

# Next generation metabolic screening (NGMS): application of metabolomics for diagnosis of inborn errors of metabolism

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*ERNDIM Workshop – 22-11-2017 – Manchester, UK*

# Biochemical diagnostics in IEM screening in 2017:





QTOF Experiment  
ESI Pos+Neg

Raw Data  
Processing



Raw Data

Analytical QC  
Check

XCMS Alignment



Sample	Retention Time	Abundance	Mass	Identified Compound
1	1.23	1000	100.05	Glucose
1	1.45	500	150.07	Fructose
1	1.67	200	200.09	Sucrose
1	1.89	100	250.11	Lactose
1	2.11	50	300.13	Maltose
1	2.33	20	350.15	Galactose
1	2.55	10	400.17	Mannose
1	2.77	5	450.19	Ribose
1	2.99	2	500.21	Arabinose
1	3.21	1	550.23	Xylose

10,000-15,000 features/sample

# NGMS workflow

Data  
Analysis

HMDB-based  
Annotation

Statistical  
Testing



Data  
Interpretation

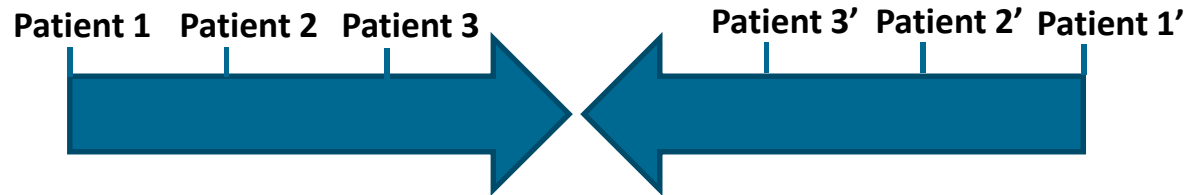
Data Filtering

Data Processing  
QC Check

Interpretation

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# NGMS workflow: run and internal QC



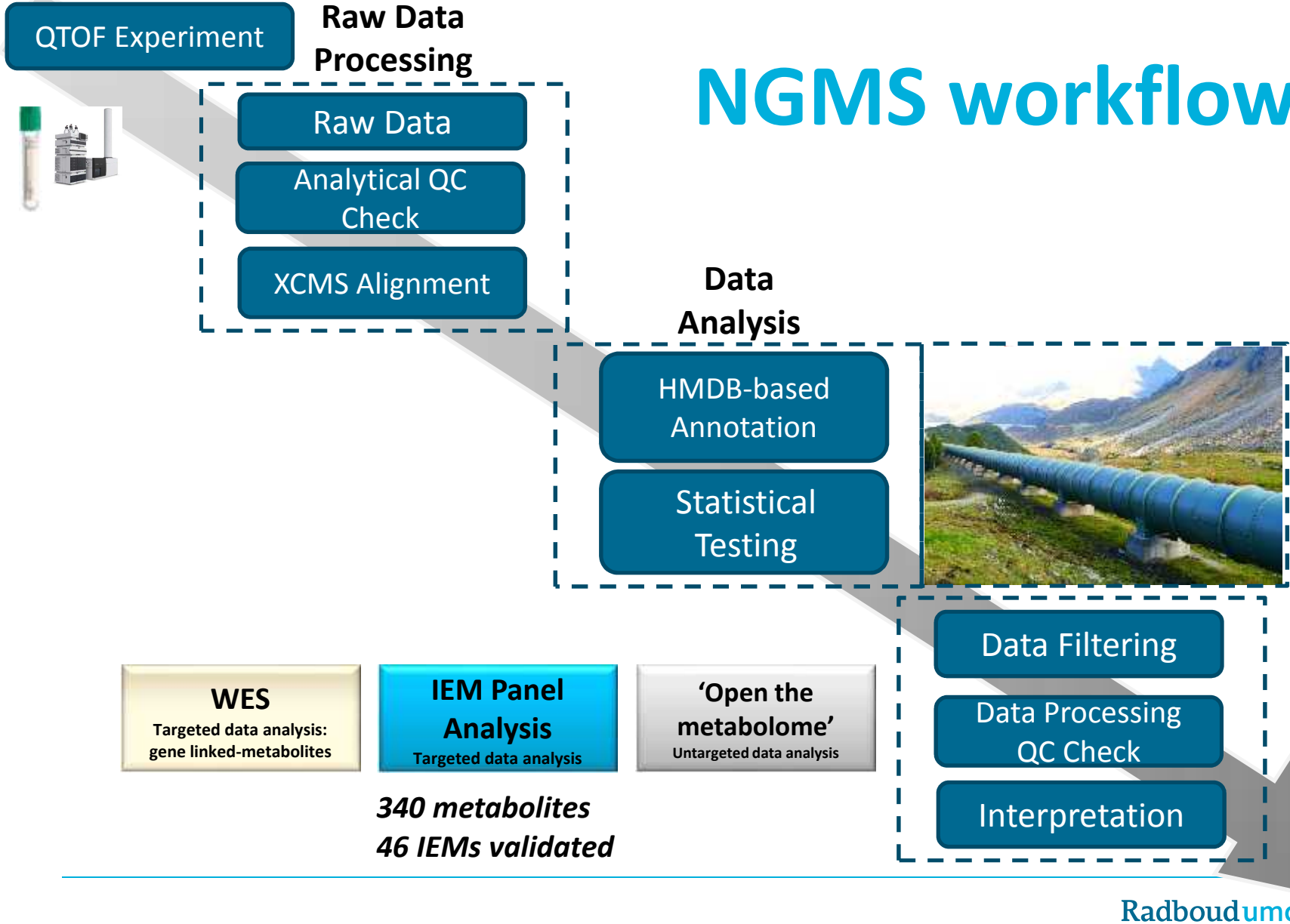
- Patient/control plasma samples in duplo in anti-parallel run order
- Performance check solution: 10(-)/11(+) standards in water, 7x/run
- Analytical QC plasma pool: pooled sample of 800 non-IEM controls, 27(-)/21(+) endogenous metabolites , 7x/run
- Analytical QC check on non-processed, unaligned data by targeted extraction of features
- ESI-mode specific sets of metabolites evaluated on retention time, intensity and mass accuracy

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# QTOF analytical performance

- Performance check solution:
  - CVs:**
    - RT<2 min: max 1% within run, 2% between-run
    - RT>2 min: max 0.5% within run, 1% between-run
    - Intensity: max 15% within run (median 30% between-run)
    - Mass accuracy: max 5 ppm error
- Analytical QC plasma pool:
  - CVs:**
    - RT<2 min: max 1% within run, 2% between-run
    - RT>2 min: max 0.5% within run, 1% between-run
    - Intensity: max 20% within run (median 30% between-run)
    - Mass accuracy: max 5 ppm error

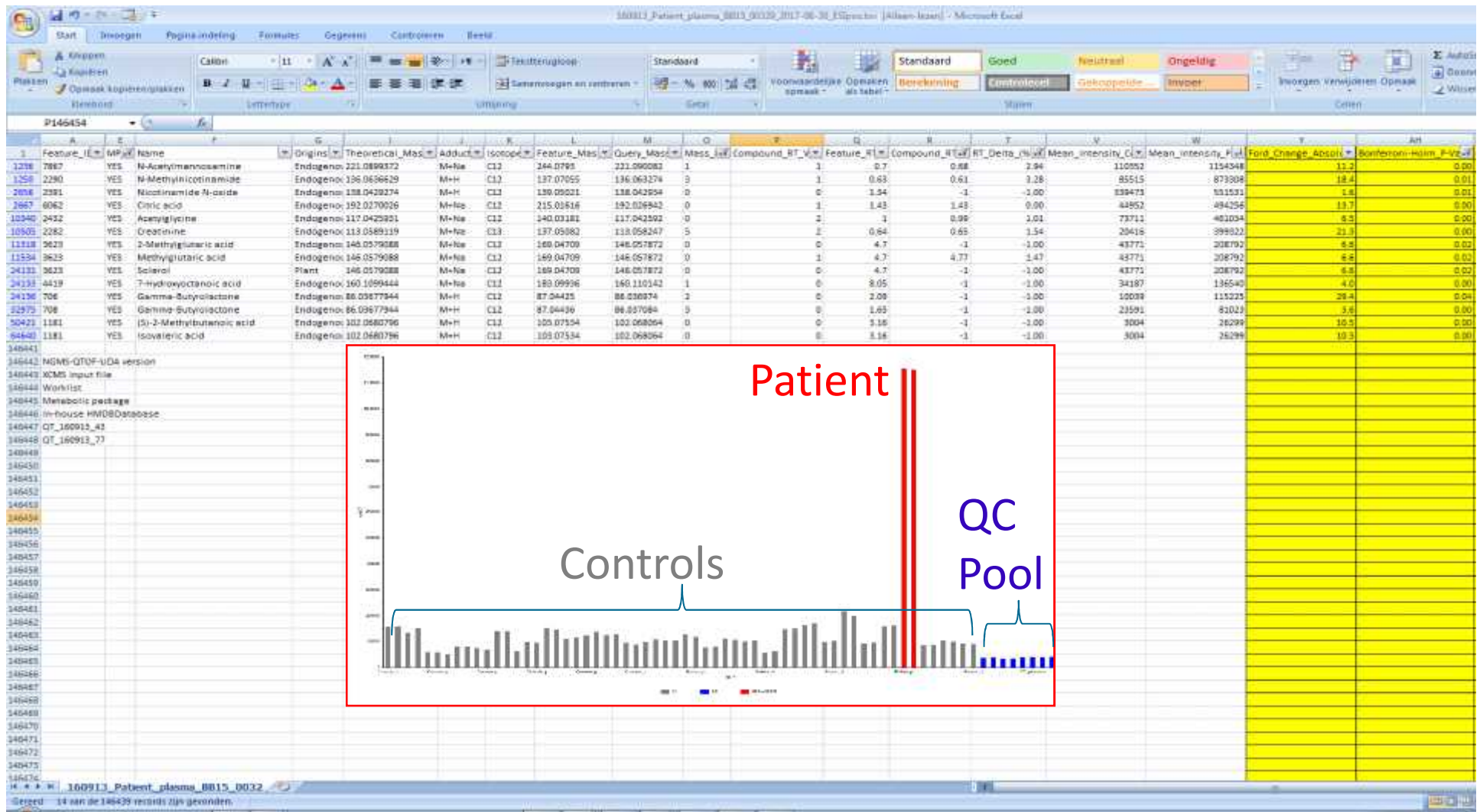
# NGMS workflow





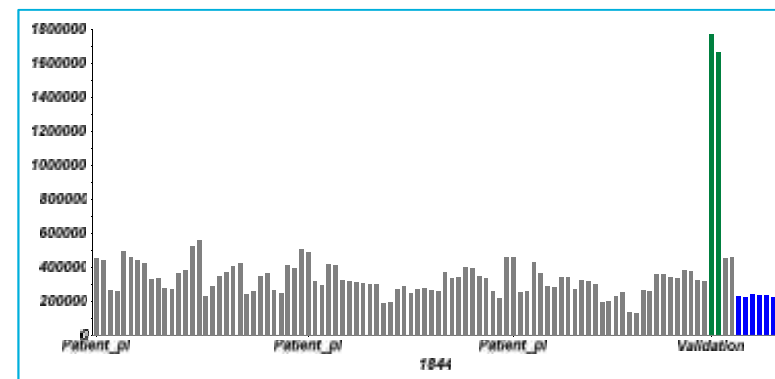
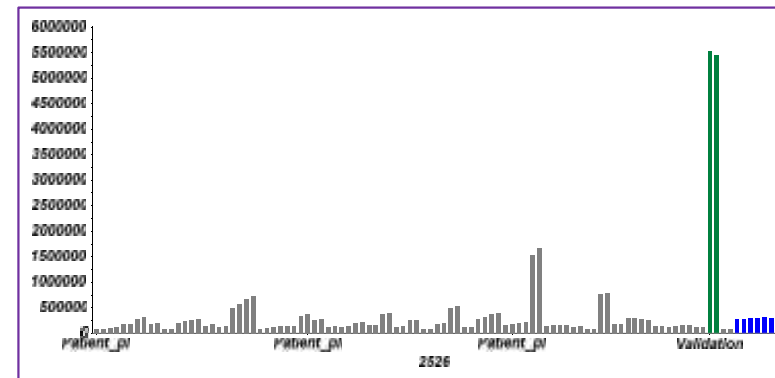


# NGMS output file - IEM panel



# NGMS workflow – Data processing QC

Name	Theoretical Mass	-M	Feature RT ESI+	Feature RT ESI-
Dihydrouracil	114.0429274	161	1.05	1.07
Glutamylphenylalanine	294.1215717	198	5.81	5.54
Palmitoylcarnitine	399.3348589	136	14.57	14.68
Phenylalanine	165.0789786	393	3.56	3.35
Tyrosine	181.0738932	494	2.03	1.64
N-Acetyl-mannosamine	221.0899372	482	0.71	0.68
Ornithine	132.0898776	581	0.49	0.78
<b>Pimelic acid</b>	160.0735589	395	6.34	6.35
<b>Xanthine</b>	152.0334254	198	1.95	2.03
Mesaconic acid	130.02661	284	ND	2.25



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## Clinical validation of IEM panel strategy:

46 IEMs, including:

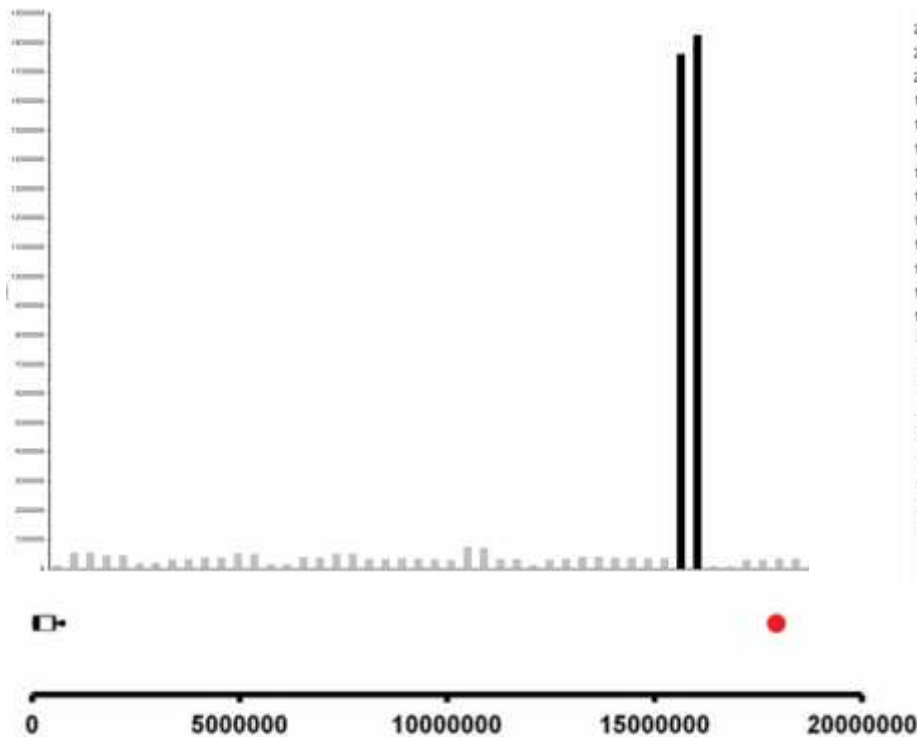
- MSUD, IVA, PA, MMA (*Amino acids, organic acids*)
- MCAD, VLCAD, LCHAD (*Acylcarnitines*)
- PKU, Tyrosinemia (*Amino acids*)
- Xanthinuria I vs II (*Purines/pyrimidines*)
- Molybdenum cofactor deficiency (*Purines/pyrimidines*)
- CTX (*Bile alcohols*)
- Refsum disease (*Very long chain fatty acids*)

*(Coene et al. Revisions submitted to JIMD 4-11-17)*

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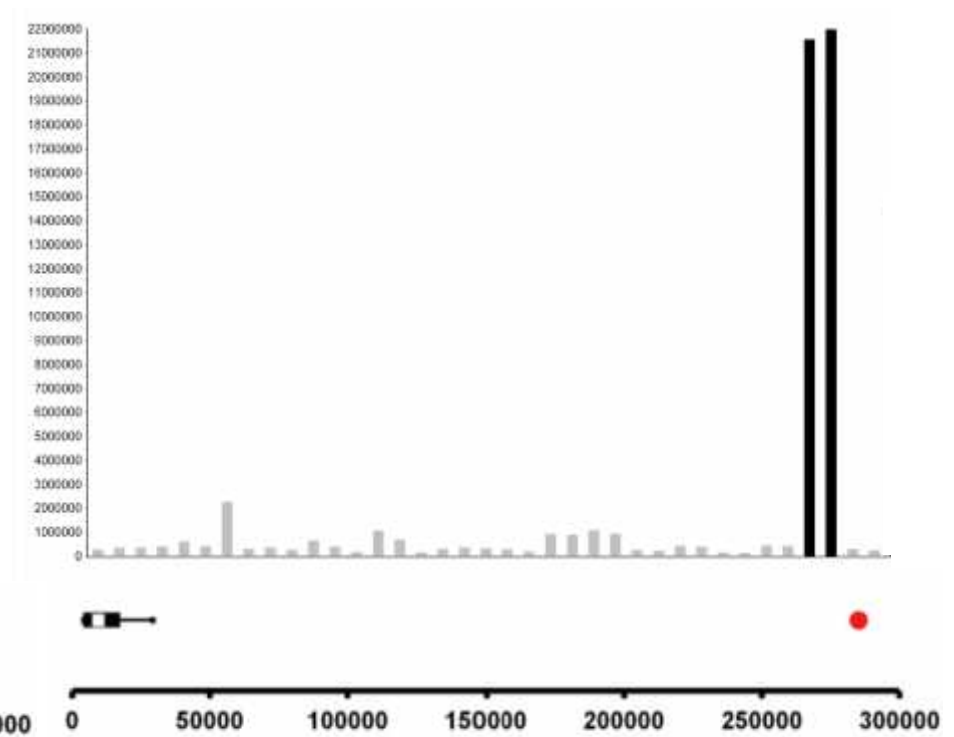
# Examples of NGMS clinical validation:

**MCAD: C8-carnitine**



Fold change 53x

**HMGCLD: C5-OH-carnitine**

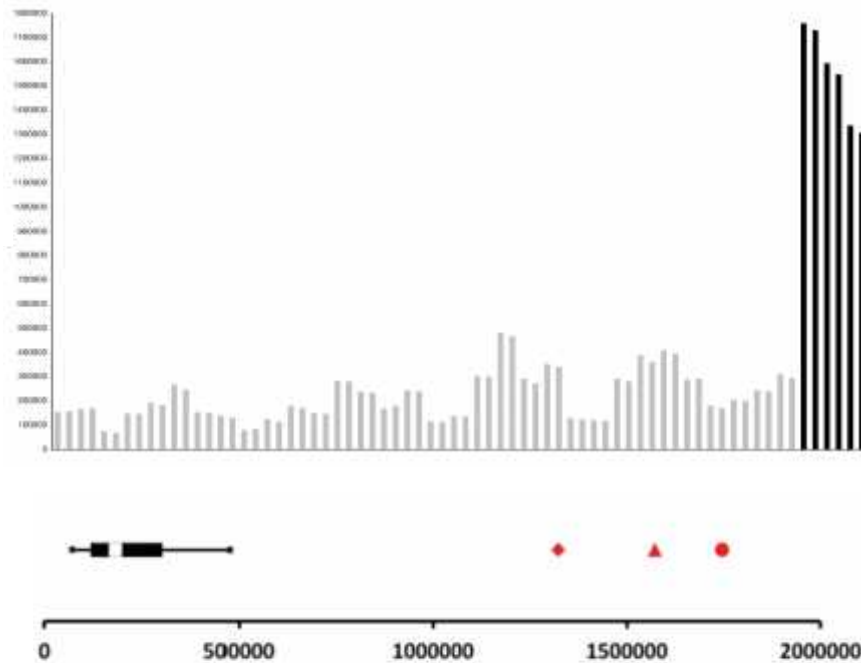


Fold change 28x

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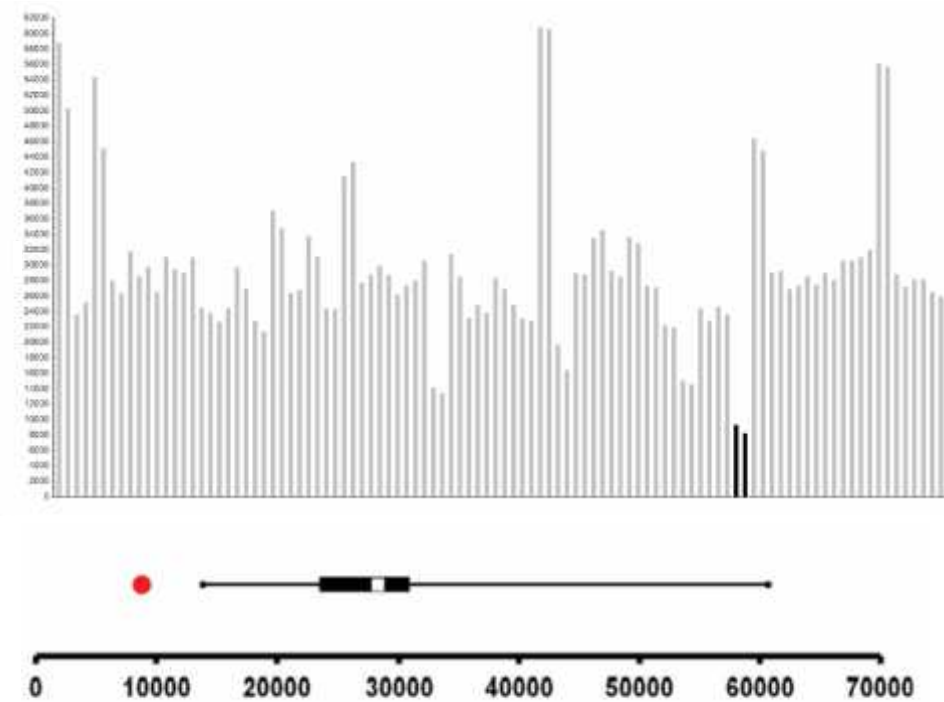
# Examples of NGMS clinical validation:

**OAT: Ornithine**



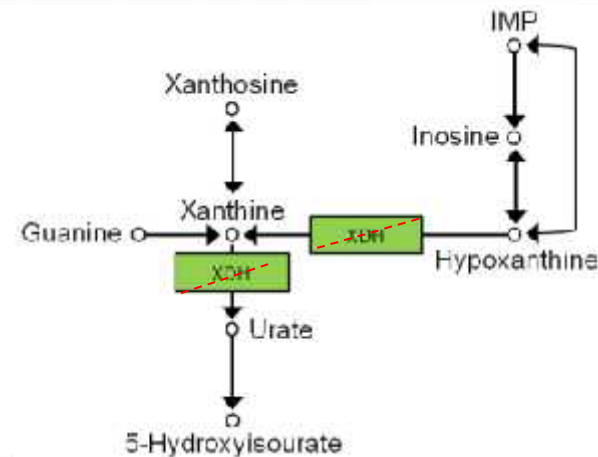
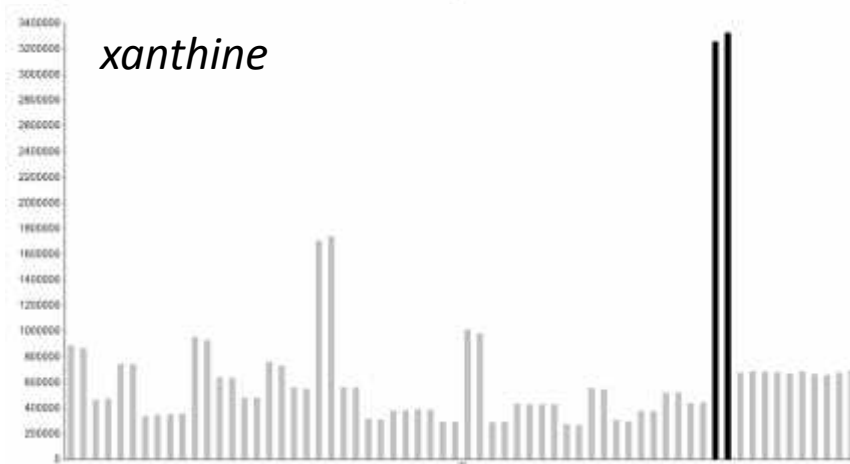
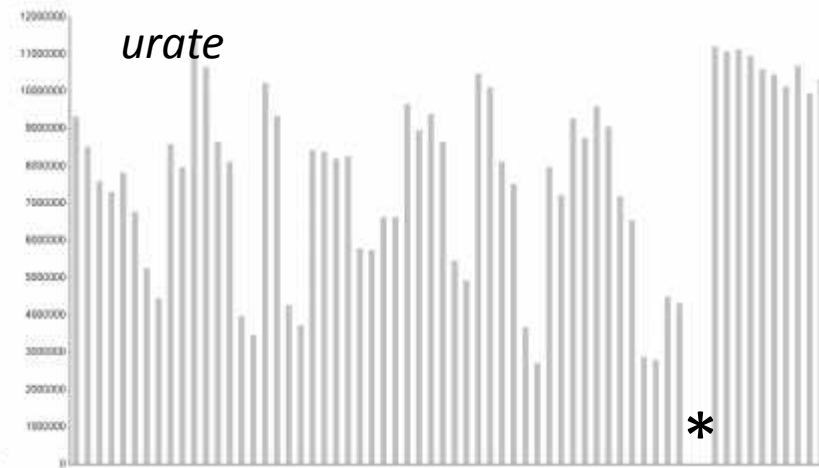
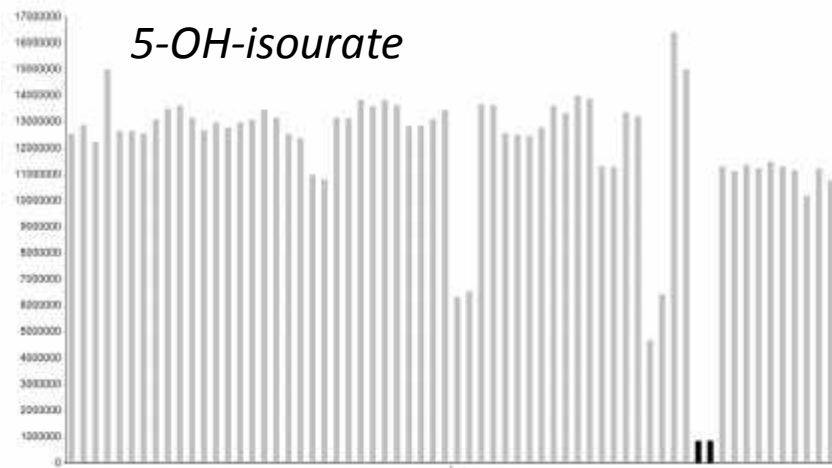
Fold change 7x

**LPI: Lysine**

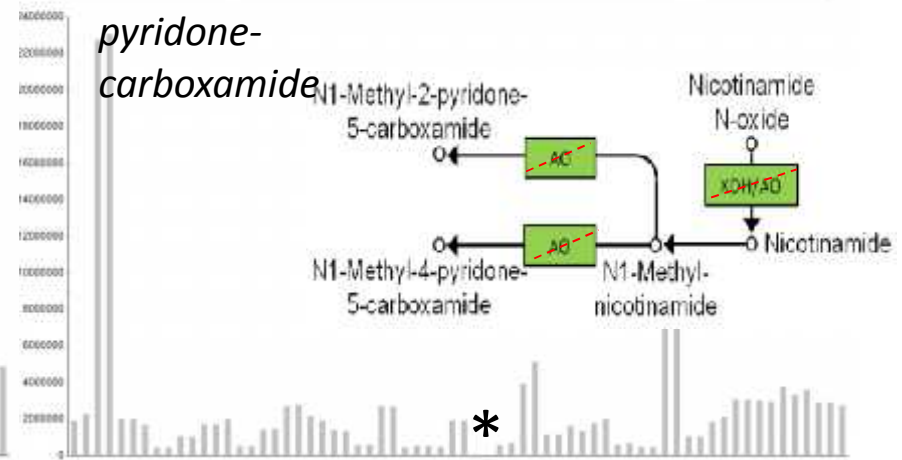
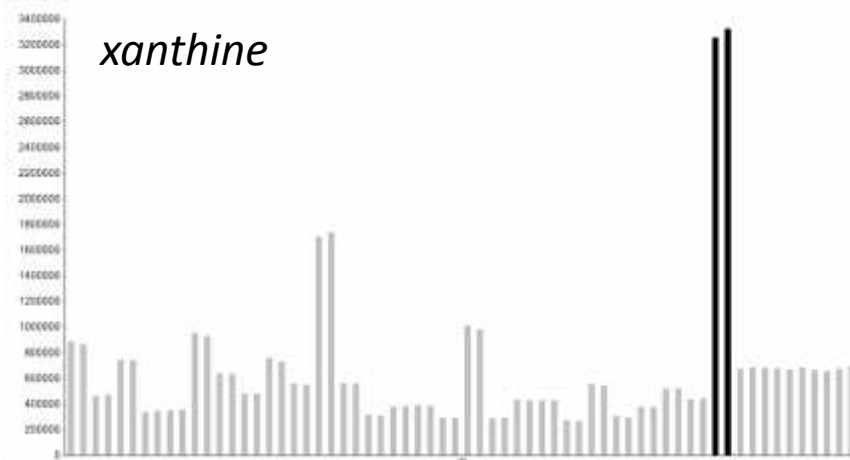
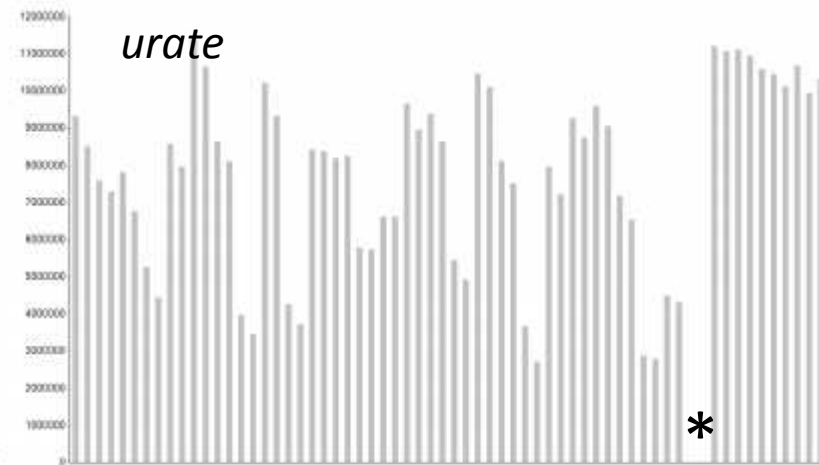
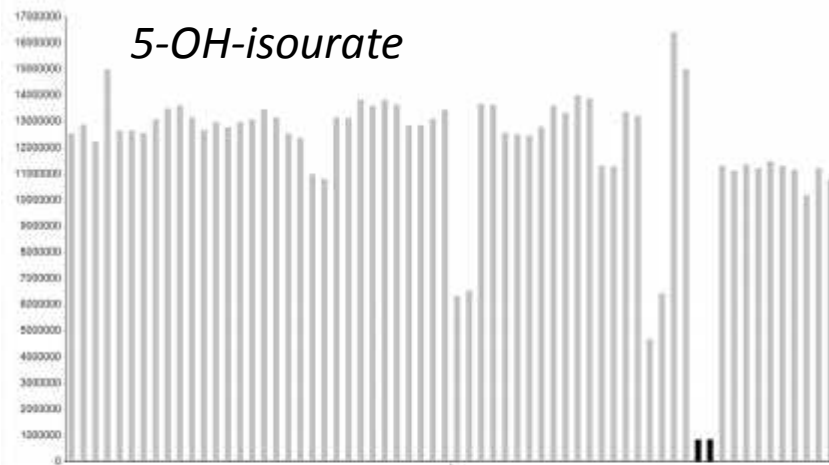


Fold change -3x

# Examples of NGMS clinical validation: Xanthinuria type I vs II?

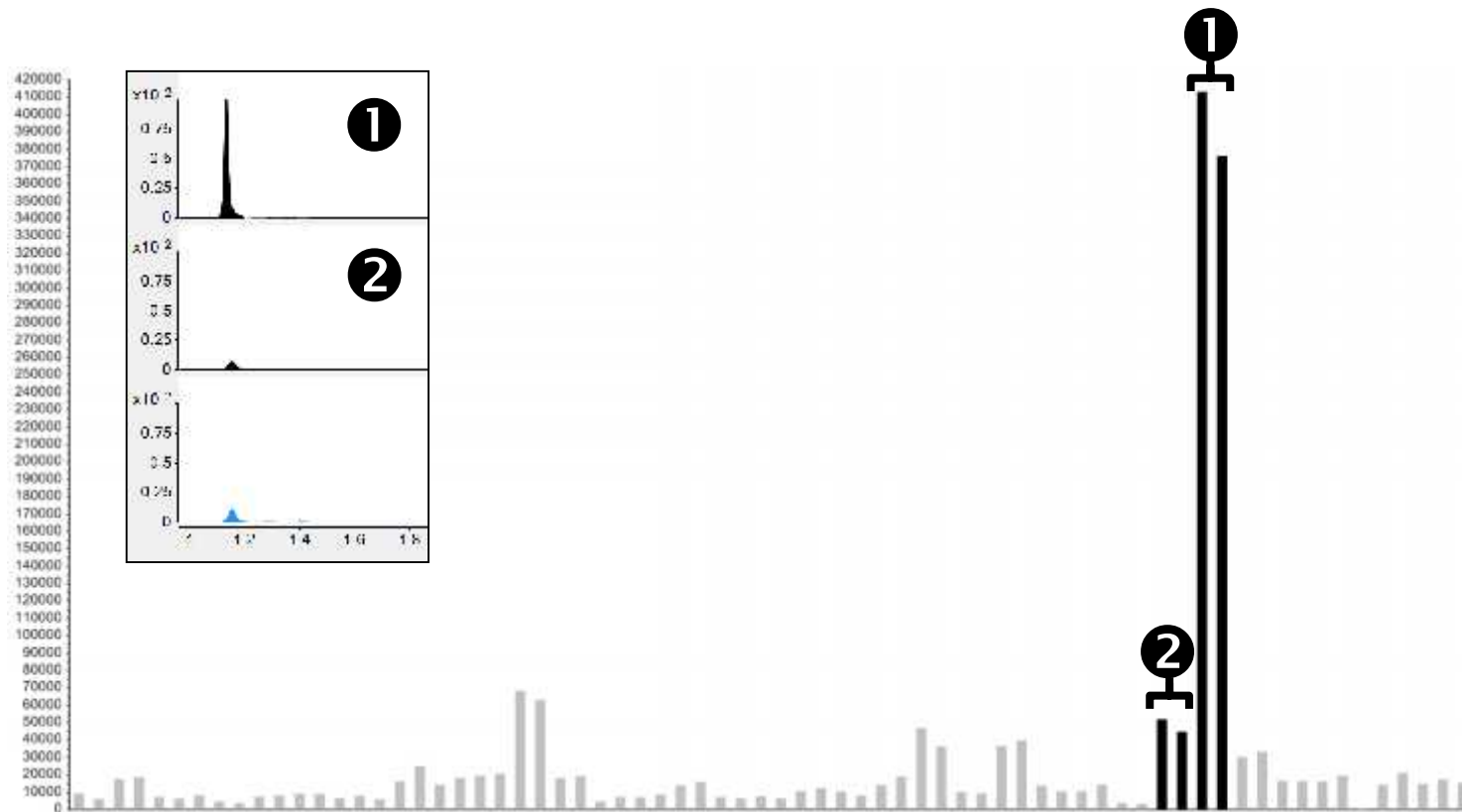


# Examples of NGMS clinical validation: Xanthinuria type II!



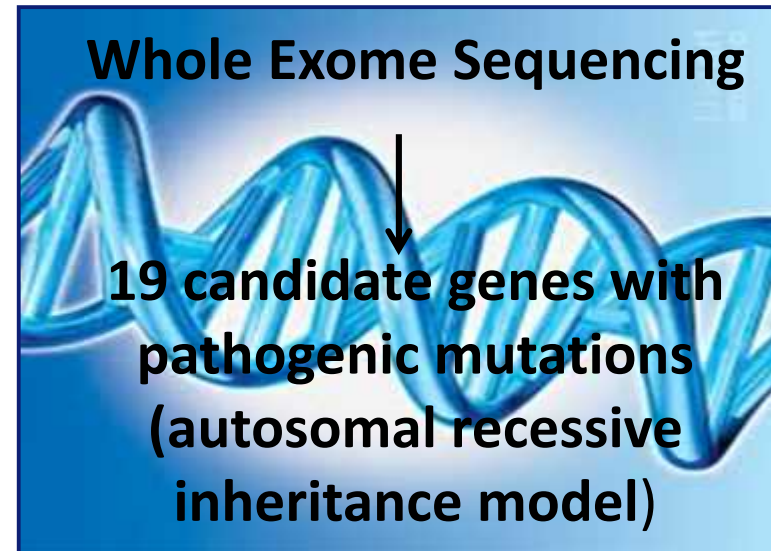
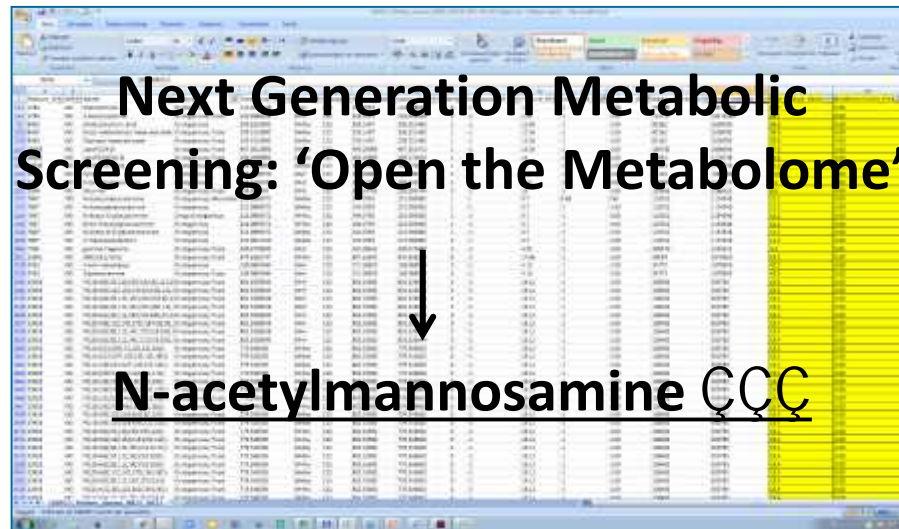
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# Integration IEM panel with WES results: VUS in *ASPA*, Canavan disease?





# Integration 'Open the Metabolome' with WES results: candidate gene



One matching gene: **NANS**

# NANS deficiency: the first novel IEM discovered through NGMS



Published online, May 23<sup>rd</sup>, 2016



NRC Handelsblad, Wetenschapsbijlage, 4 juni 2016



**Nijmegen Translational Metabolic Laboratory:**  
*Building bridges towards the diagnostic laboratory of the future*

**Metabolomics - NGMS**

**Genetics Lab**

**WES / WGS**

**Glycomics**

**Functional genomics**

**ERDNIM EQAS**

**Glycopeptidomics**

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# NGMS – External Quality Control

- **Currently:**  
3 blinded diagnostic and non-IEM plasma samples included each run (alternative for EQC)  
→ No ERNDIM DPT plasma samples available
- **Near future:**  
Exchange of blinded diagnostic and non-IEM plasma samples with MUMC
- **Future perspectives:**
  - Small scale plasma DPT?
  - Spiked plasma samples?
  - Data EQAS?



# Acknowledgements

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Marleen Huigen



Udo Engelke



Ron Wevers



Leo Kluijtmans



Clara van Karnebeek

David Wishart



Jasper Engel



Thatjana Gardeitchik

Han Brunner



Siebolt de Boer

Ed vd Heeft



Brechtje Hoegen

Christian Gilissen

