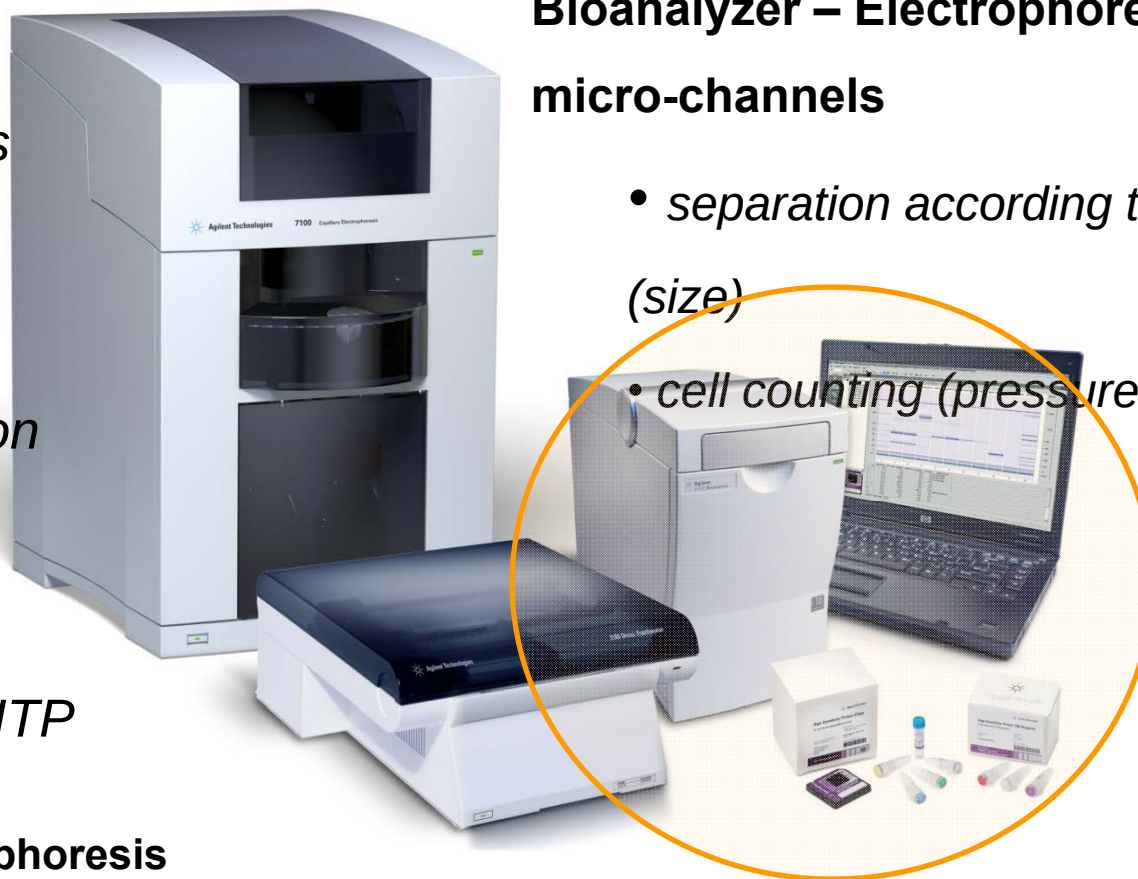
- *various detectors*
 - *UV, LIF, MS, CCD*
- *various separation modi*
 - *CZE, MEKC, CGE, CiEF, CITP*

OGE – Offgel Electrophoresis

- *separation according to iso-electric point (charge)*

Bioanalyzer – Electrophoresis in micro-channels

- *separation according to mobility (size)*
- *cell counting (pressure driven)*



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Overview Agilent Lab on a ChipTechnology

2100 Bioanalyzer Solutions



El bioanalizador adaptable a cualquier tipo de ambiente de estudio



Field deployment for on-site detection of *B. pseudomallei* in environmental samples; analysis in a mobile lab



Bioanalyzer deployed at sea for fish species identification (NOAA)



Bioanalyzer used to test 250 samples in grain silos for GMOs (UK)



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The Agilent 2100 bioanalyzer offers

Improved quality of *slab-gel-type analysis* through on-Chip electrophoresis...

...reducing the experiment to:

Easy to use analytical device that performs separation and quantitation of RNA, DNA and Proteins based on electrophoresis within a disposable glass chip.

1. Load sample



2. Run analysis



3. Analyze data



On a single Platform perform:

- Sizing, Quantitation and Purity of Proteins (5 -230 kDa)
- Sizing, Quantitation and Purity of DNA fragments (25 – 12000 bp)
- Integrity check, Separation and Quantitation of RNAs
- Cell Fluorescence Assays with stained cells (Apoptosis, Transfection, Expression,)



2100 Bioanalyzer Hardware

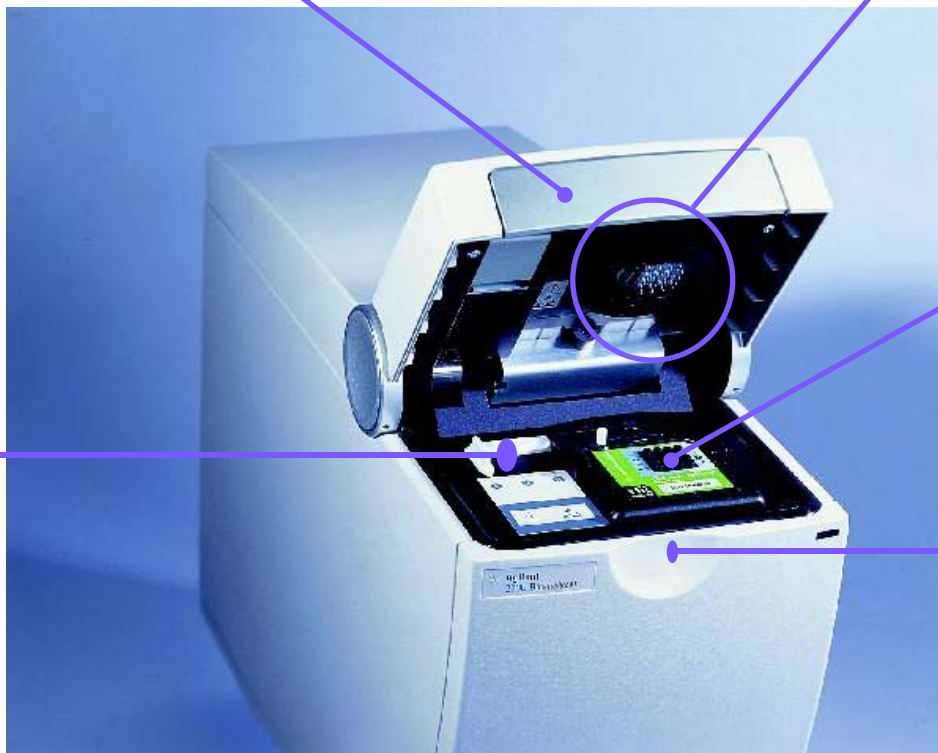
**Exchangeable cartridge
for electrophoresis or flow
cytometry assays**

**16 pin electrodes
connected to HV-sources**

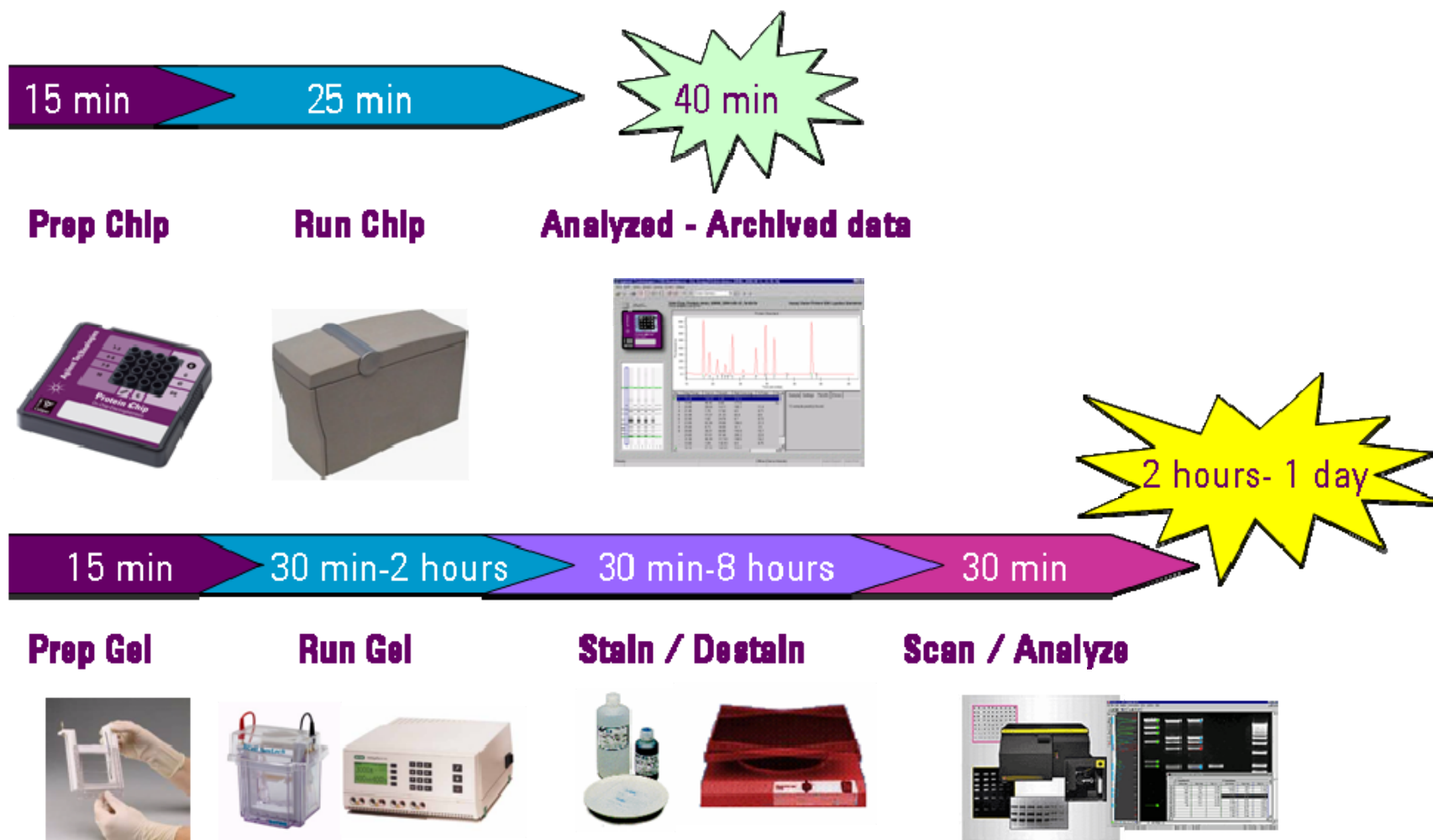
**Chip
selector**

**Chip holder with
heater plate**

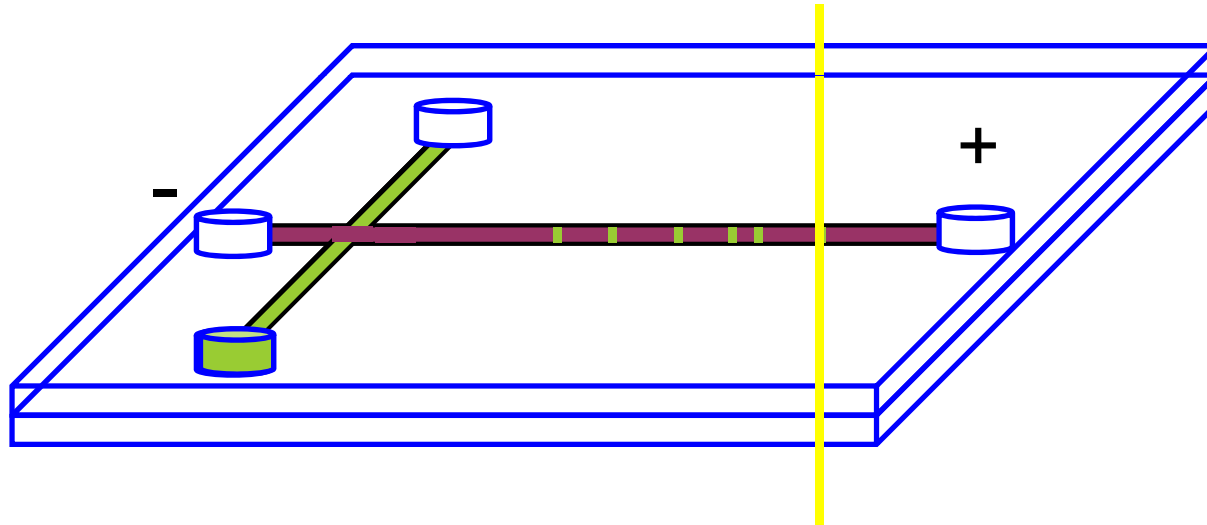
Optics for detection



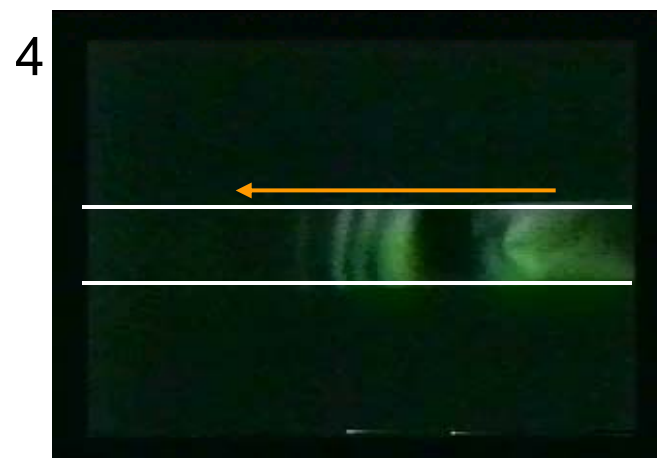
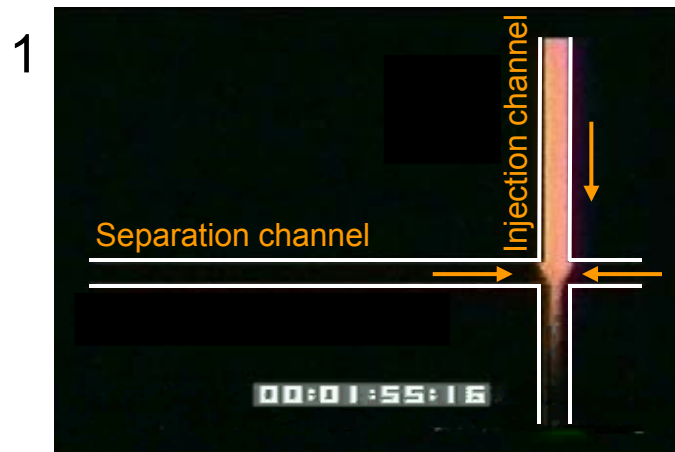
Lab-on-a-Chip or Gel - A Faster Answer !



The LabChip® Approach - Simplified Model



Lab-on-a-Chip - Principle of Injection & Separation



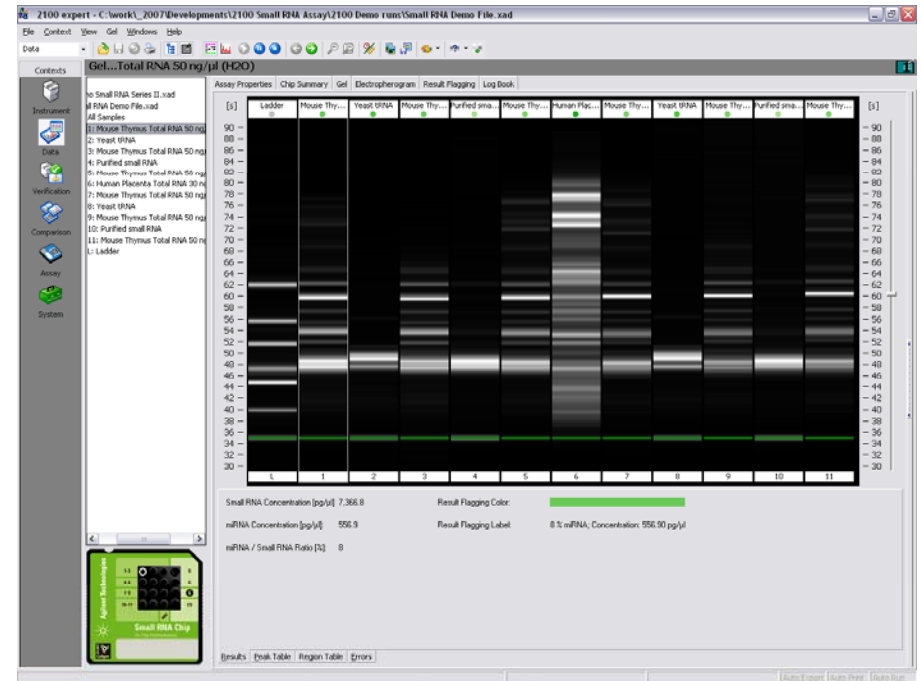
← Direction of electrodriven movement of liquids and molecules within liquids

2100 expert SW

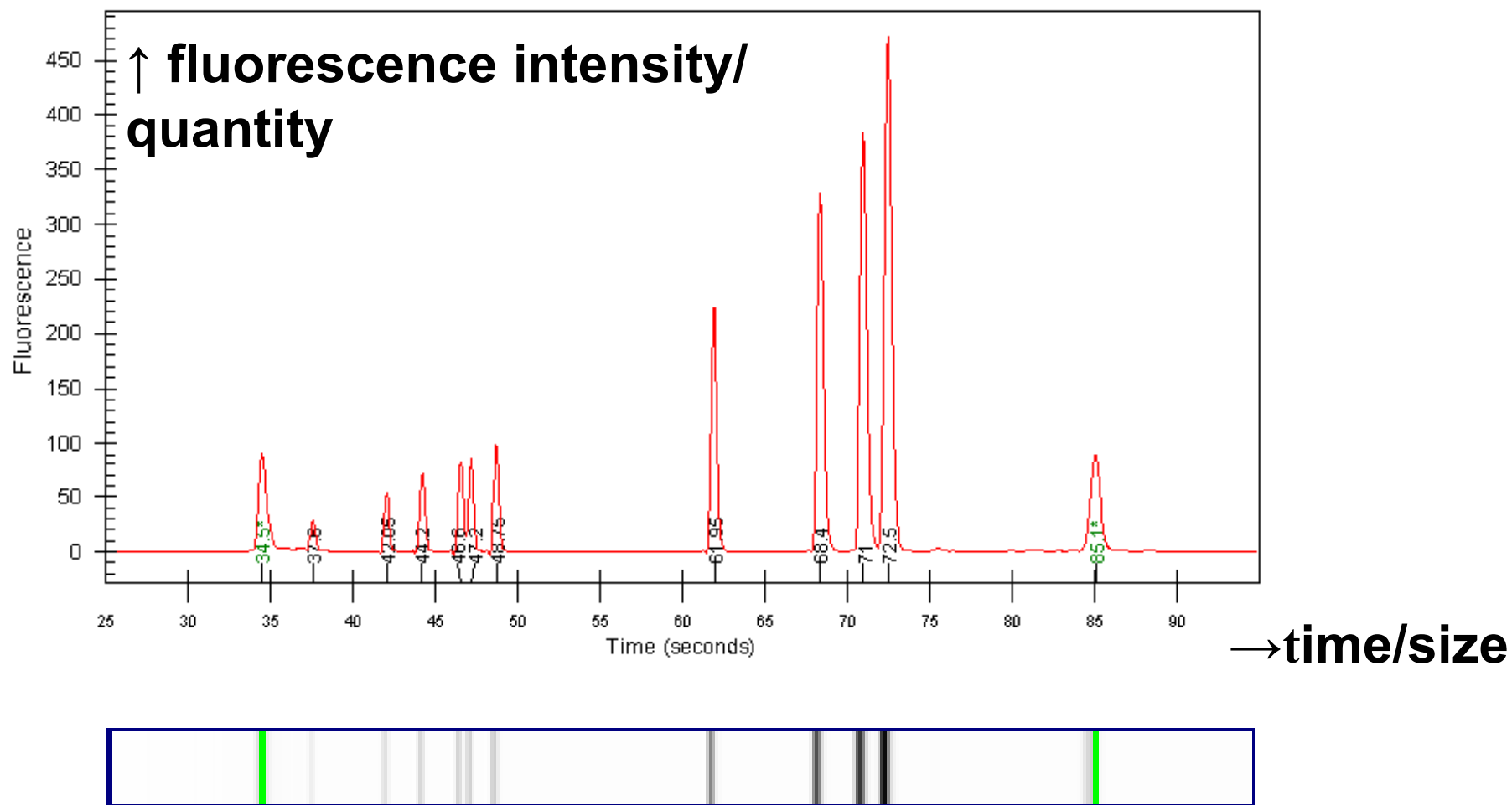
Version B.02.07

Third SW Generation

- Includes all the new Series II bioanalyzer kits
- Supporting new High Sens DNA and Protein
- Patented RIN (RNA Integrity Number)
- Color coded Result Flagging
- Allows compliance also on e-bioanalyzer (G2939AA)
- Improved comparison context (up to 48 samples per file)
- Improved manual integration
- Customizable result tables for printing and reports
- **Not compatible with A-type Instruments**



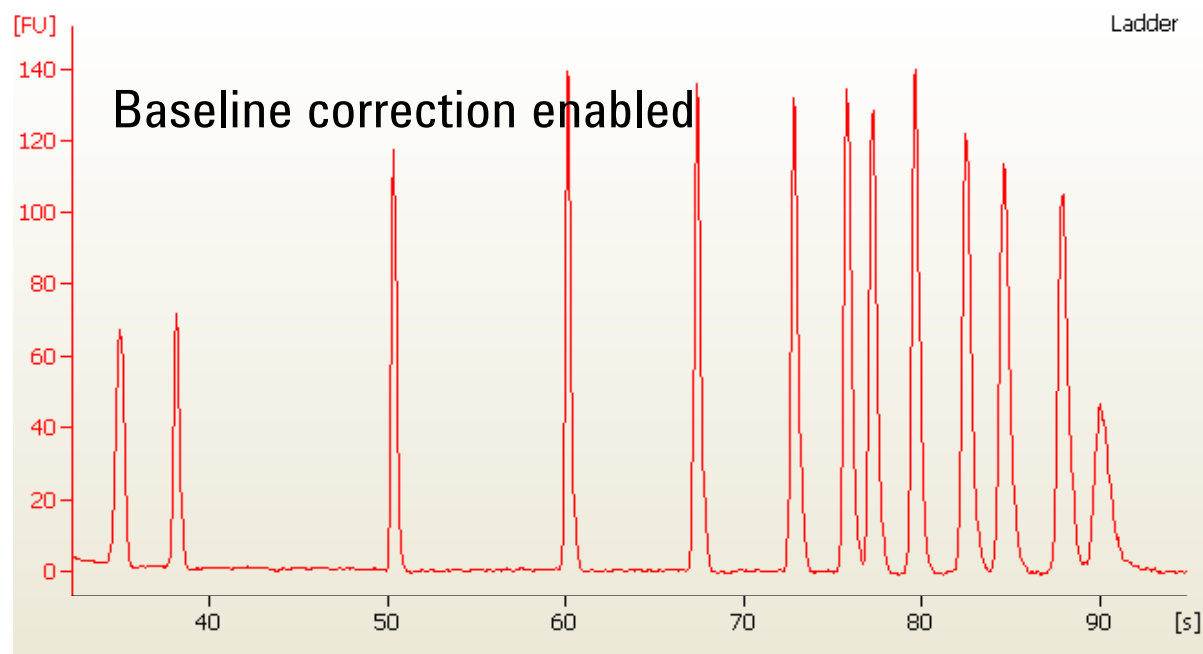
Gel view and electropherogram view



0. preparatory transformations

- Noise reduction
(Savitzky-Golay filtering)
- Spike rejection
- Baseline correction

Filter Width: (Secs)	1
Baseline Plateau: (Secs)	0.5
Polynomial Order:	6



1. Peak recognition

table of
fluorescence
intensities

Local Global

Normal Expand

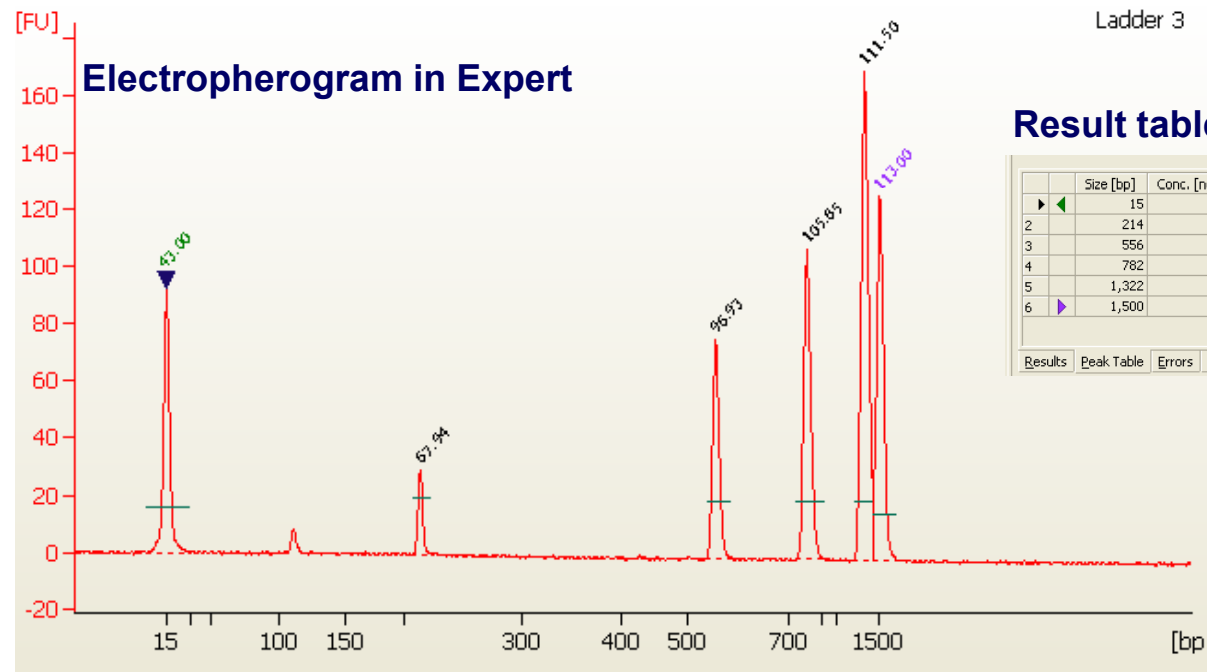
+ : General assay setpoints

- : Sample setpoints

- : Integrator

Integration start time [s]	30
Integration end time [s]	128.95
Slope Threshold	0.5
Area threshold	0.1
Height threshold [FU]	20
Width threshold [s]	0.5

table of
peaks



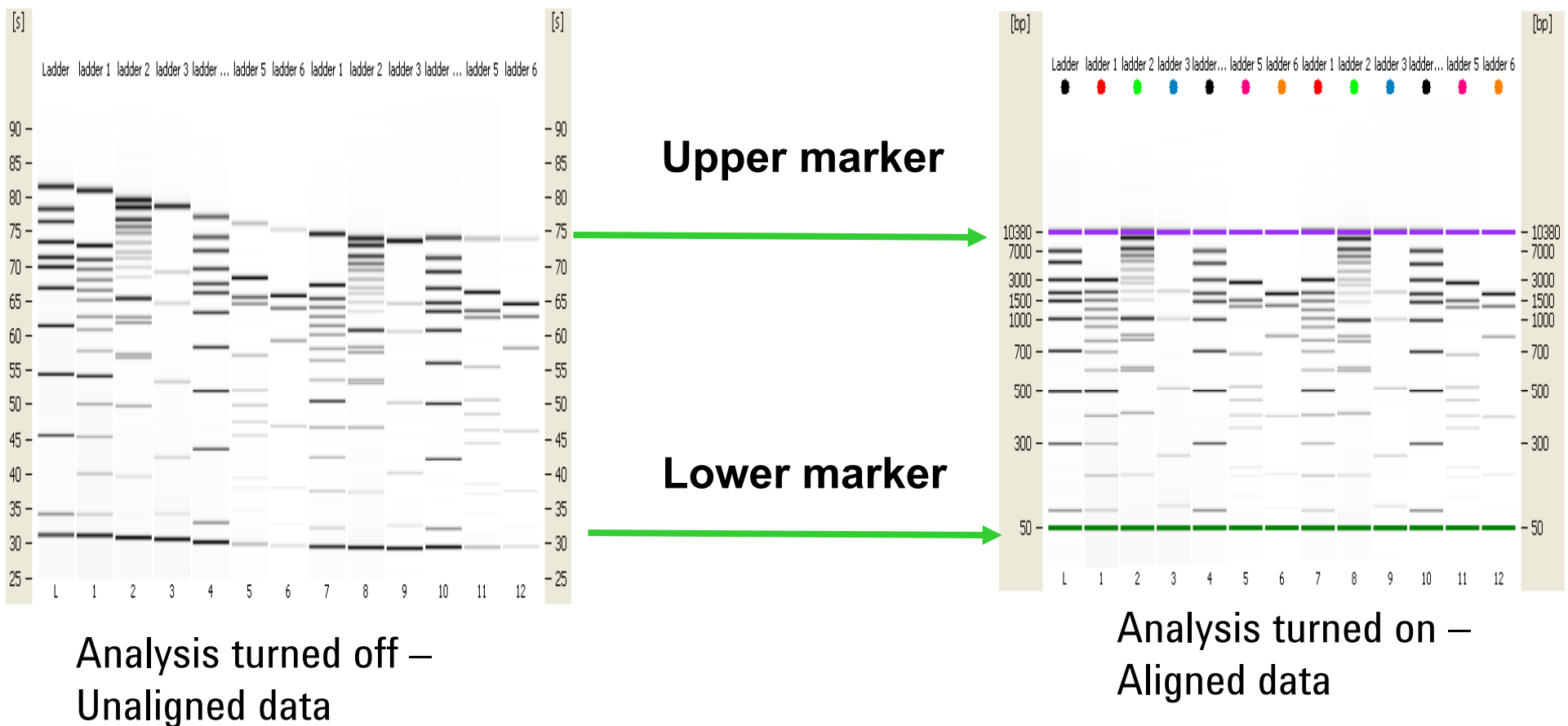
Result table in Expert

Ladder 3

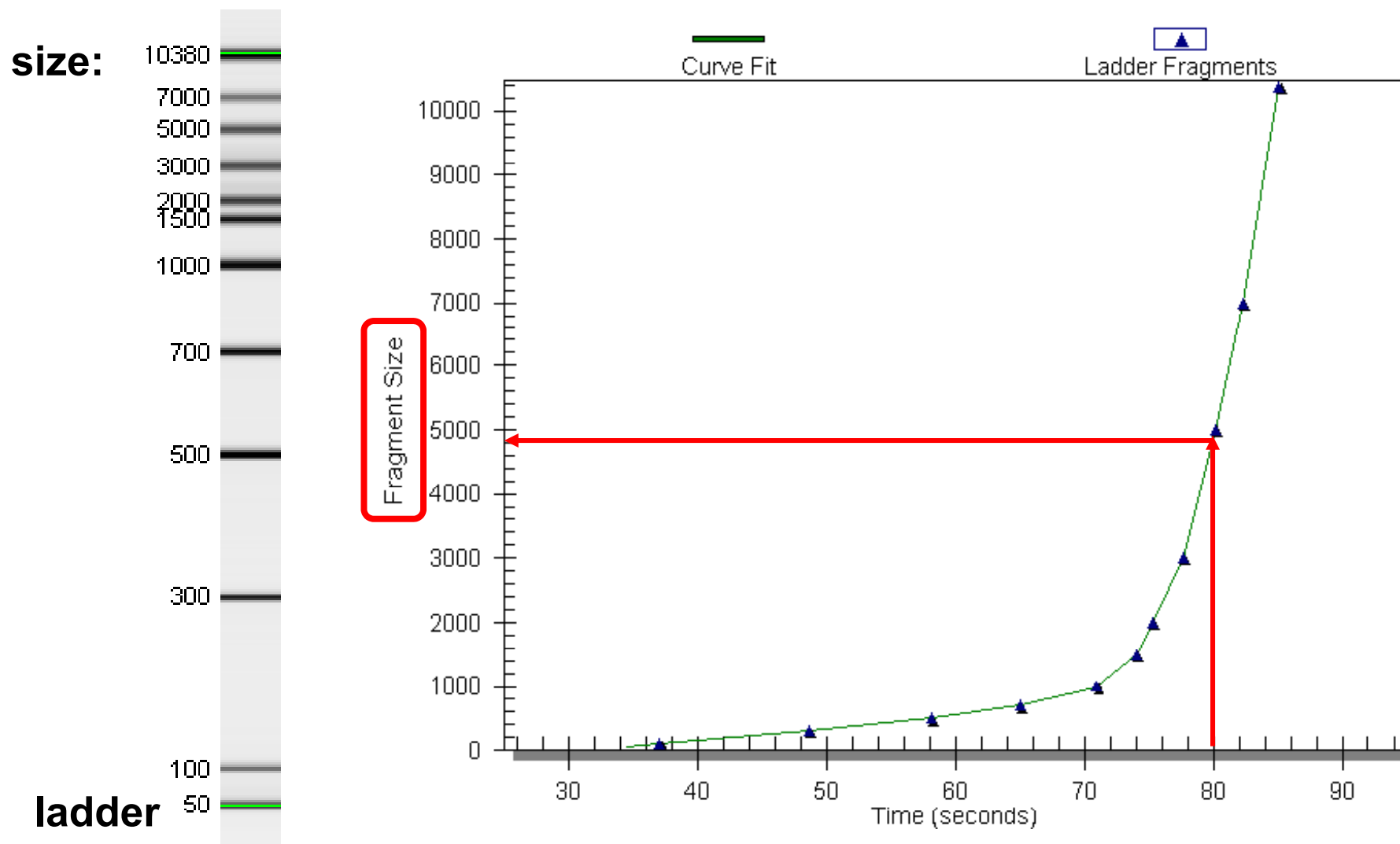
	Size [bp]	Conc. [ng/μl]	Molarity [nmol/l]	Observations
1	15	4.20	424.2	Lower Marker
2	214	0.34	2.4	
3	556	1.19	3.2	
4	782	1.84	3.6	
5	1,322	2.96	3.4	
6	1,500	2.10	2.1	Upper Marker

Results Peak Table Errors Legend

2. Alignment to markers



3. Sizing



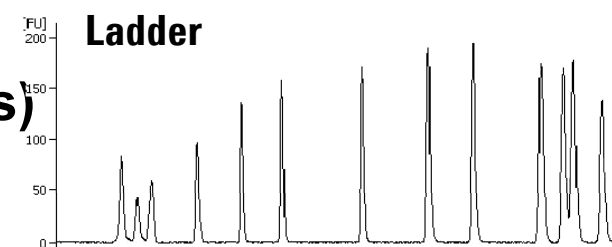
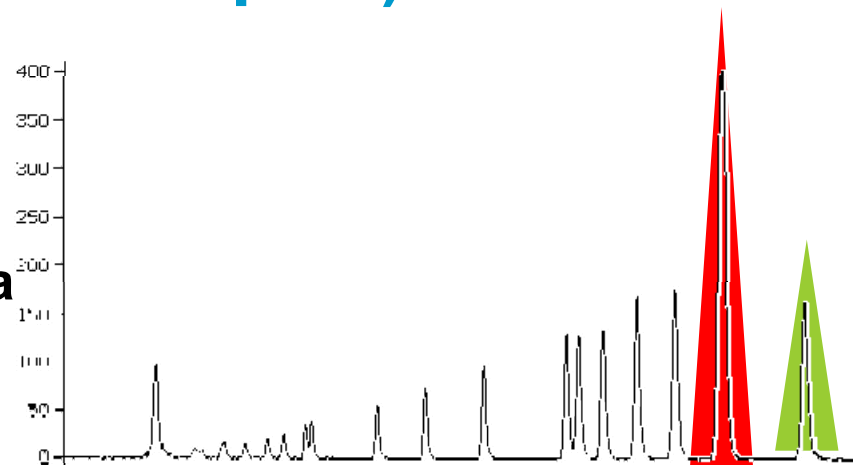
4. Quantification (DNA/Protein samples)

peak area

concentration

upper marker peak area
(known concentration)

assay-specific calibration curve
(standard areas, see assay properties)



		Size [bp]	Aligned Migration Time [s]	Time corrected area	Conc. [ng/μl]	Molarity [nmol/l]	% of Total	
1	◀	15	43.00	179.7	4.20	424.2	0.0	
2		403	87.85	83.6	1.55	5.8	9.5	
3		426	89.34	86.0	1.59	5.7	9.9	
4		466	91.93	92.2	1.70	5.5	11.0	
5		524	95.29	108.0	1.99	5.8	13.3	
6		602	99.21	116.2	2.18	5.5	14.9	
7		718	104.45	306.1	5.90	12.4	41.4	
8	▶	1,500	113.00	109.7	2.10	2.1	0.0	

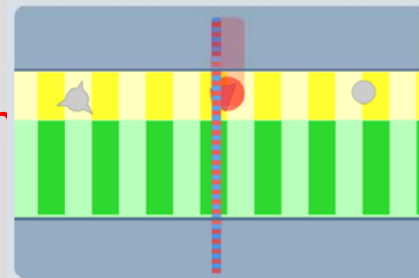


Optics & Detection

2100 Bioanalyzer

Red detection channel:

- 620-645 nm excitation with Laser (Maximum 630 nm)
- 674-696 nm detection range (Maximum 680 nm)



Blue detection channel:

- 458-482 nm excitation with LED (Maximum 470 nm)
- 510-540 nm detection range (Maximum 525 nm)

Flow
Cytometry

Standard Flow Cytometers have 3-4 fluorescence detection channels:

- FL1: excitation 488 nm, detection 530 nm
- FL2: excitation 488 nm, detection 585 nm
- FL3: excitation 488 nm, detection 661 nm
- FL4: excitation 635 nm, detection 670 nm



2100 Bioanalyzer LabChip Kits

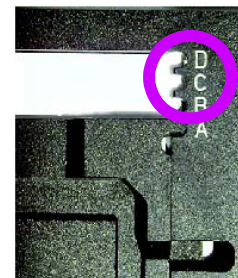
What you need to know

- Chips are disposable, they are used once and then thrown away
- Even if all wells on a chip are not been used the remaining wells cannot be used at a later time
- Some of the reagents in the LabChip kits are thermally unstable at room temperature so the kits have to be shipped cooled (on ice) and stored in a refrigerator
- The LabChip kits have a limited shelf life
 - Shelf life is 12 months from manufacture date
 - We guarantee a minimum of 4 months shelf-life when received by the customer
- Reagent kits (cooled) are available for customers who lose/waste their reagents or have reagents that exceeded their shelf-life



Chip Priming

**Set chip priming station
base plate to C**

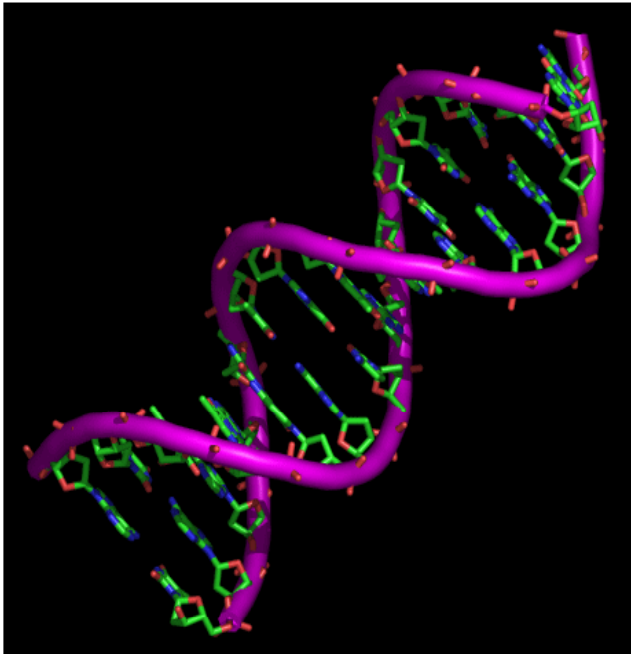


**Set metal clip to top (DNA
7500/12000)
OR
lowest (DNA 1000)
position**



**30 sec pressurization
(DNA 7500/12000)
OR
60 sec pressurization
(DNA 1000)**





APLICACIONES EN ADN



Aplicaciones plataforma DNA

Pureza de los productos de PCR

Amplificaciones multiples por PCR

Gene expression análisis via RT-PCR (validación target)

GMO testing

Detección de Patogenos (Veterinaria, hospitales, medio ambiente)

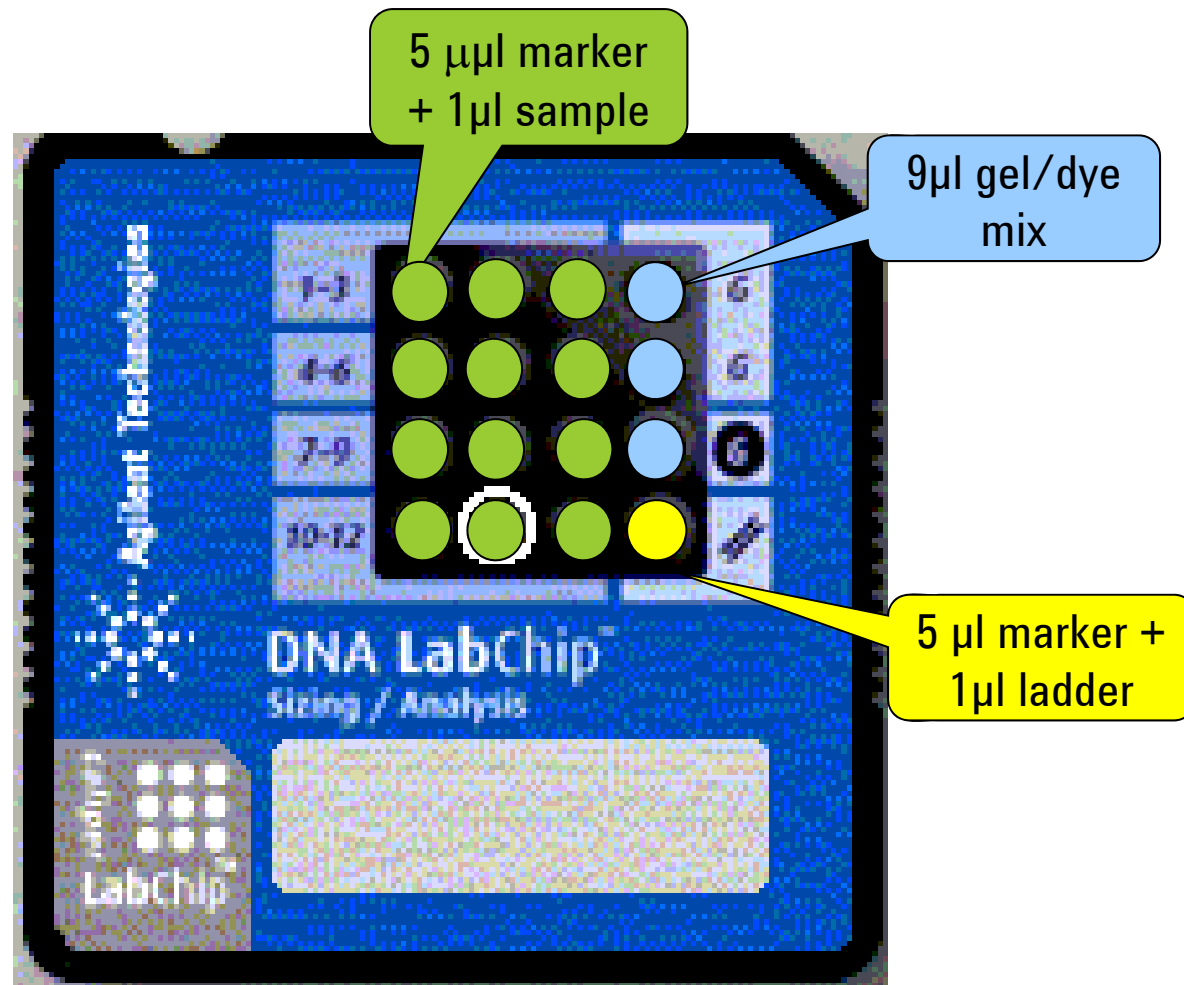
Aplicaciones en Genotipado

- **Duplicaciones/ delecciones**
- **Frecuencia alélica**
- **Sub-tipado de bacterias**
- **Forense**

Cancer diagnóstico



Chip Preparation



DNA Analysis Kits and Reagents

Order No.	Description	Order No.	Description	Order No.	Description	Order No.	Description
5067-1504	DNA 1000 Kit	5067-1506	DNA 7500 Kit	5067-1508	DNA 12000 Kit	5067-4626	High Sensitivity DNA Kit
5067-1505	DNA 1000 Reagents	5067-1507	DNA 7500 Reagents	5067-1509	DNA 12000 Reagents	5067-4627	High Sensitivity DNA Reagents

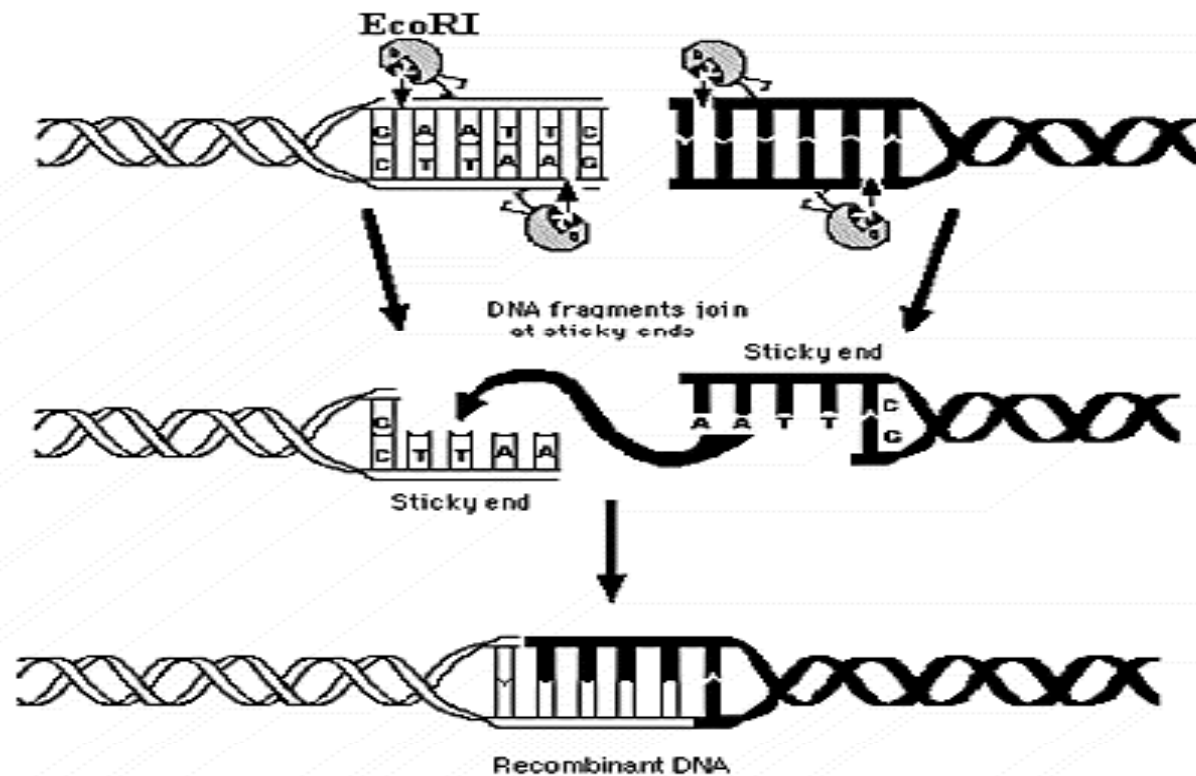
Analytical Specifications	DNA 1000 Assay	DNA 7500 Assay	DNA 12000 Assay	High Sensitivity DNA Assay
Sizing range	25–1000 bp	100–7500 bp	100–12000 bp	50–7000 bp
Sizing resolution	25–100 bp: 5 % 100–500 bp: 5 % 500–1000 bp: 10 %	100–1000 bp: 5 % 1000–7500 bp: 15 %	100–1000 bp: 5 % 1000–12000 bp: 10 %	50–600 bp: ±10 % 600–7000 bp: ±20 %
Sizing accuracy	± 10 % CV*	± 10 % CV*	± 15 % CV*	± 10 % CV*
Sizing reproducibility	5 % CV*	5 % CV*	5 % CV*	5 % CV*
Quantitation accuracy	20 % CV*	20 % CV*	25 % CV*	20 % CV*
Quantitation reproducibility	25–500 bp: 15 % CV* 500–1000 bp: 5 % CV*	100–1000 bp: 10 % CV* 1000–7500 bp: 5 % CV*	100–1000 bp: 15 % CV* 1000–12000 bp: 10 % CV*	50–2000 bp: 15 % CV* 2000–7000 bp: 10 % CV*
Qualitative range	0.1–50 ng/μL*	0.1–50 ng/μL*	0.1–50 ng/μL*	5–500 pg/μL*
Maximum salt concentration in sample	250 mM for KCl 250 mM for NaCl 15 mM for MgCl ₂	250 mM for KCl 250 mM for NaCl 15 mM for MgCl ₂	250 mM for KCl 250 mM for NaCl 15 mM for MgCl ₂	10 mM Tris and 1 mM EDTA
Physical Specifications				
Analysis time	35 minutes	30 minutes	30 minutes	45 minutes
Samples per chip	12	12	12	11
Sample volume	1 μL	1 μL	1 μL	1 μL
Kit stability	4 months	4 months	4 months	4 months
Kit size	300 samples/kit	300 samples/kit	300 samples/kit	110 samples/kit

* Determined analyzing the DNA ladder as sample



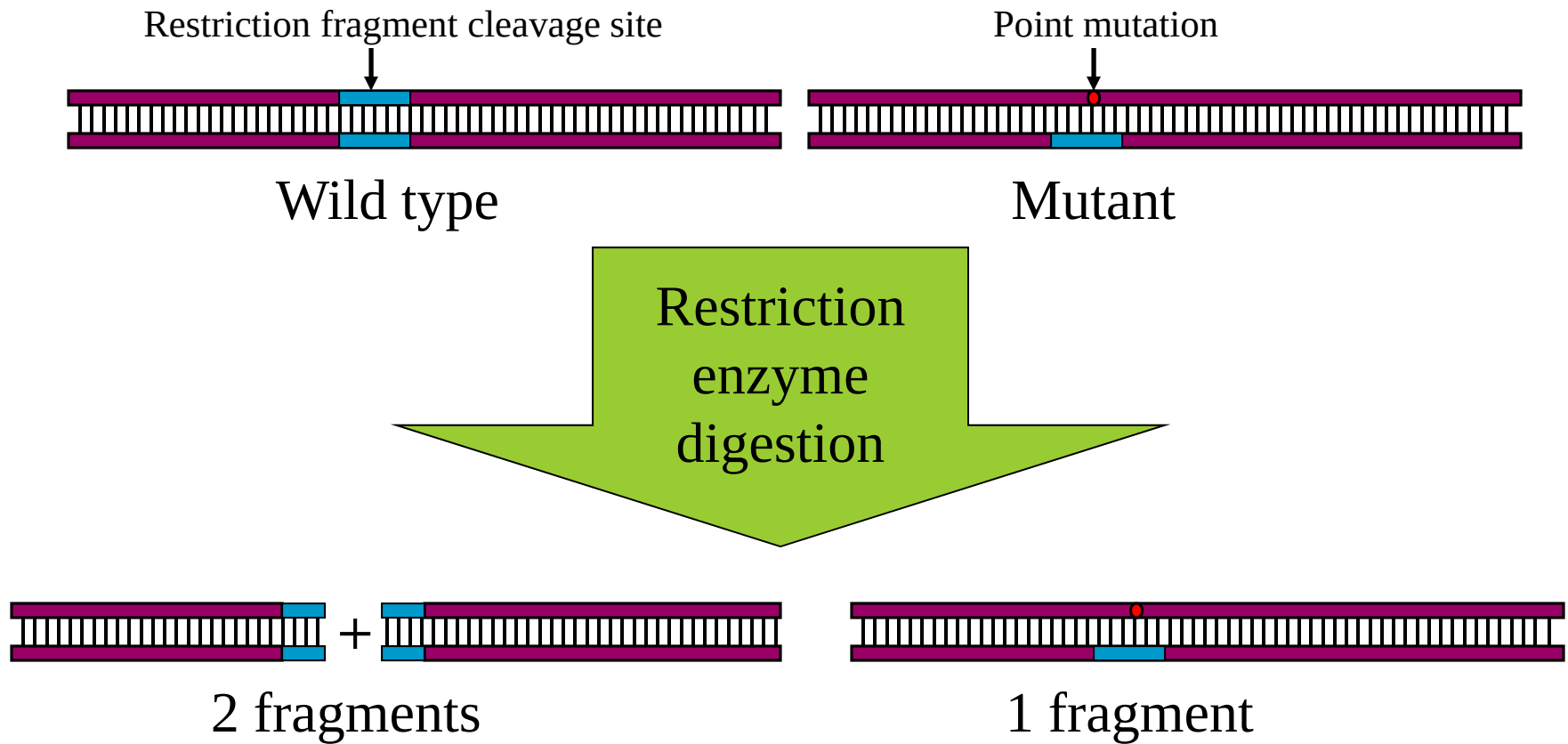
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Restriction Digests



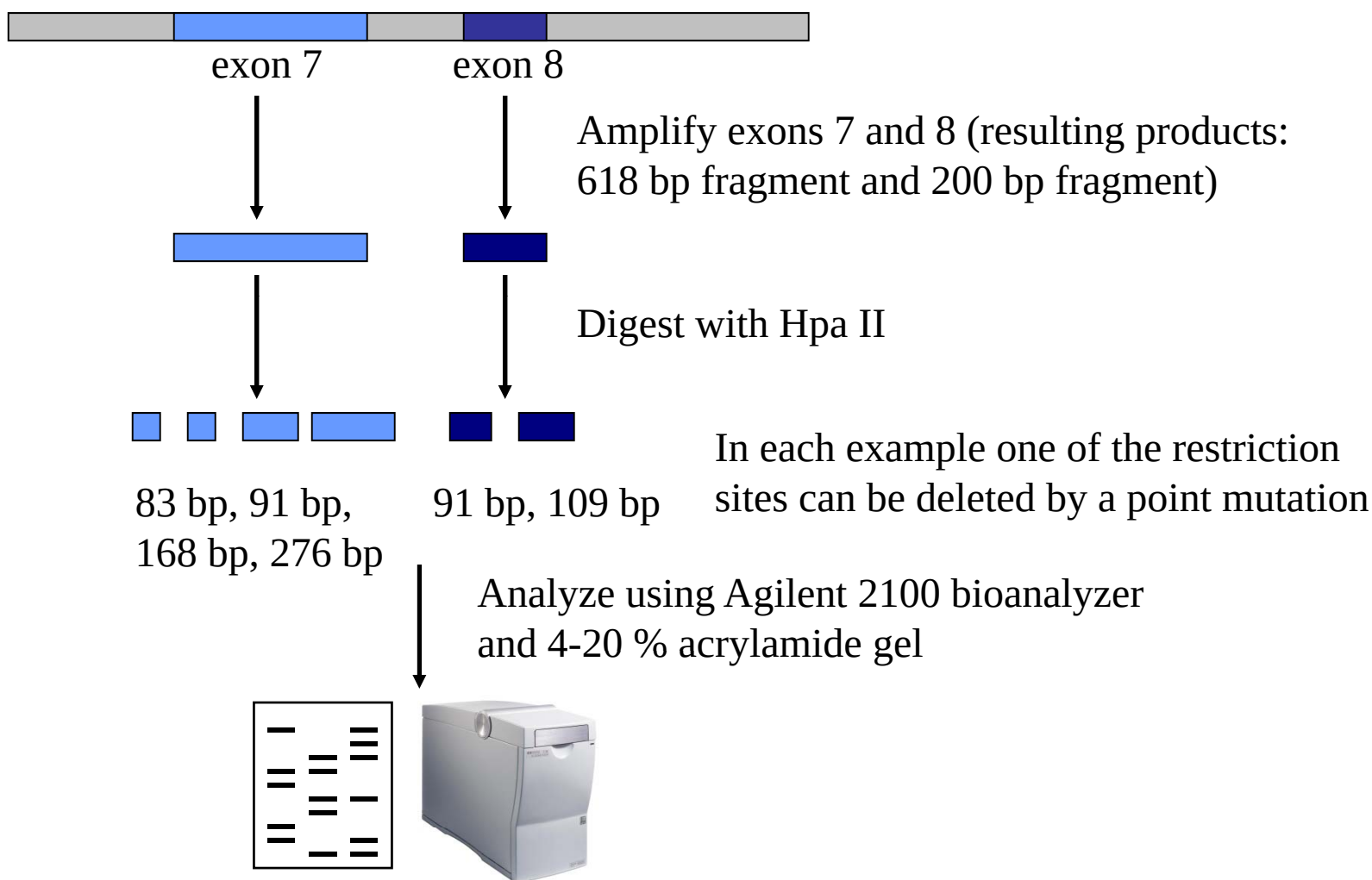
Restriction Enzyme Action of EcoRI

Mutation Detection by RFLP

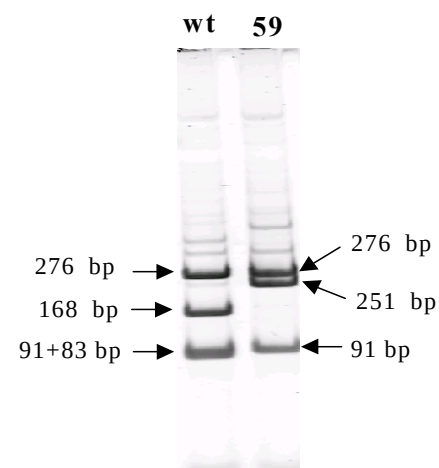
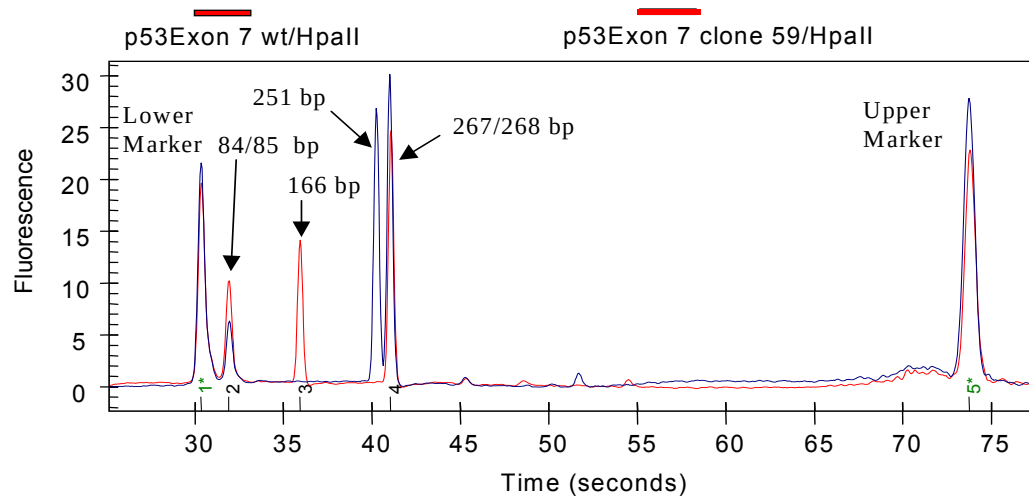
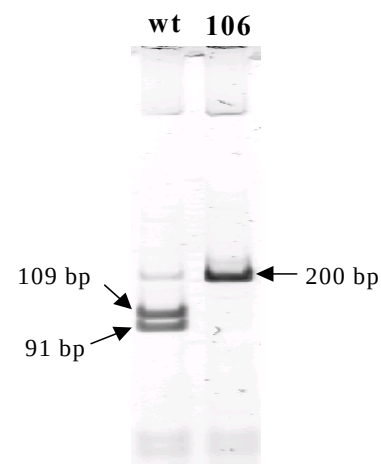
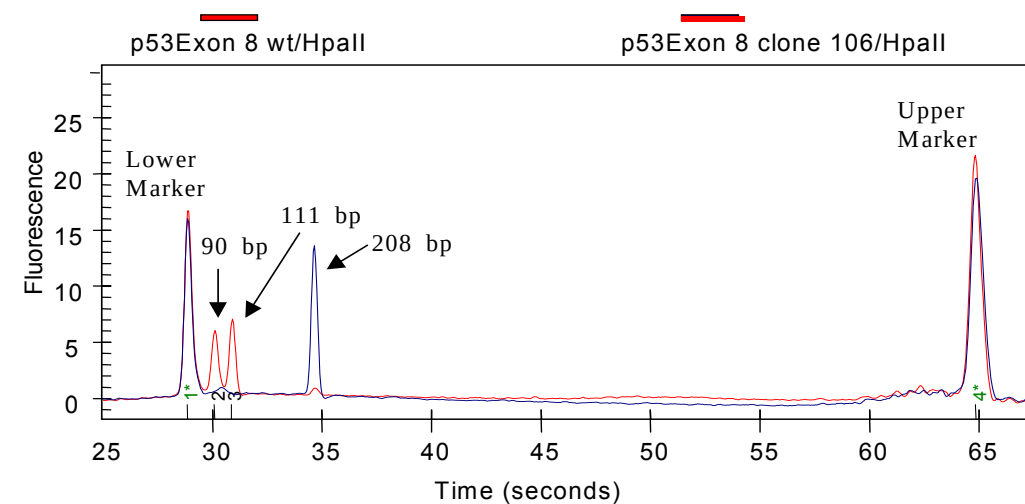


Detection of Single Base Mutations (1)

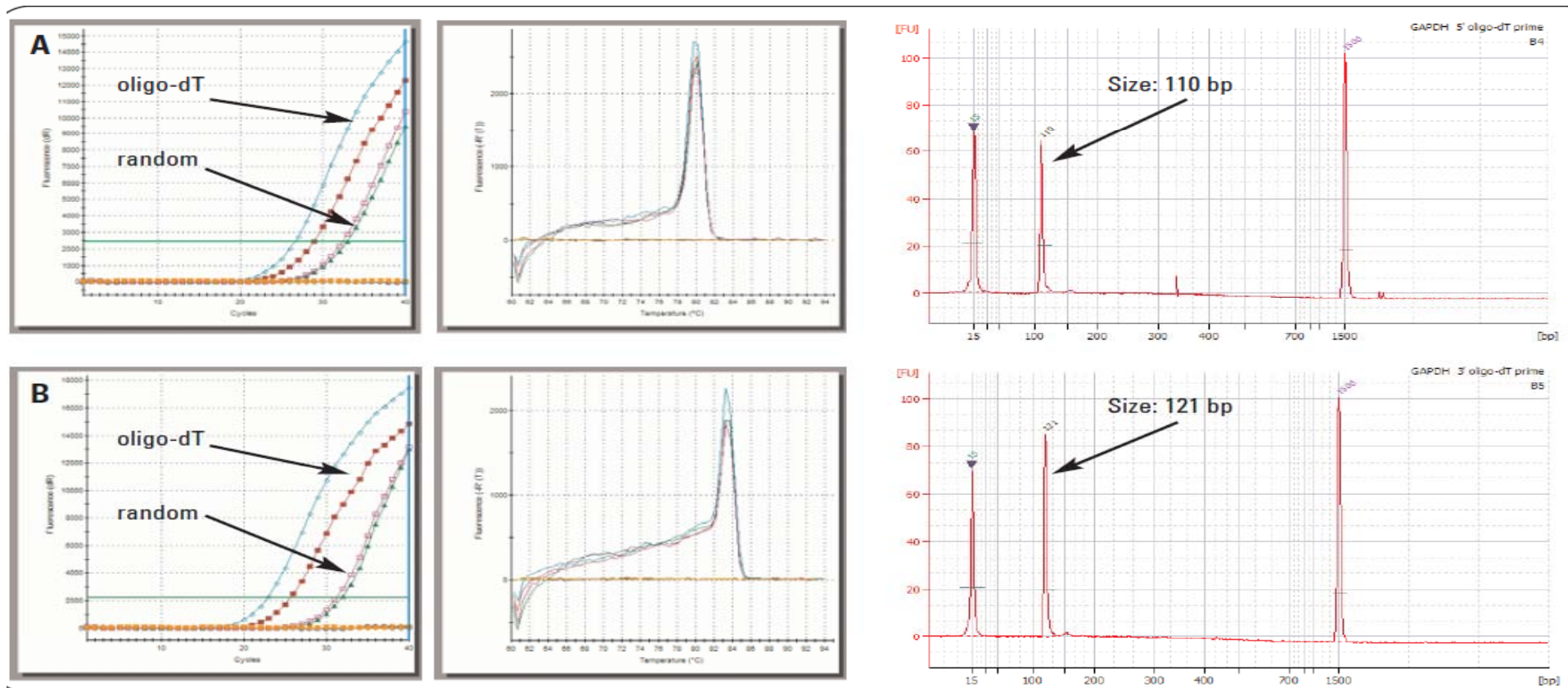
in Exons 7 and 8 of the Human p53 Gene by RFLP Mapping using the DNA 7500 kit



Detection of Single Base Mutations (2)



Optimize QPCR assay design

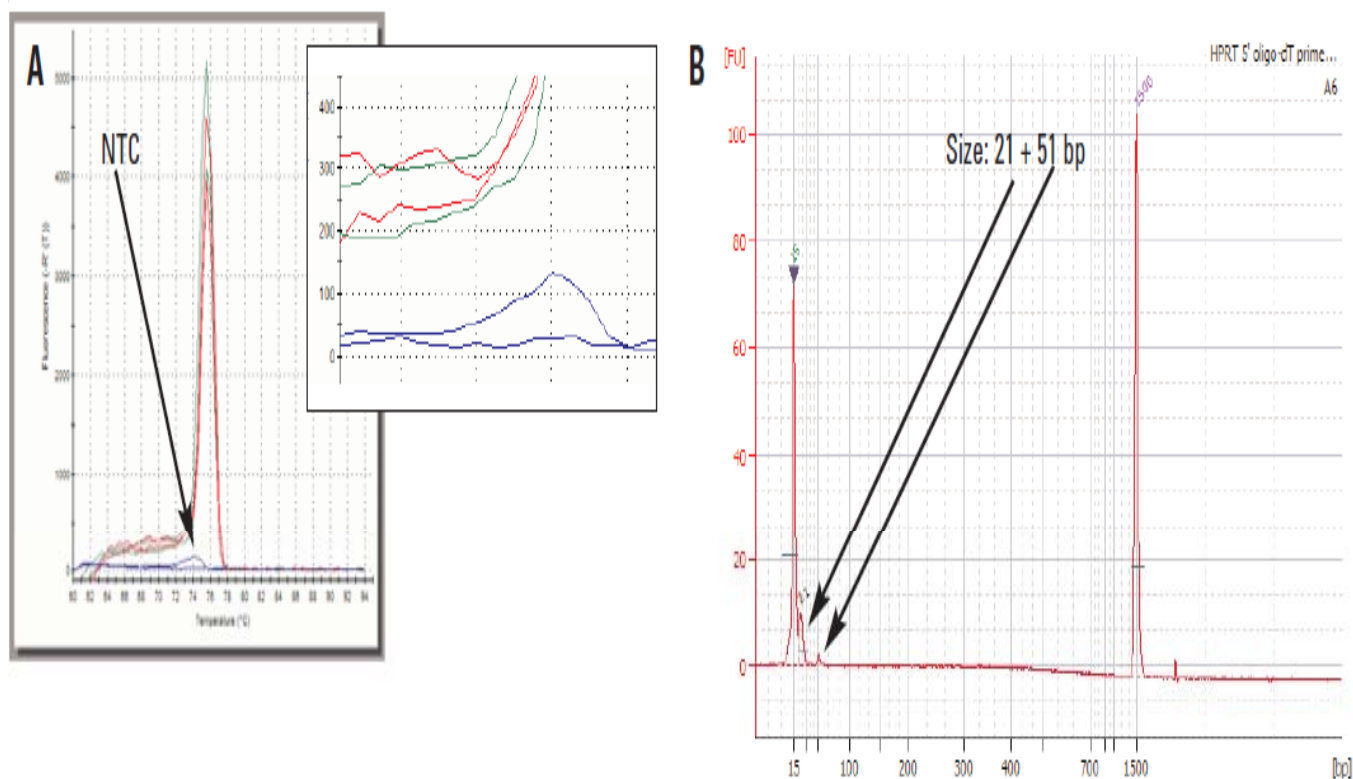


Assay Validation: Amplification plots, melt curve and bioanalyzer analysis of amplicons for GAPDH. A) 5'-assay, B) 3'-assay.



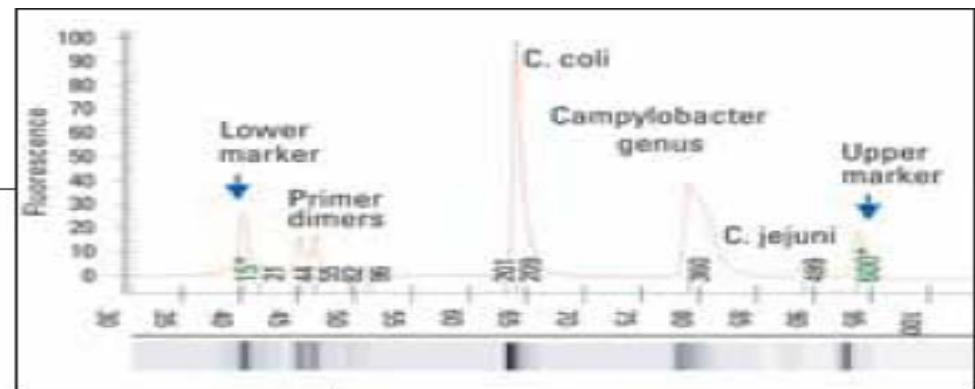
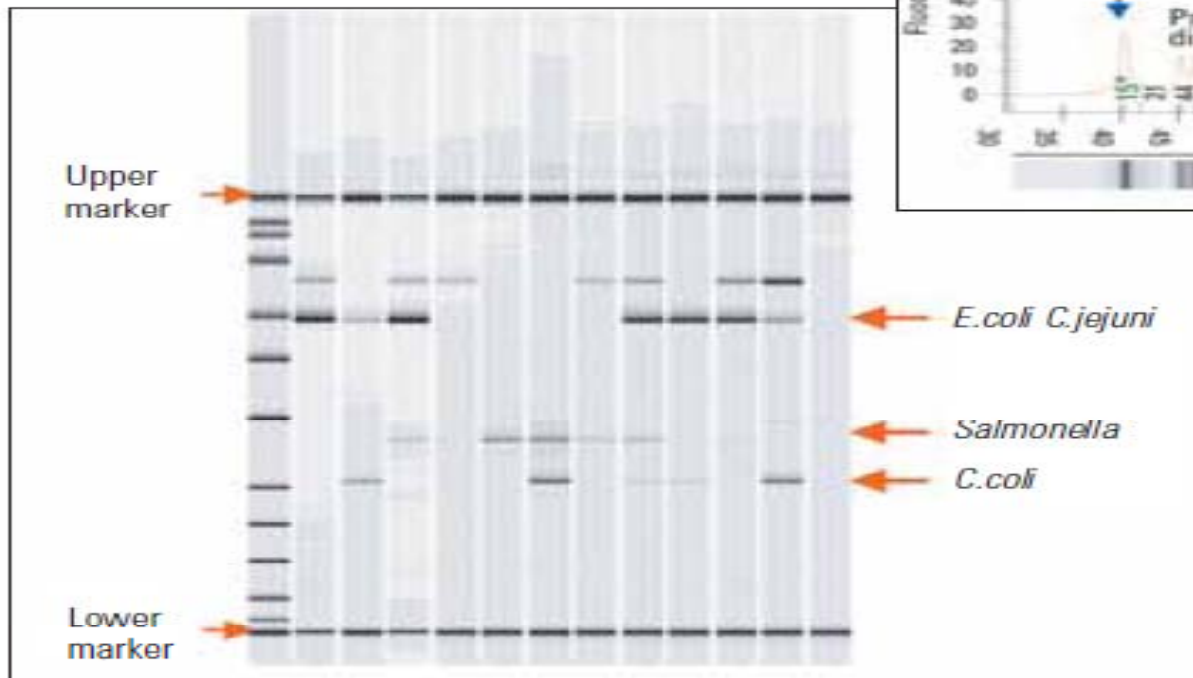
Optimize QPCR assay design

This highlights the high information content obtained by the 2100 Bioanalyzer and the poor discrimination capabilities of a SYBR Green based melt curve.



Validation of positive NTC results. Melt curve and bioanalyzer analysis of HPRT1 5'-amplicons. Enlargement of melt curve clearly shows a product in the NTC control with similar T_m to the positive control. Bioanalyzer analysis shows two minor peaks of 21 and 51 bp pointing to primer dimer formation.

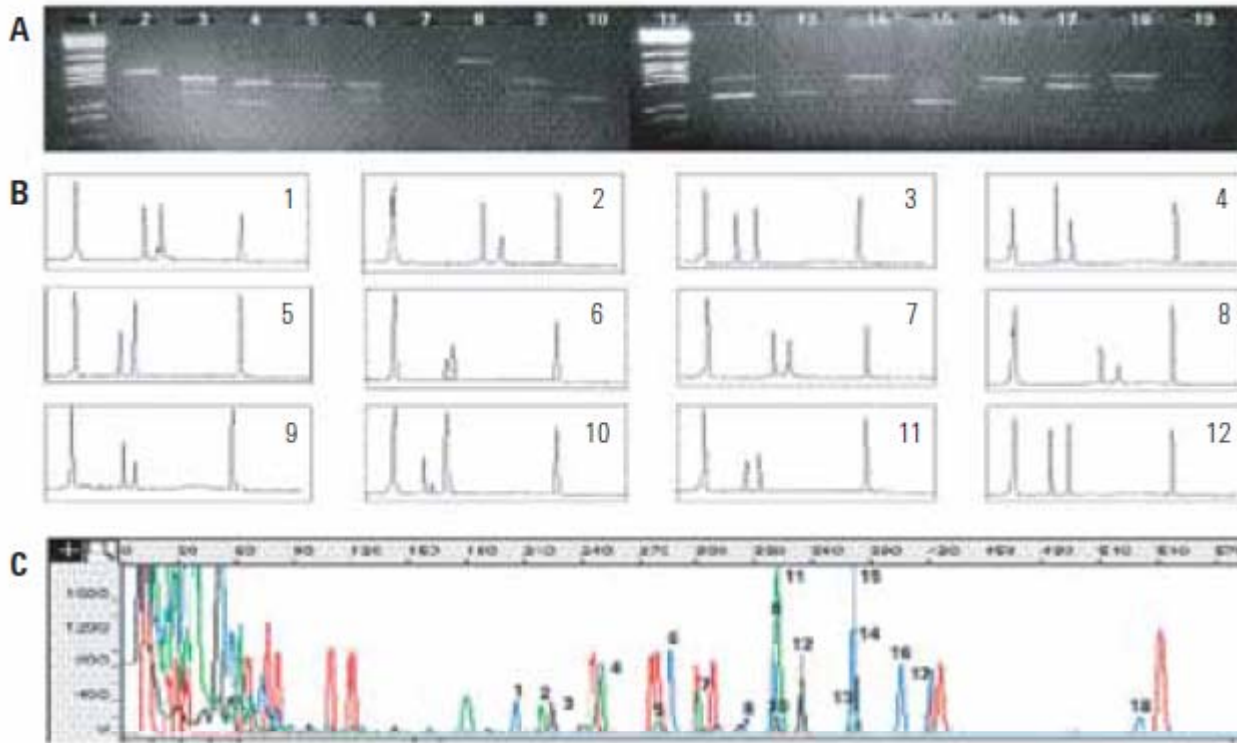
Multiplex PCR analysis of bacteria in chicken



The electropherogram is one example where bacterial DNA from two species of the *Campylobacter* genus could be detected.

Standardized end-point RT-PCR

The direct comparison of the reproducibility for agarose gel analysis (A, CV = 0.50) and the ABI Prism310 Genetic Analyzer (C, CV = 0.39) with the 2100 Bioanalyzer (B, CV = 0.29) reveals that the 2100 Bioanalyzer is superior.



Complementary DNA from bronchial epithelial cells (BEC) was analyzed by a Standardized RT-PCR (StaRT) for the expression of 15 different genes.

Agilent Technologies DNA Fish ID Solution



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Métodos de identificación de pescados - Tradicional

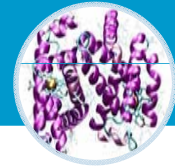
- Requiere expertos para la identificación
- Solamente aplicable a pescado total

Morfologías

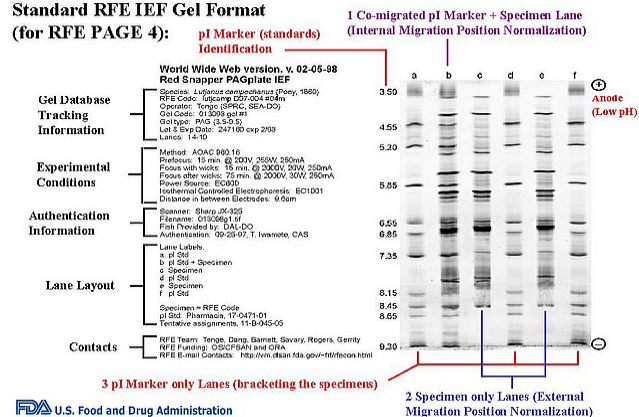


- El Procesado puede destruir proteínas.
- Polimorfismo limitado entre especies
- Dificultad de interpretación
- Influenciado por el medio ambiente
- Normalmente requiere correr muestras autenticadas en paralelo

Métodos basados en proteínas



Standard RFE IEF Gel Format (for RFE PAGE 4):



FDA U.S. Food and Drug Administration

Regulatory Fish Encyclopedia:
U.S. Food and Drug Administration, 1993-2009

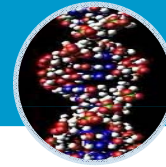


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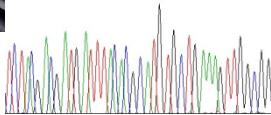
Métodos de identificación de pescados – DNA

- Resultados objetivos
- Más resistentes al procesamiento de muestras
- Fácil de utilizar
- Alta especificidad/sensibilidad

DNA métodos

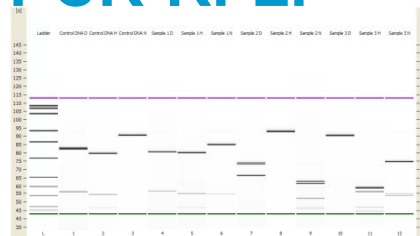


Secuenciación



- ⇒ Alta inversión inicial (> 100K \$)
- ⇒ Alto coste de mantenimiento
- ⇒ No aplicable con muestras mezcladas
- ⇒ Métodos de elección para nuevas especies.

PCR-RFLP

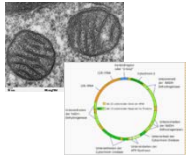


- ⇒ Discriminación entre especies sumamente relacionadas
- ⇒ Trabaja con mezclas
- ⇒ Bajo coste inicial



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Método de identificación de pescados– PCR RFLP



- ⇒ Mitochondrias: Alto número de copias
- ⇒ Comunmente empleado el gen Cytochrome B (CytB) o Cytochrome Oxidase I (COX1)
- ⇒ La secuencia del CytB aporta información para especies de pescados.



- ⇒ La PCR RFLP es un método acreditado/aprobado en muchos países.
- ⇒ Transferencia del método a 2100 Bioanalyzer para mejorar el análisis edición 2004 y 2005 por Stephen Garrett de Campden BRI (Reino Unido)

Food Control **16** (7), 601-607, (2004)

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Improved fish species identification by use of lab-on-a-chip technology

John J. Dooley, Helen D. Sage, Helen M. Brown and Stephen D. Garrett*

Biochemistry Section, Department of Chemistry and Biochemistry, Campden and Chorleywood Food Research Association, Chipping Campden, Gloucestershire GL55 6LD, UK



Determination of PCR-RFLP Profiles for Fish Species Using the Agilent 2100 Bioanalyzer

Application

Authors

Steve Garrett and John Dooley
Molecular Biology Group, Dept. of Chemistry and Biochemistry
Campden & Chorleywood Food Research Association, Chipping
Campden
Gloucestershire, GL55 6LD
UK

Fish Species Identification Using PCR-RFLP Analysis and Lab-on-a-Chip Capillary Electrophoresis: Application to Detect White Fish Species in Food Products and an Interlaboratory Study

JOHN J. DOOLEY, HELEN D. SAGE, MARIE-ANNE L. CLARKE,
HELEN M. BROWN, AND STEPHEN D. GARRETT*
Biochemistry Section, Department of Chemistry and Biochemistry, Campden & Chorleywood Food
Research Association, Chipping Campden, Gloucestershire, GL55 6LD, UK

J Agric Food Chem **53** (9), 3388-3357 (2005)

<http://www.chem.agilent.com/Library/applications/5989-2982EN.pdf>



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Agilent DNA Fish ID Solution -

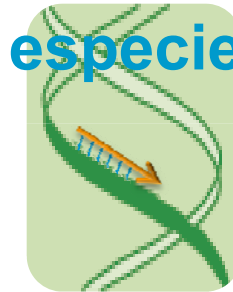
Purificación
de la muestra



< 1 h

(dependiendo # muestras)

Amplificación de secuencias
de identificación de
especies



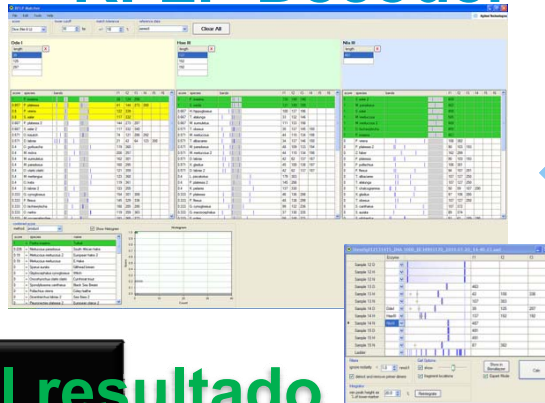
~ 1.5 h

Generación de
modelos de
especies
específicos



~2.5 h

Análisis de modelos usando el
RFLP Decoder



~ 6 h de muestra al resultado



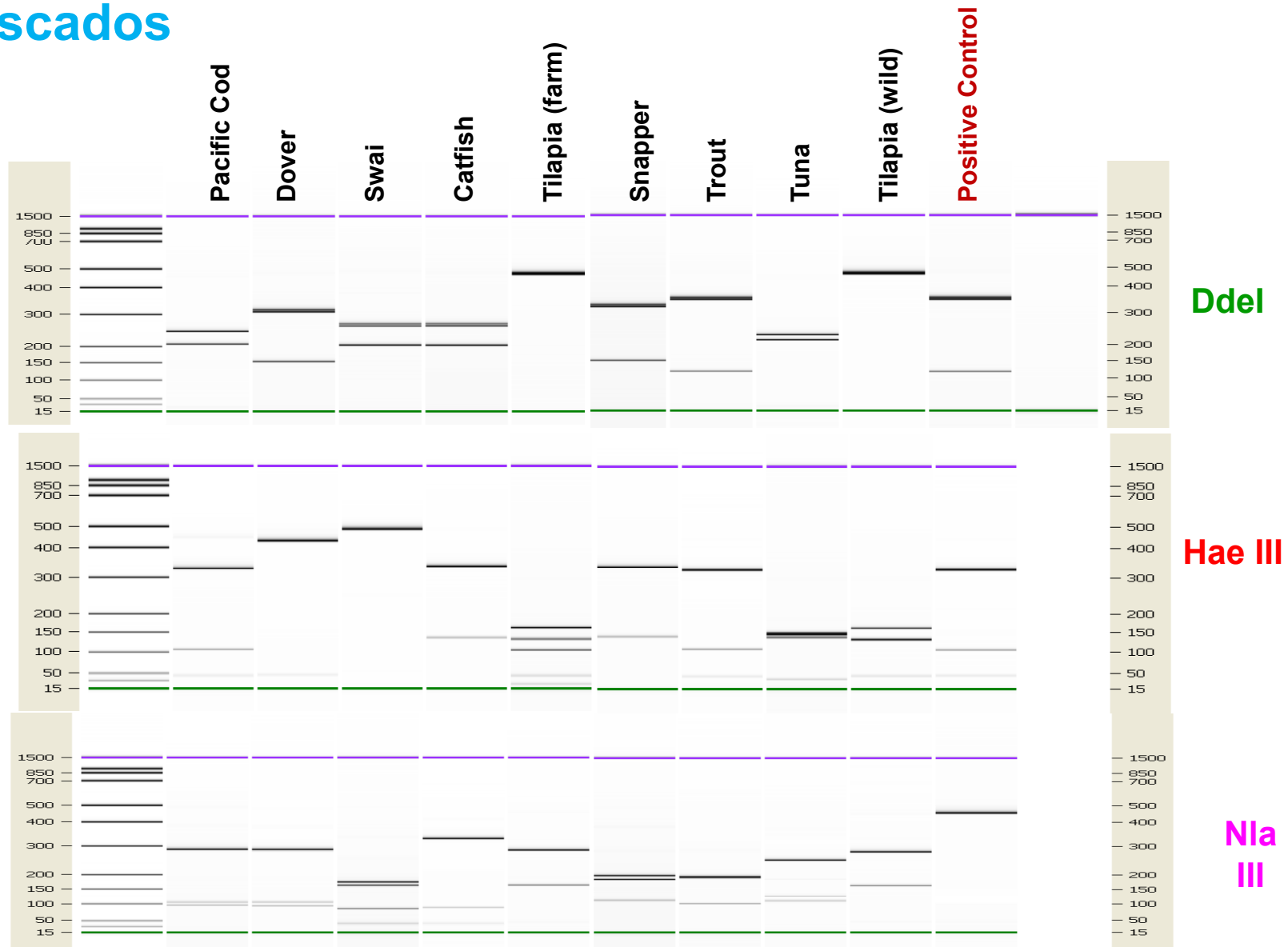
< 1 h

(dependiendo de # muestras)

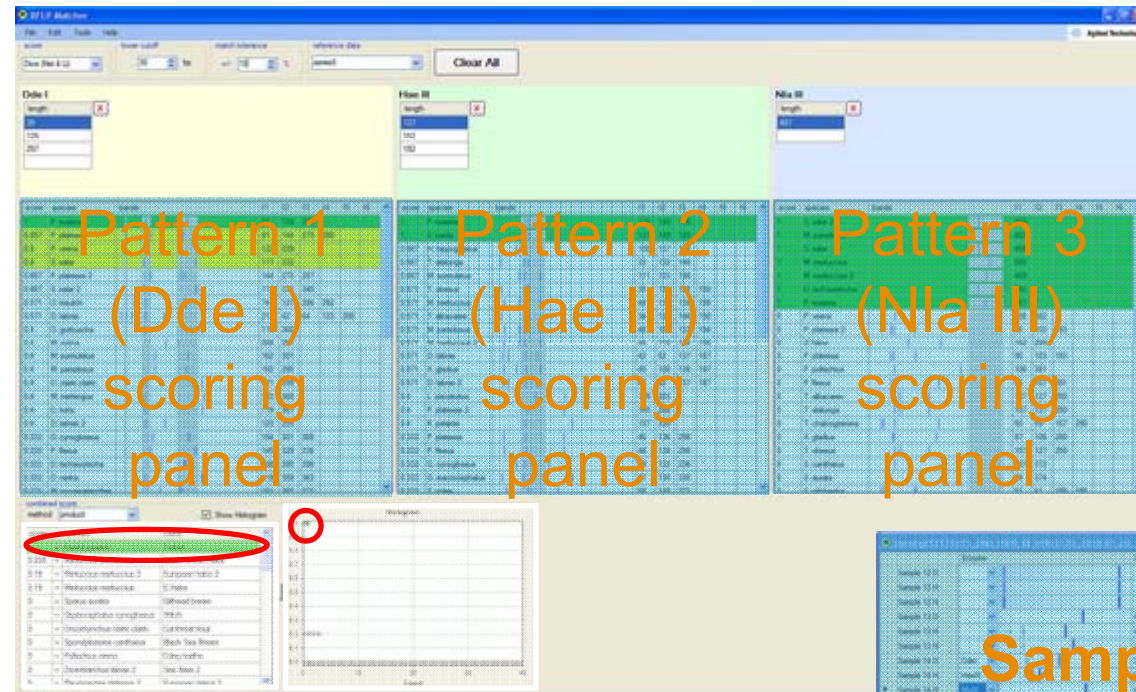


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Digestión restrictiva de los amplicons de diferentes muestras de pescados



Interpretación de Resultados – RFLP Decoder Software

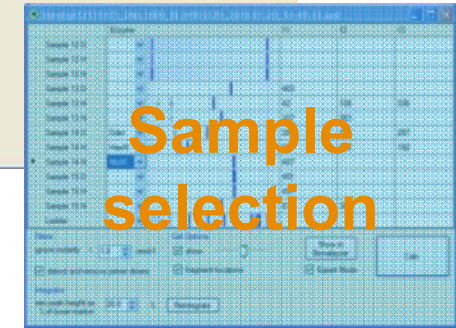


Puntuación combinada:

Indica la mayoría de las especies
El valor de la Puntuación indica la
calidad del emparejamiento.

Histograma:

La Separación de las principales
especies de aquellas con menor
puntuación ofrece una mayor
confianza en el resultado.



Agilent Technologies

Public

March

Coincidencia de patrones: RFLP Report

 **Agilent Technologies**

RFLP Decoder Report

User ID : rformosa

Date : 3/12/2010 2:44:55 PM

Score Method : Dice (Nei & Li)

Lower CutOff : 5

Combine Method : average

Tolerance : 10

Reference Database : Agilent Reference Database v1.0

S/W Version : 0.8.1.0

CSV File/Bioanalyzer XAD File : C:\Documents and Settings\rformosa\Desktop\Fish ID Training\Agilent DNA Fish ID.xad

Results

The RFLP pattern obtained for the given sample is consistent with the RFLP pattern generated from *Oncorhynchus clarkii clarkii* species.

Sample RFLP Fragments

Sample Name	Enzyme Name	Fragments
Trout_O	DdeI	121, 362
Trout_H	HaeIII	109, 329
Trout_N	NlaIII	99, 194

Species Matches

Score	Status	Species	Name
1	✓	<i>Oncorhynchus clarkii clarkii</i>	Cut-throat trout
0.933	✓	<i>Merlangius merlangus</i>	Whiting
0.767	✓	<i>Pollachius virens</i>	Coley/saithe

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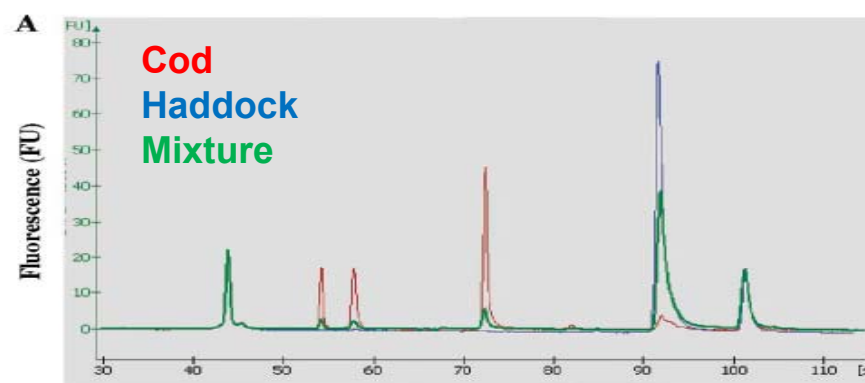
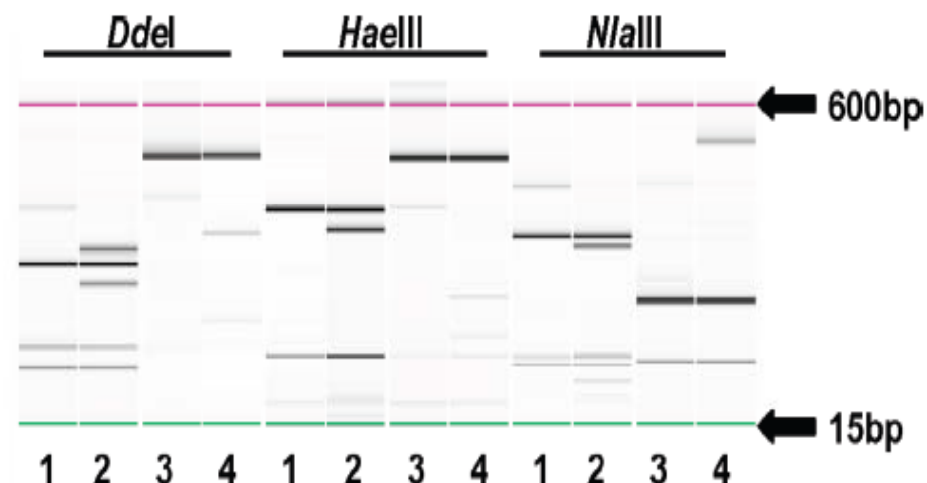


Modelos de RFLP con mezclas de pescados

(d) Details of DNA Admixtures Used in this Study

species 1	species 2
5% coley	95% Atlantic cod
5% hoki	95% Atlantic cod
5% whiting	95% haddock
5% SA hake	95% haddock
5% coley	95% Pacific cod
5% hoki	95% haddock
5% SA hake	95% Atlantic cod
5% whiting	95% Pacific cod
5% hoki	95% coley
5% whiting	95% Atlantic cod
5% A. pollock	95% Atlantic cod
5% hoki	95% Pacific cod
5% coley ^b	95% Pacific cod
5% whiting ^b	95% haddock
5% SA hake ^b	95% Atlantic cod
10% coley ^b	90% Pacific cod

^a Admixtures prepared on a w/w basis. ^b Admixture contains 59% (v/v) total fish DNA and 41% (v/v) soya DNA.



Limites de detección en mezclas: 5%

J. Agric. Food Chem. 2005, 53, 3348–3357



Agilent Technologies

Public
March 22, 2011

FOOD MARKET SINERGIAS BIOANALIZADOR Y QPCR

El Bioanalizador puede sustituir
El sistema de Fotodocumentación de geles

El QPCR complementa
Ensayos ELISA tanto en DNA como en Proteínas
Ensayos microbiológicos con patógenos

(MENOS tiempo y MAS especificidad)

ELIMINAMOS LOS NEGATIVOS EN MENOS TIEMPO

LOS POSITIVOS TENEMOS QUE CONTRASTARLOS CON MICROBIOLOGÍA

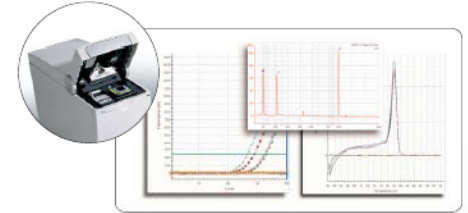
Quien ya tiene QPCR Y utiliza la tecnología **SYBR Green**, debe hacer un gel o bien un Bioanalizador para definir si lo que se amplificó es 1 sola Diana o varias. De lo contrario deberían utilizar sondas para ser selectivos



Optimizing real-time quantitative PCR experiments with the Agilent 2100 bioanalyzer

Application Note

Steffen Mueller



Abstract

This Application Note describes the benefits of the Agilent 2100 bioanalyzer in real-time quantitative PCR (QPCR) experiments. The results show that the Agilent 2100 bioanalyzer is an indispensable tool to:

- ensure experimental success by verifying RNA template quality prior to QPCR experiments
- improve the assay design and validation process by monitoring size and purity of the QPCR amplicons.

Agilent Equipment:
Agilent 2100 bioanalyzer
Stratagene Mx2005P QPCR system

Application Area:
Gene Expression

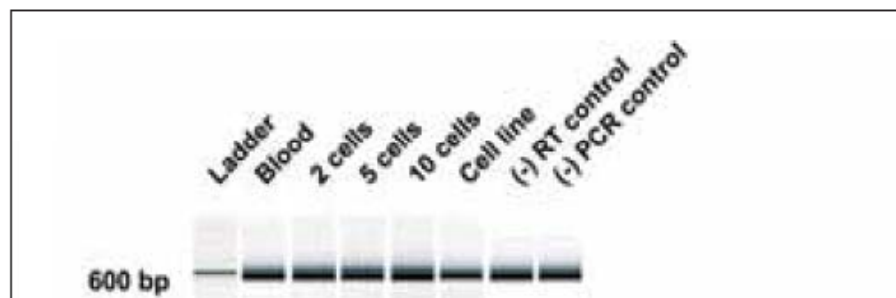
 Agilent Technologies



Agilent Technologies

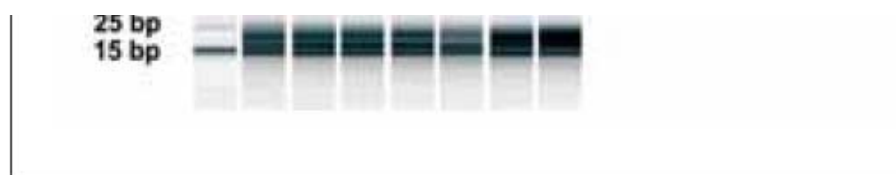
Focus en la sensibilidad: Detección de células cancerígenas en sangre total

Sangre total
5ml-EDTA



		Prior surgery	1,5 months	3 months	4,5 months	6 months
Patient 1	ELISA	+	-	-	-	-
	PCR	+	-	-	-	+
Patient 2	ELISA	-	-*	-*	-*	-
	PCR	-	-*	+*	+*	+
Patient 3	ELISA	+	-	-	-	-
	PCR	-	-	-	-	+

Gen markers cancerales

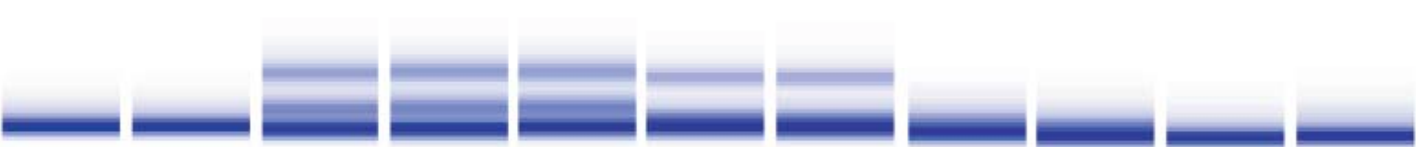


BioAnalizador

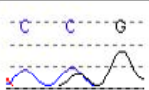
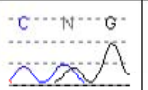
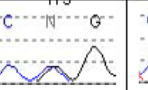
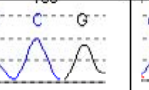
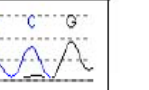
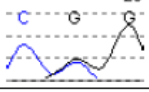
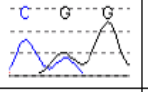
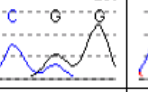
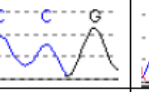
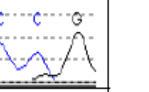
Data kindly provided by AdnaGen



Detección de SNPs en los genes p16 y K-ras

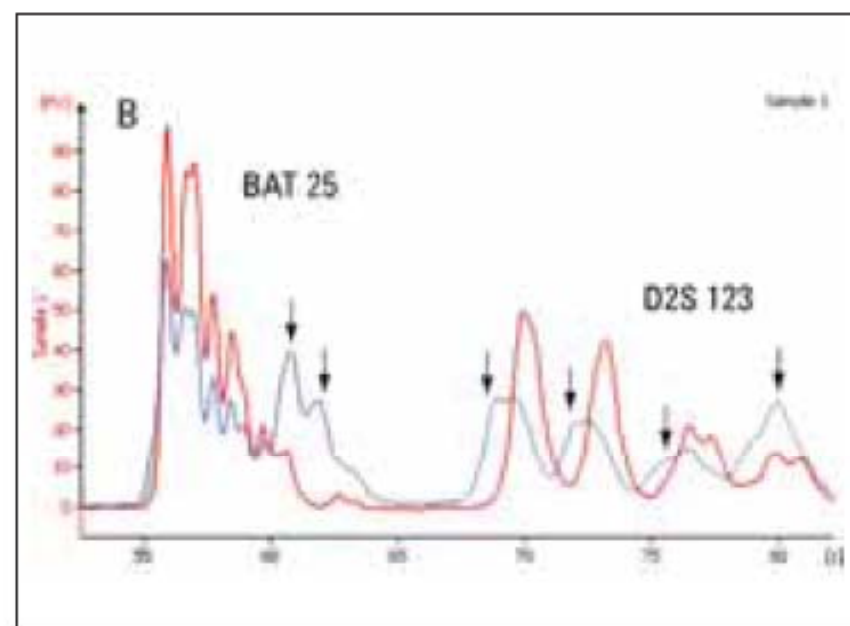
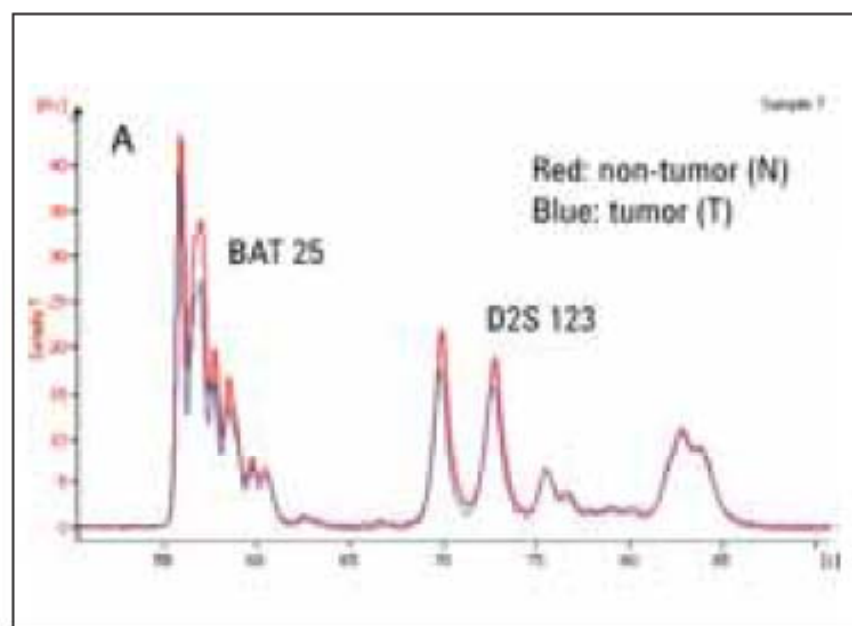
Sample	1	2	3	4	5	6	7	8	9	10	11
Genotype316	C	C	CG	CG	CG	CG	CG	C	C	C	G
Genotype356	C	C	CT	CT	CT	C	C	CT	CT	T	C
Agilent Gel											
Main Band	198	198	197	198	198	198	198	198	199	198	195
Extra Band 1			204	204	204						
Extra Band 2			216	215	215	214	214				



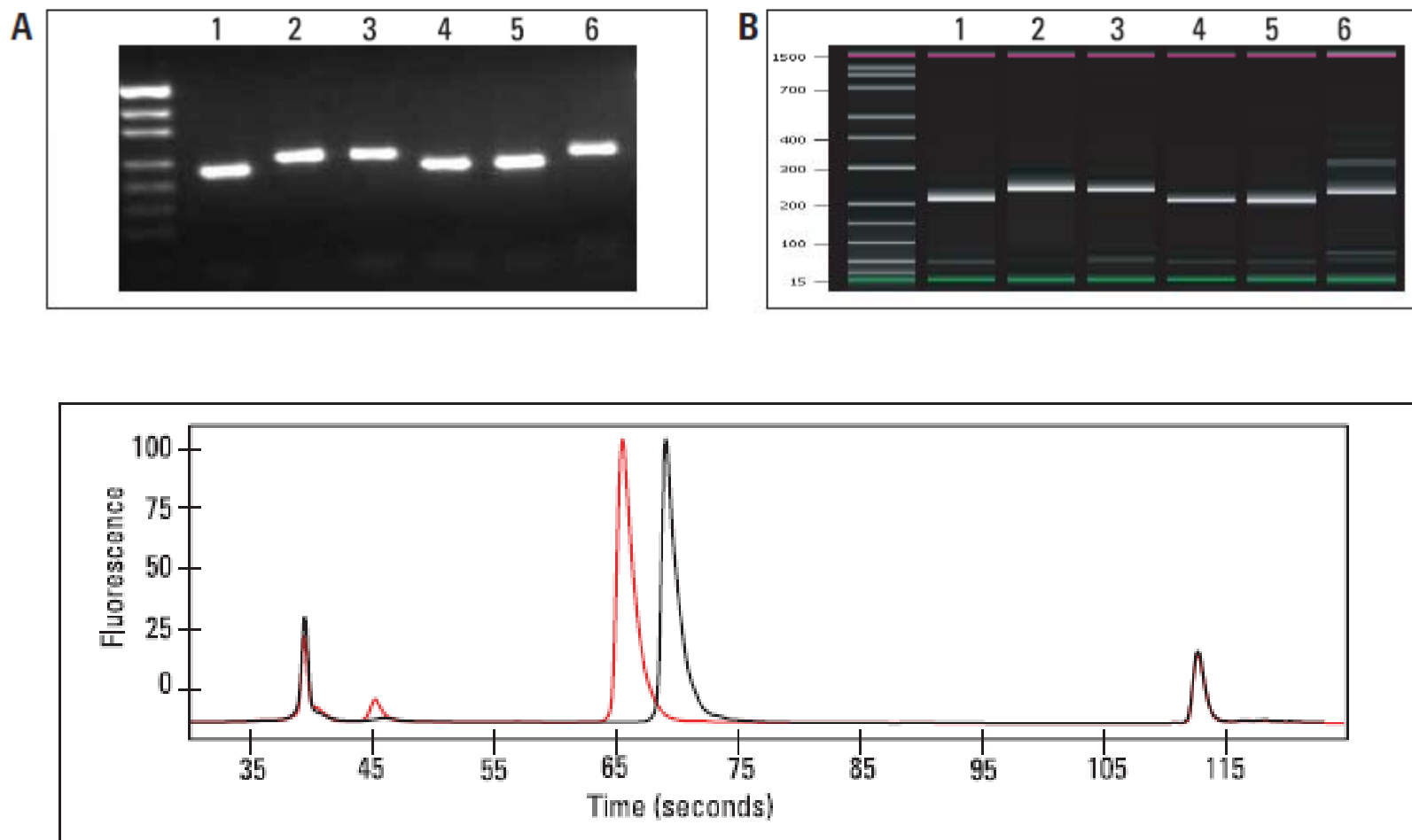
ForSeq					
RevSeq					
Genotype	CG	CG	CG	CC	CC (CG)

Inestabilidad de microsatélites en carcinoma sin marcaje adicional

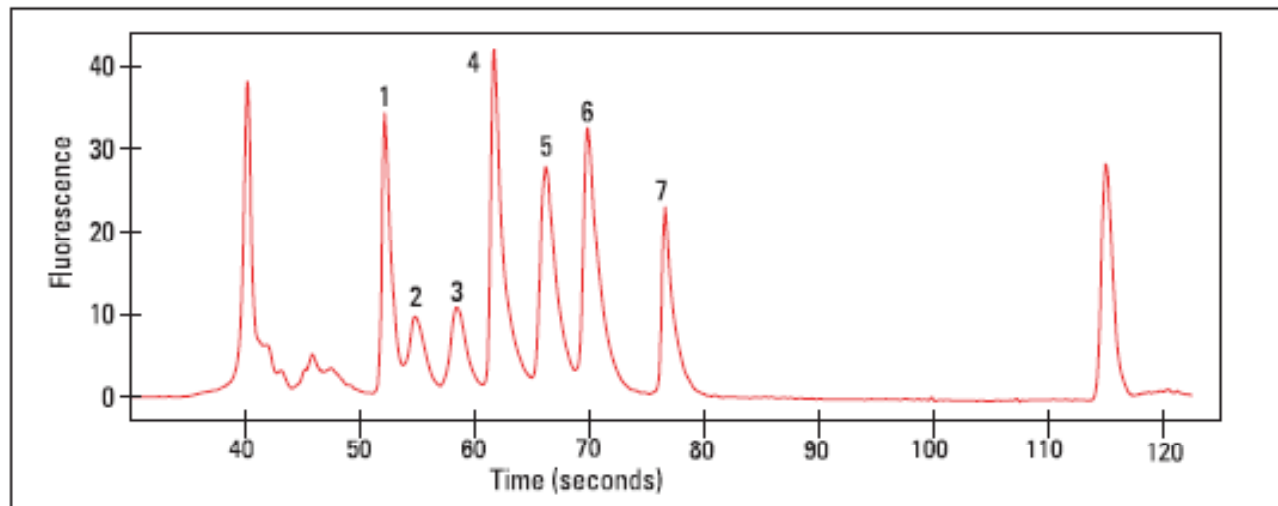
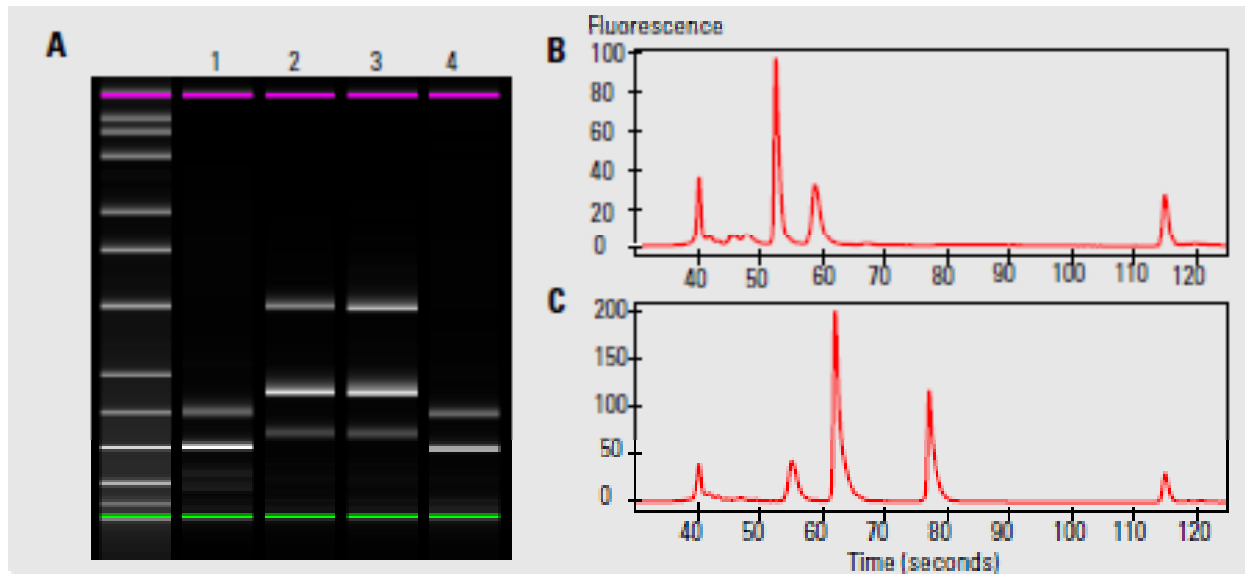
Comparación entre tejido normal y tumoral para el análisis del patrón de los microsatélites tras amplificación por PCR.



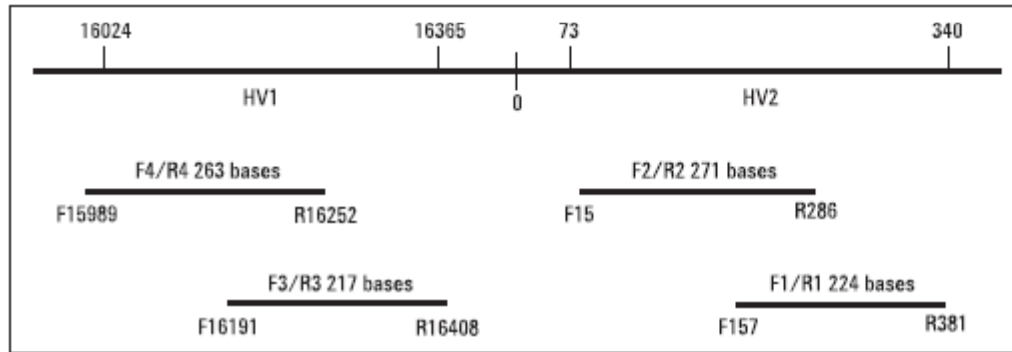
Genotipado de *H. pylori*



Genotipado de *H. pylori*

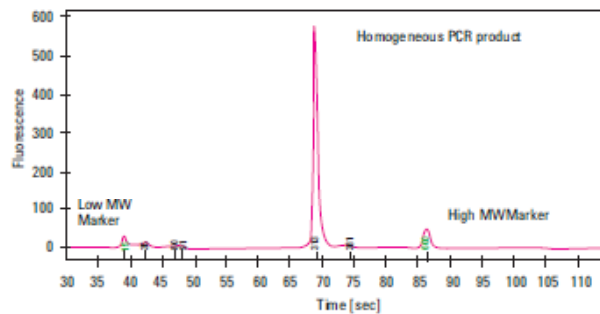


Análisis de ADN mitocondrial

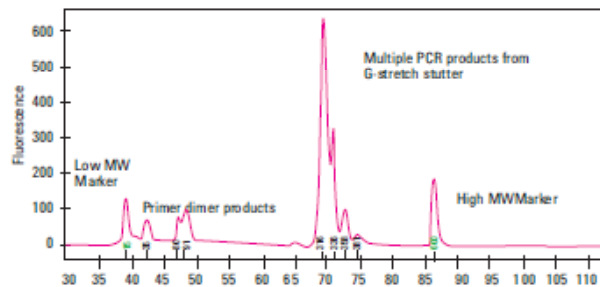
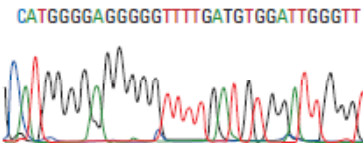


Amplified areas
in human mtDNA

mtDNA PCR product analysis



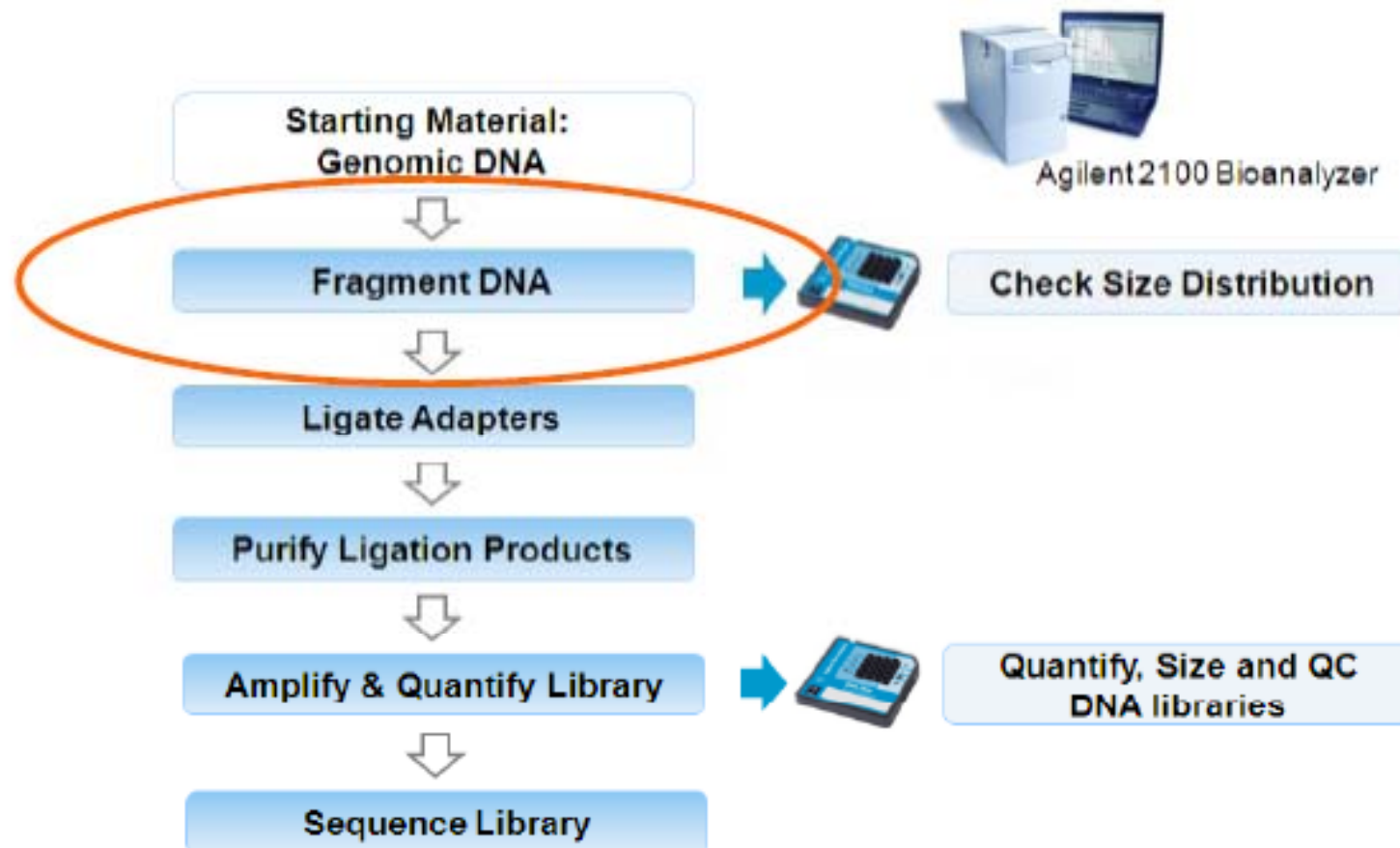
Sequence data from pure PCR product



Sequence data from multiple PCR product



Control de calidad para Next-generation sequencing



DNA Fragmentation - Monitoring the fragment size distribution

Michael A Quail, Iwanka Kozarewa, Frances Smith, Aylwyn Scally, Philip J Stephens, Richard Durbin, Harold Swerdlow & Daniel J Turner

Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. Correspondence should be addressed to D.J.T. (djt@sanger.ac.uk).

PUBLISHED ONLINE 25 NOVEMBER 2008; DOI:10.1038/NMETH.1270

NATURE METHODS | VOL.5 NO.12 | DECEMBER 2008 | 1005



- **Comparison of fragmentation by nebulization with AFA technology.**
- **Monitor performance on an Agilent Bioanalyzer 2100 DNA 1000 chip.**
- *For a 200-bp (20 bp) library, the yield produced by AFA was four- to fivefold greater than that produced by nebulization.*

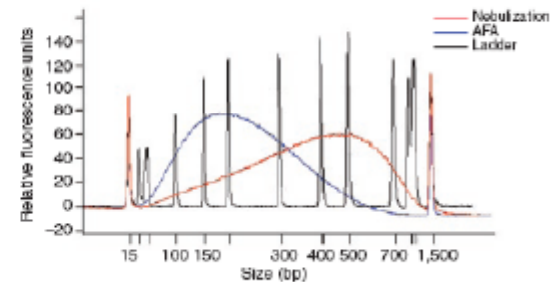


Figure 2 | Sample fragmentation. Comparison of fragmentation by nebulization with AFA technology. We fragmented 4.5 µg of human genomic DNA by nebulization or AFA, purified the samples using a spin column, eluted the DNA in 30 µl of 10 mM Tris pH 8.5, and ran 1 µl of each eluate on an Agilent Bioanalyzer 2100 DNA 100 chip. For a 200-bp (±20 bp) library, the yield produced by AFA was four- to fivefold greater than that produced by nebulization.



High sensitivity DNA kit

Para la cuantificación y discriminación por tamaño de fragmentos de dsDNA y smear de dsDNA de entre 50 – 7000 bp hasta sensibilidades de pg/ μ l.

Incrementar la sensibilidad el ADN significa:

- ☐ Muestras poco concentradas se pueden cuantificar
- ☐ La cantidad de ciclos de PCR para la amplificación de la librería se puede reducir considerablemente



Agilent High Sensitivity DNA Kit
(5067-4626)

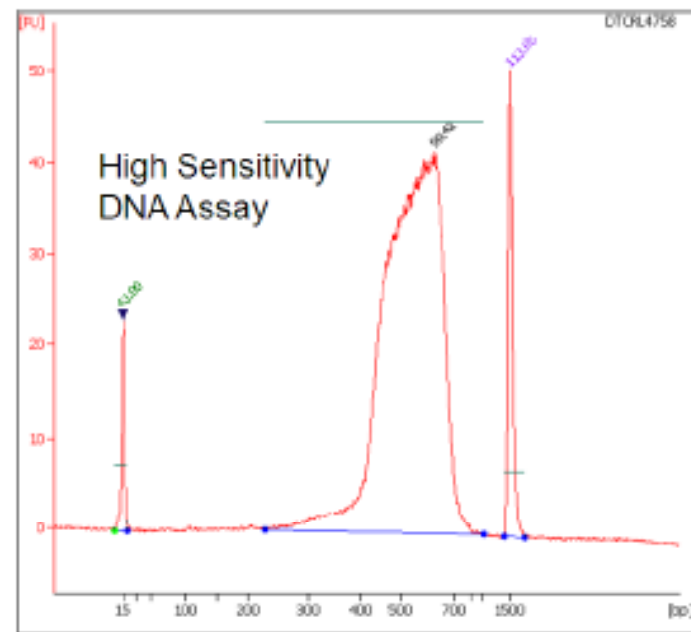
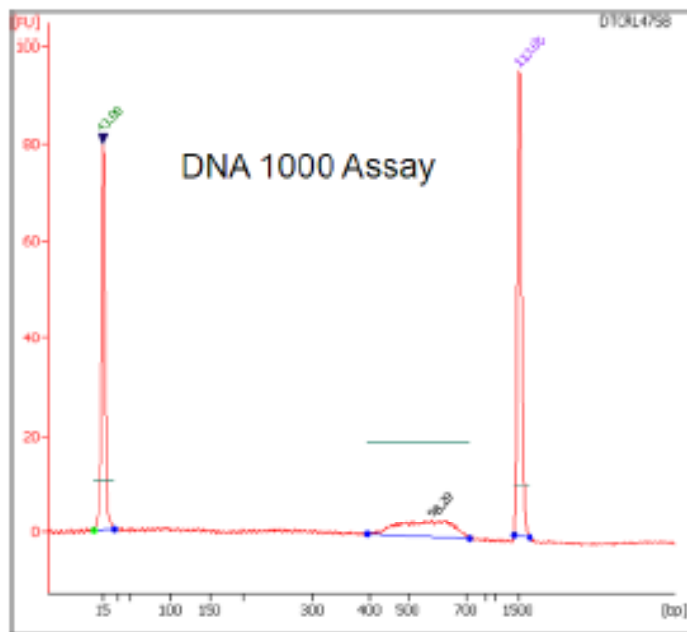


High Sensitivity DNA Reagents
(5067-4627)



High Sensitivity DNA Kit – Sensibilidad mejorada

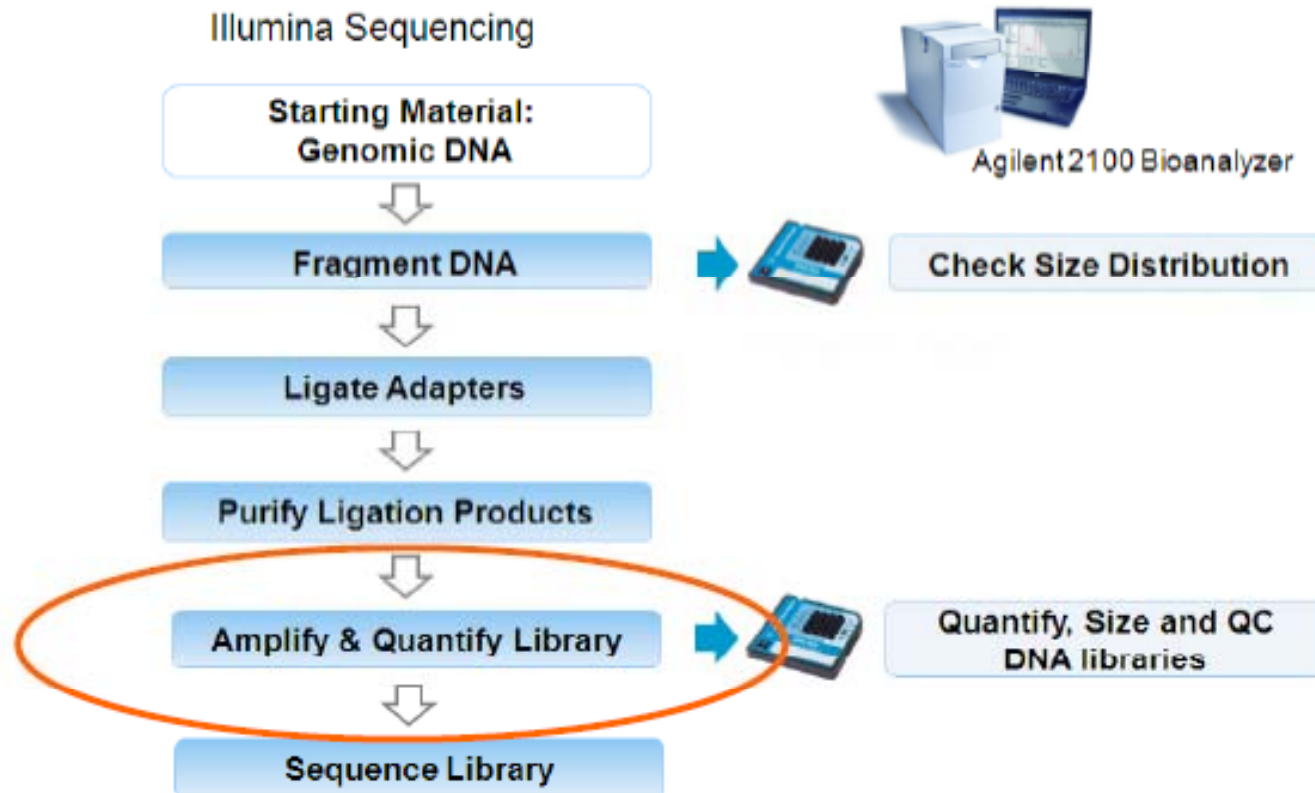
- ❑ Aumenta la sensibilidad en un factor de 20-30.
- ❑ El rango cuantitativo del High Sensitivity DNA kit se ha determinado entre 5-500 pg/μL por fragmento de DNA y entre 100-10000 pg/μl en AND fragmentado de tamaños entre 50-7000 bp.



La misma librería de ADN analizada mediante DNA 1000 kit y el High Sensitivity DNA kit

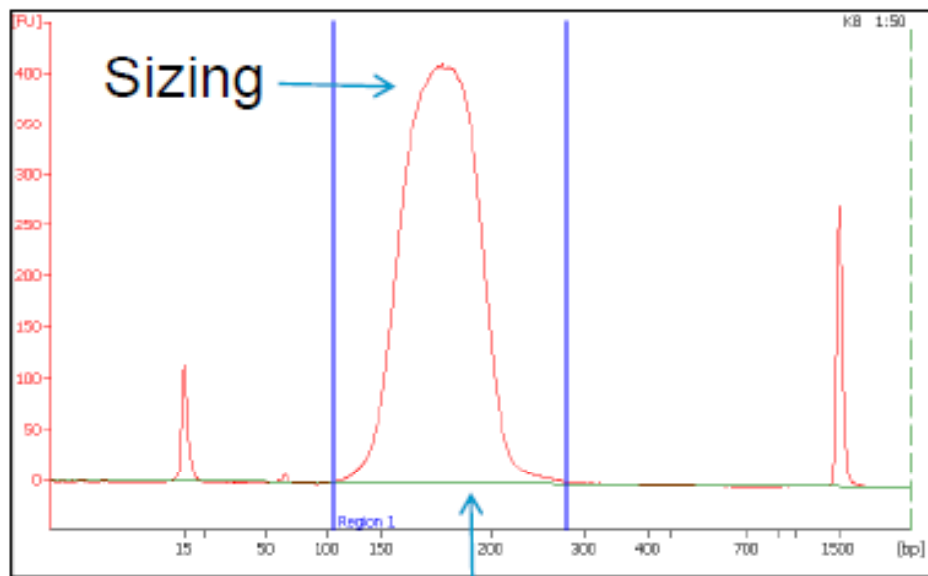


Control de calidad para Next-generation sequencing



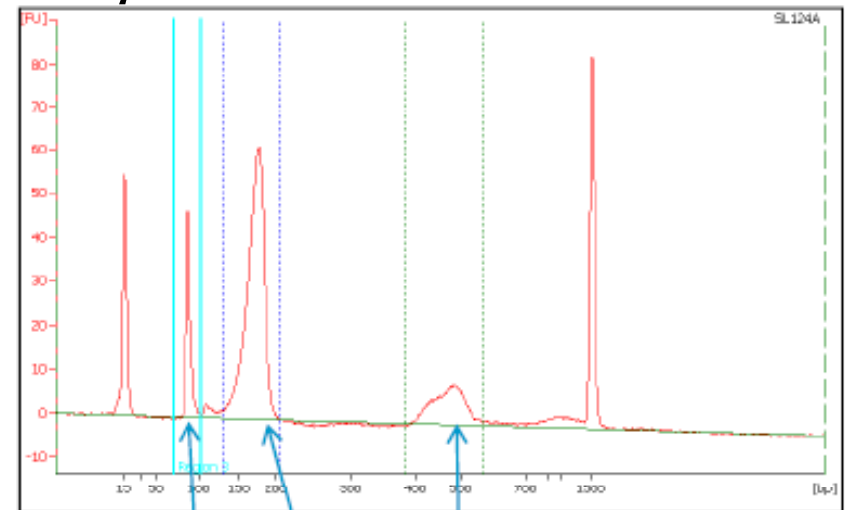
Cuantificación, tamaño y control de calidad de librerías para NGS

Librería de ADN
de alta calidad



Quantification

Identificación y cuantificación
de primer dimers
y artefactos en la PCR



Primer
dimers

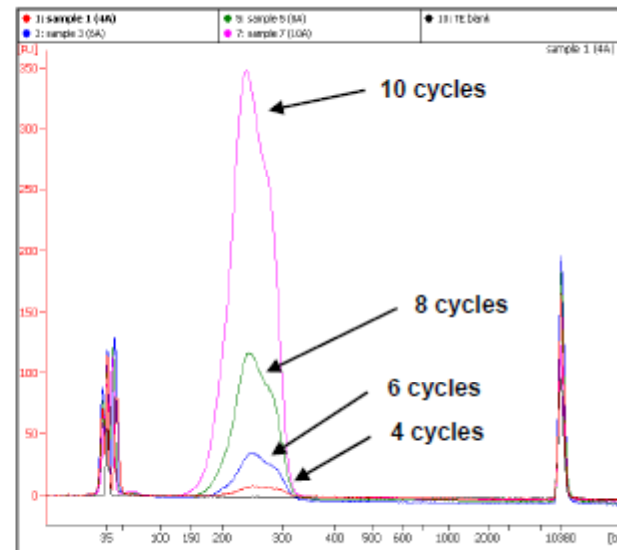
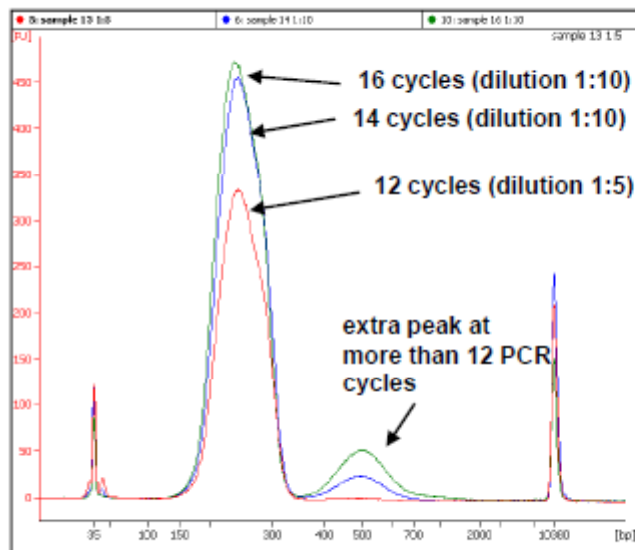
PCR artifact

DNA library

High Sensitivity DNA Kit – Reducción del número de ciclos de amplificación

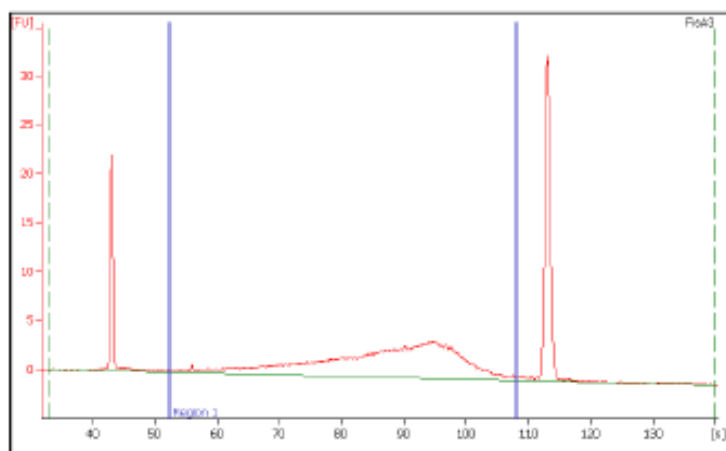
Tamaño y cuantificación para una librería de Illumina GAI. La librería se enriqueció con SureSelect Target Enrichment de Agilent y se amplificó variando el número de ciclos de PCR

- ❑ Los ciclos de amplificación a partir de cierto nivel pueden resultar en artefactos por amplificación
- ❑ Mediante el análisis con el High Sensitivity DNA se permite reducir los cliclos innecesarios de amplificación



High Sensitivity DNA Kit– Análisis de muestras con poca cantidad inicial para NGS

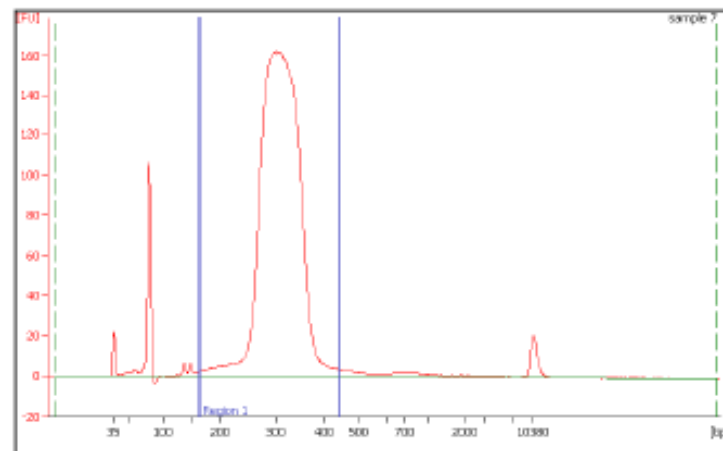
Enables the analysis of low-concentrated starting material as derived from microdissected tissues or post IP material for **ChIP-Seq**



ChIP Pre-library samples

Average Size: 827 bp

Conc: 335 pg/μl



ChIP-Seq library

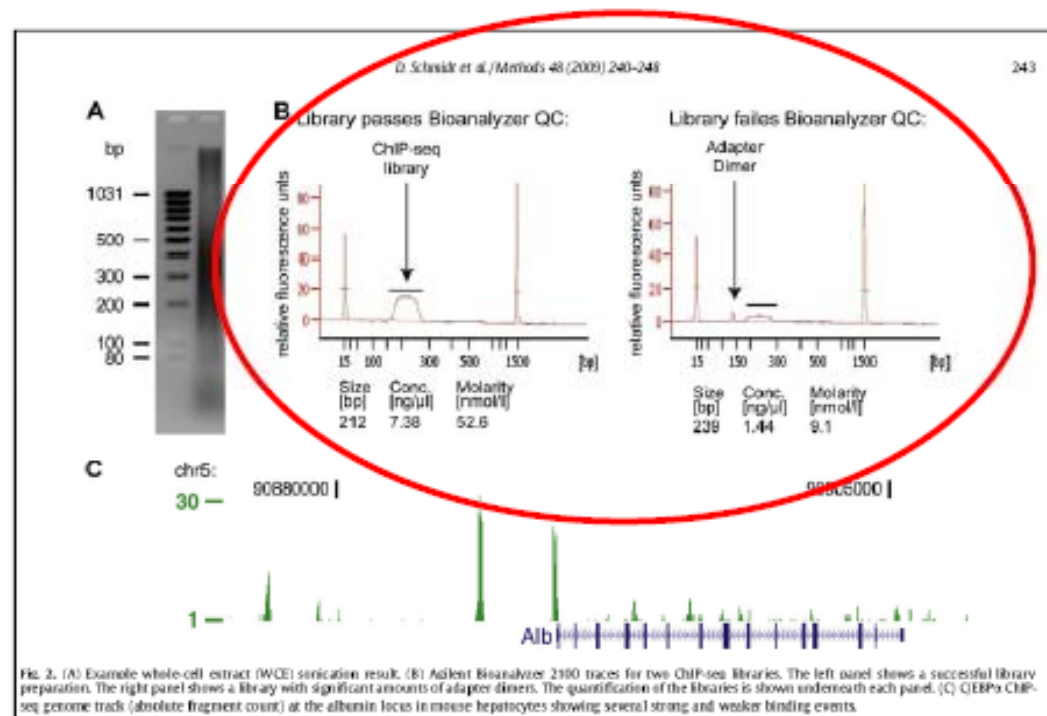
Average Size: 310 bp

Conc: 8.6 ng/μl



Control de calidad de librerías para ChIP-Seq

Schmidt et al. *ChIP-seq: Using high-throughput sequencing to discover protein–DNA interactions* Methods 48 (2009) 240–248



APLICACIONES EN ARN



Agilent RNA Analysis Kits and Reagents

Order No.	Description
5067-1511	RNA 6000 Nano Kit
5067-1512	RNA 6000 Nano Reagents
5067-1529	RNA Nano Ladder

Order No.	Description
5067-1513	RNA 6000 Pico Kit
5067-1514	RNA 6000 Pico Reagents
5067-1535	RNA Pico Ladder

Order No.	Description
5067-1548	Small RNA Kit
5067-1549	Small RNA Reagents
5067-1550	Small RNA Ladder

Analytical Specifications	RNA 6000 Nano Total RNA Assay	RNA 6000 Nano mRNA Assay	RNA 6000 Pico Total RNA Assay	RNA 6000 Pico mRNA Assay	Small RNA
Quantitative range	25–500 ng/μL	25–250 ng/μL	–	–	50–2000 pg/μL of purified miRNA in water
Qualitative range	5–500 ng/μL	25–250 ng/μL	50–5000 pg/μL in water	250–5000 pg/μL in water	50–2000 pg/μL of purified miRNA in water
Sizing range	–	–	–	–	6–150 nt
Sensitivity (signal/noise > 3)	5 ng/μL in water	25 ng/μL in water	50 pg/μL in water 200 pg/μL in TE	250 pg/μL in water 500 pg/μL in TE	50 pg/μL in water**
Quantitation reproducibility	10 % CV (within a chip)	10 % CV (within a chip)	20 % CV (within a chip)	20 % CV (within a chip)	25 % CV (within a chip)
Quantitation accuracy*	20 % CV	20 % CV	30 % CV	30 % CV	–
Maximum sample buffer strength	100 mM Tris, 0.1 mM EDTA or 125 mM NaCl or 15 mM MgCl ₂	100 mM Tris 0.1 mM EDTA or 125 mM NaCl or 15 mM MgCl ₂	50 mM Tris 0.1 mM EDTA or 50 mM NaCl or 15 mM MgCl ₂	50 mM Tris, 0.1 mM EDTA or 50 mM NaCl or 15 mM MgCl ₂	10 mM Tris, 0.1 mM EDTA

Physical Specifications					
Analysis time	30 minutes	30 minutes	30 minutes	30 minutes	30 minutes
Samples per chip	12	12	11	11	11
Sample volume	1 μL	1 μL	1 μL	1 μL	1 μL
Kit stability	4 months at 4 °C	4 months at 4 °C	4 months at 4 °C	4 months at 4 °C	4 months at 4 °C
25 chips per kit	RNA Nano 12/chip = 300 samples/kit	RNA Nano 12/chip = 300 samples/kit	RNA Pico 11/chip = 275 samples/kit	RNA Pico 11/chip = 275 samples/kit	–

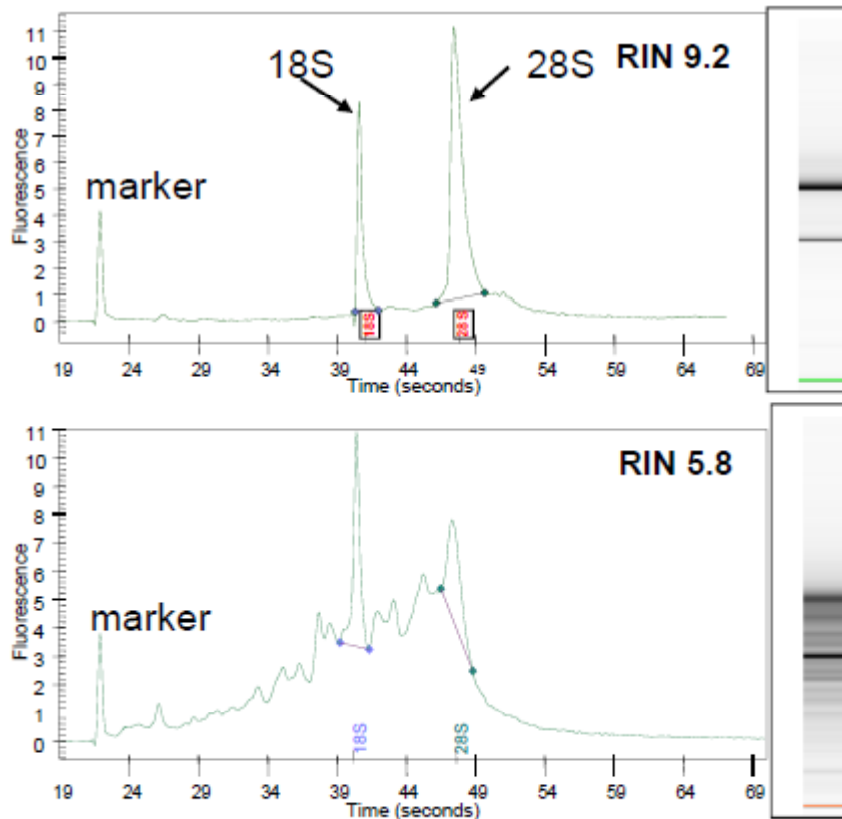
* Determined analyzing the RNA ladder as sample

** Measured for the 40 nt fragment of the Small RNA ladder



Integridad del ARN – Calidad del ARN total de la muestra

Paso clave en trabajo tras la preparación de la muestra de ARN anterior a realtime-PCR o microarrays



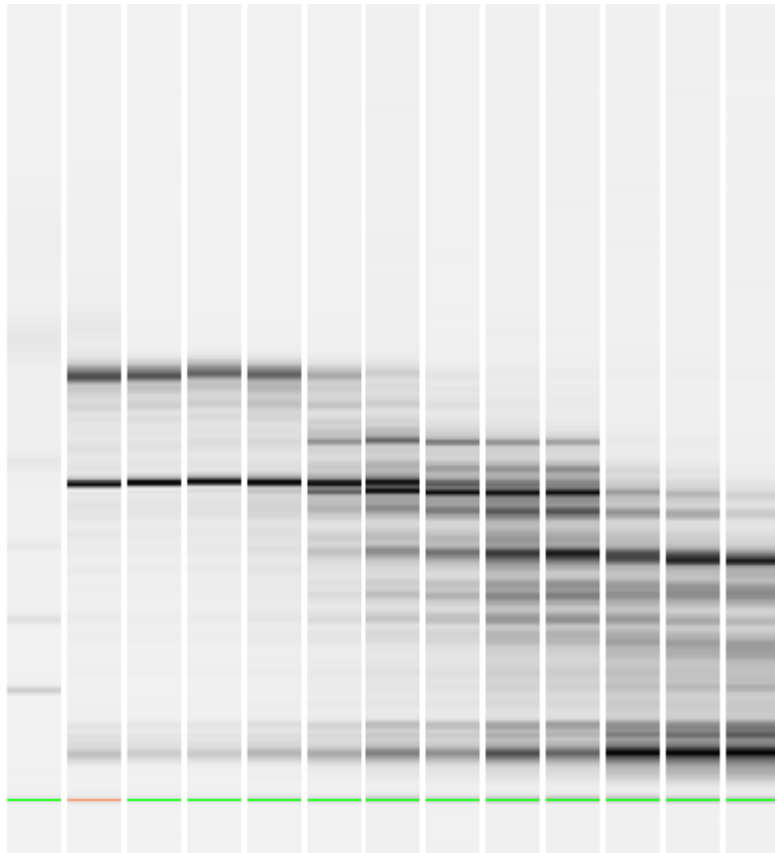
ARN de alta calidad

ARN de baja calidad

Schroeder et al.: The RIN: an RNA integrity number for assigning integrity values to RNA measurements, BMC Mol Biol. 2006 Jan 31;7:3.



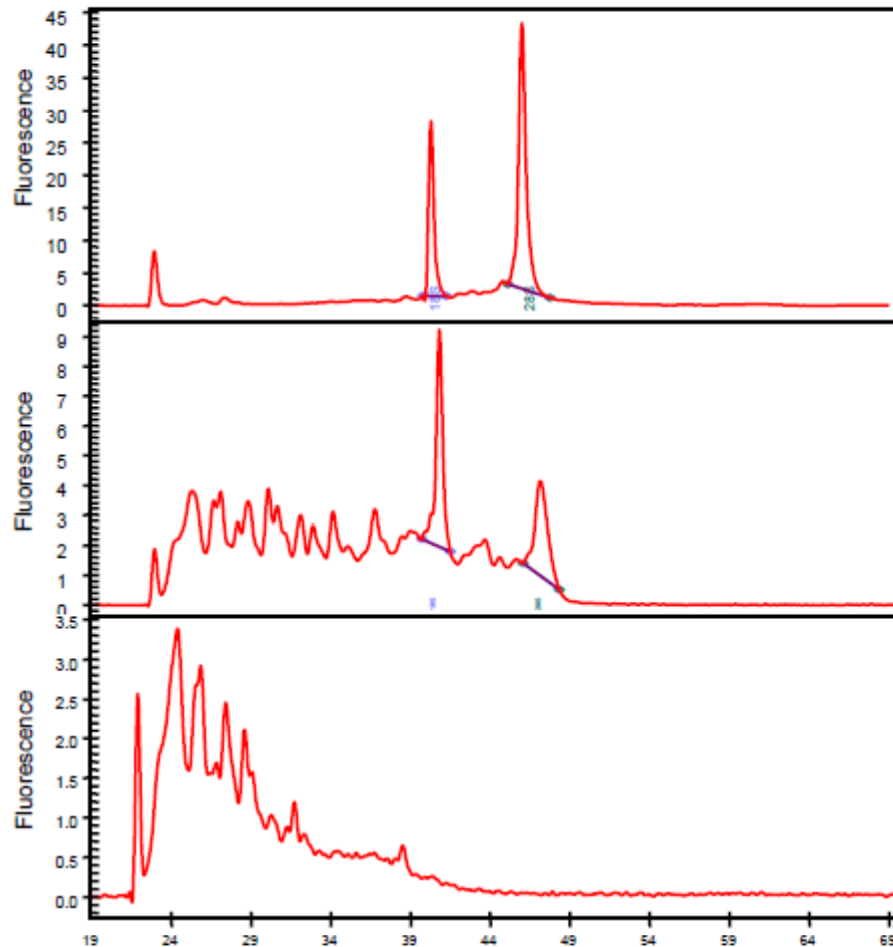
RIN – RNA Integrity Number



- ☐ The ratio of ribosomal bands is not sufficient to describe RNA integrity!
- ☐ RNA degradation is a gradual process.
- ☐ Results have to be interpreted by visual inspection.
- ☐ Overlay of electropherograms only works well for samples with the same concentration.
- ☐ Instrument dependency in signal height



RIN –Integridad del ARN



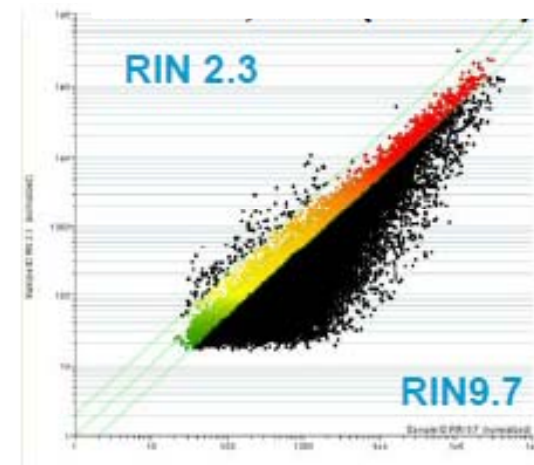
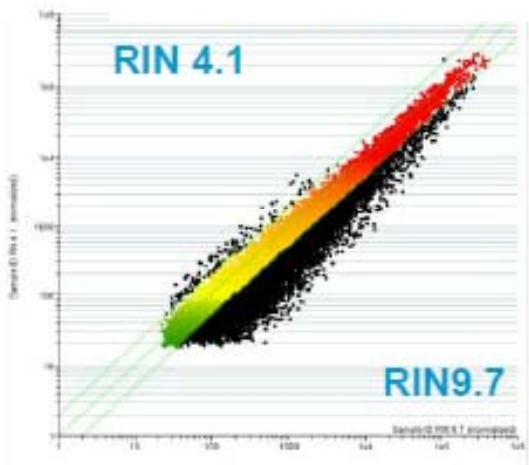
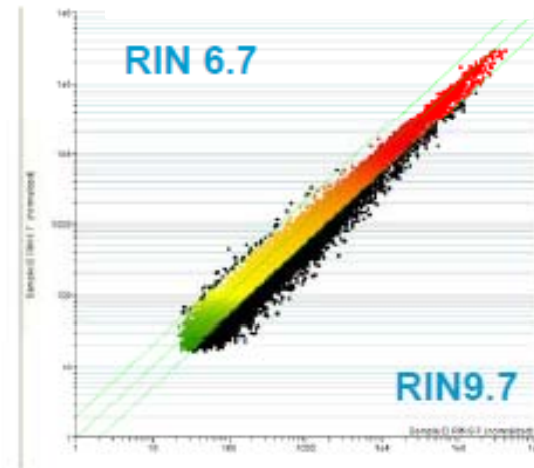
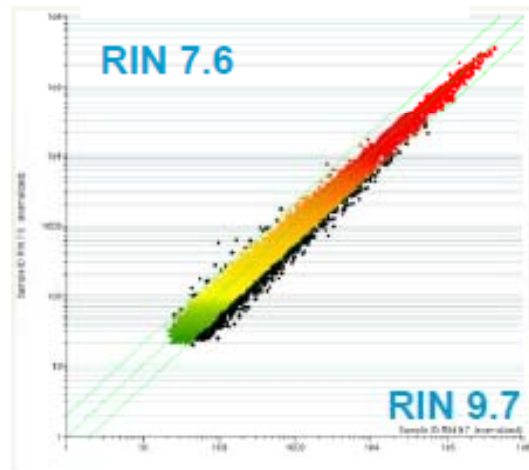
Intact RNA: RIN 10

Partially degraded RNA: RIN 5

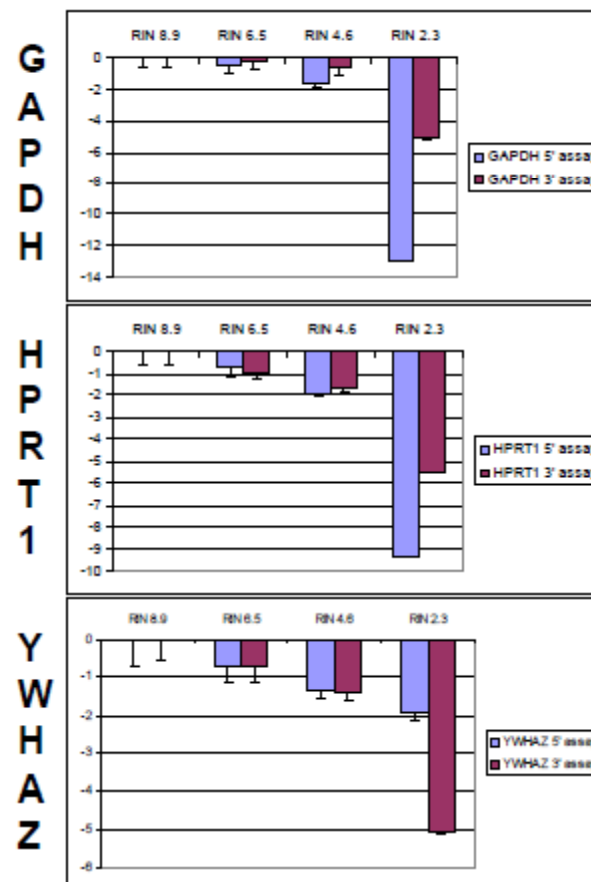
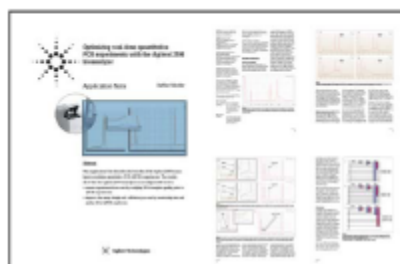
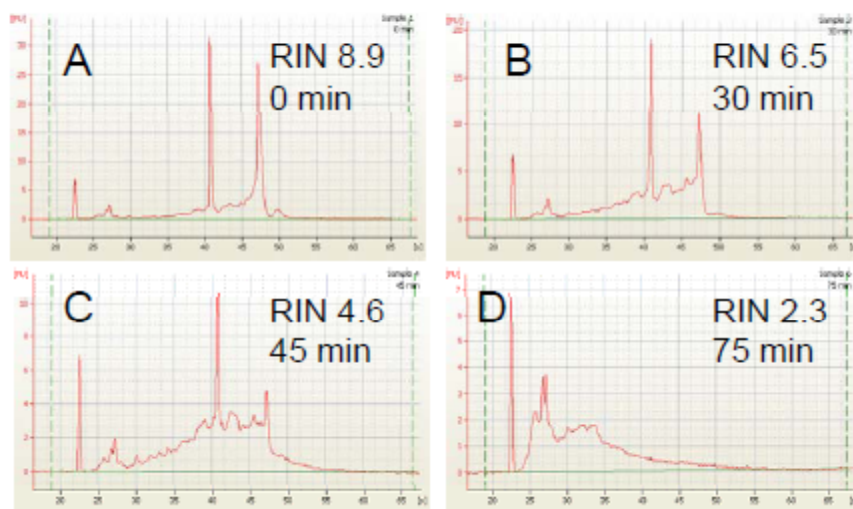
Strongly Degraded RNA: RIN 3



Porqué la calidad sí importa – Efectos en los resultados de expresión génica



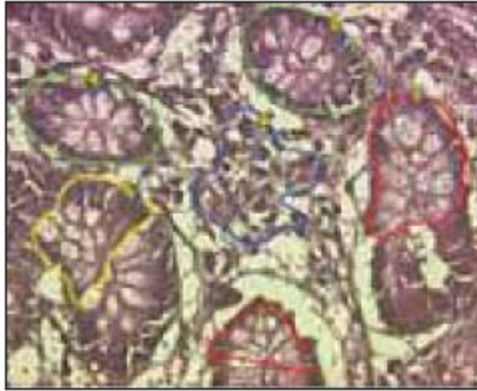
RNA QC/QPCR – Calidad del ARN y niveles de expresión génica



RNA QC/qPCR Application Note (5989-7730EN)



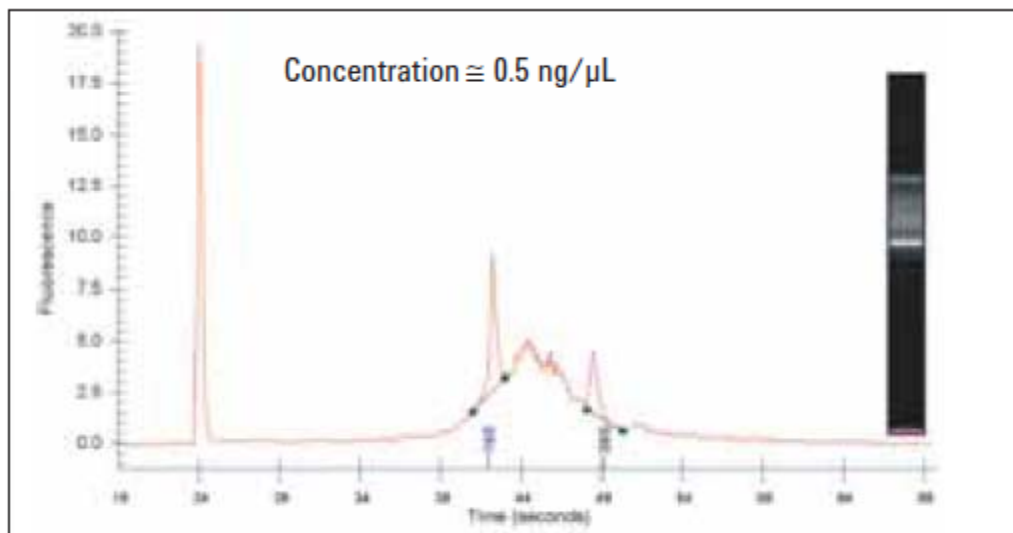
Microdissección y análisis de ARN



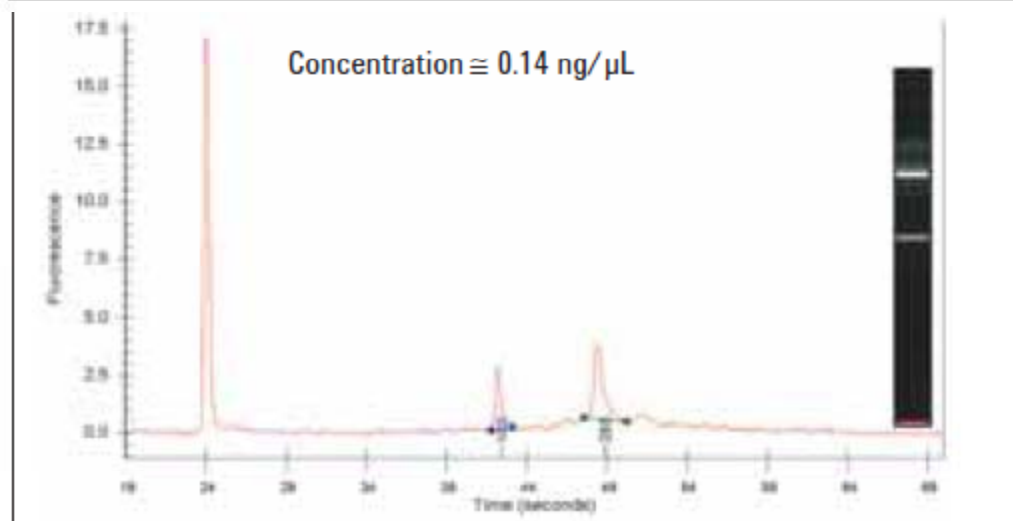
Laser micro dissection



Microdissección y análisis de ARN: contaminación por ADN de la muestra



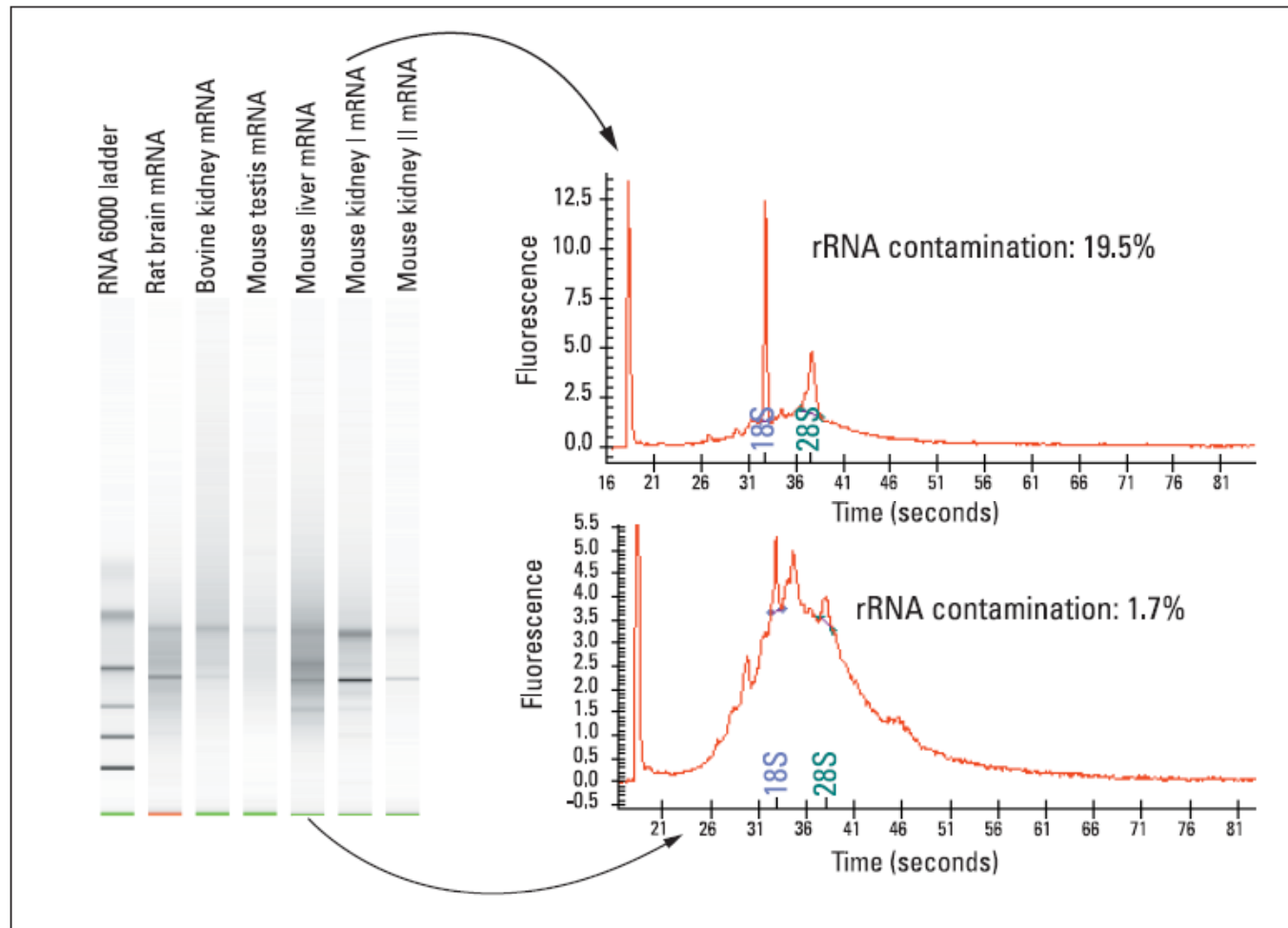
Efectos de la digestión de ADN en
columna con DNasa



Sobreestimación
de la concentración

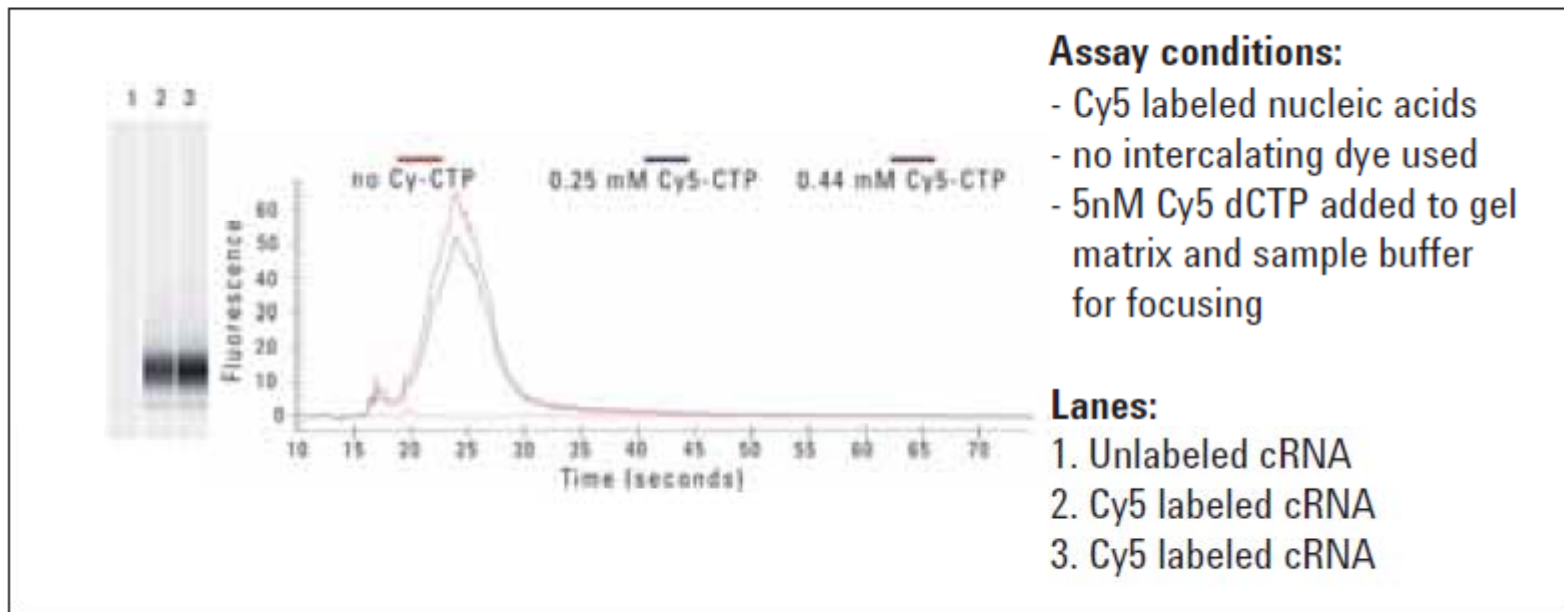
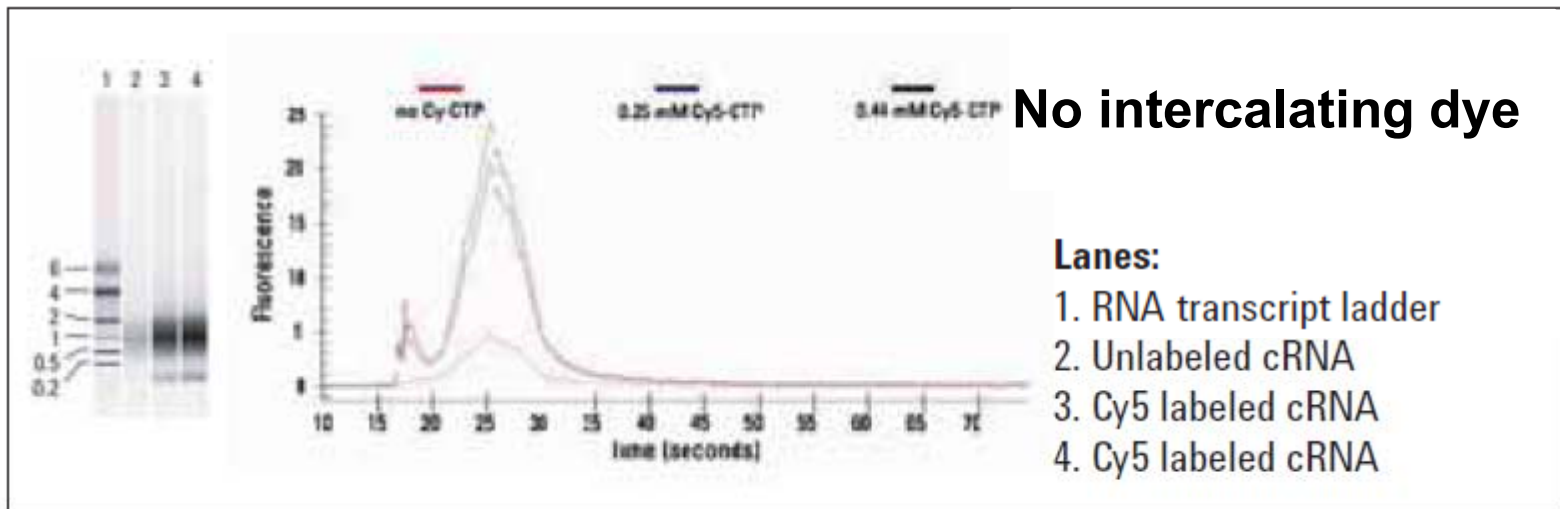
Análisis del mRNA

Contaminación con rRNA de muestras de mRNA

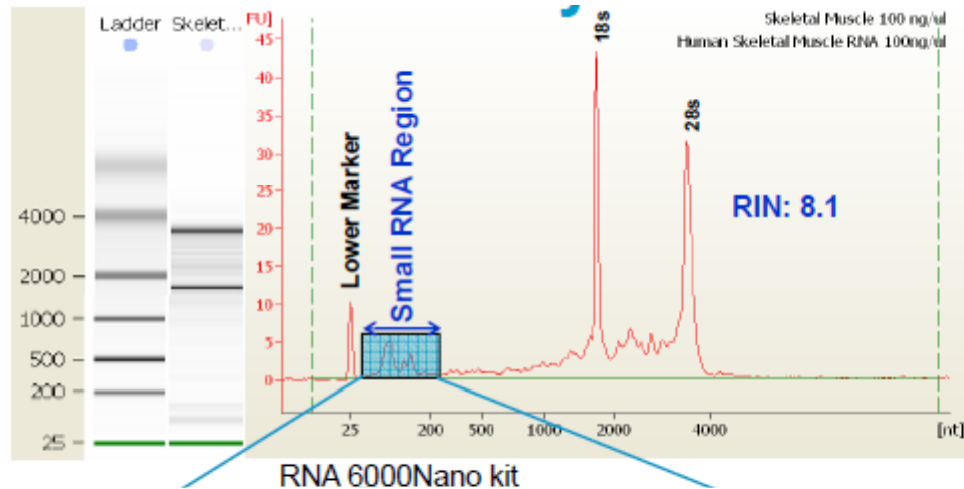


Analisis de muestras marcadas con Cy5

Muestras de cRNA con o sin tinción incorporado en la matriz de gel



Small RNA kit



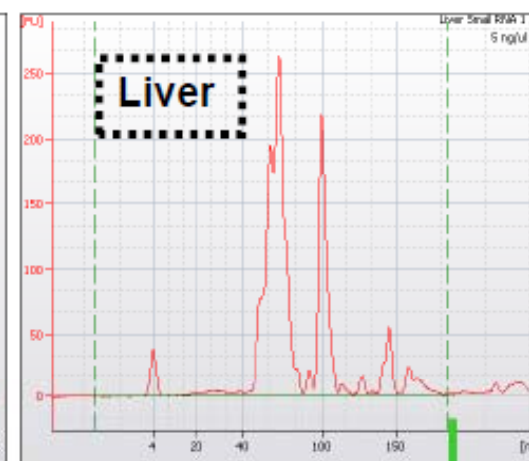
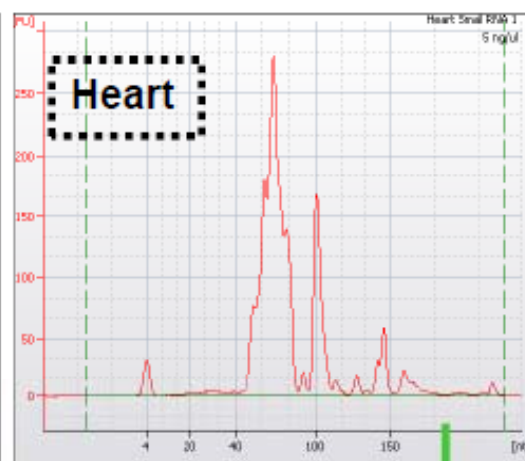
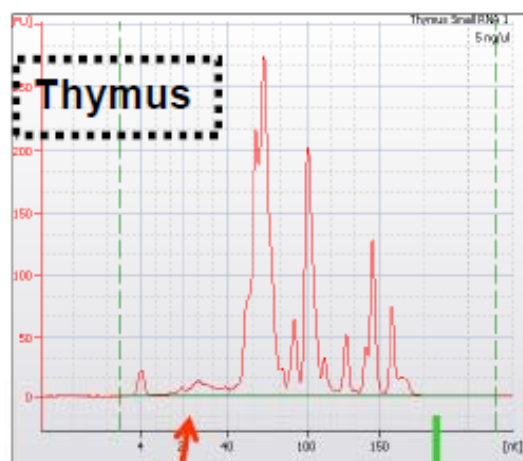
RNA 6000Nano

Size range: 25-6000nt

Results: Integrity, Total RNA amount, gDNA contamination

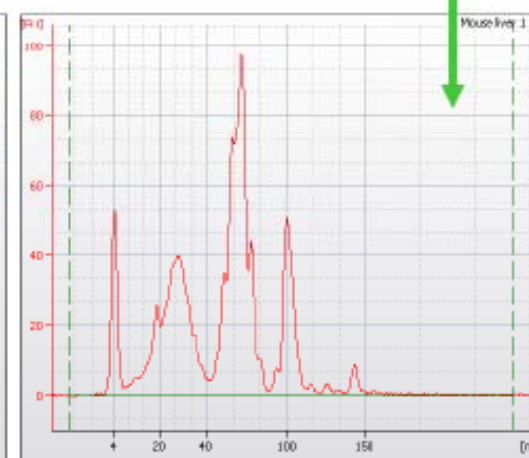
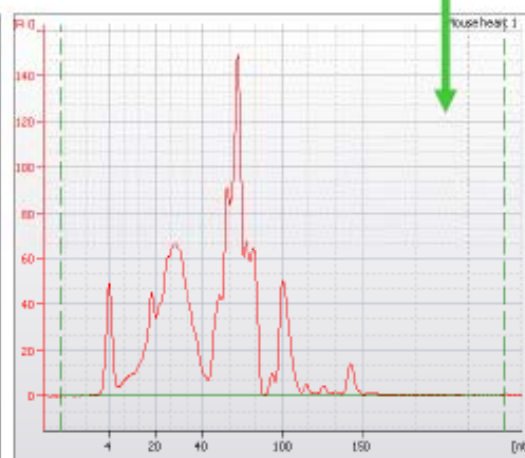
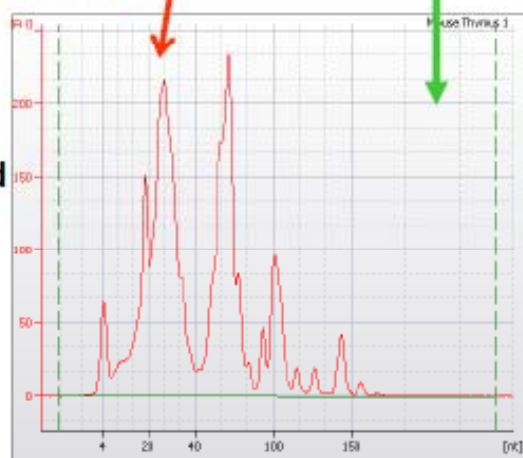
Small RNA Extraction - Monitoring the enrichment of miRNA

Pre-purified small RNA
(0-150 nt)

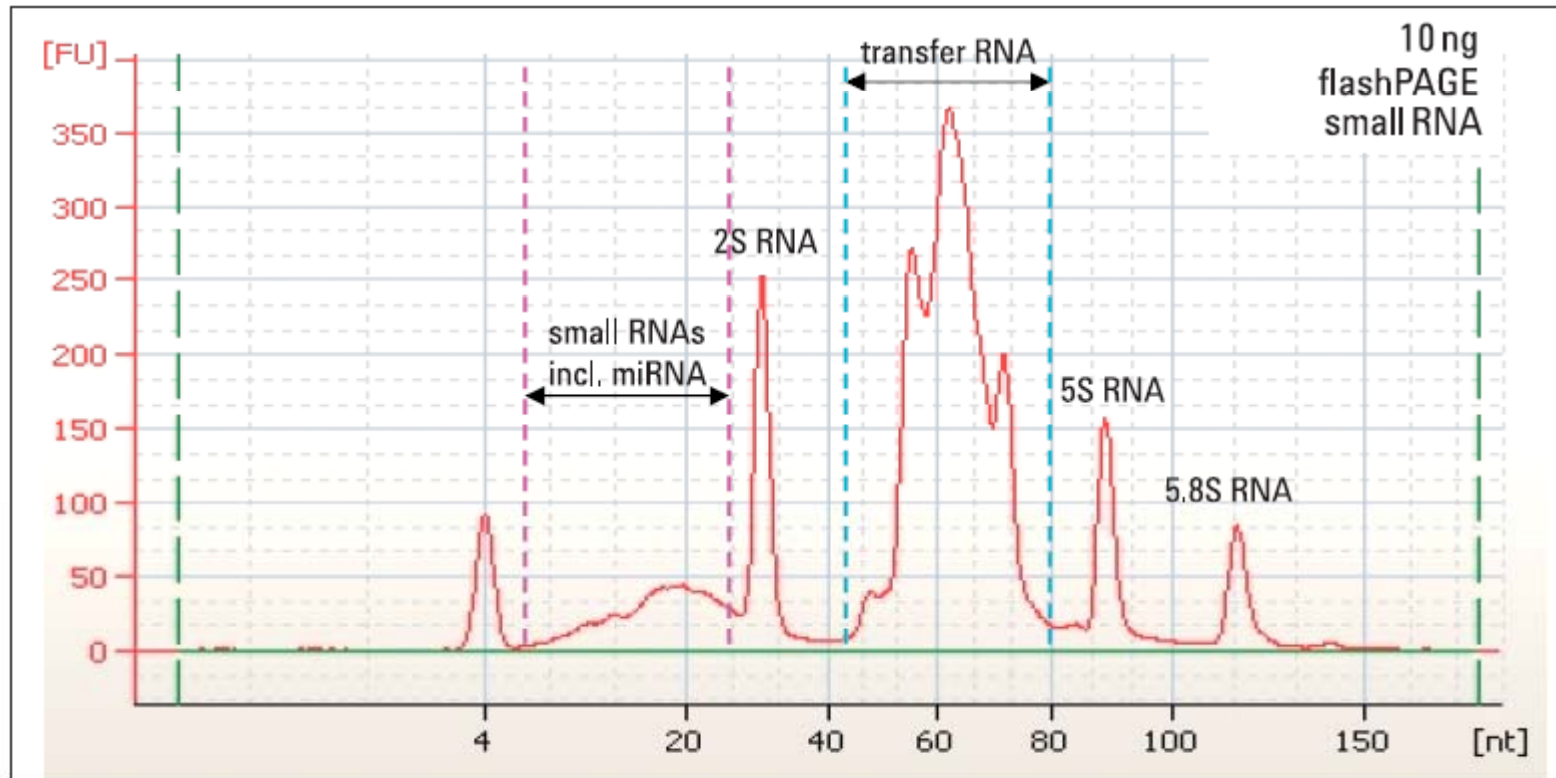


miRNA Peak

PAGE-based
enrichment
of miRNA



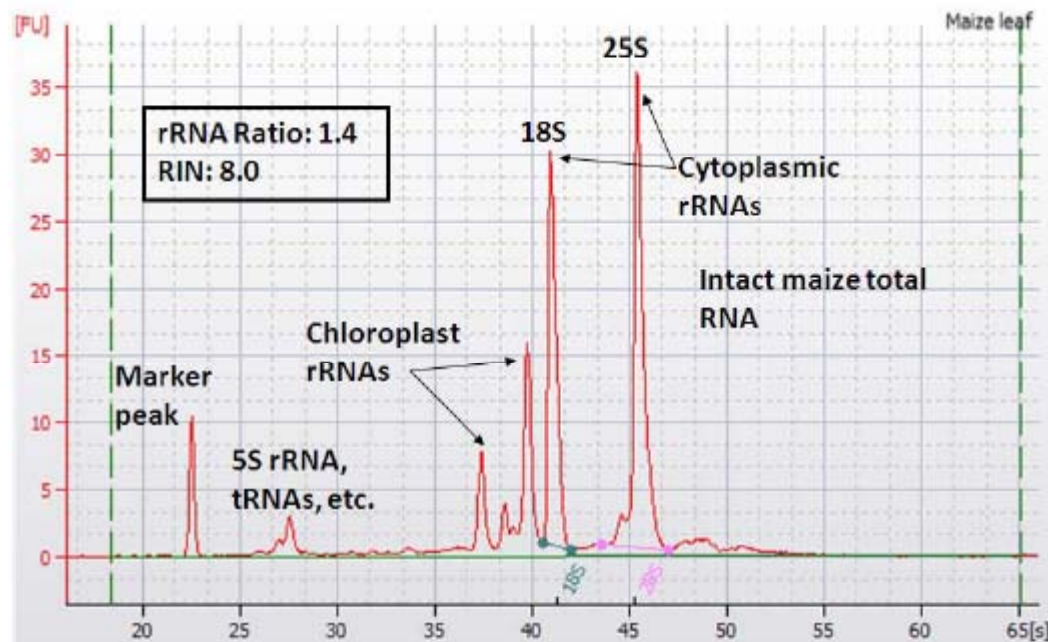
Small RNA – distinción de especies de small RNA



Analisis de RNAs de células Schneider de *Drosophila* (10ng RNA total)

Nuevo test de ARN para plantas

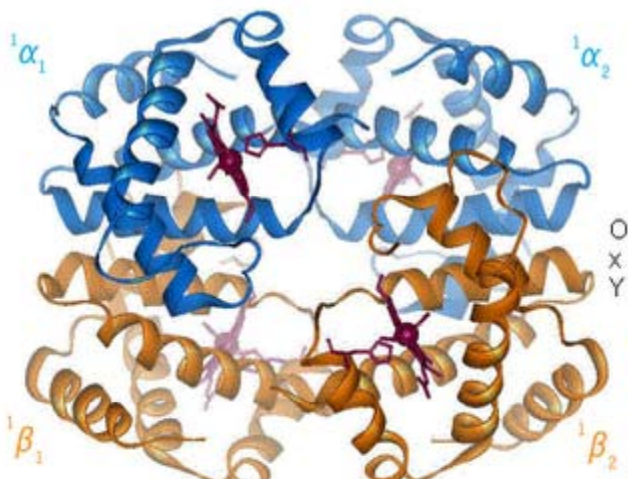
- ❑ Nuevo test para ARN de plantas en el 2100 Expert software B.02.07
- ❑ Método de identificación reproducible de fragmentos de rRNA de diferentes muestras de plantas para determinar la integridad del ARN
- ❑ Algoritmo RIN estándar
- ❑ Compatible con los kits estándar de ARN



Data kindly provided by D Morrow, Stanford University



Agilent Technologies



APLICACIONES EN PROTEINAS



Protein Analysis Kits and Reagents

Order No.	Description
5067-1515	Protein 80 Kit
5067-1516	Protein 80 Reagents

Order No.	Description
5067-1517	Protein 230 Kit
5067-1518	Protein 230 Reagents

Order No.	Description
5067-1575	High Sensitivity Protein 250 Kit
5067-1576	High Sensitivity Protein 250 Reagents
5067-1577	High Sensitivity Protein 250 Labeling Reagents
5067-1578	High Sensitivity Protein 250 Ladder

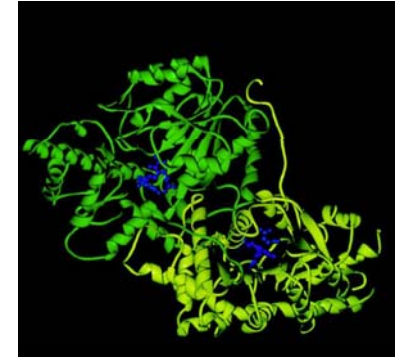
Analytical Specifications	Protein 80 Assay	Protein 230 Assay	High Sensitivity Protein 250 Assay
Sizing range	5–80 kDa	14–230 kDa	10–250 kDa
Typical sizing resolution	10 %	10 %	10 %
Typical sizing accuracy	10 % CV (CAII, BLG)	10 % CV (BSA, CAII)	10 % CV (BSA)
Sizing reproducibility	3 % CV (CAII, BLG)	3 % CV (BSA, CAII)	3 % CV (BSA)
Sensitivity (signal/noise > 3)	6 ng/μL CAII (15 ng/μL BSA) in PBS 10 ng/μL (CAII) in 0.5 M NaCl (30 ng/μL BSA in 0.5 M NaCl)	6 ng/μL CAII (15 ng/μL BSA) in PBS 30 ng/μL (BSA) in 0.5 M NaCl	1 pg/μL (labeled BSA) in water on chip 5 pg/μL (labeled BSA) in PBS on chip Labeling reaction at 1 ng/μL of total protein
Quantitative range	60–2000 ng/μL CAII in PBS	15–2000 ng/μL CAII, 30–2000 ng/μL BSA in PBS	Up to 4 orders of magnitude (0.3 to 3000 ng/μL BSA)
Qualitative range	6–4000 ng/μL CAII and BLG	6–5000 ng/μL CAII, 15–5000 ng/μL BSA in PBS	–
Quantitation reproducibility	20 % CV (CAII, BLG)	20 % CV (BSA, CAII)	20 % CV (BSA)

Physical Specifications			
Analysis time	30 minutes	25 minutes	30 minutes
Samples per chip	10	10	10
Sample volume	4 μL	4 μL	5 μL
Kit stability	4 months	4 months	6 months
Kit size	250 samples/kit	250 samples/kit	100 samples/kit

CAII = Carbonic Anhydrase, BSA = Bovine Serum Albumin, BLG = beta-Lactoglobulin



Aplicaciones del Protein LabChip



Células lisadas

- Identificación sobre proteínas expresadas
- Comparación de diferentes formas de expresión

Fracciones de columna

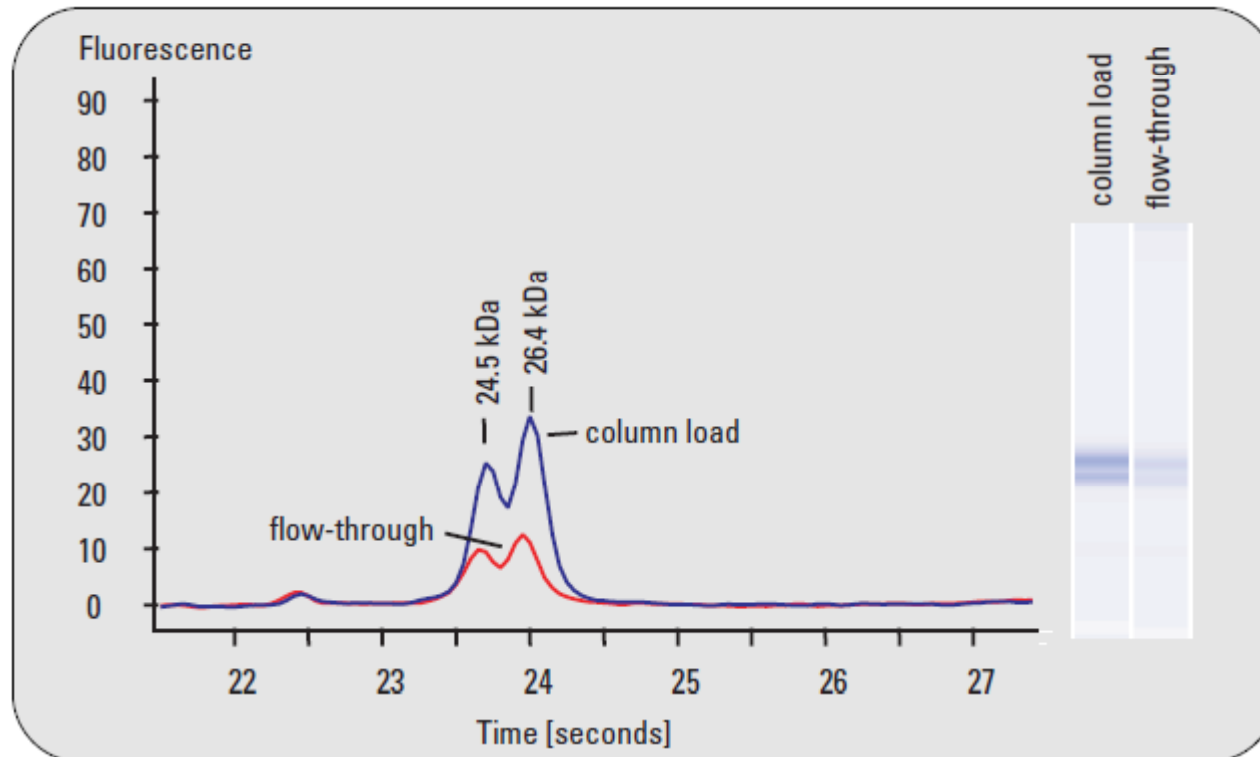
- Monitorización de aislamiento de proteínas y purificación.
- Comprobación de fracciones(impurezas)

Purificar proteínas

- monitorizar impurezas
- QC de anticuerpos monoclonales y policlonales



Análisis de la capacidad de las columnas



Optimization of a Protein Purification Workflow



Application Note 5990-6153EN

The Bioanalyzer Protein 250 Kit is used to distinguish between His-tagged and cleaved protein species during a protein purification process. It helps with:

- Optimization of the sample purification process: cleavage of the His-tag
- Final sample QC.

Optimization of on-column cleavage

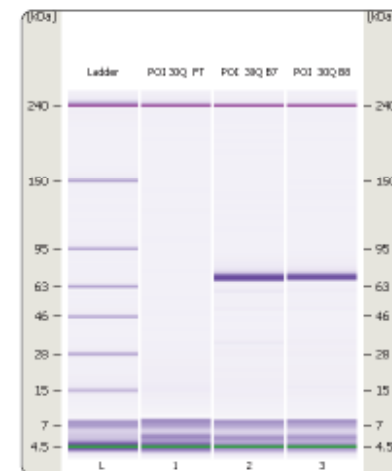


	Size [kDa]	Rel. Conc. [ng/μL]	% Total
Unop.	71.9	310.2	38.3
cleavage	81.9	414.7	51.3
Optimized	70.9	993.0	78.0
cleavage	83.2	11.4	0.9

➔ Initial purity of the target protein: 38%

Final QC from optimized process

Size [kDa]	Rel. Conc. [ng/μL]	% Total
4.5	0.0	0.0
6.0	0.0	0.0
8.0	0.0	0.0
16.2	10.9	0.7
33.8	11.8	0.8
50.4	12.8	0.8
60.6	13.0	0.8
70.9	1,484.8	96.9
240.0 (marker)	60.0	0.0
324.8	0.0	0.0

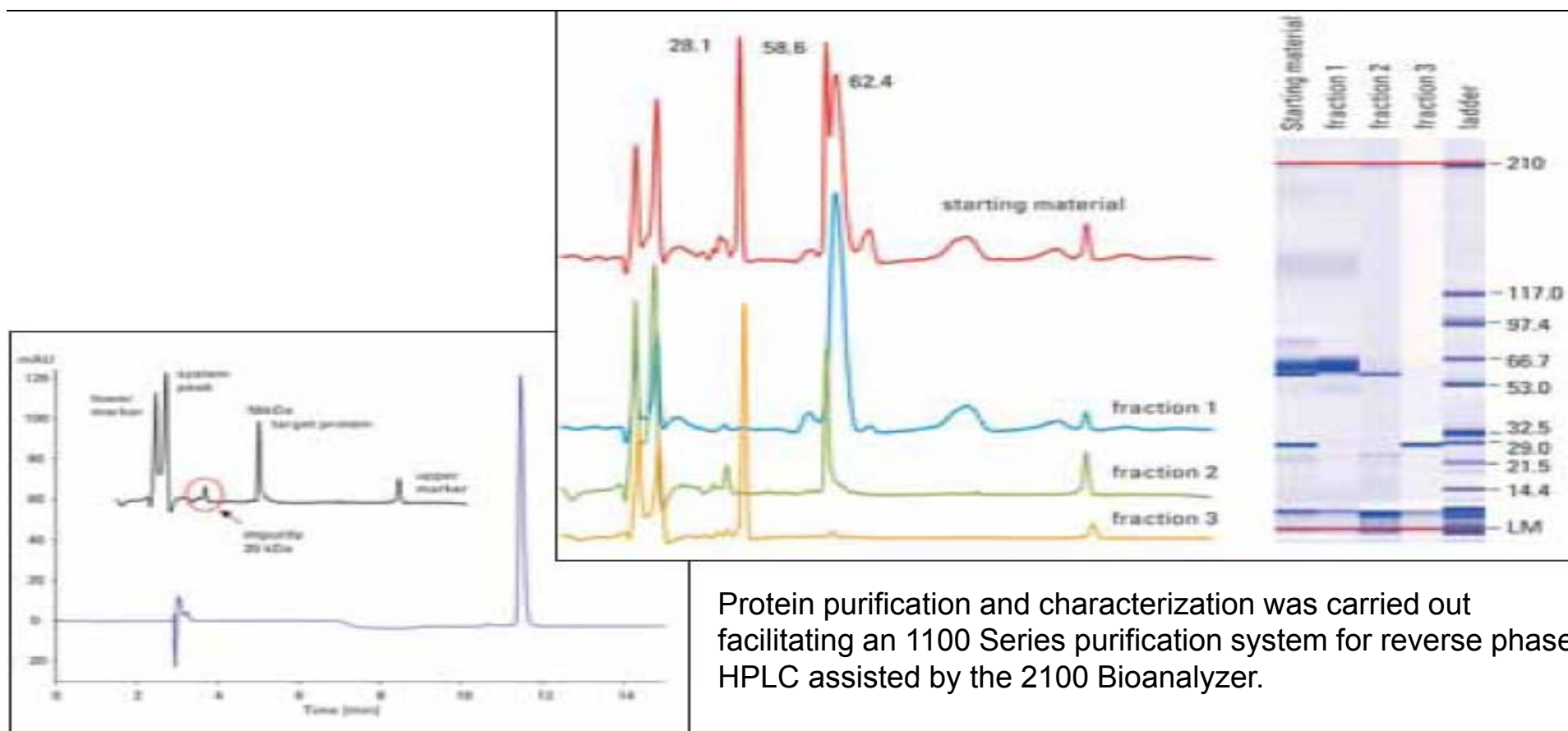


➔ Final purity of the target protein: 97%



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Complementing RP-HPLC protein purification



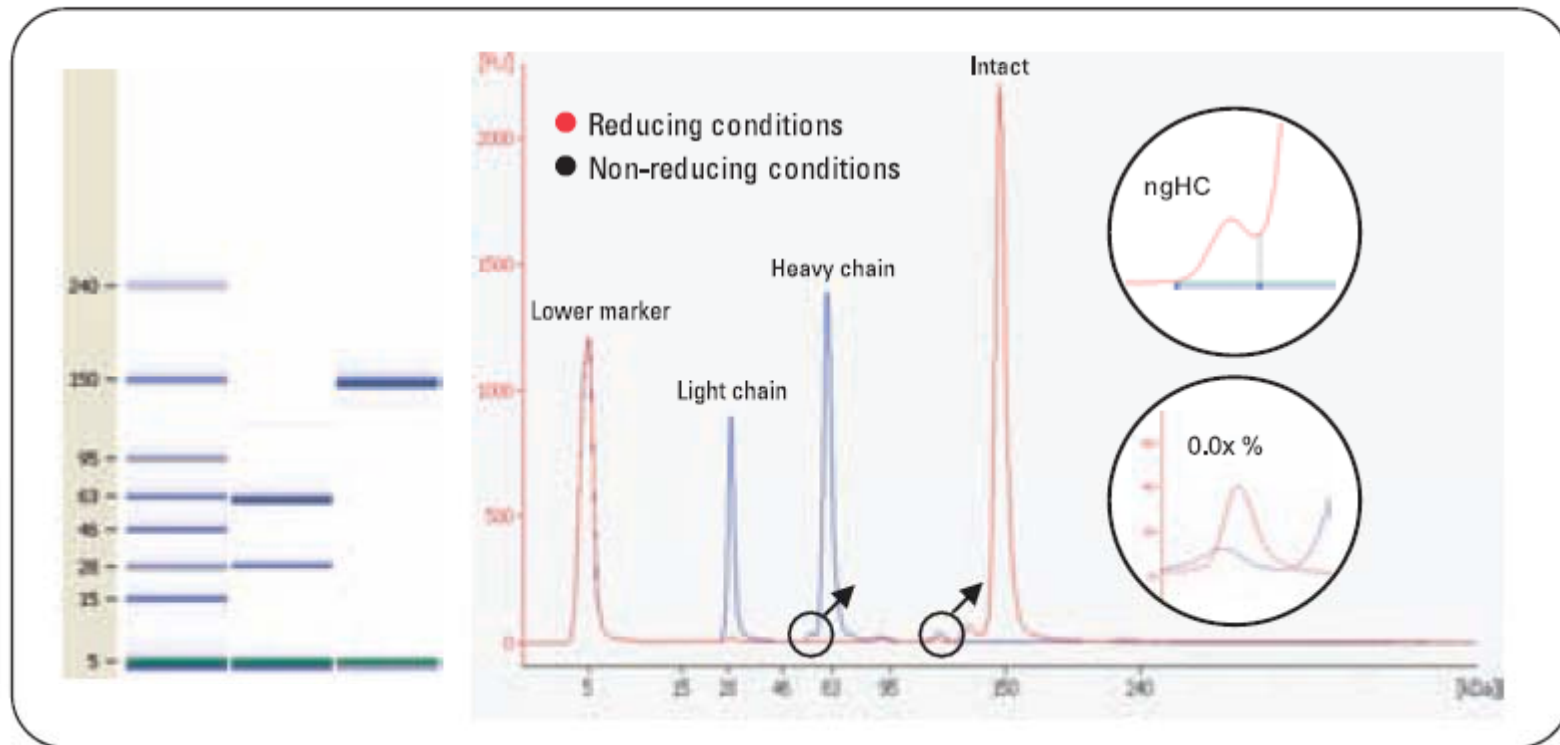
Protein purification and characterization was carried out facilitating an 1100 Series purification system for reverse phase HPLC assisted by the 2100 Bioanalyzer.



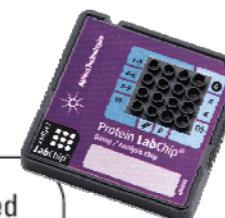
Análisis de anticuerpos



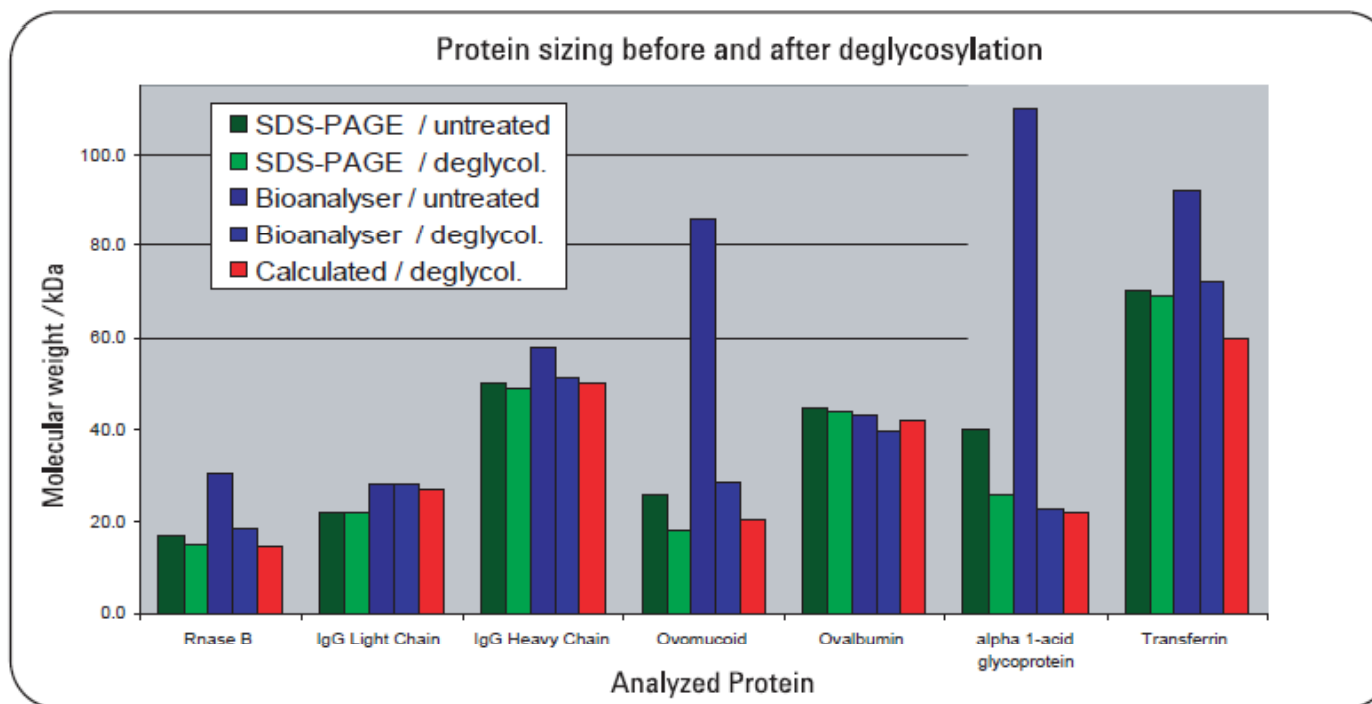
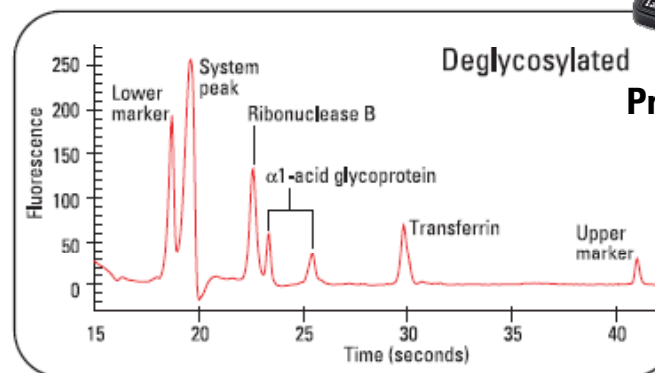
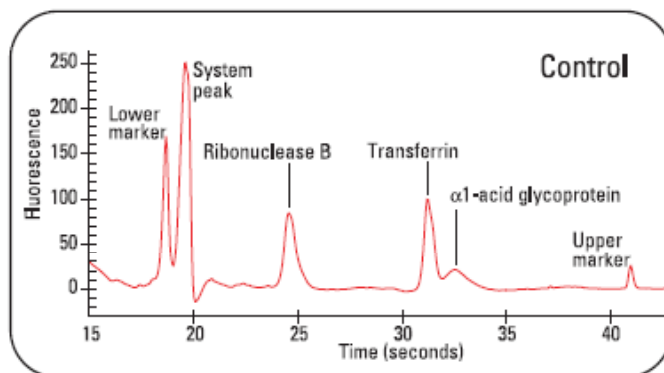
**High sensitive
Protein 250 kit**



Glicosilación de proteínas



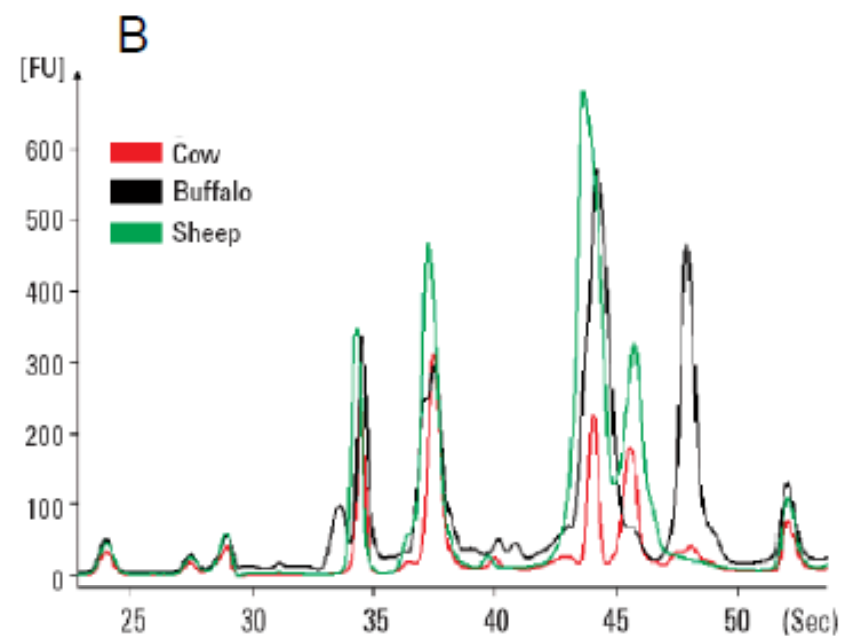
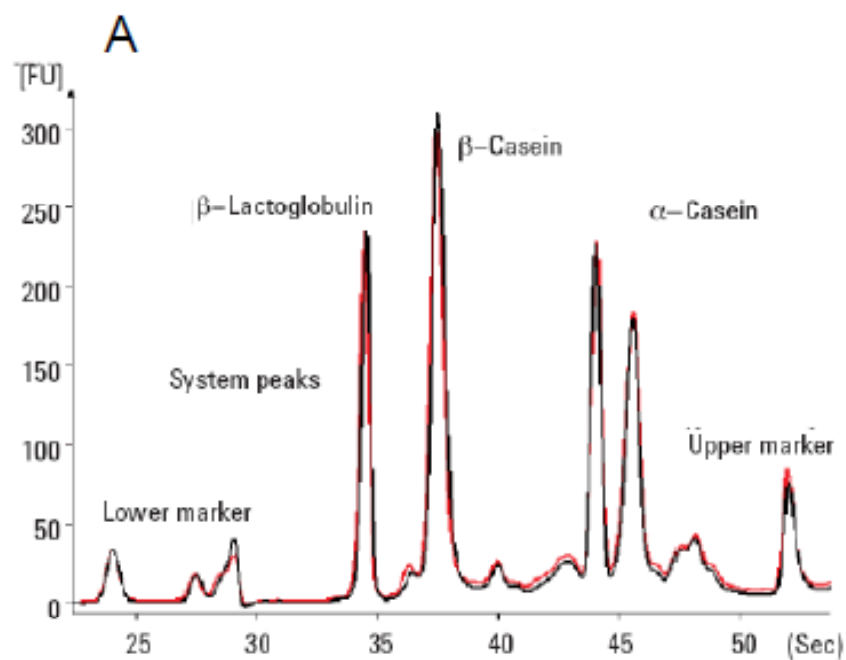
Protein 230 kit



Análisis de proteínas en leche



Protein 80 kit



Immunoprecipitation for quantification of β - galactosidase from crude *E. coli* cell lysate

Products:

2100 Bioanalyzer

Industry:

Academia

Author:

Ela Herwig, Technical University of Vienna

Application note publication number: 5990-7008EN

Publication date: January 1st, 2011



Highly sensitive and specific methods for the detection of target proteins in crude sample:

- Traditional method: Western Blot of SDS-PAGE slab gels
- New alternative method: Immunoprecipitation in combination with the High Sensitivity Protein 250 kit for the 2100 Bioanalyzer.

Advantages (see also 5989-4097EN):

→ Feature Combination of Western Blot and ELISA!

<i>Sensitive:</i>	HSP-250 Kit for Bioanalyzer
<i>Selective:</i>	Antibody-based in-solution pull-down
<i>Quantitative:</i>	Electronic data from Bioanalyzer

and secondary antibodies)

- Semi-quantitative & reproducible!
- ➔ Customer application example with β -Galactosidase

Immunoprecipitation for the specific detection of β -Galactosidase (β -Gal)

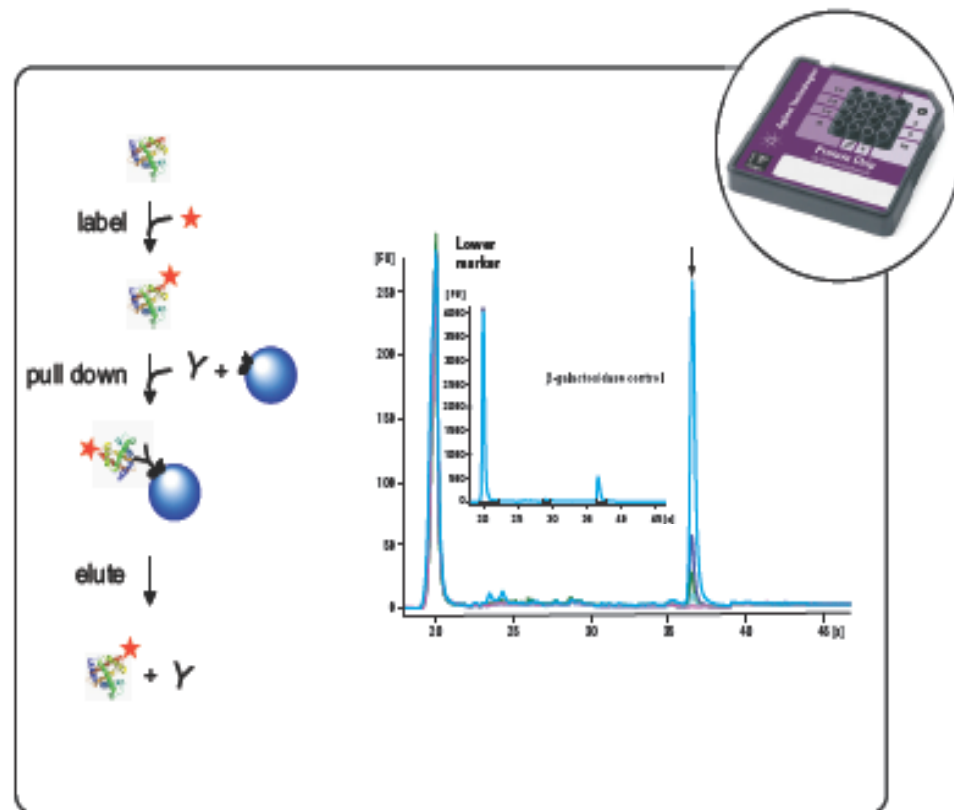
This application example from the Technical University of Vienna shows:

- How to set up the **immunoprecipitation method**
- **Tuning** of the method:
 - Effects of Antibody selection
 - Effects of Antibody concentration
- How to establish a **calibration curve** for quantification
- **Reproducibility** of the method in determining the level of endogenously expressed target protein β -Gal



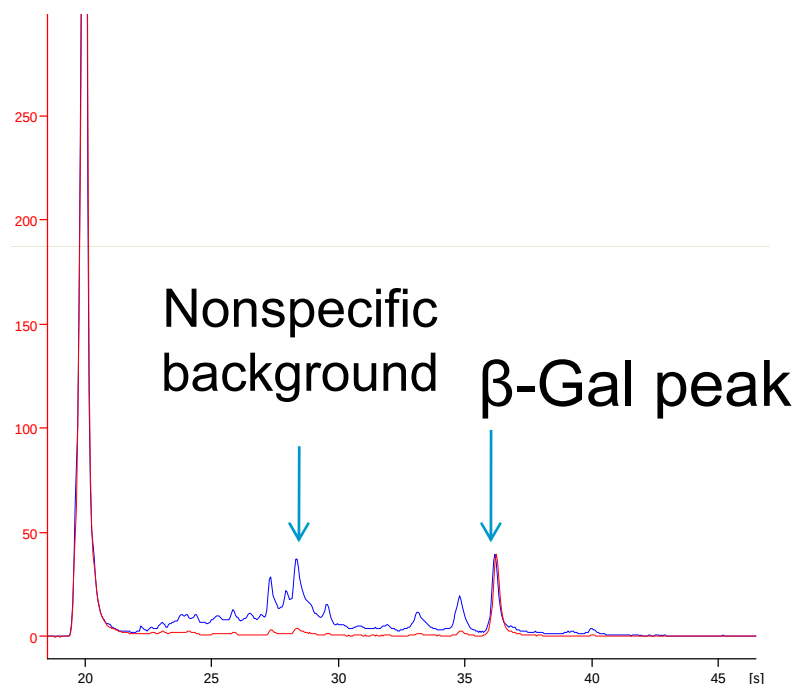
1. Immunoprecipitation workflow

1. Labeling of crude lysate expressing the target protein using reagents of the HSP-250 kit (5067-1575).
2. Immunoprecipitation of the target protein with specific antibody and Protein G coupled to magnetic beads.
3. Elution of all bead-bound proteins with SDS sample buffer of the HSP-250 kit.
4. Direct analysis on the 2100 Bioanalyzer using the HSP-250 Protein Chip and reagents.



2. Set-up

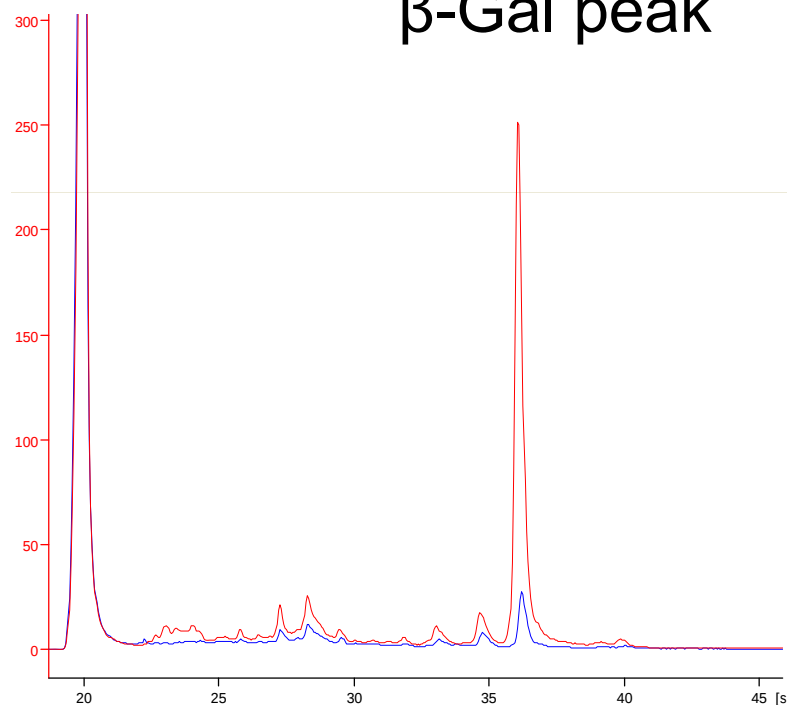
A. Antibody Selection



One antibody shows significantly more non-specific background (blue) than the other (red)!

B. Antibody Concentration

β -Gal peak

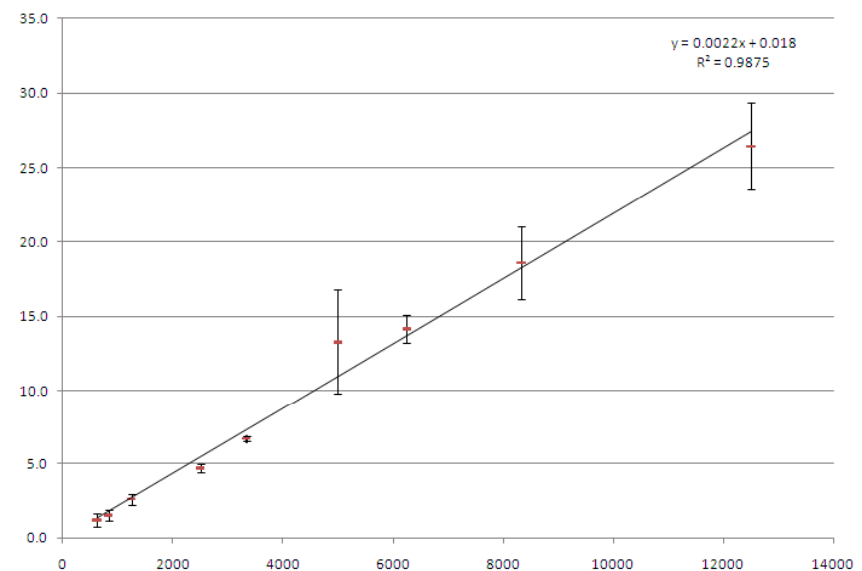
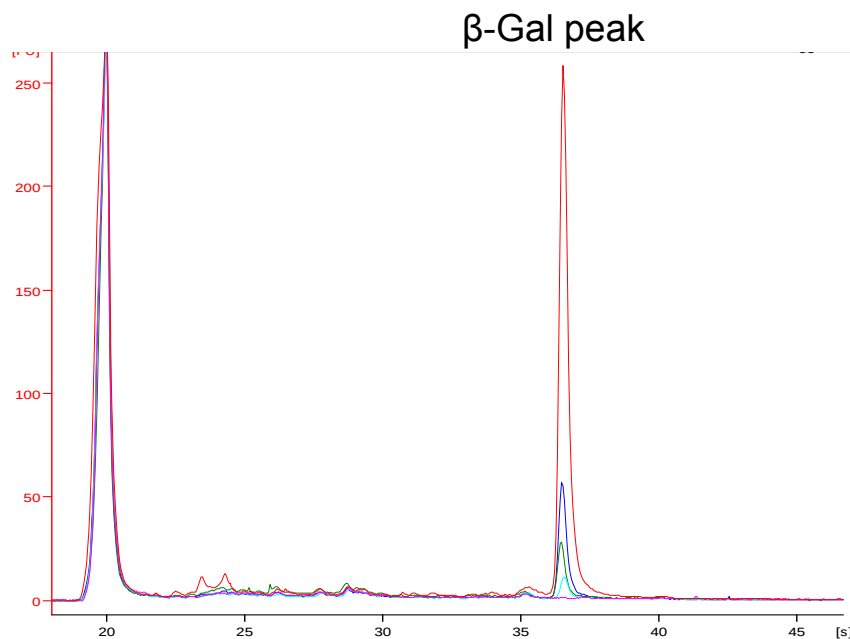


Antibody concentration influences target signal and non-specific background.

3. Calibration curve for quantification

Increasing concentration of spiked-in β -Gal into crude lysate returns increasing signal from IP.

➔ Calibration Curve based on the linear relationship between initial β -Gal concentration in the lysate and peak intensities.



4. Detection of endogenously expressed β -Gal

Detection and quantification of endogenously expressed β -Galactosidase in crude lysate:

Dilution factor of applied antibody	Migration time corrected area	Calculated amount of β -galactosidase (ng/ μ L)	Mean value (ng/ μ L) (n = 3)
1000	54,4	24,8	22,5 $\pm$ 1,9
2000	23,5	21,4	
5000	9,4	21,4	

Approach is proving its reliability as results are consistent and reproducible, even across experiments in which the antibody concentration was varied.

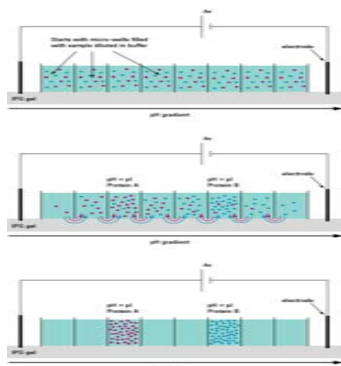
Geles en 2D: Combinación de Offgel y Bioanalizador

E. coli lysate
(50 µg)



Protein clean up and labeling

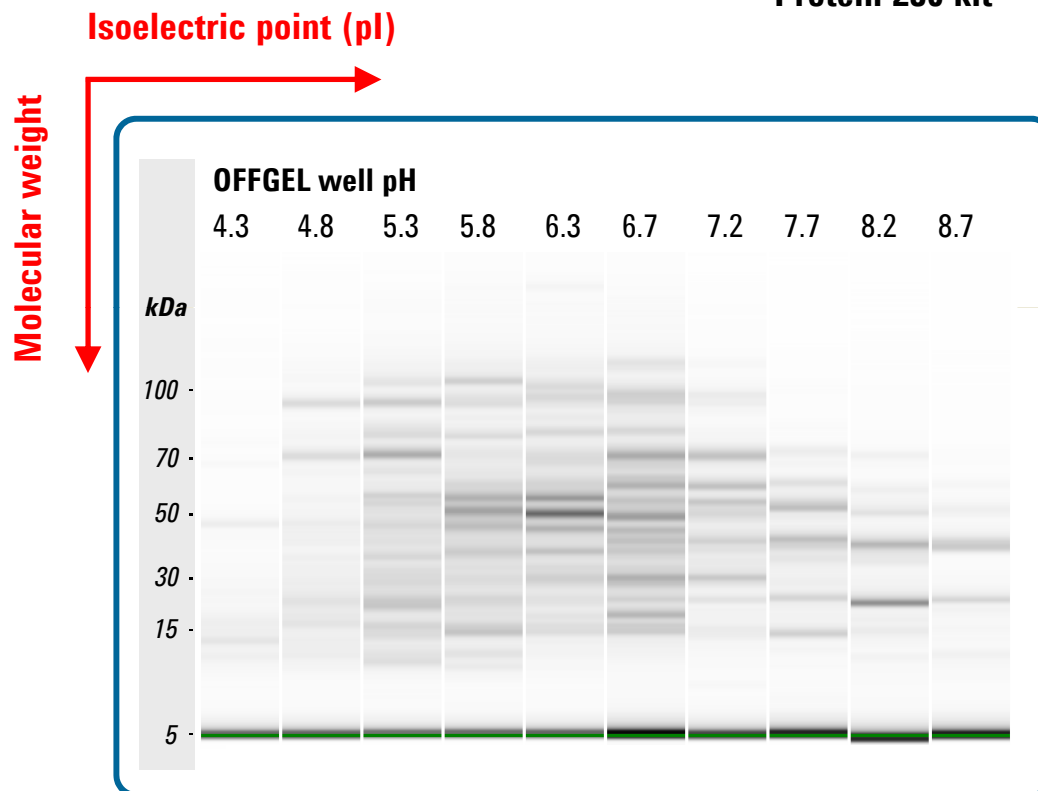
OFFGEL Electrophoresis



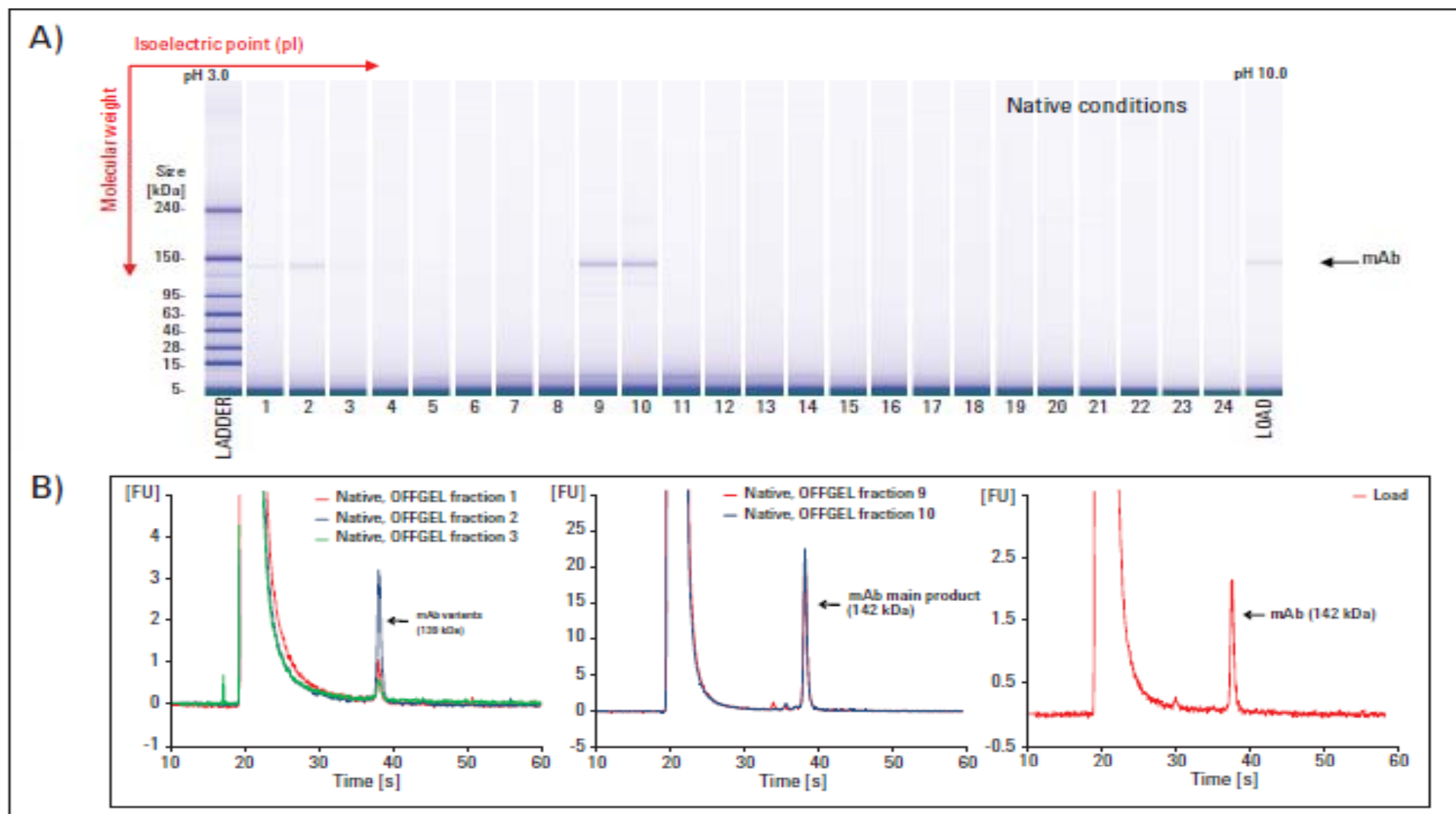
2100 Bioanalyzer
HiSens Assay



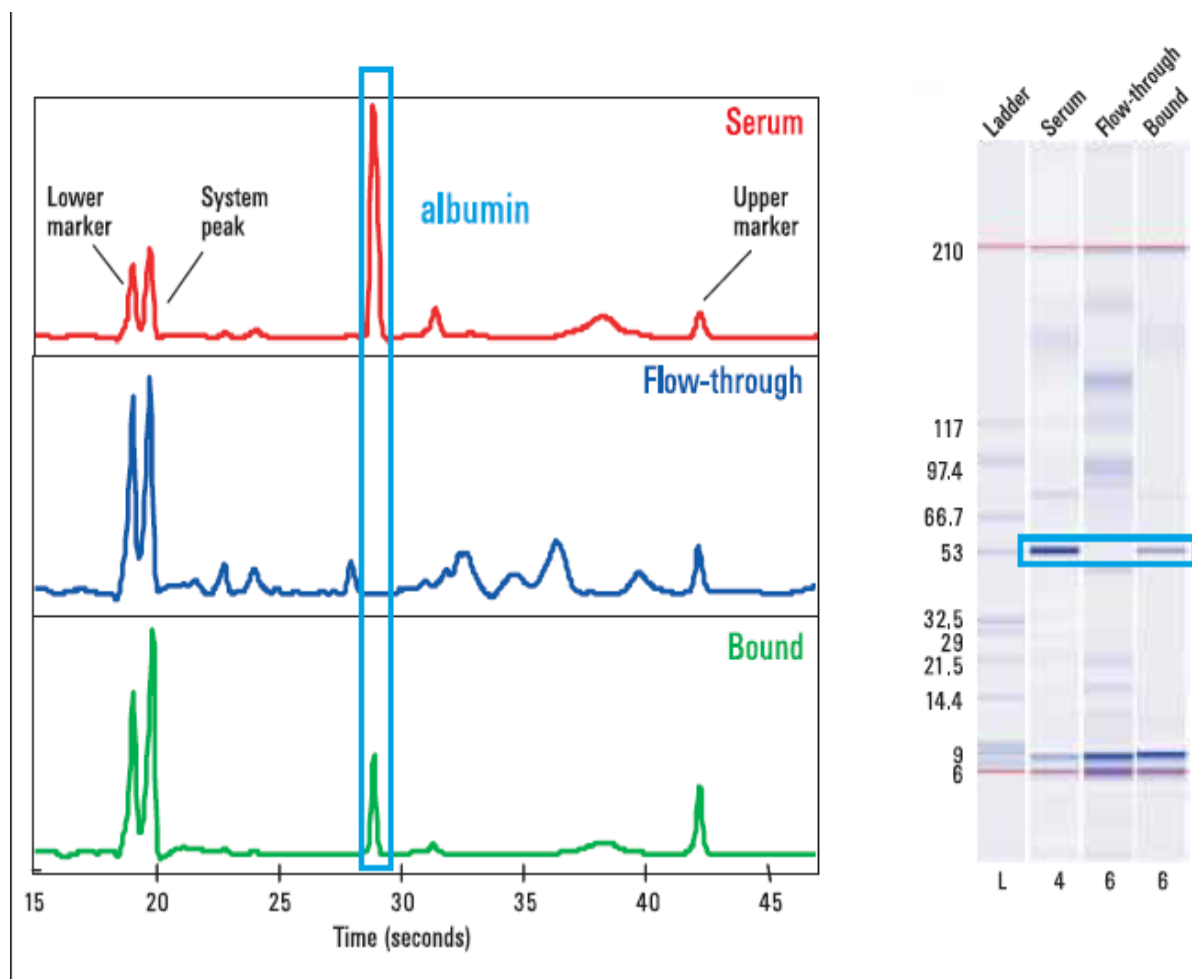
High sensitive
Protein 250 kit



Monitoring antibody charge variants



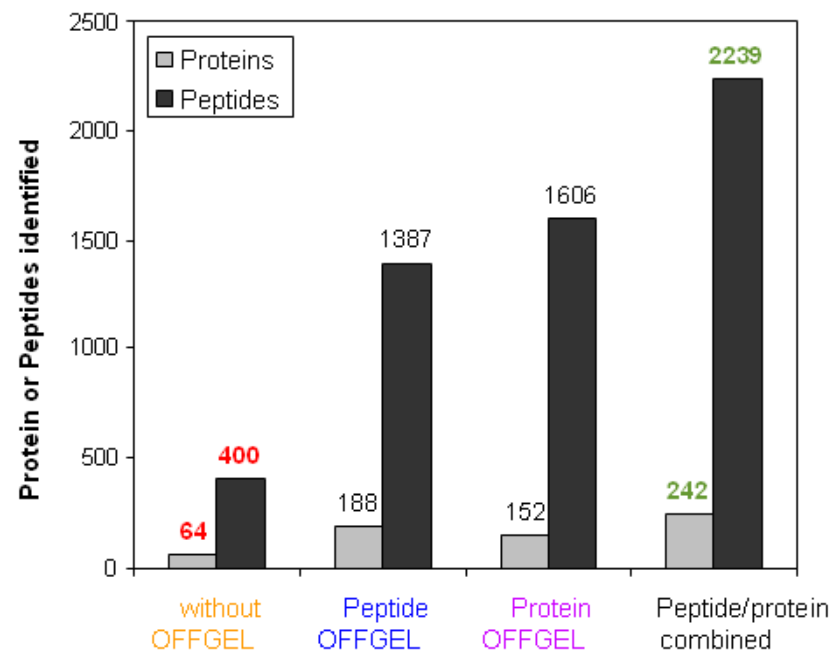
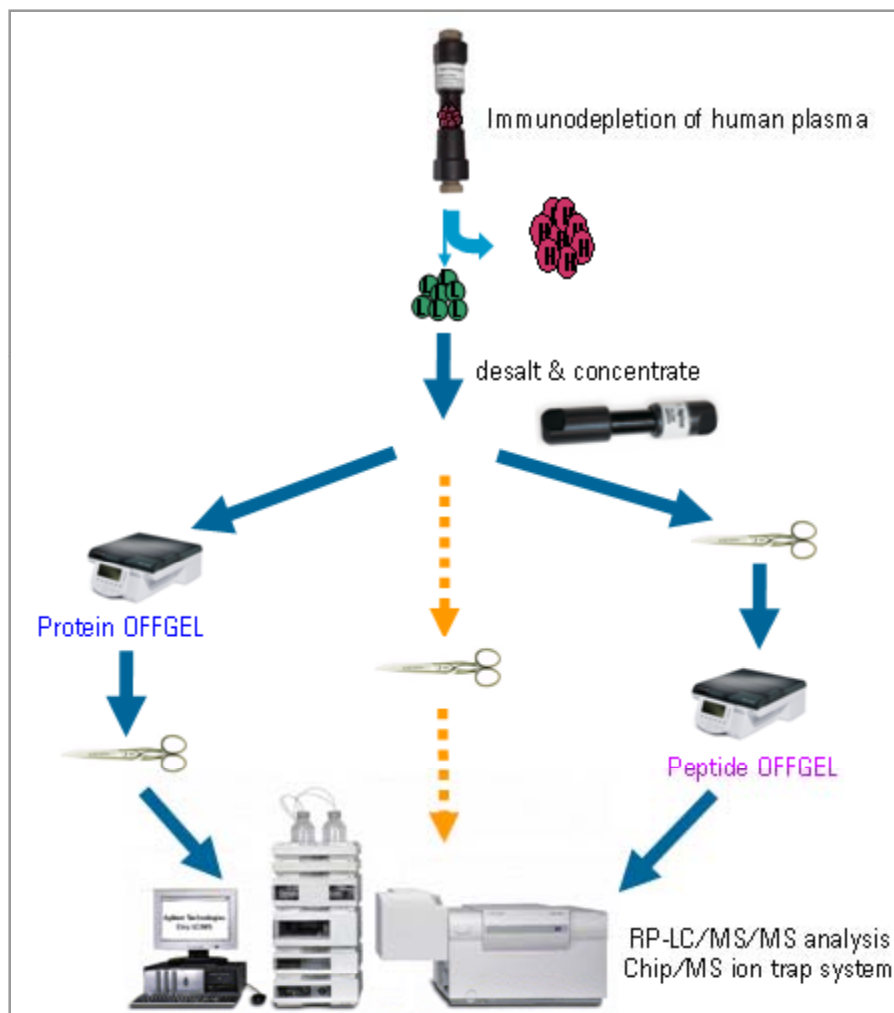
Depletion of high abundant proteins from blood samples



Depletion of high abundant proteins in human blood plasma was facilitated by the Agilent Multiple Affinity Removal System

OFFGEL Incremento de la sensibilidad en MS

ejemplo de trabajo



Incremento de 4x en la
detección de proteínas tras
el fraccionamiento con el
OFFGEL



Bioanalyzer Literature



Bioanalyzer Application Compendium 5990-6987EN Now with all the latest applications in NGS!

#	Doc.	Author	Title	Year	Journal	Owner
11174	Article	Zhang et al.	Genome-wide expression of Lysine-2-oxoglutarate (Lys-2-oxoglutarate) in glioblastoma	2010	Journal of Neurology	
11175	Article	Zhang et al.	Gene expression profiling in peripheral blood mononuclear cells from patients with sporadic amyotrophic lat.	2010	Journal of Neurology	
11176	Article	Zhang et al.	The gut transcriptome of a pig model: metabolic dysfunction	2010	Journal of Neurology	
11177	Article	Zhang et al.	Four stress-induced miRNAs differentially regulated in the embryonic and non-embryonic	2010	Biochemical and Biophysical Research Communications	
11178	Article	Zhang et al.	Combined fibroblast growth factor and epidermal growth factor receptor inhibitors affect tumor growth	2010	Pharmacology and Therapeutics	
11179	Article	Zhang et al.	Do cellular pathways directly affect human embryonic stem cell gene expression?	2010	Pharmacology and Therapeutics	
11180	Article	Zhang et al.	Similarities and differences between circulating related gene expression in nasal and bronchial epithelium	2010	Physiology and Biochemistry	
11181	Article	Zhang et al.	Minimally invasive detection of colorectal cancer using circulating tumor cells	2010	Investigative Ophthalmology and Visual Science	
11182	Article	Zhang et al.	Acute and chronic blood pressure changes in cardiac autonomic nervous system	2010	Frontiers in Physiology	
11183	Article	Zhang et al.	The impact of tumor phase on gene expression of epithelial cells and adhesion molecules	2010	Frontiers in Physiology	
11184	Article	Zhang et al.	PGC-1α: A Potential Therapeutic Target for Early Intervention in Parkinson's Disease	2010	Genetics and Molecular Biology	
11185	Article	Zhang et al.	Dynamic transcriptomic profiles of embryonic stem cells in response to zinc depletion	2010	BMC Genomics	
11186	Article	Zhang et al.	Retinal vascular leakage occurring in SABA-Rho-1 mutant deficient mice	2010	Experimental Eye Research	
11187	Article	Zhang et al.	Traditional Chinese medicine processing using heat treatment of medicinal material	2010	Experimental Eye Research	
11188	Article	Zhu et al.	Genetically cell nuclear protein-1, a novel depression-related protein, regulates corticosterone-releasing factor	2010	Brain	
11189	Article	Zhu et al.	Genome-wide gene expression in a transgenic mouse line carrying the mouse resistance gene Hsd-1 to the rice b.	2010	BMC Genomics	
11190	Article	Zhu et al.	Prognostic and Predictive Gene Signatures for Advanced Chemotherapy in Resected Non-Small Cell Lung Can.	2010	J. Clin. Oncol.	
11191	Article	Zhu et al.	Identification of novel human target genes in the adult female hippocampus	2010	Investigative Ophthalmology and Visual Science	
11192	Article	Zhu et al.	Differential gene expression in human cells infected with wild type and attenuated foot-and-mouth disease vi.	2010	Virology	
11193	Article	Zhu et al.	Genetic Evidence of an Adipogenic Drug Regulates Adipogenic PPARγ for Increased Activity of Peroxisome γ	2010	Chem. Res. J. of C.	
11194	Article	Zhu et al.	Environmental Damage to the Retina and Preconditioning: Contrasting Effects of Light and Hyperoxia Stress	2010	Investigative Ophthalmology and Visual Science	
11195	Article	Ziegler et al.	A human neuron injury model for molecular studies of axonal regeneration	2010	Experimental Neurology	
11196	Article	Zhang et al.	Production of Fibrocyte-Associated Protein with Optimal Physical Properties	2010	Artificial Cells and Biomimetic Materials	
11197	Article	Zhang et al.	The heat-shock protein 1 inhibits P53 expression in prostate cancer cells	2010	Int. J. Cancer	
11198	Article	Zhang et al.	Impact of microRNA-101 on physiological performance of male Wistar (Rattus norvegicus) rats	2010	Environmental Toxicology and Chemistry	
11199	Article	Zhang et al.	Let-7a-1-Dependent Regulation of miR-101 and MicroRNA-101 Expression: Implications for Dis.	2010	Mol. Pharmacol.	
11200	Article	Zhang et al.	miR-101 dynamic control enhances efficiency in monitoring for patients treated with sorafenib, imatinib, and	2010	Journal of Hepatology	
11201	Article	Zhang et al.	Transcriptional Activation Reveals a Mechanism for a Proinflammatory Phenotype in STX11 Knockout Mice during Is.	2010	J. Virol.	
11202	Article	Zhang et al.	Technical Advances: The rat retina contains isolated mononuclear phagocytes with proliferative capacity and p.	2010	J. Leukoc. Biol.	
11203	Article	Zhang et al.	Alterations of the Transcriptional Region of IL-13A2 Lead to Age-Related Cataract	2010	Investigative Ophthalmology and Visual Science	
11204	Article	Zhang et al.	Acute leukemia with t(11;21)(p11;p15.5) Karyotype: Poor prognosis and potential origin	2010	Genes Chromosomes and Cytogenetics	
11205	Article	Zhang et al.	MicroRNA profiling of multiple osteochondromas: identification of disease-specific and normal cartilage sign.	2010	Genes Chromosomes and Cytogenetics	
11206	Article	Zhang et al.	Expression of T-cell markers during Adenovirus-induced Hepatocellular Carcinoma in Mice	2010	Developmental Biology	
11207	Article	Zhang et al.	Evaluation of potential reference genes for real-time RT-PCR studies in Adenovirus-induced Hepatocellular Carcinoma	2010	BMC Genomics	
11208	Article	Zhang et al.	Comparative characterization and expression patterns of Adenovirus-induced Hepatocellular Carcinoma	2010	Frontiers in Molecular Biosciences	
11209	Article	Zhang et al.	Verification Method for Rapid Polymerase Chain Reaction Systems to Detect Bacteria in Agave	2010	Frontiers in Molecular Biosciences	
11210	Article	Zhang et al.	MicroRNA in the Clinical Laboratory: Will It Be a Game Changer? Prospects and Pitfalls	2010	Clin. Chem.	

Article (Zhang et al. 2010)
van Zyl, T., Berman, R., Durrant, K., de Jong, A., Hager, O., Vennart, M. & van der Klei, I.
Adaptation of *Haemaphysalis* to methanol: a transcriptome analysis
BMC Genomics 2010, 11, 1

Abstract BACKGROUND: Methanophilic yeast species (e.g. *Haemaphysalis*, *Pichia pastoris*) can grow on methanol as sole source of carbon and energy. These organisms are factories for the production of recombinant proteins, but are also used in functional research to model organisms to study peroxisome biology. During peroxisome growth, glucose, polyphosphates typically contain a single, small peroxisome that is redundant for growth while on methanol multiple, enlarged peroxisomes are present. These organelles are crucial to supply methanol, as they contain key enzymes of methanol metabolism. In this study, changes in the transcriptome profile during adaptation of *H. pastoris* cells from glucose to methanol media were investigated using DNA-microarray analyses. RESULTS: Two hours after the shift of cells from glucose to methanol nearly 20% (1184 genes) of the approximately 8000 annotated polyphosphates genes were significantly upregulated with at least a two-fold differential expression. Highest upregulation (> 500-fold) was observed for the genes encoding the transcription and translation machinery, an enzyme of the methanol degradation pathway. Upregulated genes also included genes encoding other enzymes of methanol metabolism as well as of glycolysis. A moderate increase in transcriptional levels (up to 4-fold) was observed for several PEX genes, which are involved in peroxisome biogenesis. Only PEX11 and PEX12 were highly upregulated. In addition, an increase was observed in several ATO genes, which encode proteins involved in autophagy and autophagy processes. The strongest up-regulation observed for ATO8 and ATO11. Approximately 20% (1246 genes) of the genes were downregulated. These included glycolytic genes as well as genes involved in transcription and translation.

Bioanalyzer Reference Database

- includes publications in scientific journals and books
- 11211 references
- updated every 6 months
- available for download under Bioanalyzer Resources:

<http://www.genomics.agilent.com/GenericA.aspx?PageType=Custom&SubPageType=Custom&PageID=2153>



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- Mejora de la exactitud y fidelidad en las mediciones.
- Resultados comparables entre experimentos y laboratorios
- Datos digitales para la facilidad del análisis, presentación y archivo de datos



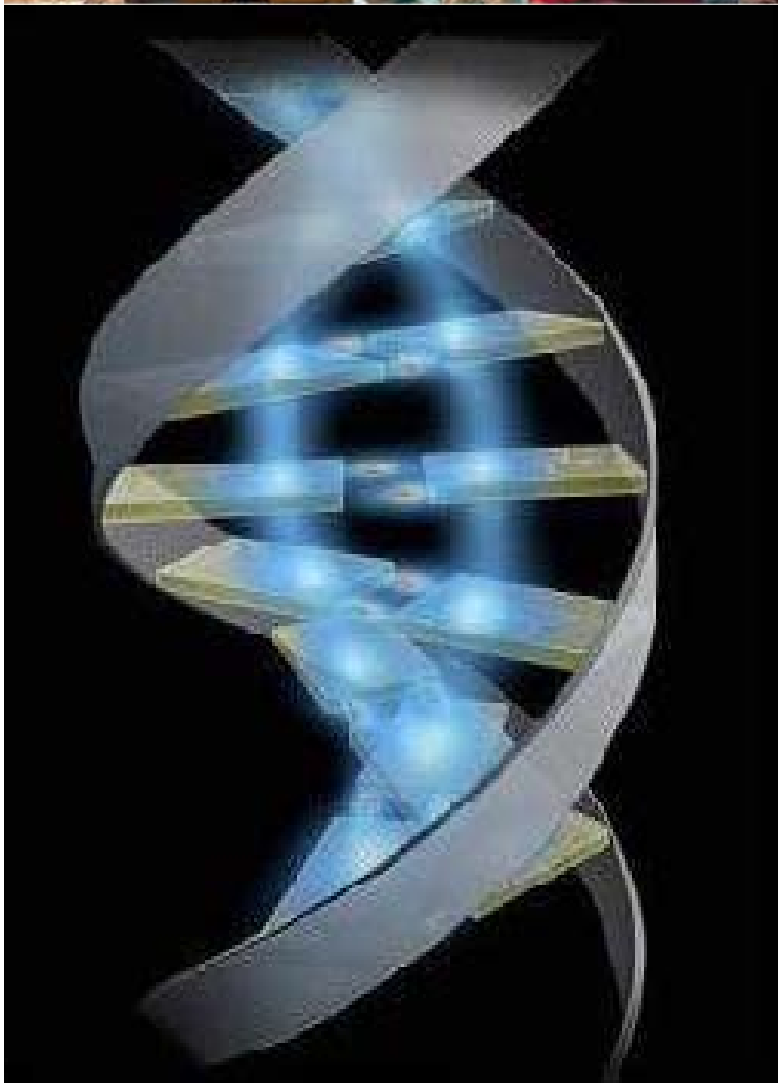
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*hasta el 31 de marzo de 2011 en Agilent Technologies



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Muchas gracias!!

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