

*Comparison of QuantiGene and LC-MS/MS technologies for quantification of antisense oligonucleotides in tissue and plasma matrices*

*Davy Guignard, Evotec*



# Disclaimer

This presentation (including any information which has been or may be supplied in writing or orally in connection herewith or in connection with any further inquiries) is being delivered on behalf of Evotec SE (the “Company”, “we,” “our” or “us”). This presentation is made pursuant to Section 5(d) and/or Rule 163B of the Securities Act of 1933, as amended, and is intended solely for investors that are qualified institutional buyers or certain institutional accredited investors solely for the purposes of familiarizing such investors with the Company. This presentation shall not constitute an offer to sell or the solicitation of an offer to buy Evotec securities, nor shall there be any sale of these securities in any state or jurisdiction in which such offer, solicitation or sale would be unlawful prior to registration or qualification under the securities laws of any such state or jurisdiction. No representations or warranties, express or implied, are made as to the accuracy or completeness of the statements, estimates, projections or assumptions contained in the presentation, and neither the Company nor any of its directors, officers, employees, affiliates, agents, advisors or representatives shall have any liability relating thereto.

## **Cautionary Note Regarding Forward-Looking Statements**

This presentation contains forward-looking statements concerning our business, operations and financial performance and condition, as well as our plans, objectives and expectations for our business operations and financial performance and condition. Many of the forward-looking statements contained in this presentation can be identified by the use of forwardlooking words such as “anticipate,” “believe,” “could,” “estimate,” “expect,” “intend,” “may,” “might,” “plan,” “potential,” “should,” “target,” “would” and other similar expressions that are predictions of or indicate future events and future trends, although not all forward-looking statements contain these identifying words. Forward-looking statements are based on our management’s beliefs and assumptions and on information currently available to our management. Such statements are subject to risks and uncertainties, and actual results may differ materially from those expressed or implied in the forwardlooking statements due to a variety of factors. The forward-looking statements contained in this presentation speak only as of the date of this presentation, and unless otherwise required by law, we do not undertake any obligation to update them in light of new information or future developments or to release publicly any revisions to these statements in order to reflect later events or circumstances or to reflect the occurrence of unanticipated events.



# Agenda

1. Quantification of ASOs in biological matrices
2. Objectives & Methods
3. Development of the QuantiGene methods
4. Sample analysis
5. Method comparison: QuantiGene vs LC-MS/MS
6. Conclusion & Perspectives





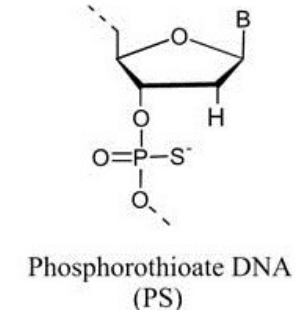
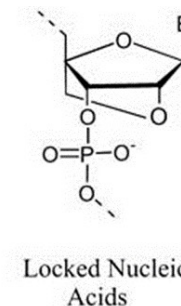
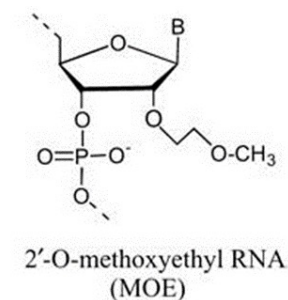
# *Context - Quantification of ASOs in biological matrices*

# Pharmacokinetics of antisense oligonucleotides

## Peculiarities of ASOs compared to small molecules

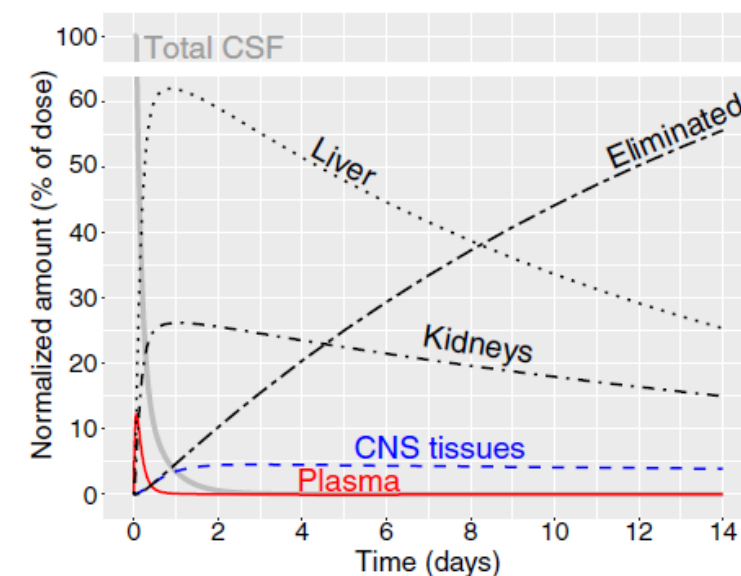
### • ASO = antisense oligonucleotide

- Synthetic short sequence (15-25 nt) of RNA, DNA or a mix
- Single strand
- Can modulate the expression of a gene through different mechanisms of action
- Back bone chemistries that increase stability and potency (↓ dose)



### • PK evaluation

- High concentration in tissues (kidneys and liver)
- Fast elimination from systemic circulation → very low concentration in plasma
- Need a very sensitive bioanalytical method to quantify ASOs in plasma (accessible matrix for repeated samplings)





# Quantification of oligonucleotides

## Overview of the current technologies

Chromatography-based methods	Hybridization-based methods
<ul style="list-style-type: none"> <li>• LC-UV</li> <li>• LC-MS/MS</li> </ul>	<ul style="list-style-type: none"> <li>• Single-probe hybridization ELISA</li> <li>• Dual-probe ECL (MSD technology)</li> <li>• RT-qPCR</li> </ul>
<ul style="list-style-type: none"> <li>• Hybridization–LC-MS/MS</li> <li>• Hybridization–LC-UV</li> </ul>	

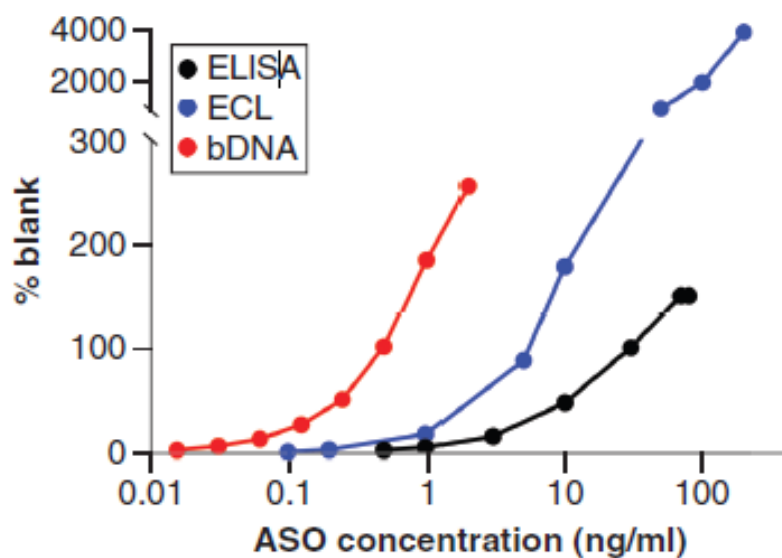
### ***Limitation of some technologies: lack of sensitivity***

(especially when low-dose and non-intravenous ASOs are administered)

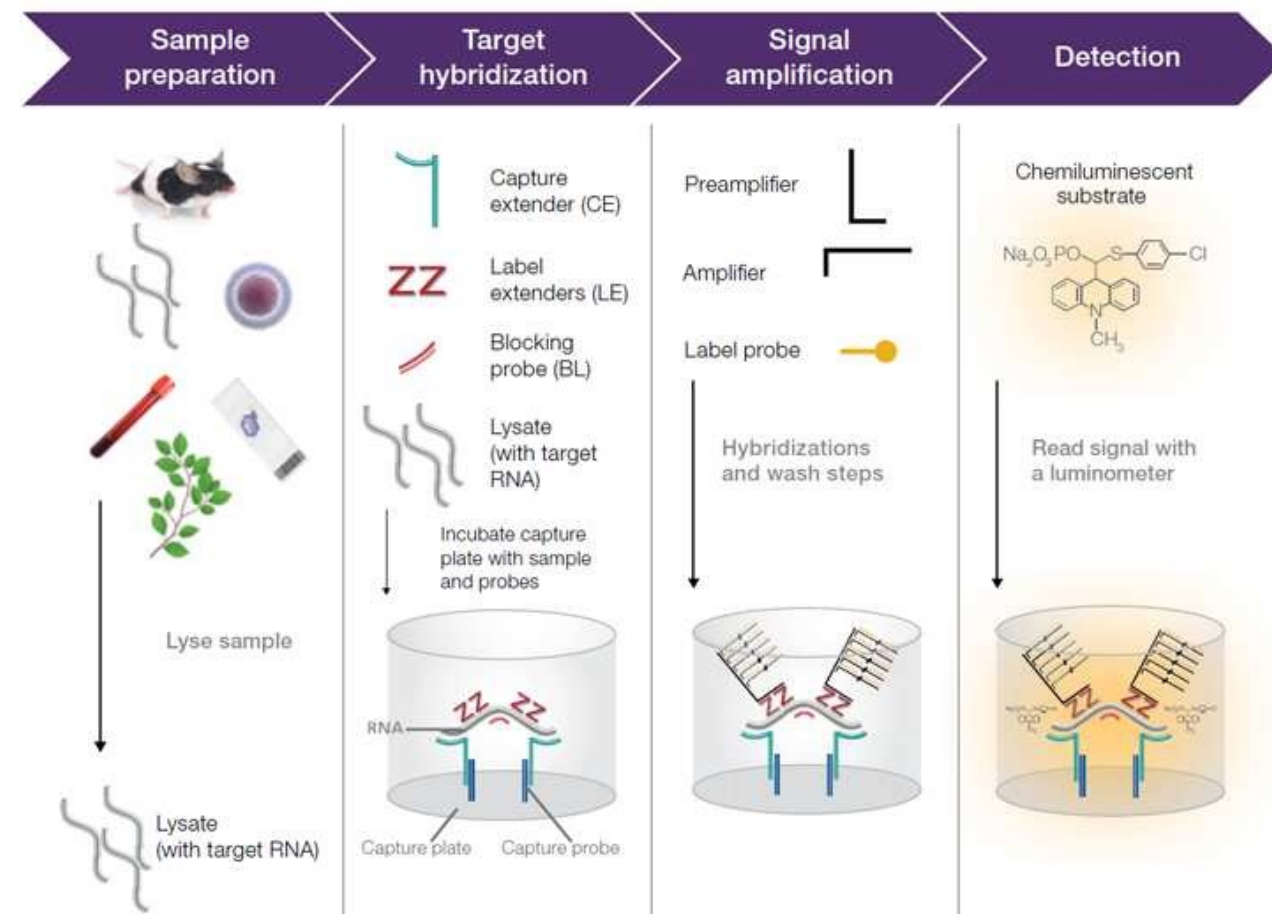
# Quantification of oligonucleotides

## QuantiGene technology

- Hybridization-based gene expression assay that uses branched DNA for signal amplification
- The luminescent signal is proportional to the number of RNA molecules present in the sample
- Originally designed for detection of mRNA molecules; adapted for ASO quantification
- Directly applicable to a biological matrix (no sample purification)
- Highly sensitive



**ThermoFisher**  
SCIENTIFIC





# *Objectives & Methods*





## Questions & Objectives

Is the QuantiGene technology

- Applicable for the quantification of ASOs in solid tissues?
- Applicable for the quantification of short sequence ASOs (>16 nt)?
- Applicable for the quantification of ASOs with chemical modifications (PS; LNA)?
- Comparable with the LC-MS/MS technology?



## Objectives

- Compare the QuantiGene and the LC-MS/MS technologies (reliability)
- Characterize the PK profiles of different anti-Malatl1 antisense oligonucleotides (tool ASOs) after a SC administration in mouse

QuantiGene



LC-MS/MS



# Material & Methods

## In vivo study design

- Model**

- C57Bl/6JRJ female mice (6-8 weeks old)
- N=3 /group

- Administration**

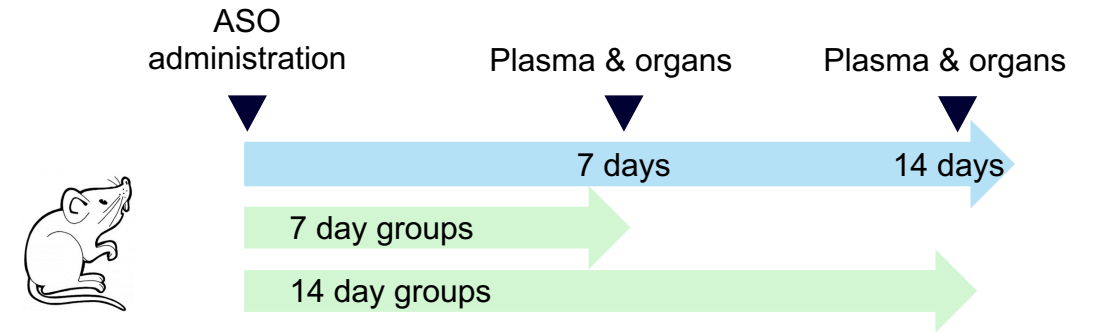
- single SC administration
- 3 ASOs anti-Malat1: MM1 – MM2 or MM5
- 3 dose levels: 8.3 – 25 or 75 mg/kg

- Samplings**

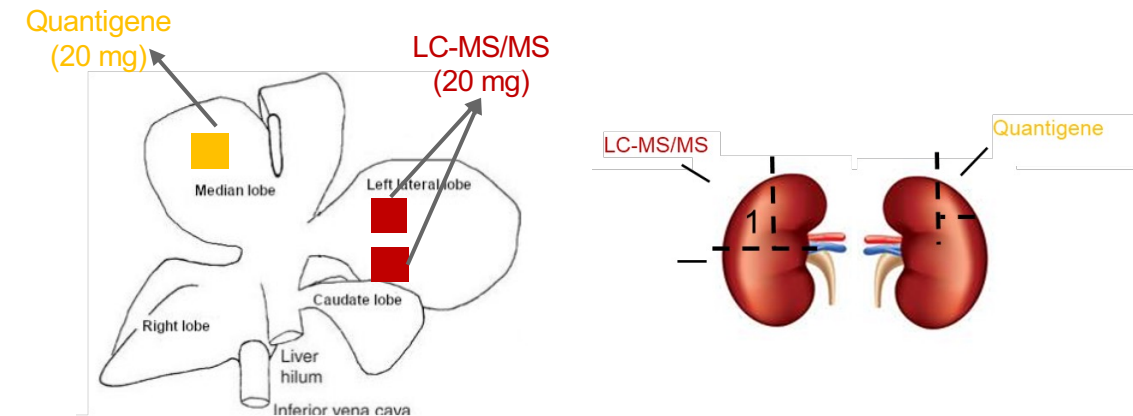
- Timepoints: 7 and 14 days post-administration
- Blood sampling
- Organ collection: : liver, kidneys

Quantification of the ASOs by:

- QuantiGene
- LC-MS/MS



ASO	Length	Chemistry
MM1	16 nt	LNA-Gapmers (3 LNA at each end) and full PS backbone
MM2	20 nt	
MM5	16 nt	



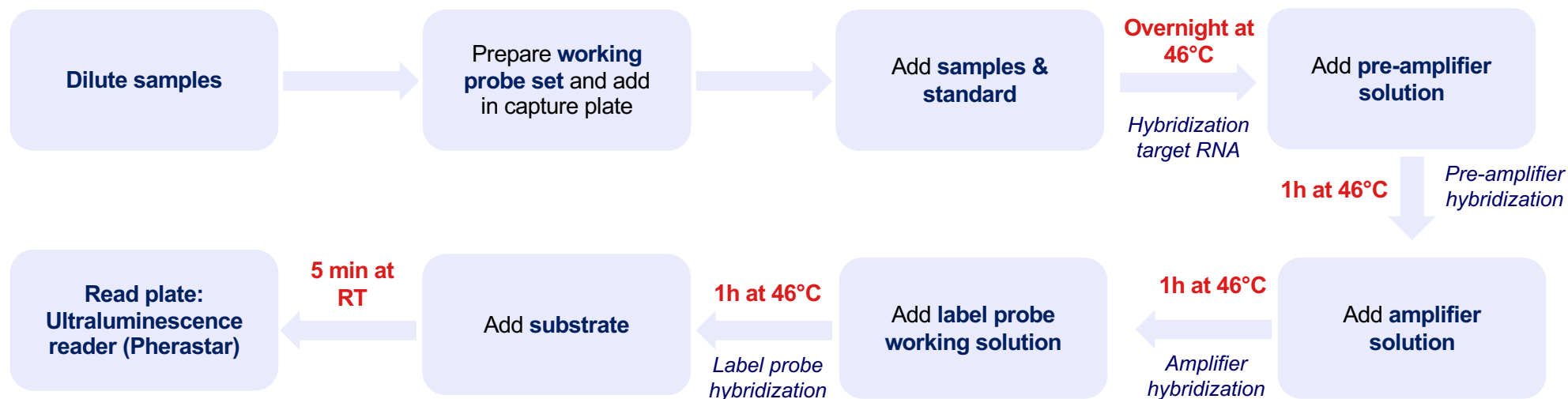


# *Development of the QuantiGene methods*

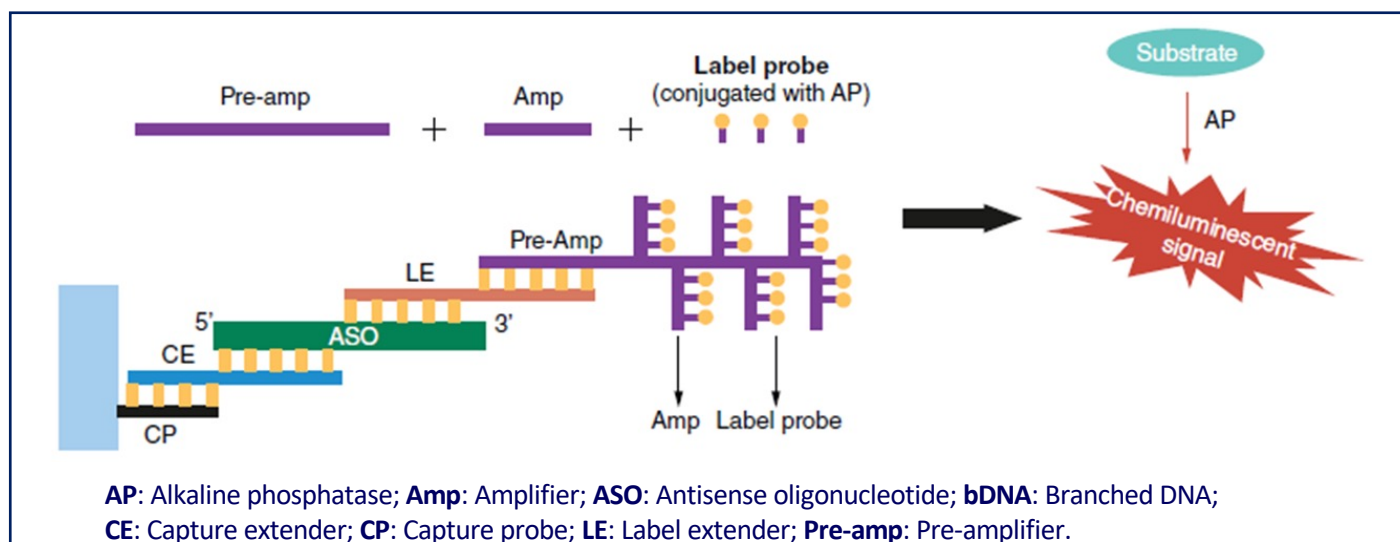


# QuantiGene Kit

## Optimized protocol - Assay



Use of “QuantiGene™ Singleplex assay kit”, but protocol from “QuantiGene® 2.0 miRNA Assay”





# Development of the QuantiGene methods

## Matrix effect and dilution linearity

### 1) Definition of the MRD

- Standard curves in buffer (PBS), plasma, liver homogenate and kidney homogenate
- Comparison of the blank signal and the SNR
- Test of few samples at different dilutions



For the 3 ASOs, preparation of a standard curve:

- in mouse plasma 1/10
- in tissue homogenate 1/100

### 2) Possibility to use a pool (50/50) of « liver – kidney homogenate »

Comparison of the concentration obtained with a calibration curve prepared in liver homogenate or in kidney homogenate

### 3) Dilution linearity

- Up to 1/10 000 for plasma samples
- Up to 1/250 000 for liver and kidney samples

MM1 - Analysis of liver samples with calibration curve in kidney				
Sample ID	Dilution	Concentration with the calibration curve in liver (ng/mL)	Concentration with the calibration curve in kidney (ng/mL)	%Difference
#14-D7	100	164	142	-14
#12-D14	100	16	13	-19

MM1 - Analysis of kidney samples with calibration curve in liver				
Sample ID	Dilution	Concentration with the calibration curve in kidney (ng/mL)	Concentration with the calibration curve in liver (ng/mL)	%Difference
#14-D7	100	173	199	14
#12-D14	100	214	245	14

MM5 - Kidney samples			
Sample ID	Dilution	Final concentration (µg/mL)	Accuracy (%RE) versus smallest dilution
#55 – D7	25 000	4.44	N/A
	50 000	4.67	5
	100 000	4.76	7
	250 000	5.00	13
#51 – D7	50 000	7.87	N/A
	100 000	8.55	9
	250 000	8.31	6



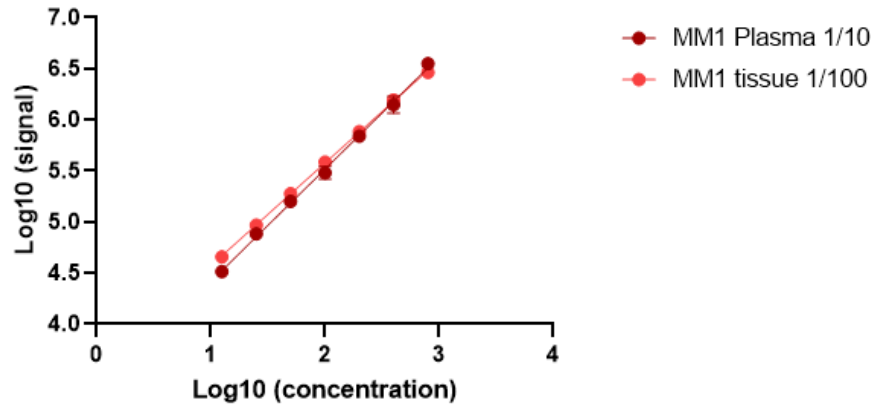
# Development of the QuantiGene methods

## Qualification of the methods

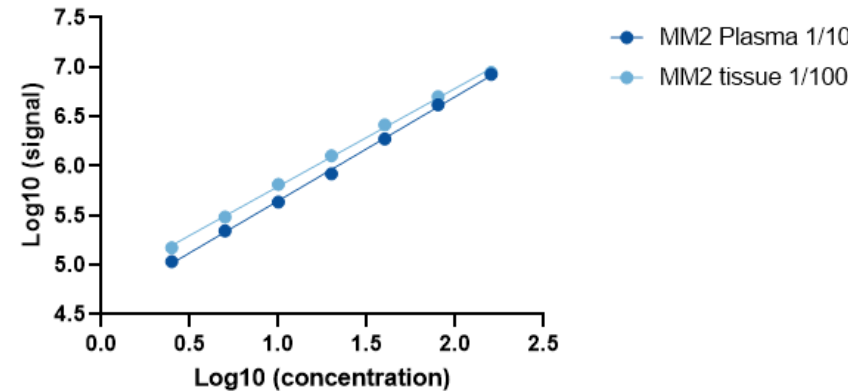
For discovery purpose

- Based on the criteria described in the EMA and FDA bioanalytical guidelines but criteria may be slightly adapted
- Standard curve and QCs (LLOQ, low QC, mid QD, high QC, ULOQ)
- Evaluation of the precision and the accuracy

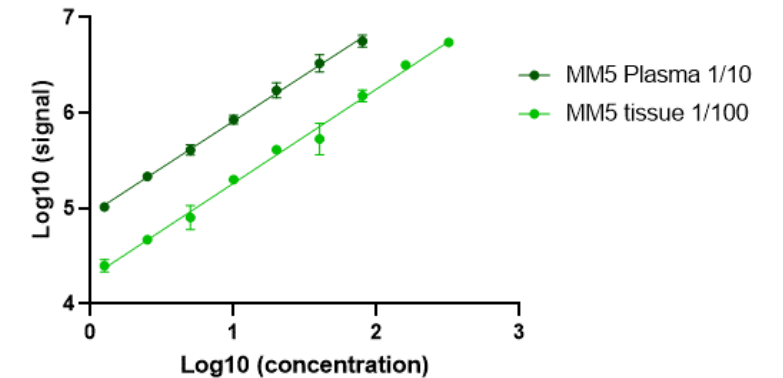
MM1



MM2



MM5



→ Calibration range for MM1 ASO in both matrices:

**Range: ~ 25 – 800 pg/mL**

→ QCs slightly more variable in plasma for lower concentrations

→ Calibration range for MM2 ASO in both matrices:

**Range: 2.50 - 160 pg/mL**

→ QCs slightly more variable in plasma for lower concentrations

→ Calibration range for MM5 in both matrices:

- **Plasma 1/10: ~ 1.25 - 80 pg/mL**
- **Tissue homogenate 1/100: ~ 1.25 - 320 pg/mL**

→ Inter-run variability with this ASO (high background signal with this probe)

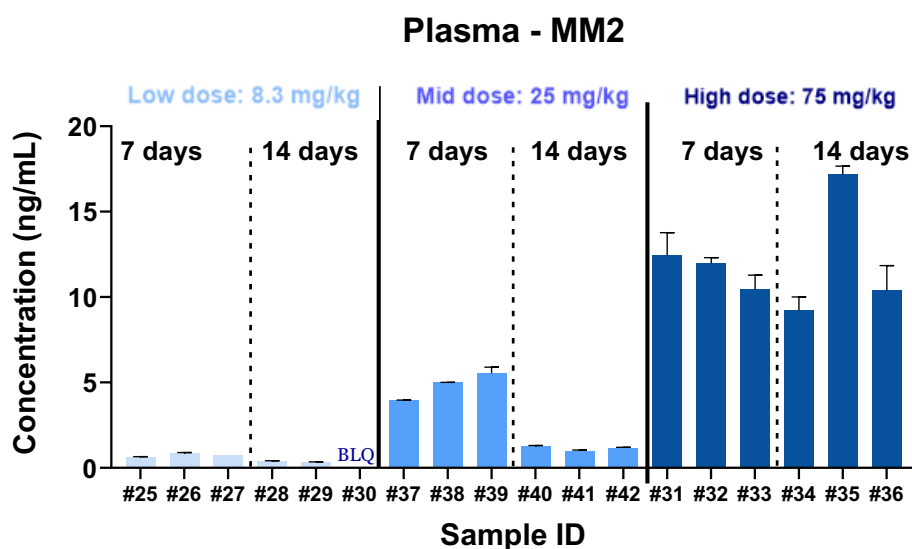
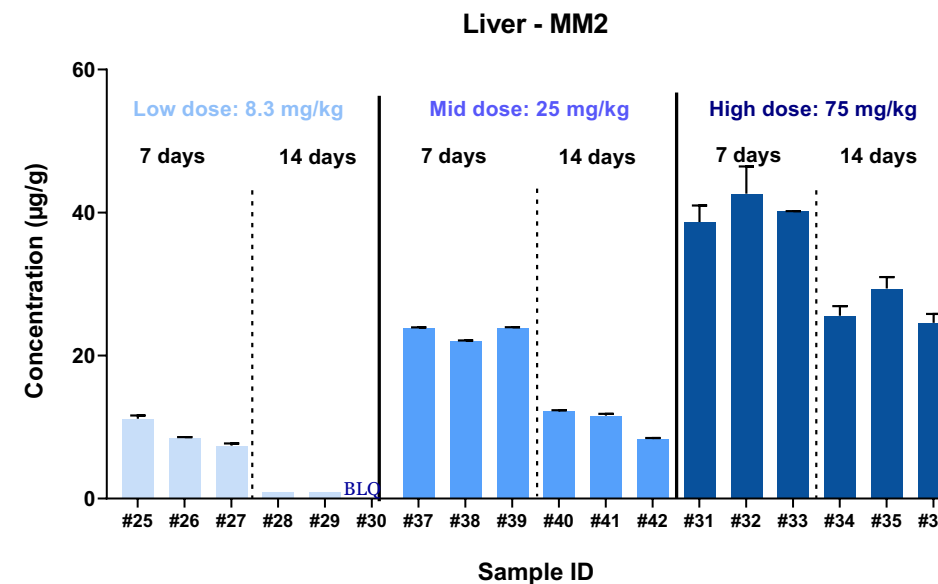
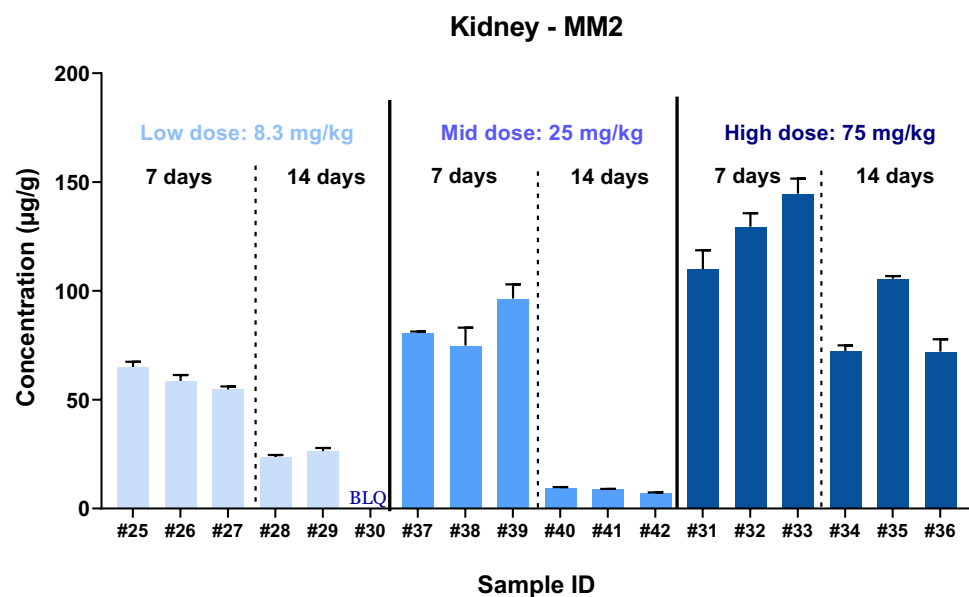


# *Sample analysis*



# Sample analysis with the QuantiGene technology

## Concentrations of the ASO MM2



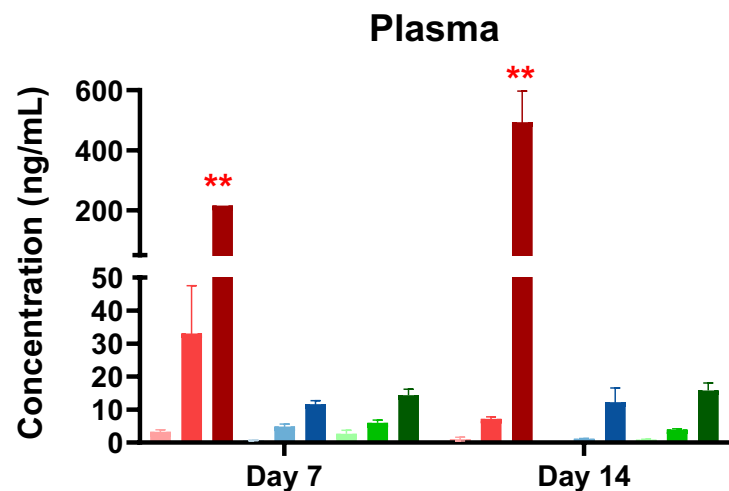
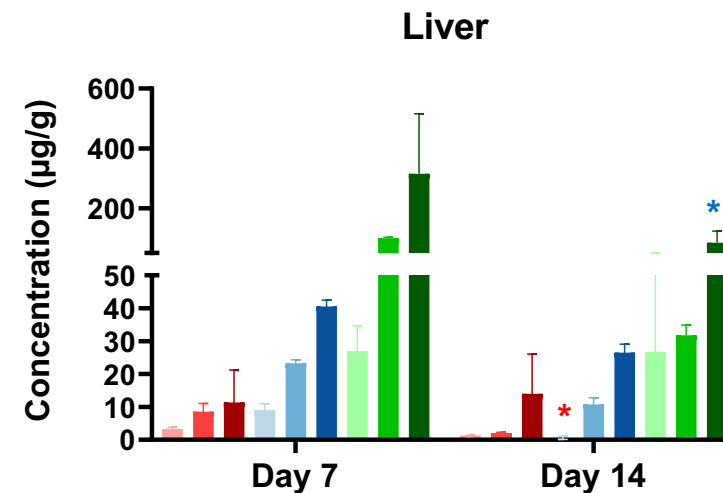
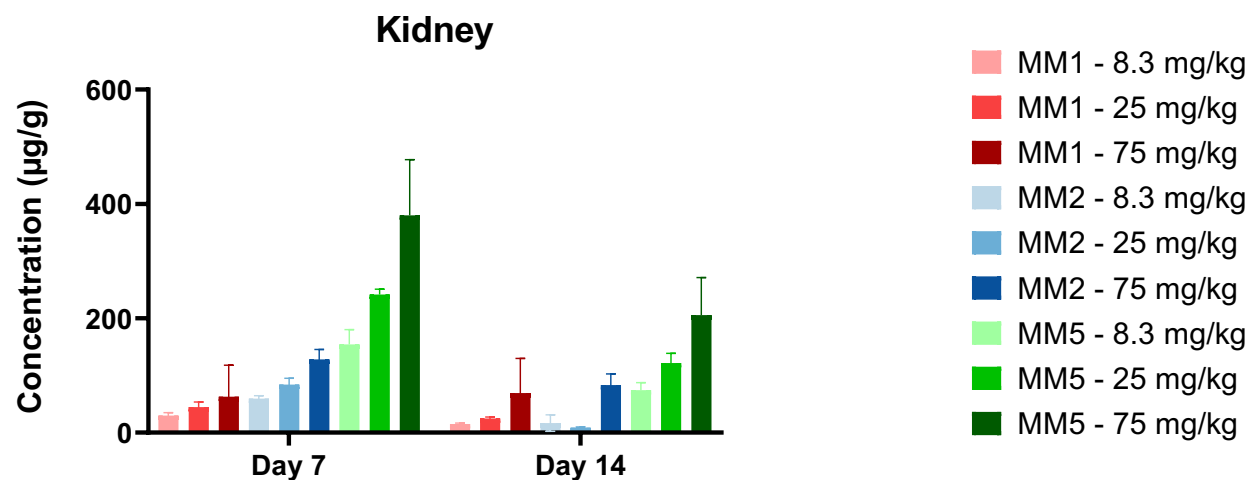
- All samples could be quantified except for the mouse #30
- Very low variability between technical replicates
- Kidney and liver: concentrations in the range of µg/g of tissue  
→ high dilution needed (up to 1/250 000)
- Plasma: concentration in the range of ng/mL
- Dose-dependent concentrations
- Time-dependent concentrations
- Low inter-animal variability





# Sample analysis with the QuantiGene technology

## Summary of the 3 ASOs



\* Data above ULOQ after dilution 1/100 for two samples (> 867 ng/mL)  
 \* Extrapolated data for one sample (<LLOQ of the run)

\*\* Data above ULOQ after dilution 1/250 (> 200 ng/mL)

- Dose-response observed for all ASOs in all matrices
- High exposure in kidneys and liver for the 3 ASOs
- Higher exposure for MM5 ASO in solid tissues
- High MM1 level in plasma observed, especially at higher dose:  
 → Hepatic cell lysis? Clear colored spotted liver for samples from this group; ↑ ALT & AST



***Method comparison:  
QuantiGene vs LC-MS/MS***



# Method comparison: QuantiGene vs LC-MS/MS

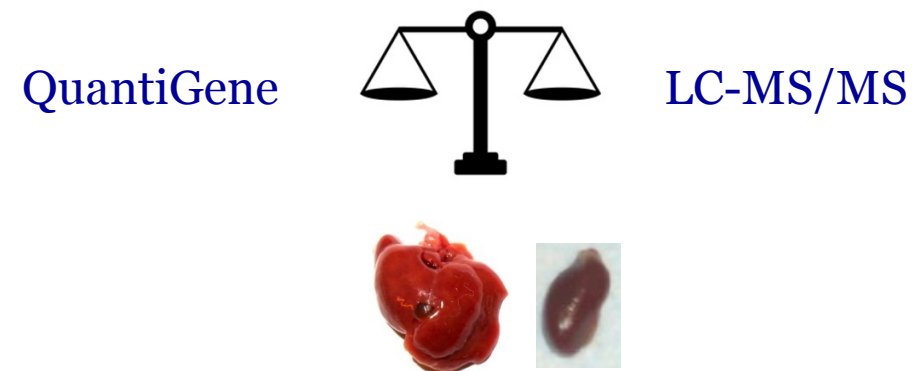
LC-MS/MS conditions – Generic method

UPLC Conditions	
<b>Instrument</b>	Agilent 1290 Bio
<b>Phase A:</b>	water 0.02%DPA, 0.1% HIFP
<b>Phase B:</b>	acetonitrile/MeOH (75/25)
<b>Column:</b>	Acquity™ Premier Oligonucleotide BEH C18 2.1X50; 130A, 1.7um
<b>Column Temperature:</b>	50 °C
<b>Flow rate</b>	0.7 mL/min
<b>Injection Volume</b>	5 µL



Gradient profile	
Time (min)	%B
0	1
1.1	30
1.2	80
1.4	80
1.6	1
2.2	1

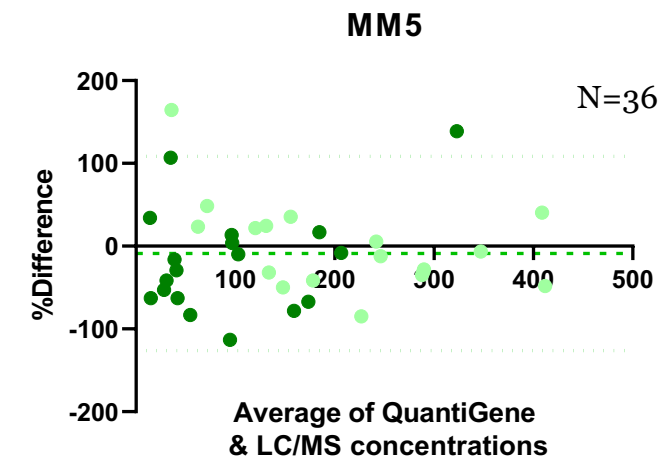
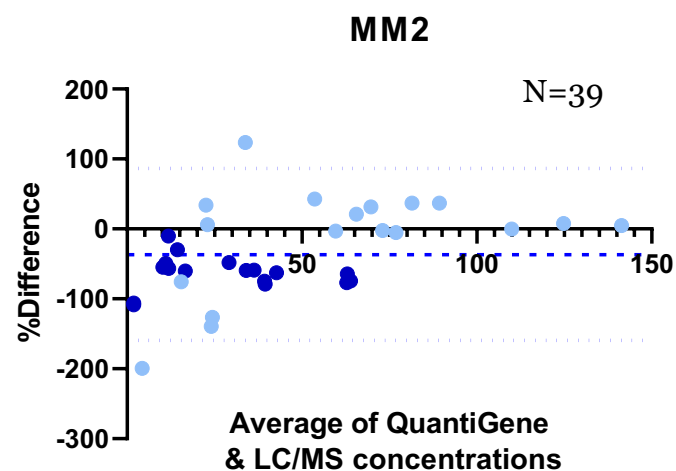
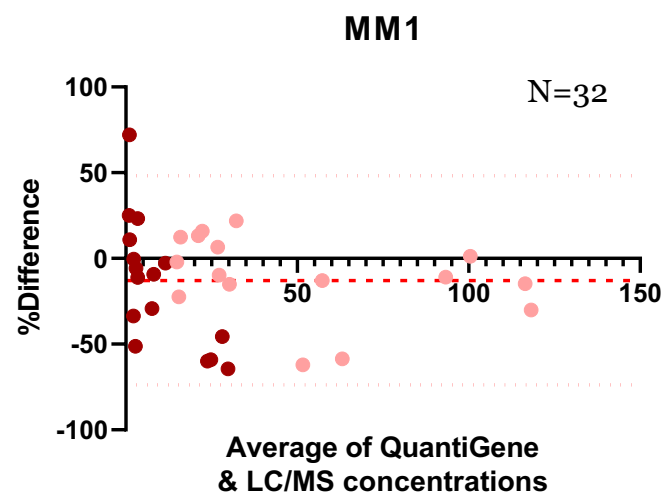
Mass Spec Conditions	
<b>Instrument</b>	Sciex API 6500+
<b>Ionization</b>	TIS
<b>Temperature</b>	550 °C
<b>Mrm for MM1</b>	658.5>95.00
<b>Mrm for MM2</b>	733.2>95.00
<b>Mrm for MM5</b>	660.5>95.00
MM2 and MM5 used as internal standard for MM1/MM5 and MM2, respectively	





# Method comparison: QuantiGene vs LC-MS/MS

Bland Altman: % difference vs average



<b>MM1: QuantiGene – LC-MS/MS</b>	
Average of bias	-13 %
SD of bias	31 %
95% Limits of Agreement	
From	-74 %
To	48 %

<b>MM2: QuantiGene – LC-MS/MS</b>	
Average of bias	-37 %
SD of bias	63 %
95% Limits of Agreement	
From	-160 %
To	86 %

<b>MM5: QuantiGene – LC-MS/MS</b>	
Average of bias	-9 %
SD of bias	60 %
95% Limits of Agreement	
From	-126 %
To	108 %

- Fold change < 2 for the majority of samples → **acceptable for discovery purpose** (especially regarding the very high dilutions applied)
- Comparable at high concentrations; QuantiGene slightly lower than LC-MS/MS especially for liver samples
- Note: samples were not exactly collected from the same area (liver: different lobes)



# Method comparison: QuantiGene vs LC-MS/MS

## Pros & Cons

Parameter	QuantiGene	LC-MS/MS
<b>Sensitivity</b>	Probe-dependent and matrix dependent About 50 pg/mL in plasma About 500 - 1000 pg/g in solid tissue	Matrix dependent About 150 ng/g in tissue
<b>Specificity</b>	Dependent on the design of the probes, may recognize the parent and some metabolites	High selectivity: possibility to distinguish parent and metabolites
<b>Dynamic range</b>	Medium; 2 orders of magnitude (Hook effect at high concentration)	Wide (3 orders of magnitude)
<b>Applicability</b>	ASOs shorter than 16 nt → potential difficulties for optimal binding	Better with ASOs < 40 nt
<b>Time of development</b>	3 weeks per ASO + delay due to probe design	1 week per ASO
<b>Price</b>	High (about 1200 € per 96-well plate)	Low
<b>General comment</b>	Method is <b>highly dependent on the design of the probe</b> by ThermoFisher	<b>Generic method</b> with minor fine tuning applicable



# *Conclusion & Perspectives*



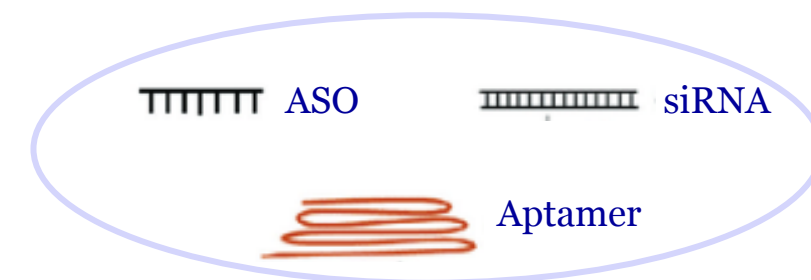
## Conclusion & Perspectives

- The QuantiGene technology can be used to quantify ASOs in different matrices
- It can be used for LNA-PS –ASOs (>16nt)
- Results obtained in the current study showed comparable data between the QuantiGene and the LC-MS/MS technologies (for discovery purpose)
- The QuantiGene technology is highly sensitive (may be useful to quantify very low concentrations) but not specific (parent and truncated metabolites)
- Development of method with the QuantiGene technology is more expensive and time-consuming than with the LC-MS/MS technology

➔ **QuantiGene technology may be used as an alternative of LC-MS/MS** in case of technical issues with LC-MS/MS (administration of a low dose; use of a non-intravenous route)

### Continue to explore the capabilities of the QuantiGene technology

- Test other biological matrices (brain tissue)
- Test ASOs with different chemical modifications (MOEs)
- Test other oligonucleotide-based modalities (siRNA, aptamers...)





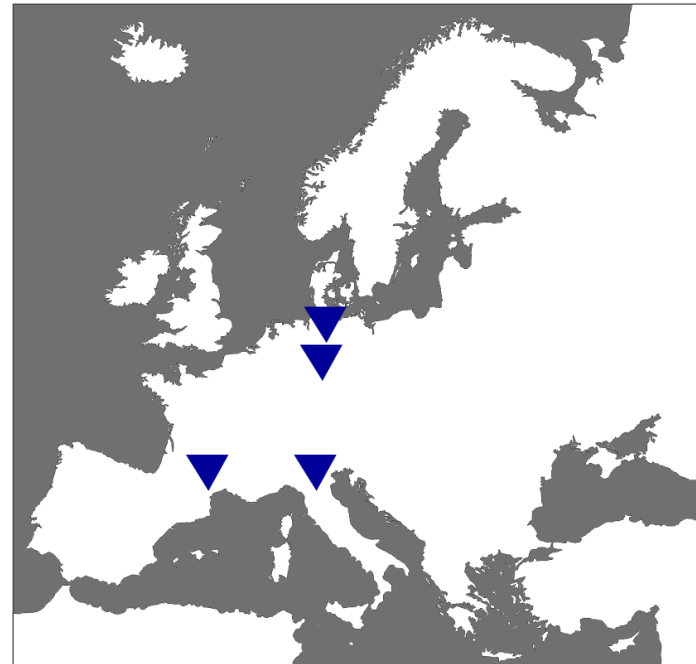
# Acknowledgements

## *A collaborative effort*

Toulouse (France)



- **Estelle Cochet**
- Flore Grandin
- Laurie Joucla
- Hermine Gandon
- Déborah Delpéuch
- Hilary Brooks



Hamburg (Germany)



- Yalda Sedaghat

Göttingen (Germany)



- Elisabetta De Filippo

Verona (Italy)



- **Marco Michi**
- Annalisa Mercuri



QUESTIONS  
AND ANSWERS

