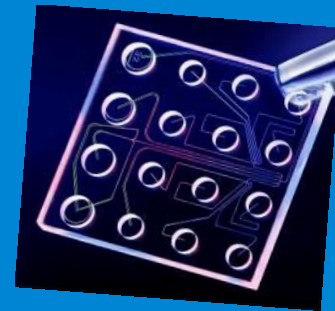


The Importance of Reliable Sample Quality Control in Multiple Workflows

2100 Bioanalyzer System



Outline

Importance of Quality Control

Sample QC in Next Generation Sequencing

Sample QC in Gene Expression

Sample QC in Proteomics

... and even more!

Outline

Importance of Quality Control

Sample QC in Next Generation Sequencing

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Sample QC in Proteomics

... and even more!

Quality of Samples is Critical for Experimental Success

Garbage in, garbage out!



A. Impact on sequencing:

Good DNA library quality helps ensure good quality reads and maximizing sequencing output

B. Impact on gene expression arrays and generation of RNAseq libraries:

Quality of input RNA will determine success of library preparation and reproducibility of microarrays

C. Impact on data analysis:

Integrity of RNA helps assure accurate determination of relative gene expression levels, support for existence of variants, transcripts and splice forms

- across different genes
- across alternatively spliced variants

Outline

Importance of Quality Control

Sample QC in Next Generation Sequencing

Sample QC in Gene Expression

Sample QC in Proteomics

... and even more!

Quality of DNA Libraries is Critical for Sequencing Success

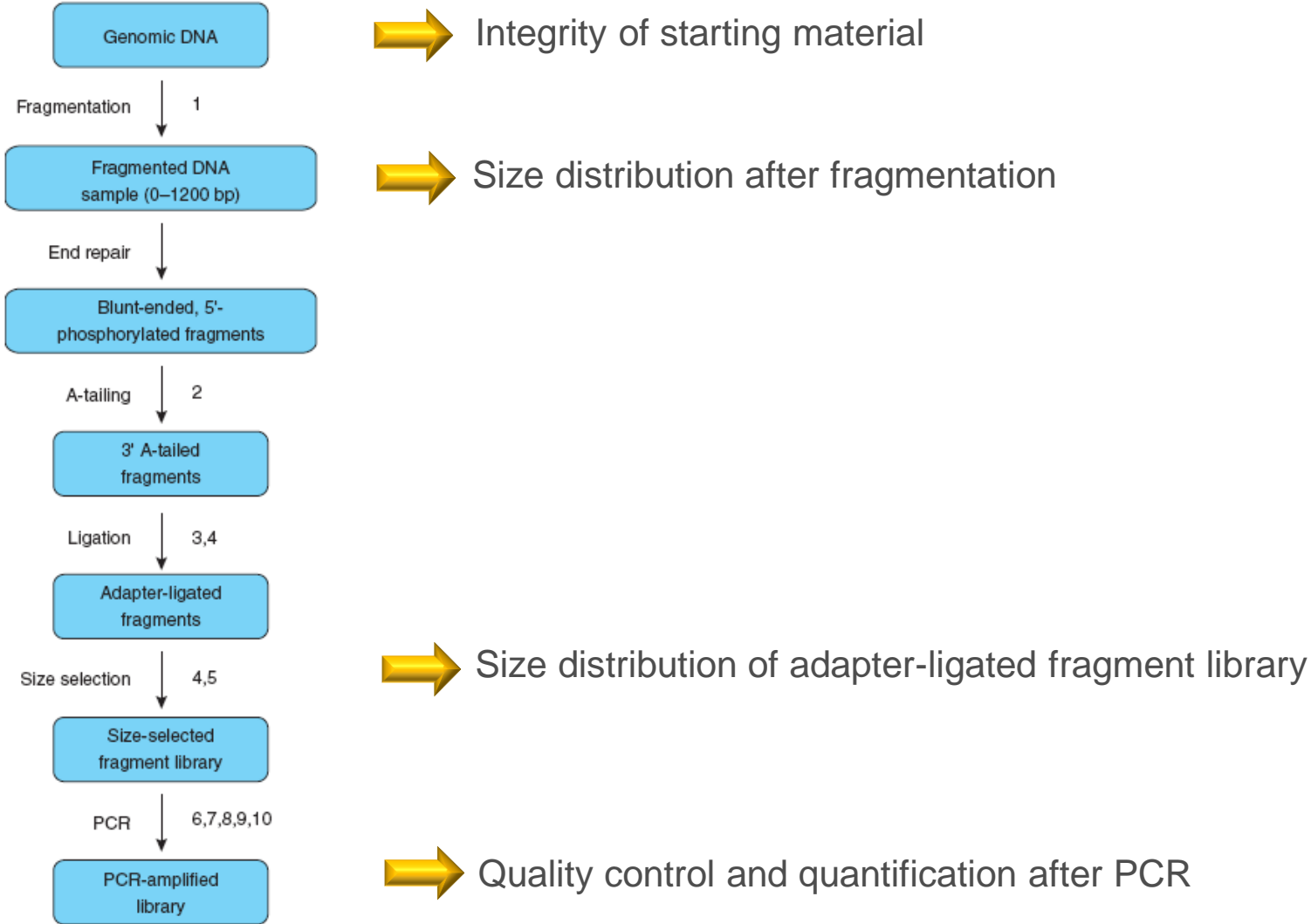
Garbage in, garbage out!



For every application of next-gen sequencing, eg. genome sequencing, transcriptome sequencing (RNA-seq), chromatin immunoprecipitation sequencing (ChIP-seq) or targeted resequencing, there is a specific protocol to convert the source nucleic acid to standard DNA libraries.

The aim of recent developments in library preparation methods is to produce a high-quality representative, non-biased DNA library from small amounts of starting material.

Quality Control during Library Preparation

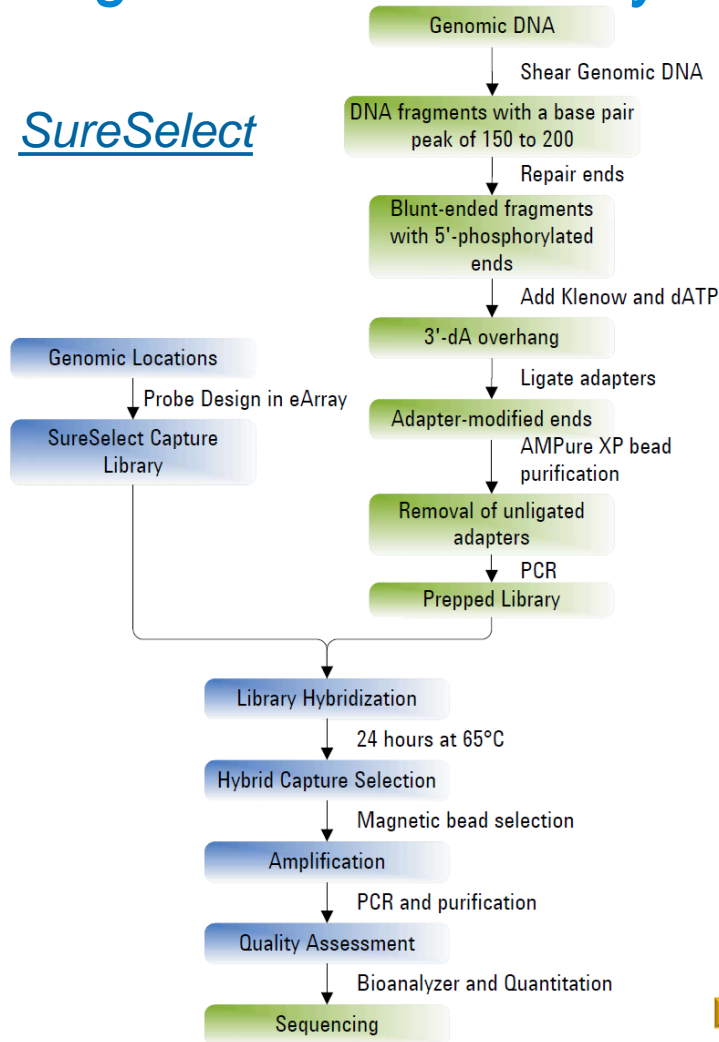


Adapted from Quail et al (2008) Nature Methods)

Quality Control during Library Preparation

Target Enrichment Systems

SureSelect



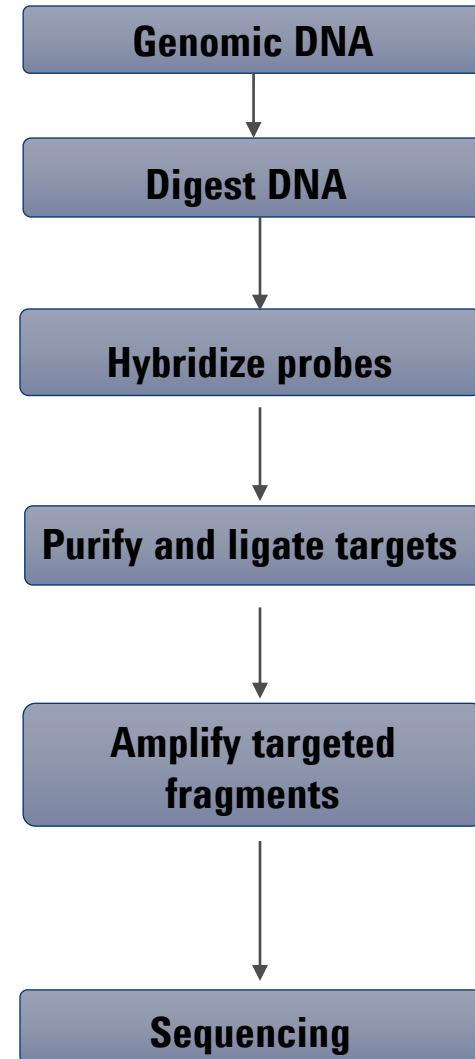
Integrity of starting material

Size distribution after fragmentation

Size distribution of adapter-ligated fragment library

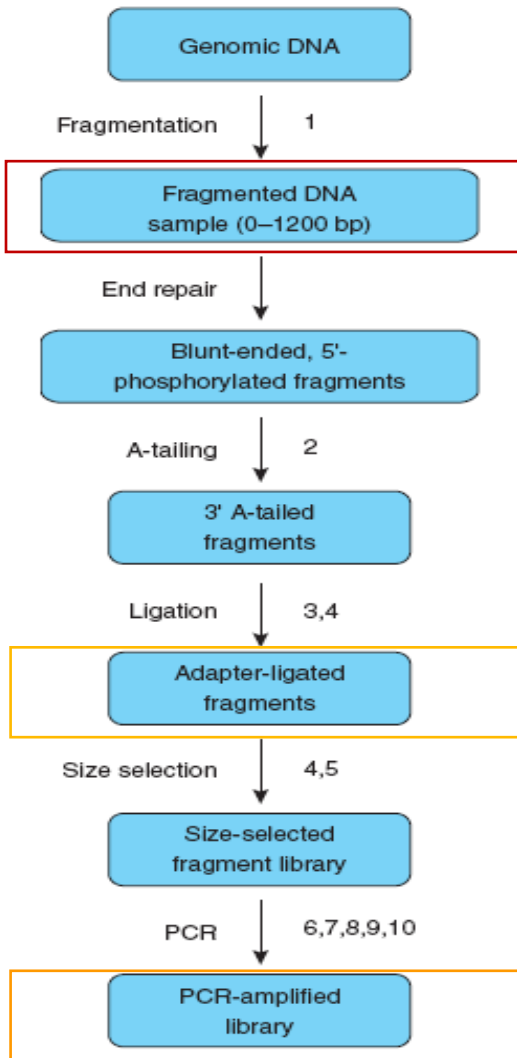
Quality control and quantification after PCR

HaloPlex

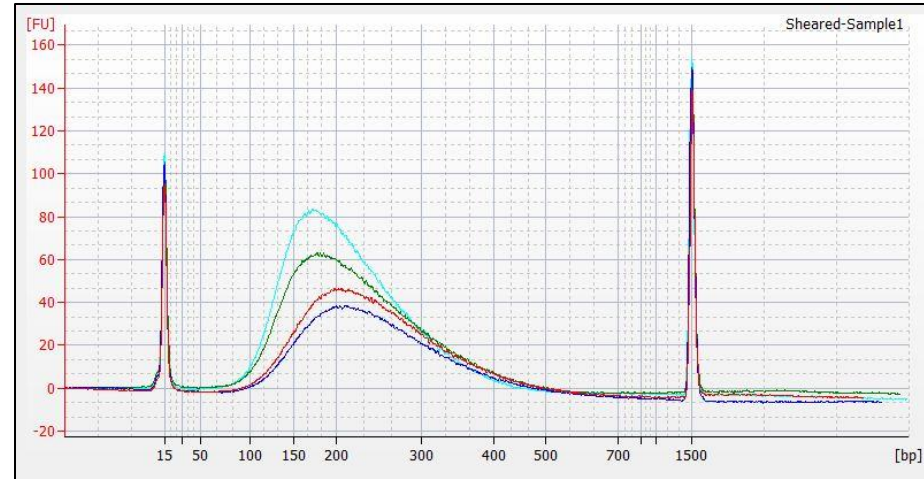


Next Generation Sequencing

□ Steps where QC assessment is critical and Bioanalyzer analysis is recommended

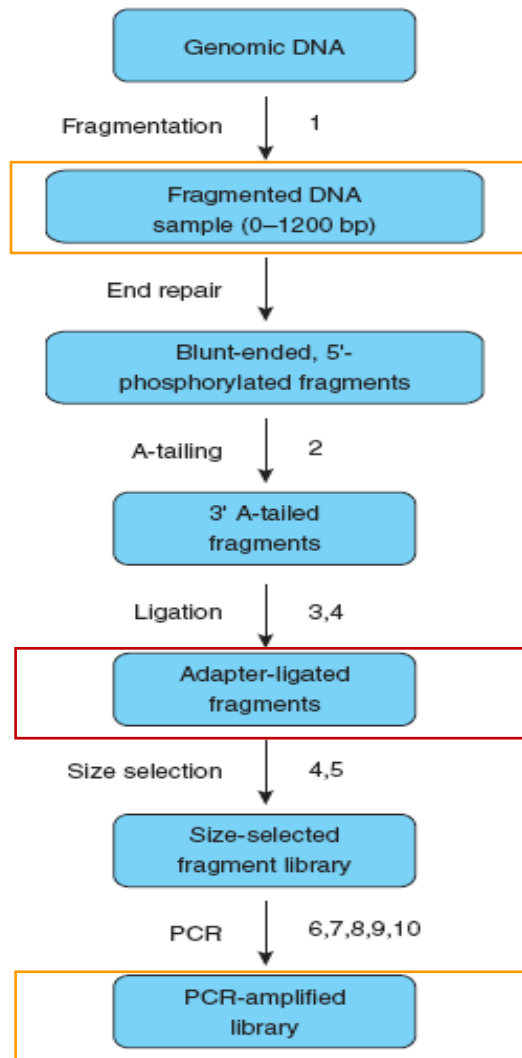


Samples sheared on Covaris and run on the Bioanalyzer DNA 1000 Kit:

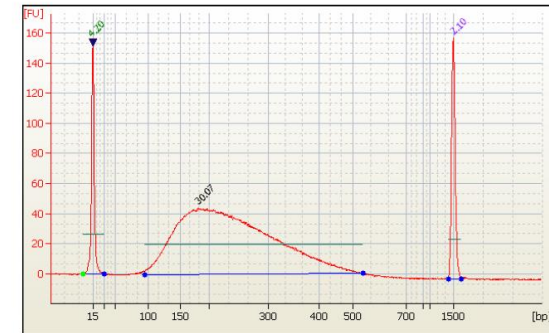


Next Generation Sequencing

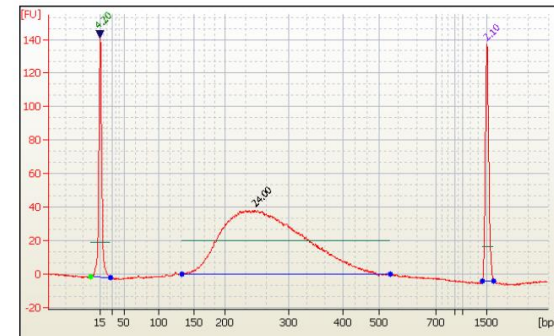
□ Steps where QC assessment is critical and Bioanalyzer analysis is recommended



Post – shearing – peak size of 190bp



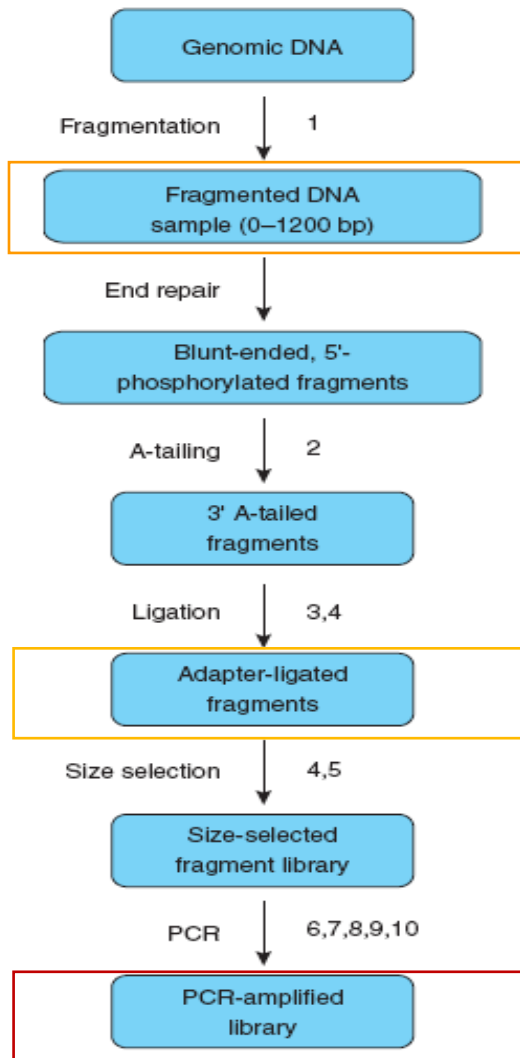
After adaptor ligation – peak size of 250± 10bp



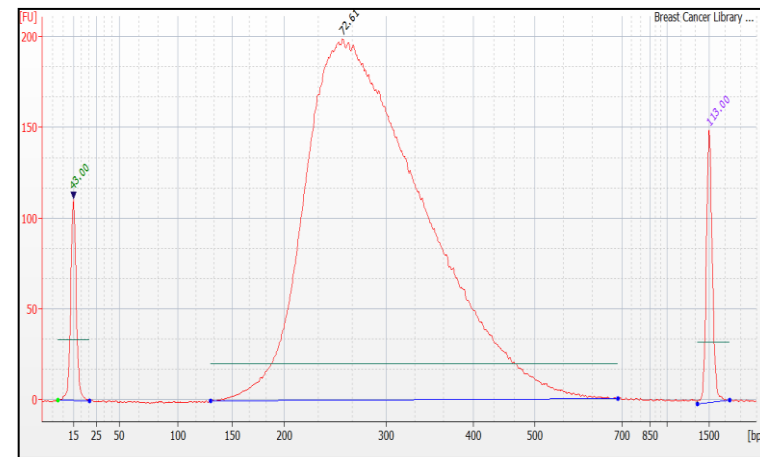
Inefficient adaptor ligation will result in reduced library complexity after PCR.

Next Generation Sequencing

□ Steps where QC assessment is critical and Bioanalyzer analysis is recommended

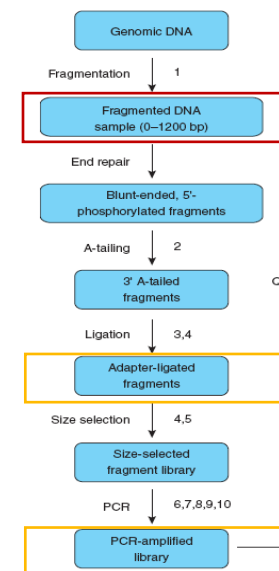


Amplified library run on the Bioanalyzer DNA 1000 Kit:



The Importance of Monitoring Size Distribution

- Choice of fragmentation can significantly affect the recovery of desired fragments and hence the amount of starting material required.
- Sequencing fragments that do not fall within the recommended size distribution may lead to low read depth or even a lack of read coverage for specific portions of the sequence.
- When performing SureSelect target enrichment, fragment size distribution can affect final % on-target capture.
- Probe-based sonication methods routinely introduce sample-to-sample variability and are not recommended.



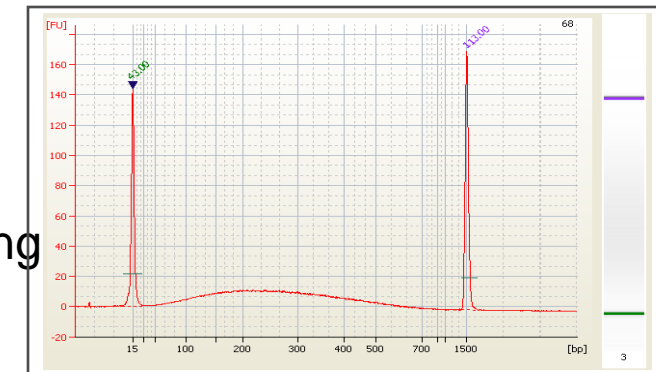
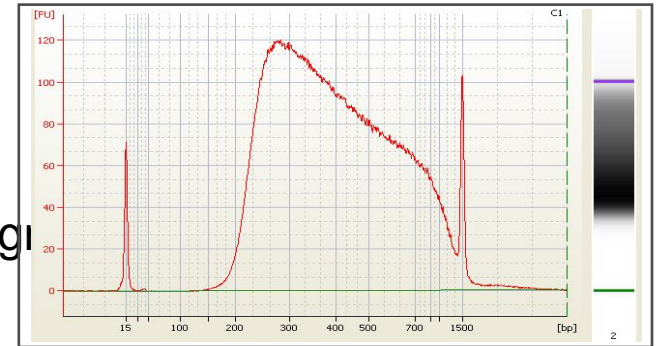
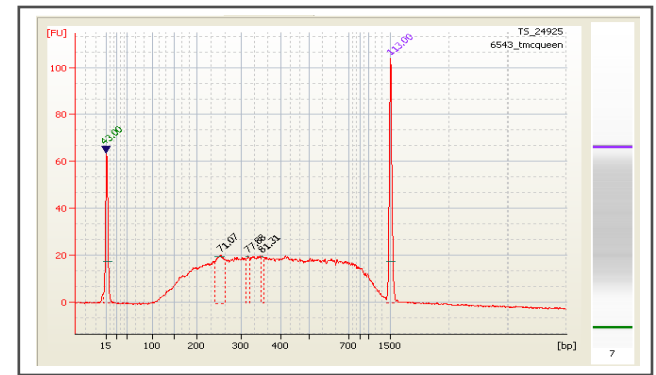
Shearing - Common issues

Uneven shearing

- Poor DNA quality
 - DNA eluted in incorrect buffer (not TE).
- Covaris issues
 - Bubbles in microtube will cause inconsistent fragi
 - Water level is too high/low.
 - Temperature of water bath is not between 6-8°C.
 - Insufficient degassing

Extended size range

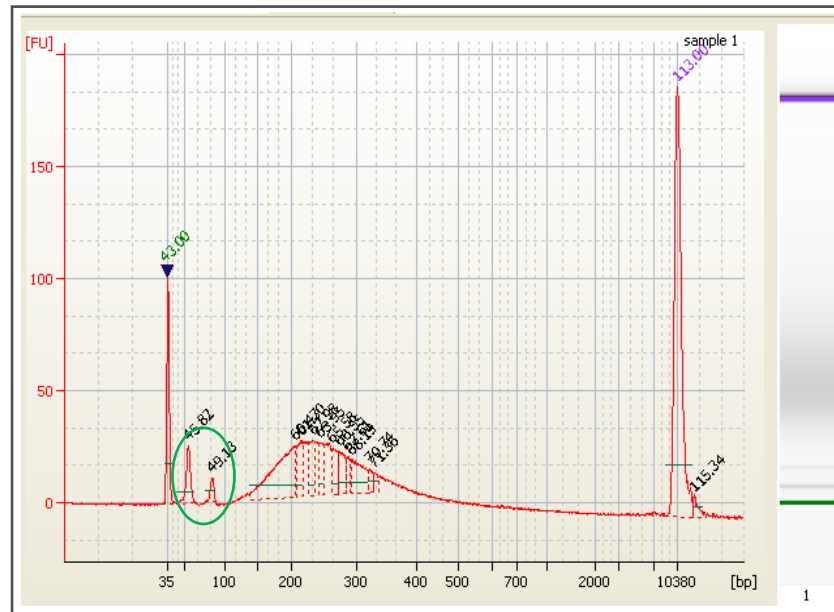
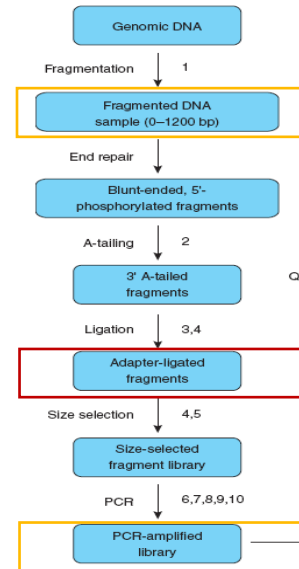
- Covaris issues. Perform a control experiment using as commercially available lambda DNA.



Adapter Ligation - Common issue

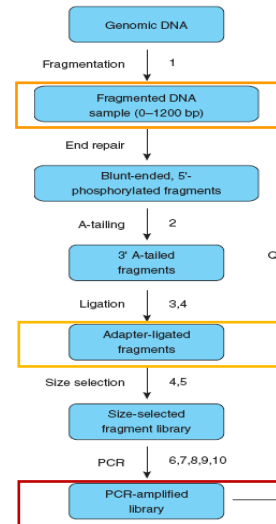
Excess Adapters

- Inefficient ligation due to too much input DNA or the use of incorrect ligation temperature (ligation is performed at 20-25°C. When using a PCR machine, make sure the lid is not heated).

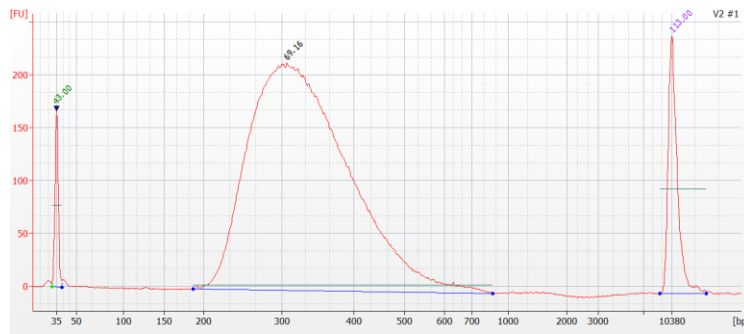


Quality Control after PCR Amplification

- PCR amplification is required for enrichment of adapter-ligated fragments, as well as to add indexes.
- In the SureSelect and HaloPlex protocols, PCR is also used to amplify captured DNA for final QC and quantification. *Libraries are analyzed on the Bioanalyzer High Sensitivity DNA assay*



SureSelect Libraries



HaloPlex Libraries



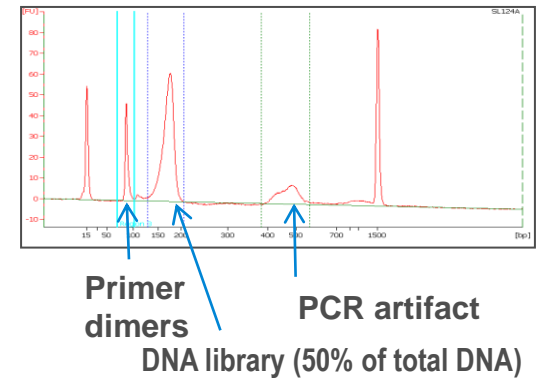
- PCR can create bias. PCR artifacts caused by overamplification or primer dimers can also affect sequencing coverage and accuracy.



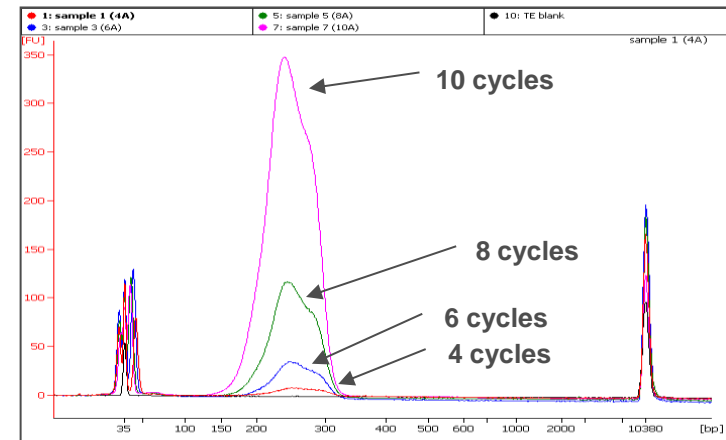
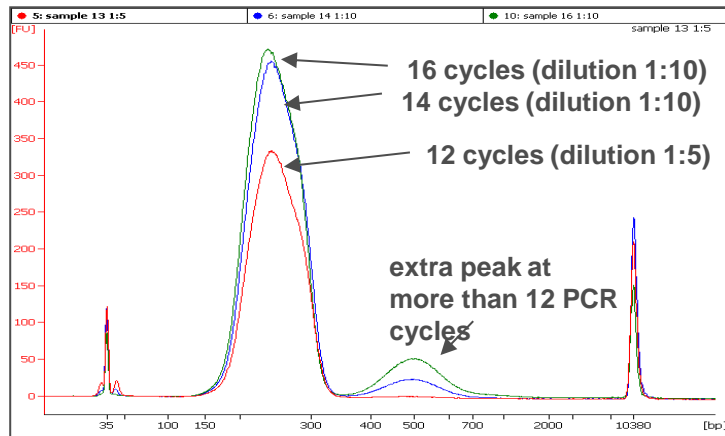
PCR Amplification – Common issues

Primer dimers and artifacts

- Primer dimers present in the library will be sequenced.
 - Primer dimers may be removed by performing additional bead clean-up steps.
 - Gel-based size selection can also remove primer dimers.



- Repeat PCR with fewer cycles to prevent formation of artifacts using remaining library.



PCR Amplification – Common issues

Bead carryover –

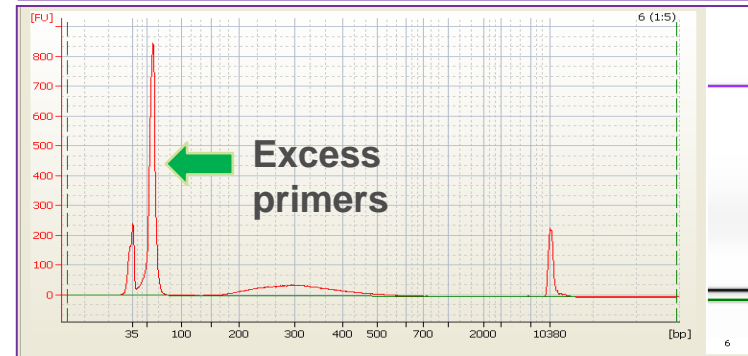
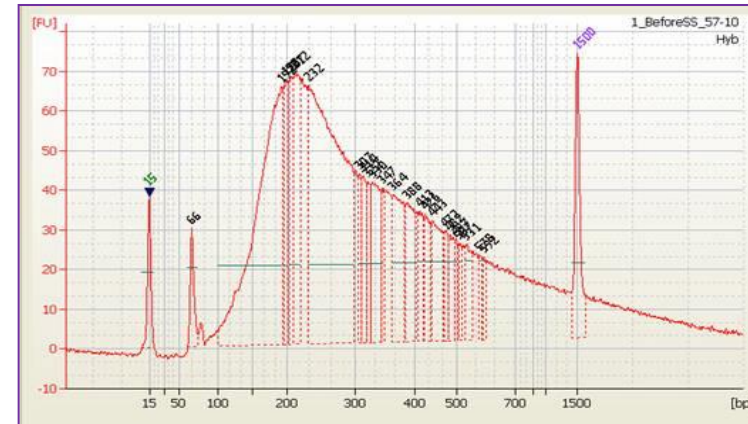
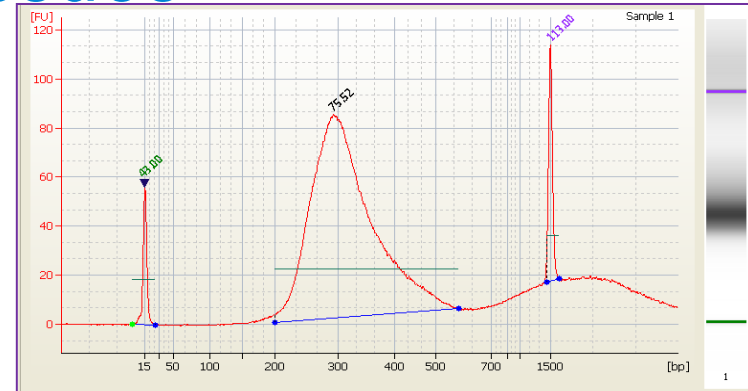
- SPRI bead carryover from post-PCR clean-up step.
- Use a strong magnet for bead separation and pipette carefully during elution to avoid disturbing beads.

Residual buffer –

- Likely due to buffer carryover from post-PCR clean-up using columns.

Low PCR yield –

- Inefficient PCR cycling results in low yield and an excess of primers.
- Can be a result of poor adapter ligation, low DNA quality, inefficient bead clean-up, use of too few cycles or PCR instrument is not well-calibrated.
- When performing target capture, low yields after post-capture PCR can also indicate suboptimal hybridization.



Outline

Importance of Quality Control

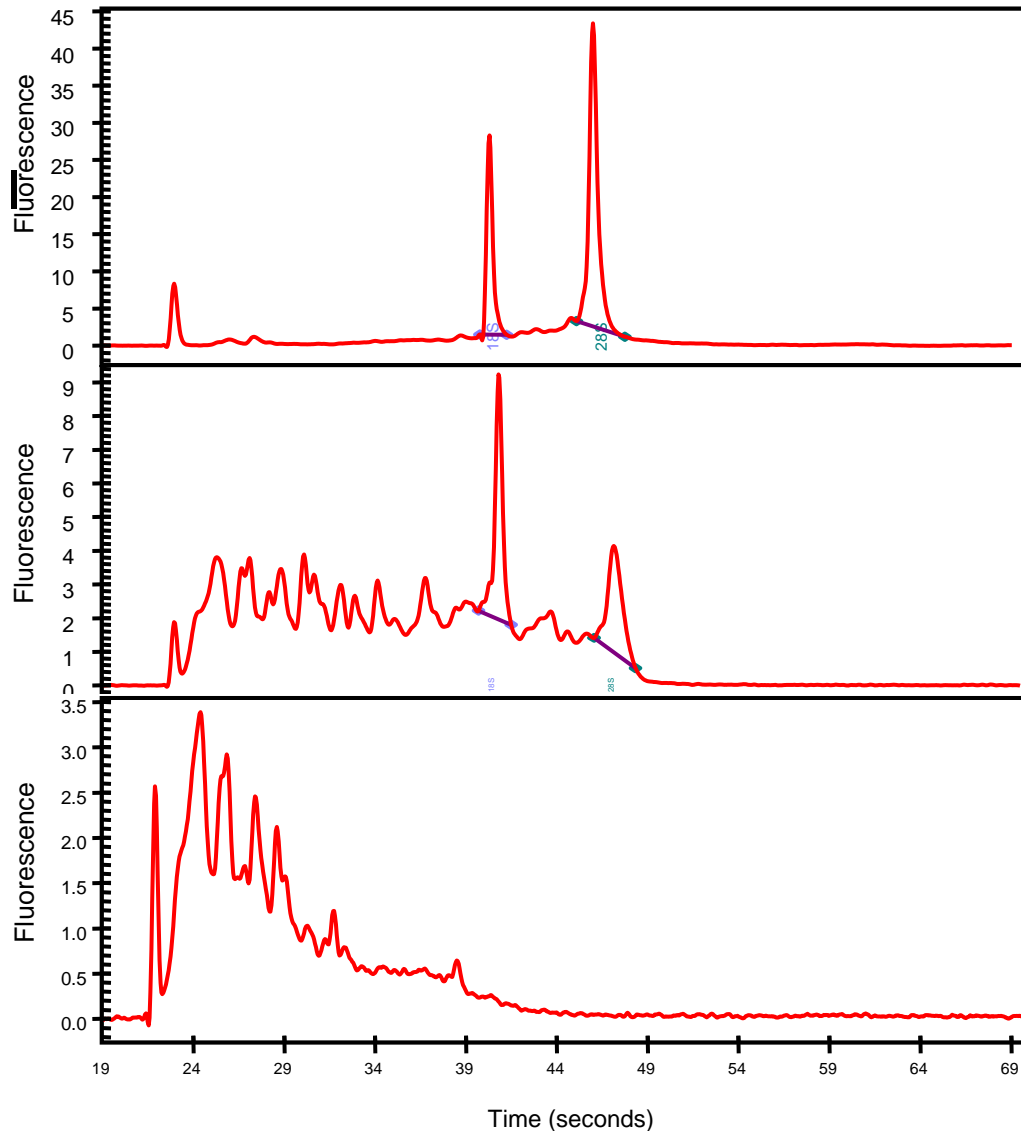
Sample QC in Next Generation Sequencing

Sample QC in Gene Expression

Sample QC in Proteomics

... and even more!

RIN – Standardized Assessment of RNA Integrity



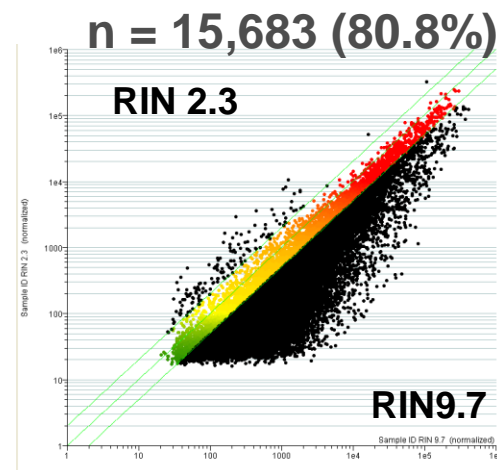
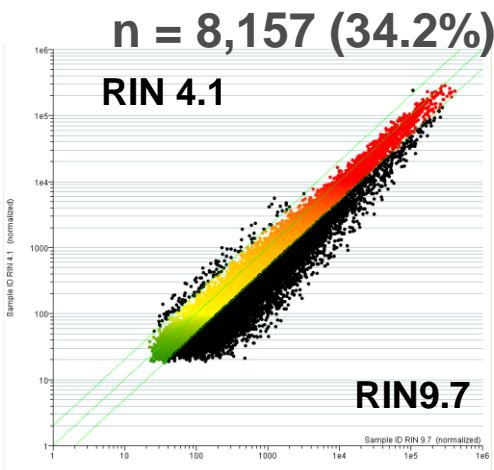
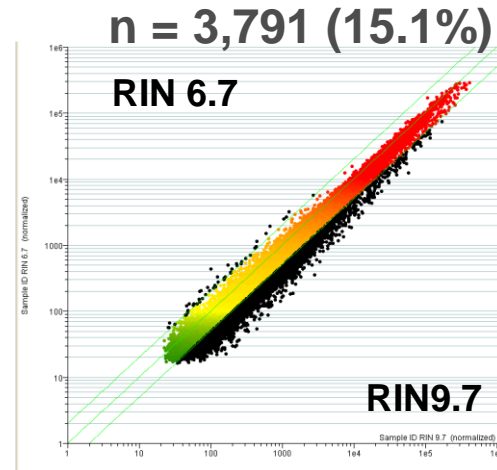
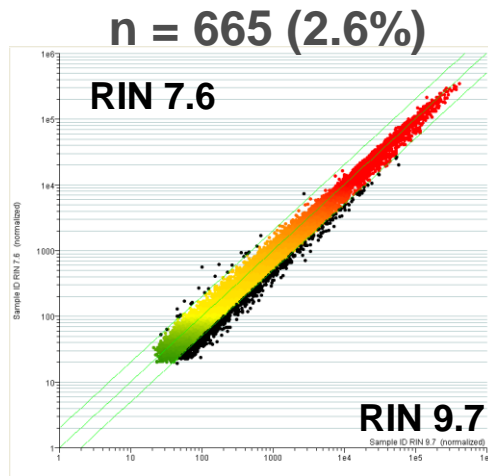
Intact RNA: RIN 10

Partially degraded RNA: RIN 5

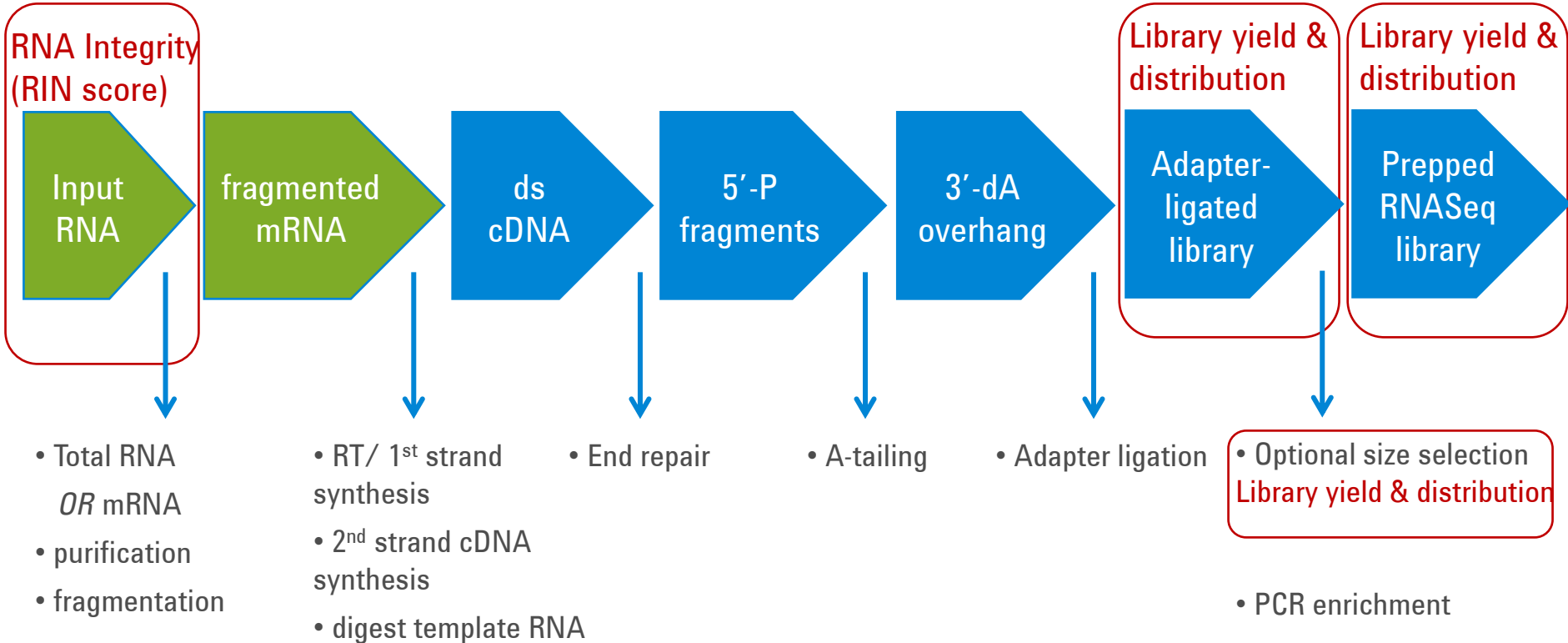
Strongly Degraded RNA: RIN 3

RNA QC is Critical for Microarray Success

Garbage in, garbage out!



QC is Important for RNA-seq, too!



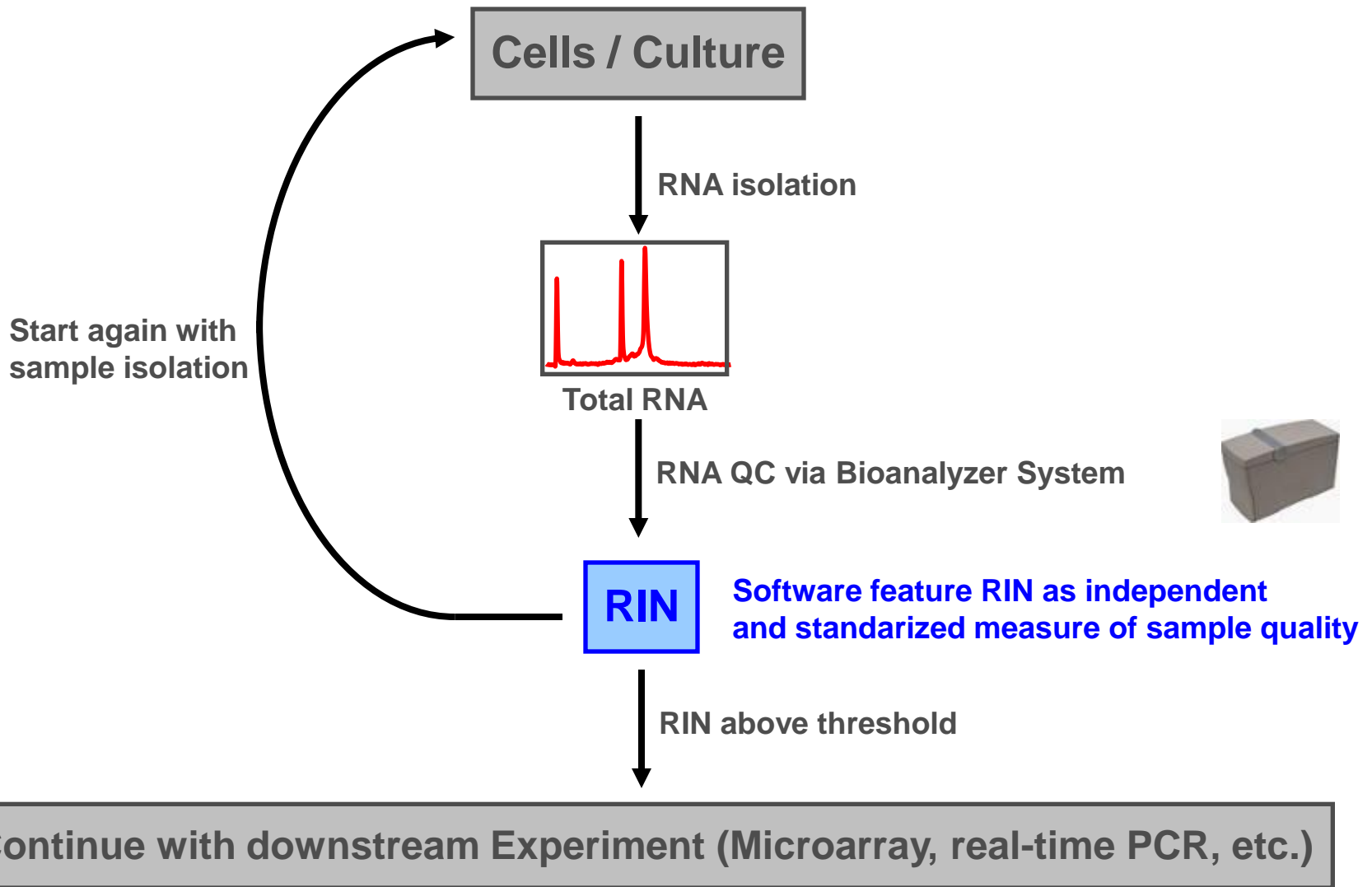
Tutorial: "2100 Bioanalyzer: The Gold Standard for RNA QC – Focus on RNASeq" by Maria Celeste Ramirez, Ph.D. Application Scientist Agilent Technologies, Inc.



"Preparation of High Quality RNA-Seq Libraries for Next-Generation Sequencing" by Michael H. Farkas, Ph.D. Ocular Genomics Institute Massachusetts Eye and Ear Infirmary Harvard Medical School



RNA QC in Routine Gene Expression Workflow



MIAME Guidelines for GEx Microarrays:
<http://compbio.dfci.harvard.edu/pubs/MIAME.pdf>

MIQE Guidelines for QPCR:
<http://www.clinchem.org/cgi/reprint/55/4/611>



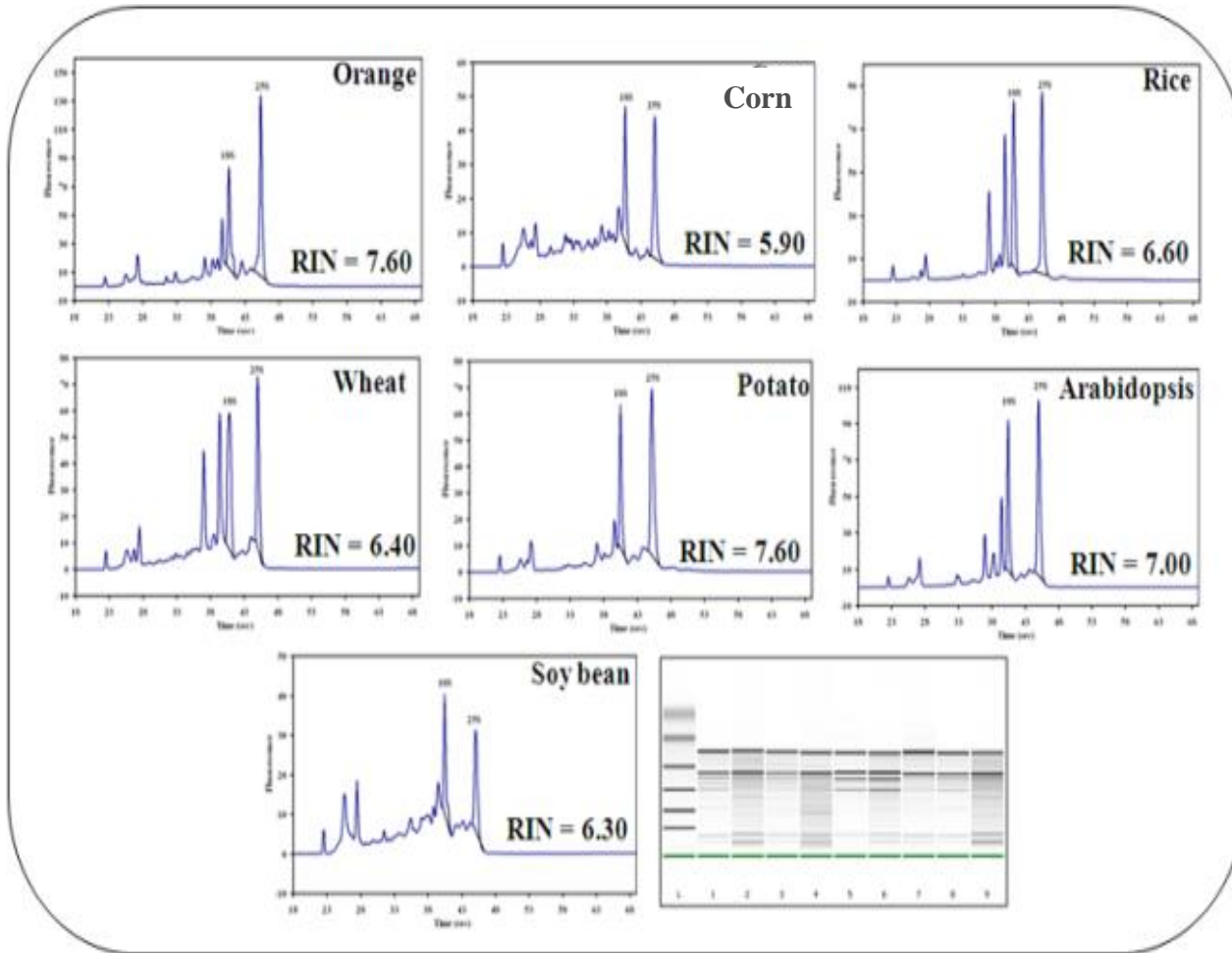
Agilent Technologies

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Application Plant RNA



Application Note: 5990-8850EN



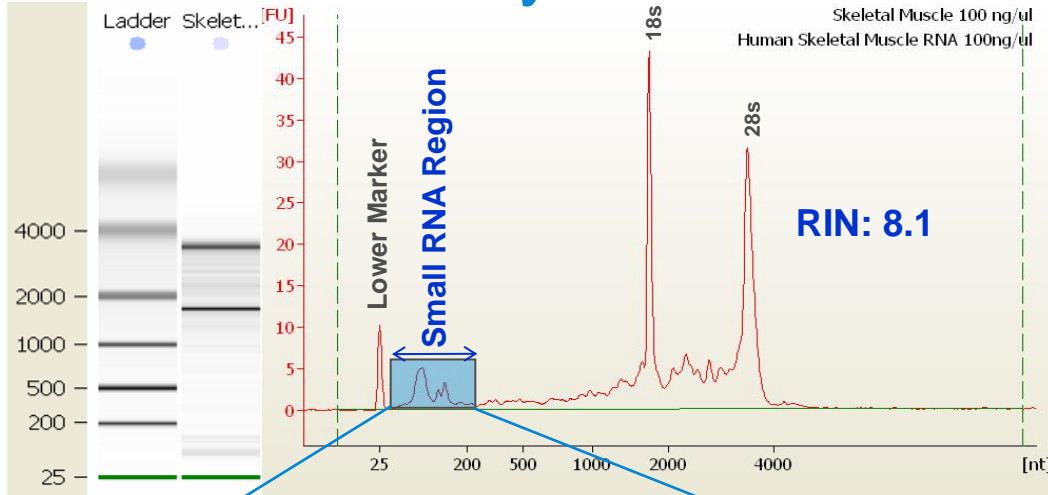
Plant RNA

RNA from green tissue contains additional rRNA units (e.g. 25S) in contrast to other cells.

- new software feature (assay) as of **B.02.07**
- now the 2100 can analyze different tissue plant RNA samples to assess integrity of plant RNA from a variety of sources

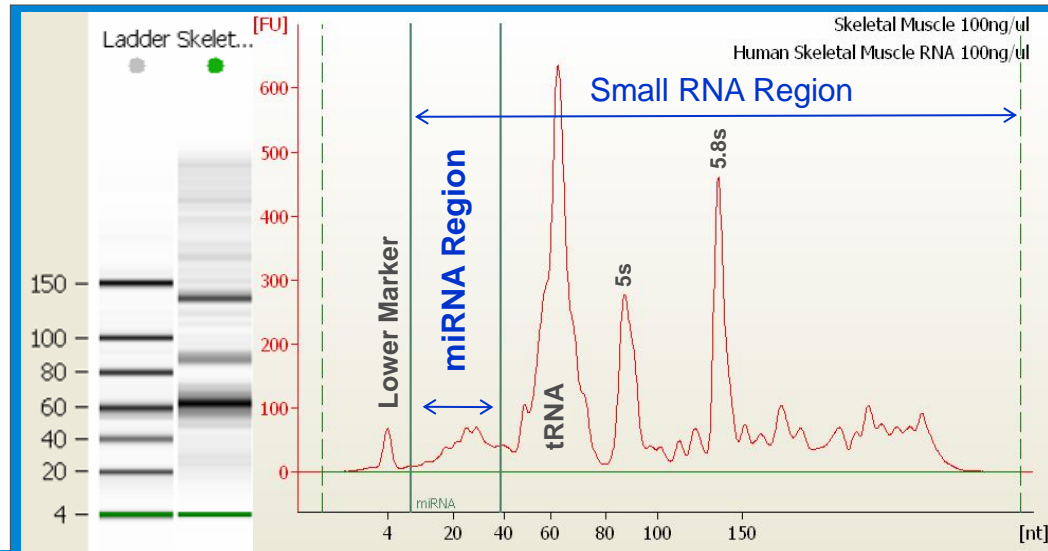


Small RNA Assay versus RNA Nano Assay



RNA 6000Nano kit

Small RNA Kit



RNA 6000 Nano

Size range: 25-6000nt

Results: Integrity, Total RNA amount, gDNA contamination



Changed multiple parameters:

- Dye composition
- Gel formulation
- Electronic Script
- Analysis setpoints in SW



Small RNA

Size range: 6-150nt

Results: miRNA amount, Ratio and amount of other Small RNA

No RIN for small RNA!



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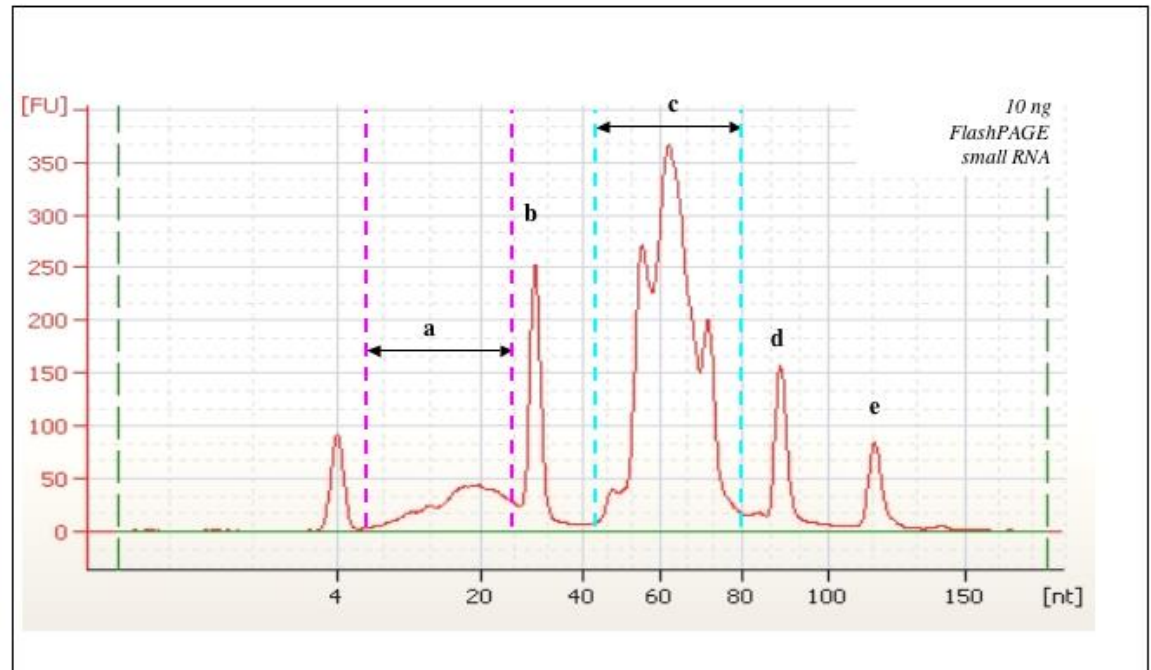
Establishing Individual QC Criteria Analysis of Small RNAs from *Drosophila* Schneider Cells



Analysis of small RNAs from *Drosophila* Schneider cells

Small RNA electropherogram:

- a) miRNA region
- b) 2S RNA region
- c) transfer RNA
- d) 5S rRNA
- e) 5.8S rRNA



The presence of sharp individualized 5S and 2S rRNA peaks can be used to directly evaluate the quality of small RNA samples.

Odile Sismeiro, Institut Pasteur, Paris, France

Outline

Importance of Quality Control

Sample QC in Next Generation Sequencing

Sample QC in Gene Expression

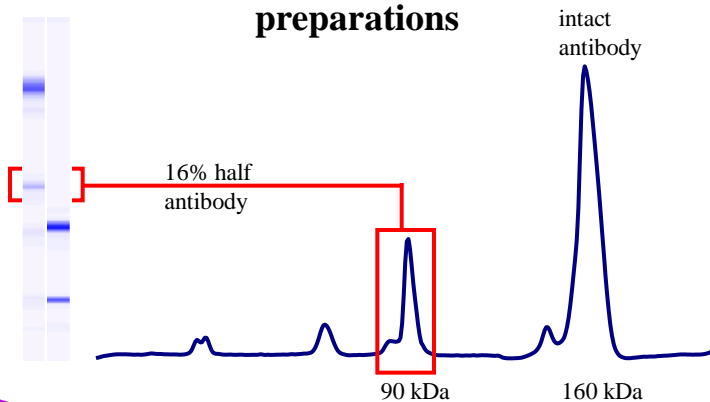
Sample QC in Proteomics

... and even more!

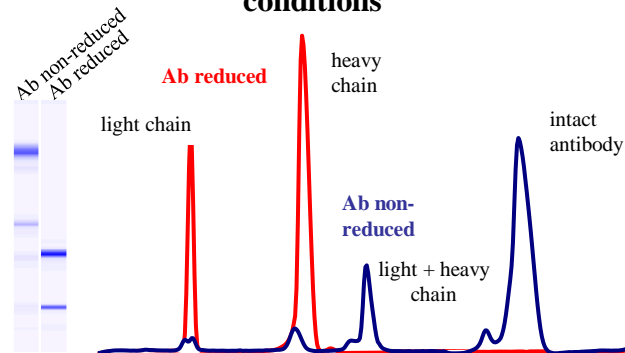
Quality Control of Antibodies



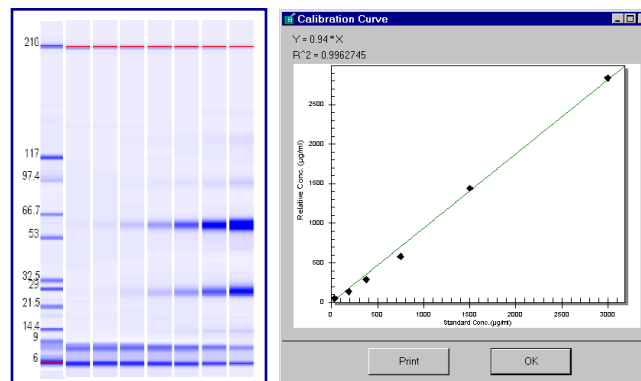
Determine the half antibody content in IgG preparations



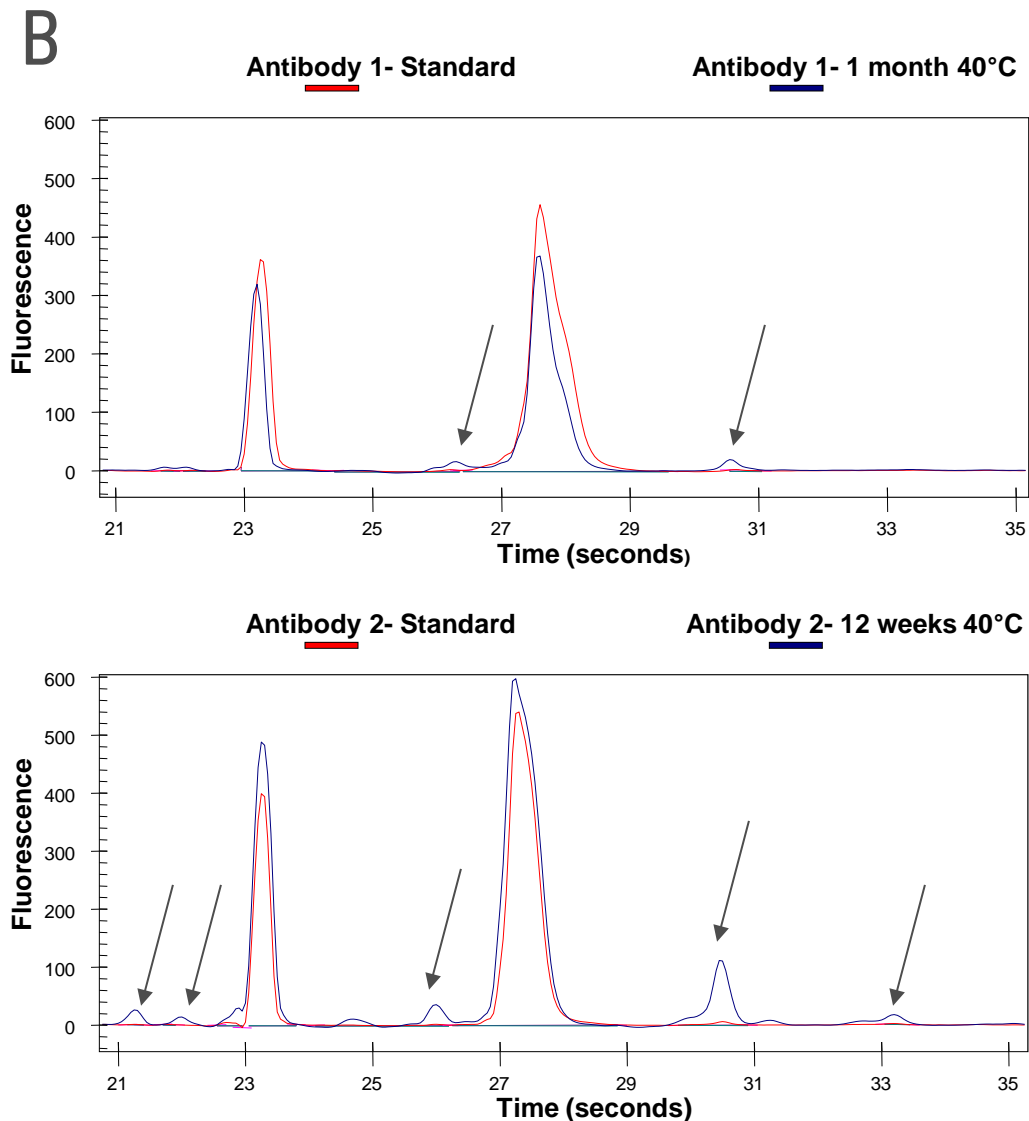
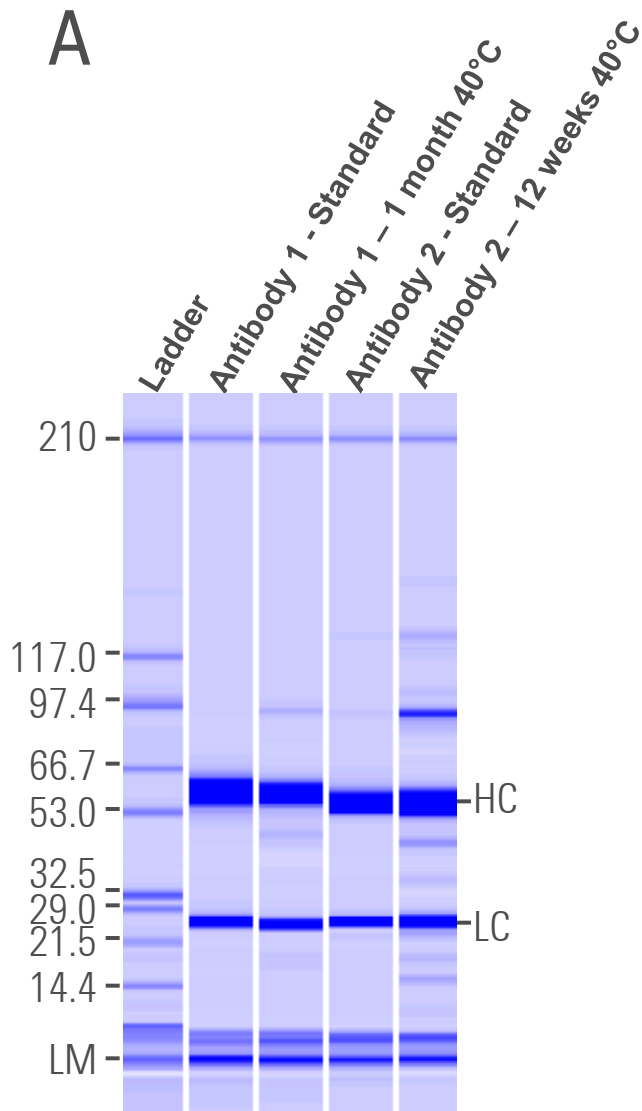
Antibody analysis under reducing and non-reducing conditions



Absolute Quantitation of IgG samples



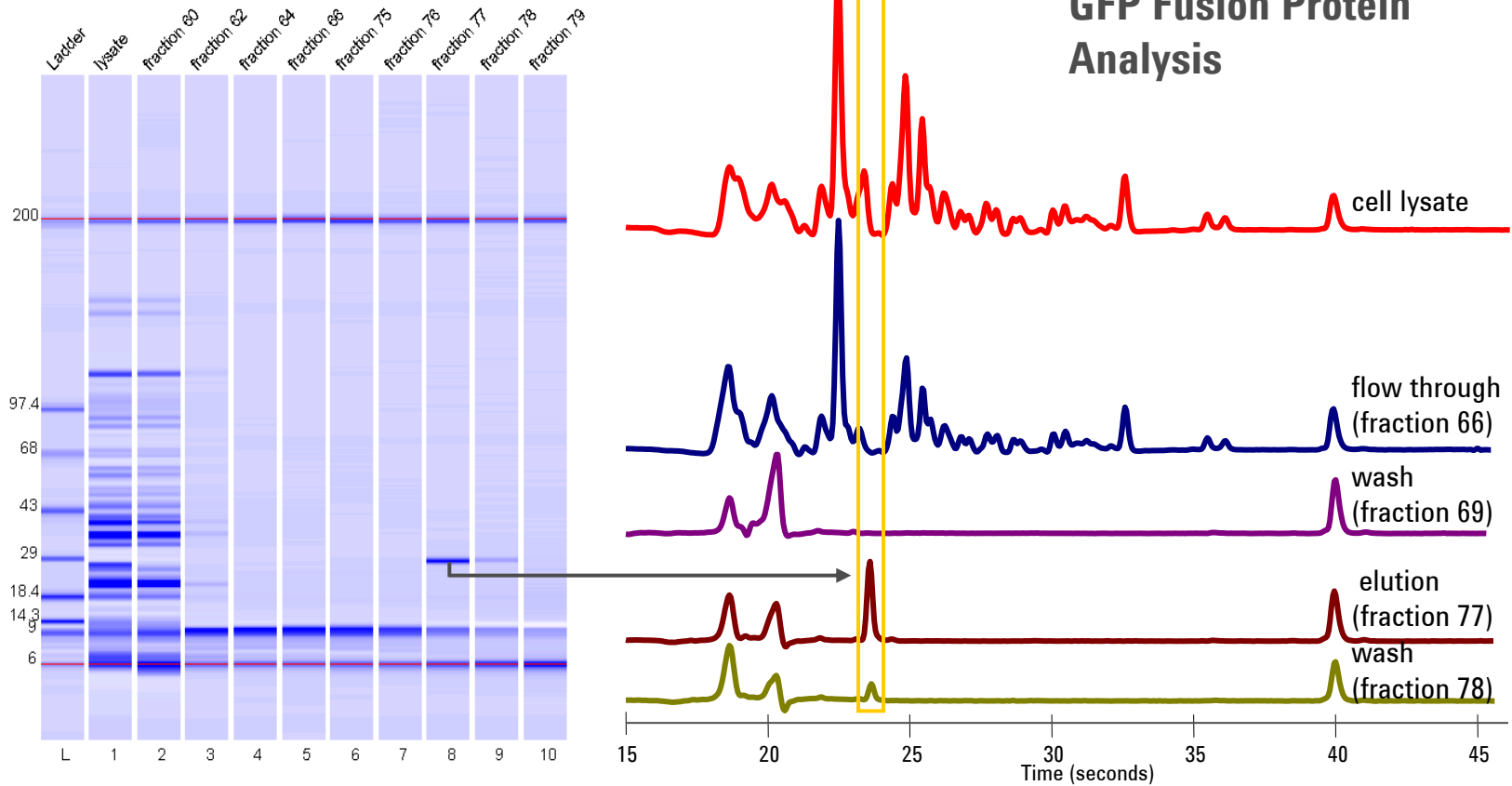
Analysis of Antibody Stability – Stress Test



Monitoring of Protein Purification Process



GFP Fusion Protein Analysis



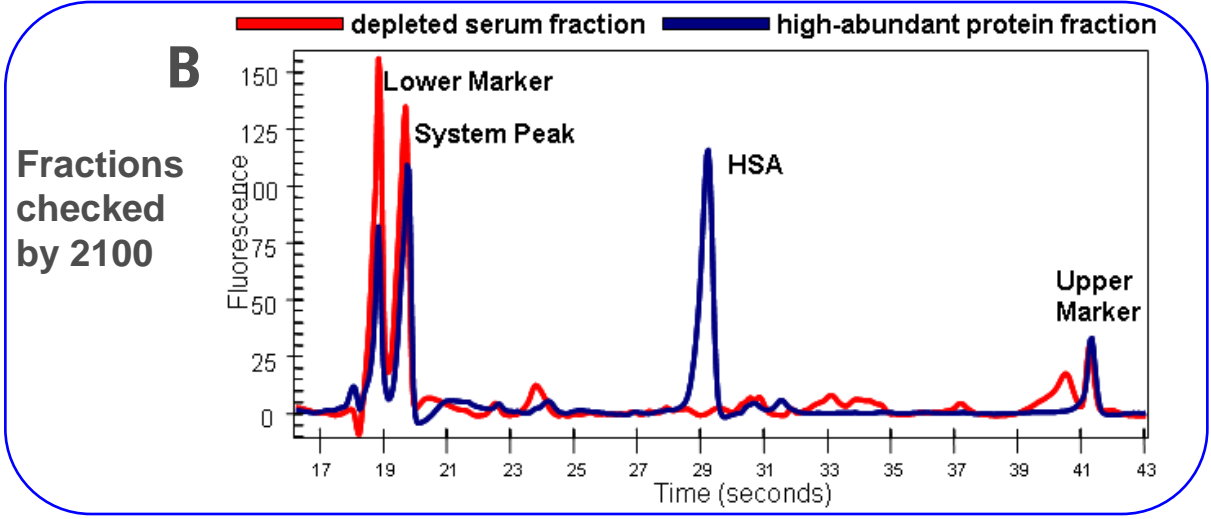
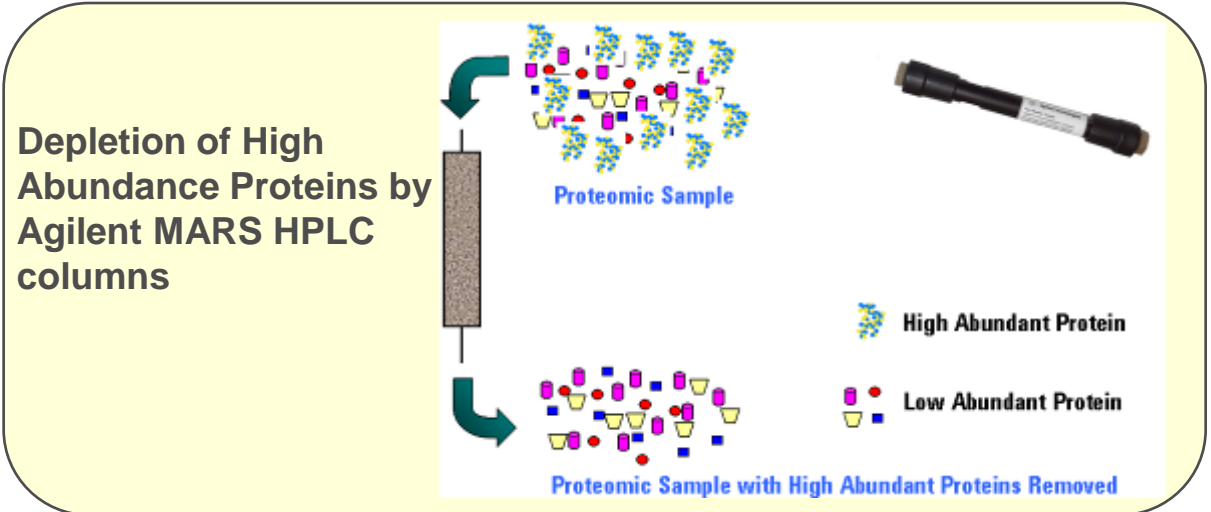
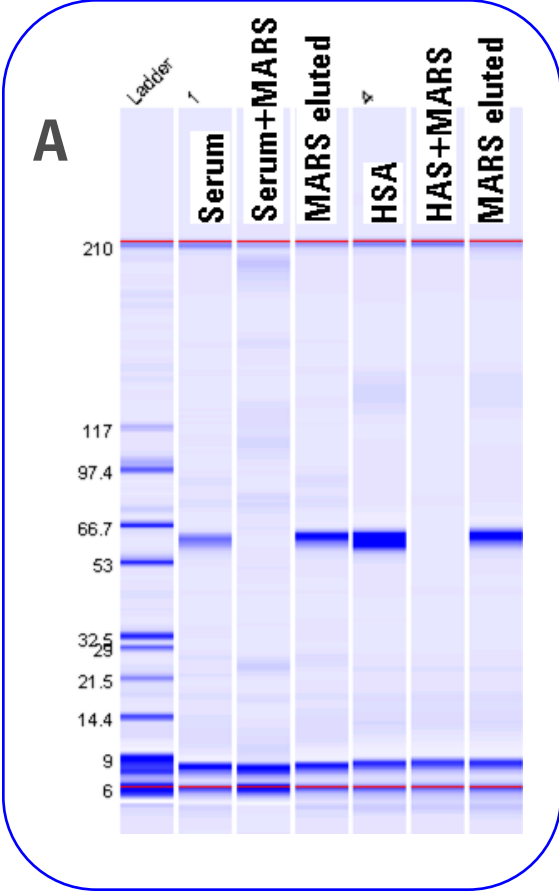
↑ 2100 Bioanalyzer gel-like image

↑ 2100 Bioanalyzer electropherogram

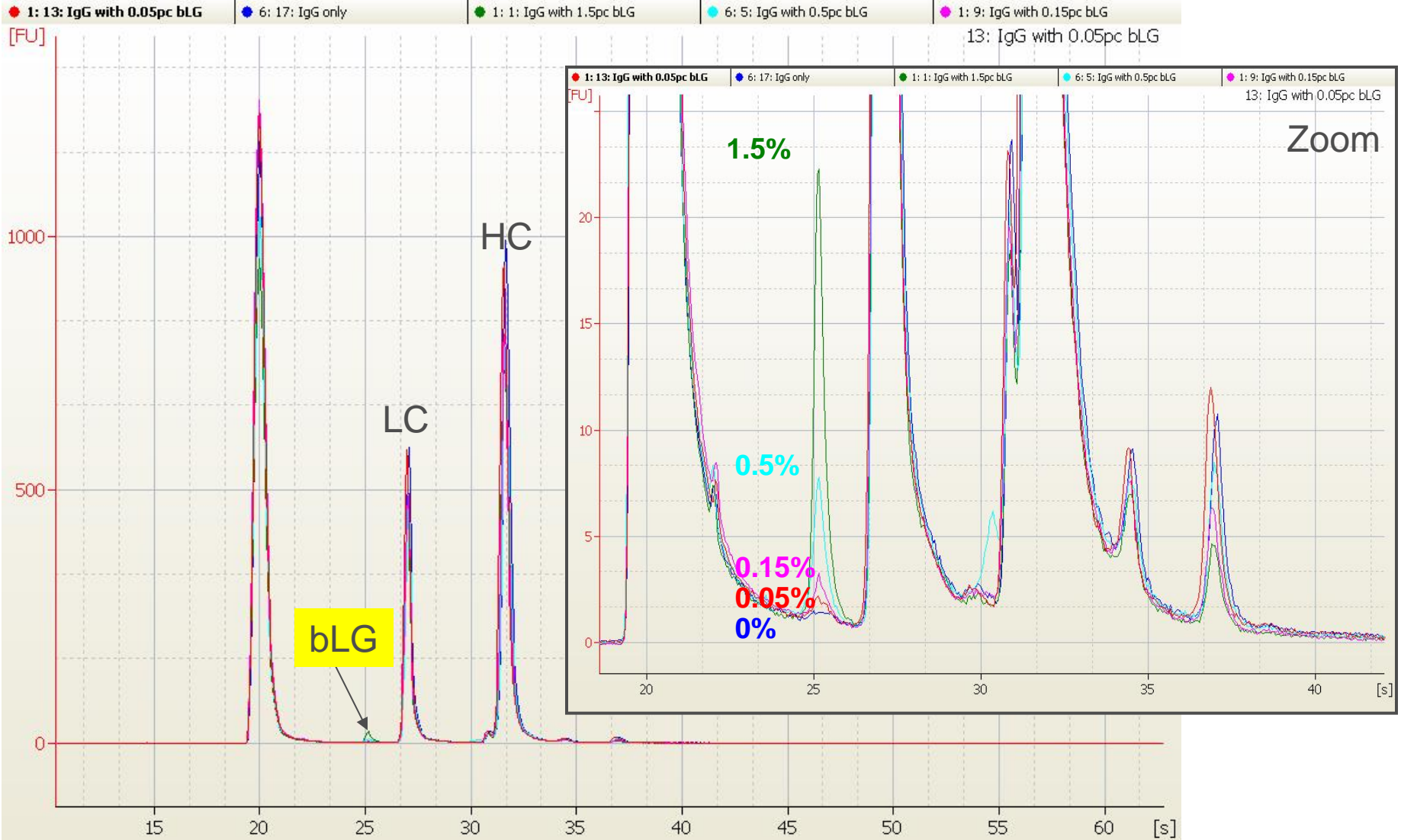
Courtesy of P. Sebastian and S.R. Schmidt
GPC-Biotech AG, Martinsried, Germany



Depletion of High Abundance Proteins in Human Serum



ICH Guidelines: Simulation of Impurity Detection



C. Wenz, et. al., *Electrophoresis* 31, 2010



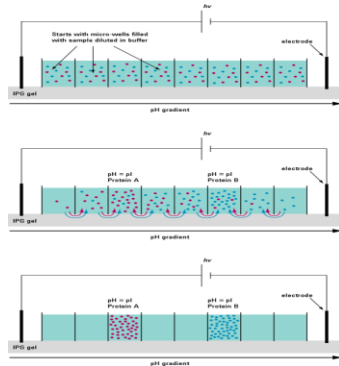
2-DG Equivalent: HSP250 + OFFGEL Fractionation (IEF)

E. coli lysate
(50 μ g)



Protein clean up and labeling

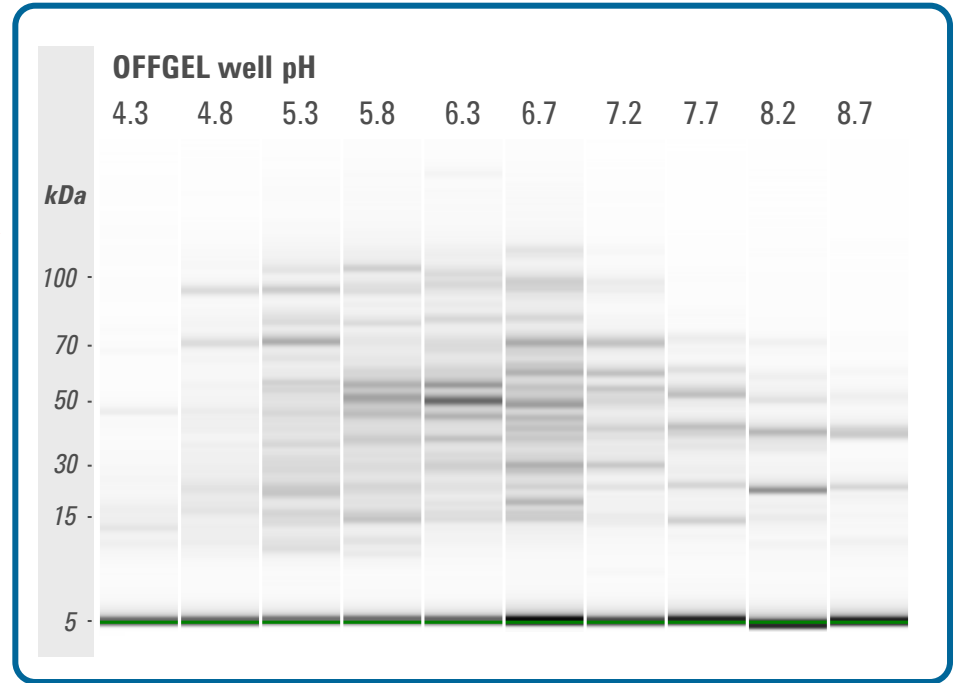
OFFGEL Electrophoresis



2100 Bioanalyzer
HSP-250 Assay



Isoelectric point (pI)
Molecular weight



Application Note: 5989-8419EN



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Outline

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Sample QC in Next Generation Sequencing

Sample QC in Gene Expression

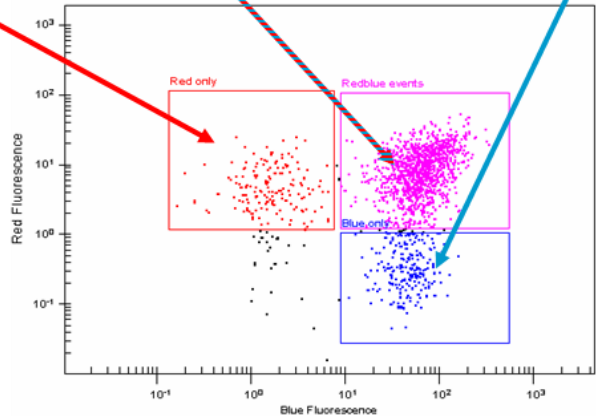
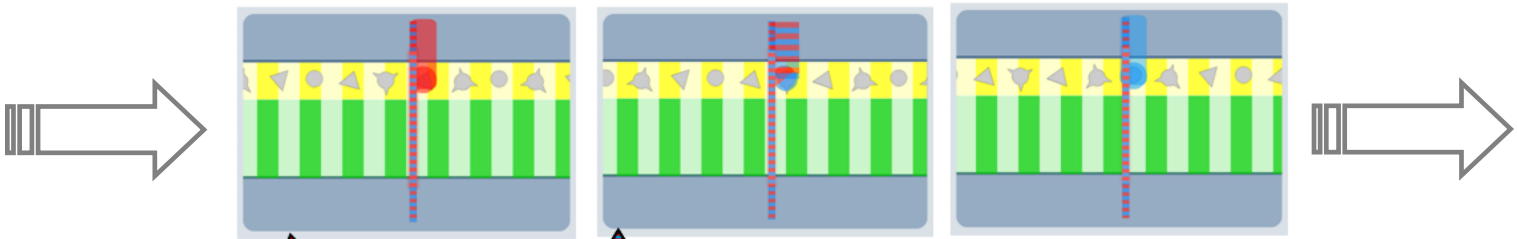
Sample QC in Proteomics

... and even more!

Cell Applications



- Protein Expression
- Apoptosis Detection
- Gene Silencing
- Transfection Monitoring
- Cell Staining



Dot plot view for easy data evaluation

Flow Cytometry on a Chip - 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)

SYNTHETIC BIOLOGY

DNA & RNA Applications in Genome Editing



PCR products

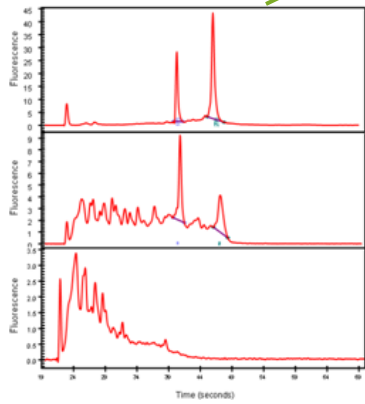
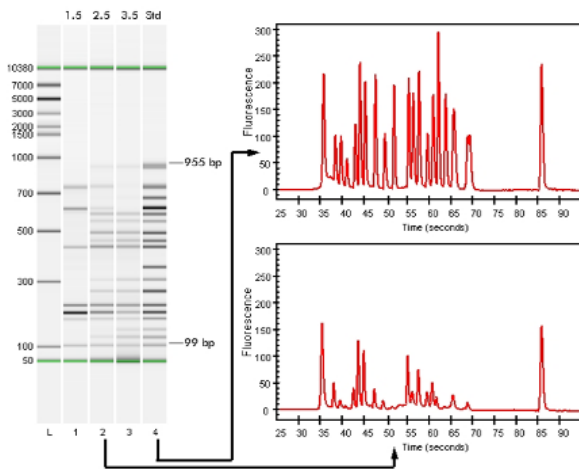
gDNA integrity

Restriction Digest Analysis

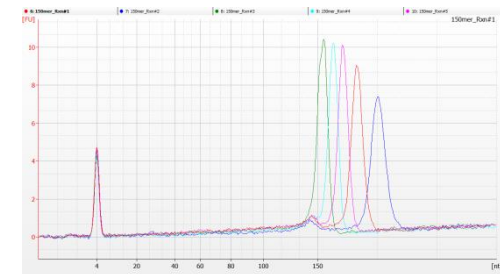
Quality Control in NGS

Total RNA integrity

Quality Control of Oligos



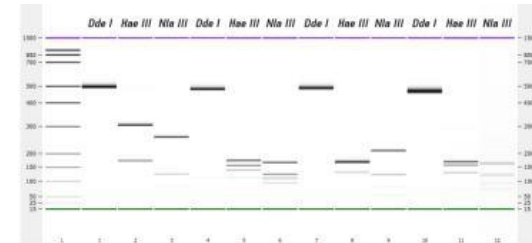
Oligo tailing reaction



Examples of Electrophoresis in Synthetic Biology workflows

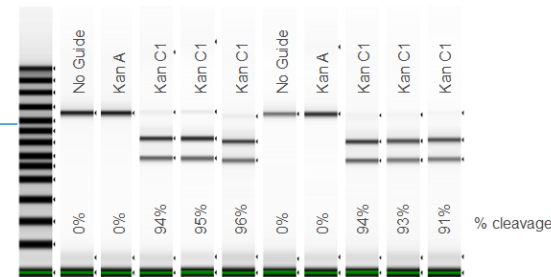
Vector Assembly

- ❑ Starting material QC: Gene of interest after PCR amplification
- ❑ Verifying vector composition with restriction analysis
- ❑ Vector analysis by NGS (including multiple QC steps)



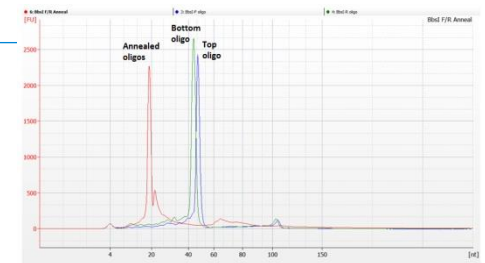
CRISPR/ Cas9

- ❑ DNA target after PCR amplification
- ❑ Cleavage efficiency of digestion with Cas9 Nuclease (Detection and Quantitation)



guide RNA synthesis

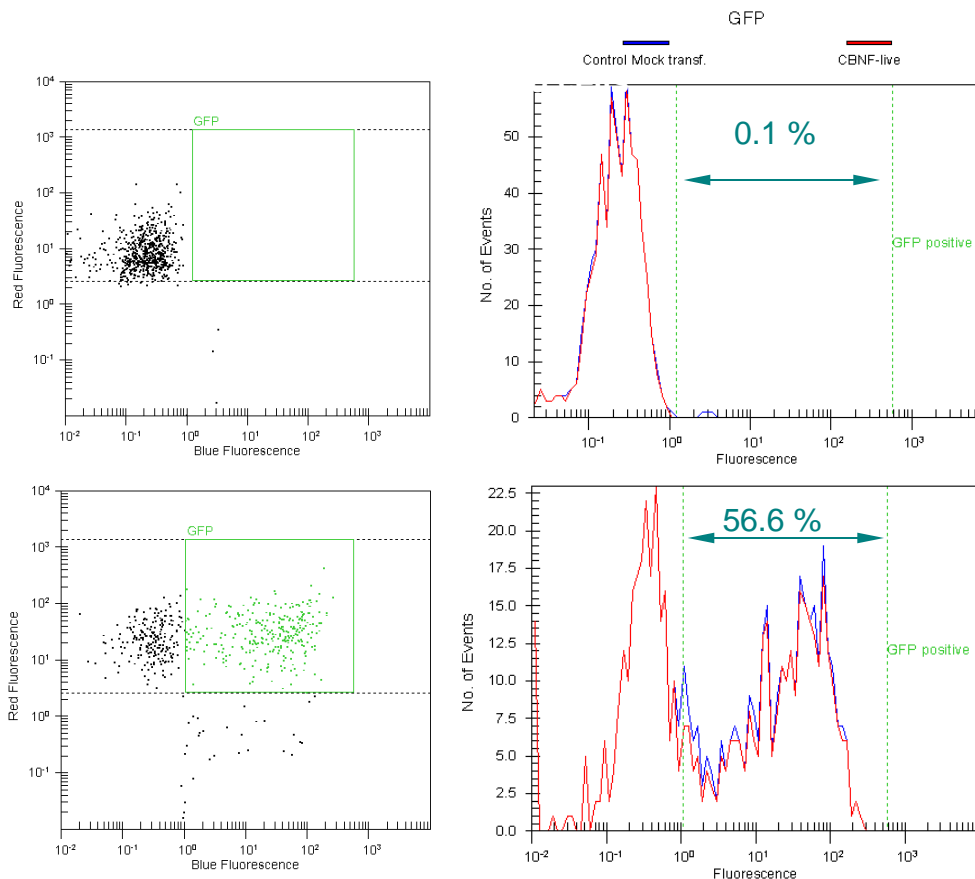
- ❑ Starting material QC: oligo templates*
- ❑ Monitoring oligo annealing reactions
- ❑ Quantitation and QC of gRNA product*



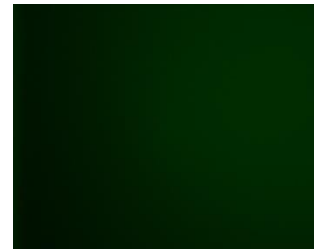
* Utilizes Small RNA Assay on the 2100 Bioanalyzer System

Applications: Protein Expression Analysis

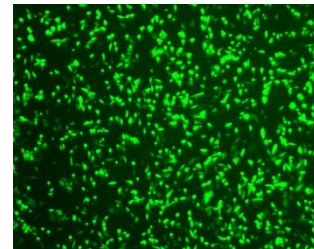
GFP Transfection Efficiency Control



CHO-K1 cells were transfected with EGFP DNA and Lipofectamine.



Control



EGFP transfected



More Information

www.agilent.com/genomics/bioanalyzer

- Application Notes
- Publications
- Data Sheets
- Videos
- Brochures
- Special Offers
- Free Software Downloads



Alternative to 2D gel electrophoresis – OFFGEL electrophoresis combined with high-sensitivity on-chip protein detection


Application Note

Christian Wanz
Andreas Pflüger




Performance characteristics of the High Sensitivity Protein 250 assay for the Agilent 2100 bioanalyzer


Technical Note

Quantification Strategies Using the High Sensitivity Protein 250 Assay for the Agilent 2100 Bioanalyzer

Technical Note

Agilent Technologies

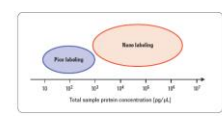


Additional Pico protocol for the High Sensitivity Protein 250 assay with the Agilent 2100 Bioanalyzer

Optimized procedure for lowest concentrated samples

Technical Note

Protein Electrophoresis



Abstract

The Agilent High Sensitivity Protein 250 assay for the Agilent 2100 Bioanalyzer analyzes proteins from 10 to 250 kDa. This assay is based on the detection of fluorescently labeled proteins that are separated electrophoretically on microfluidic chips. Fluorescence labeling and quantification of proteins with a linear dynamic range spanning four orders of magnitude. The sensitivity is superior to color-based 2D-PAGE, allowing it to detect concentrations as low as 1 pg/μL. Labeled protein serum albumin (BSA) on-chip. However, the fluorescent labeling requires a minimum total protein concentration of 1 ng/μL in the total sample.

This technical note describes a new Pico labeling protocol, which extends the applicability to protein samples with concentrations below 1 ng/μL.

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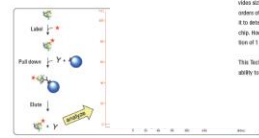
Immunoprecipitation Sensitivity Protocol Combining Specific Proteins with the Agilent 2100 Bioanalyzer

Application Note

Protein Electrophoresis

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Abstract

A new method for the targeted analysis of proteins is presented that combines the specificity of immunoprecipitation with the sensitivity of protein detection on microchips using the High Sensitivity Protein 250 assay for the Agilent 2100 Bioanalyzer. As an alternative to Western blotting, this method is valuable for researchers required, for example, in protein expression and purification in pharma, biotech or academic labs. Advantages of this new method in comparison to Western blotting are:

- More reliable results: higher specificity and sensitivity
- Better accuracy and precision: less manual steps and direct availability of quantitative data
- Increased productivity: 3 hours versus 1 day analysis time
- Lower spending for antibodies: 10x less primary and no secondary antibody are needed
- Lower reagent consumption: environmentally friendly process

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