

Medical Delta Metabolomics XL Fieldlab for better treatments and healthcare

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Our Vision:

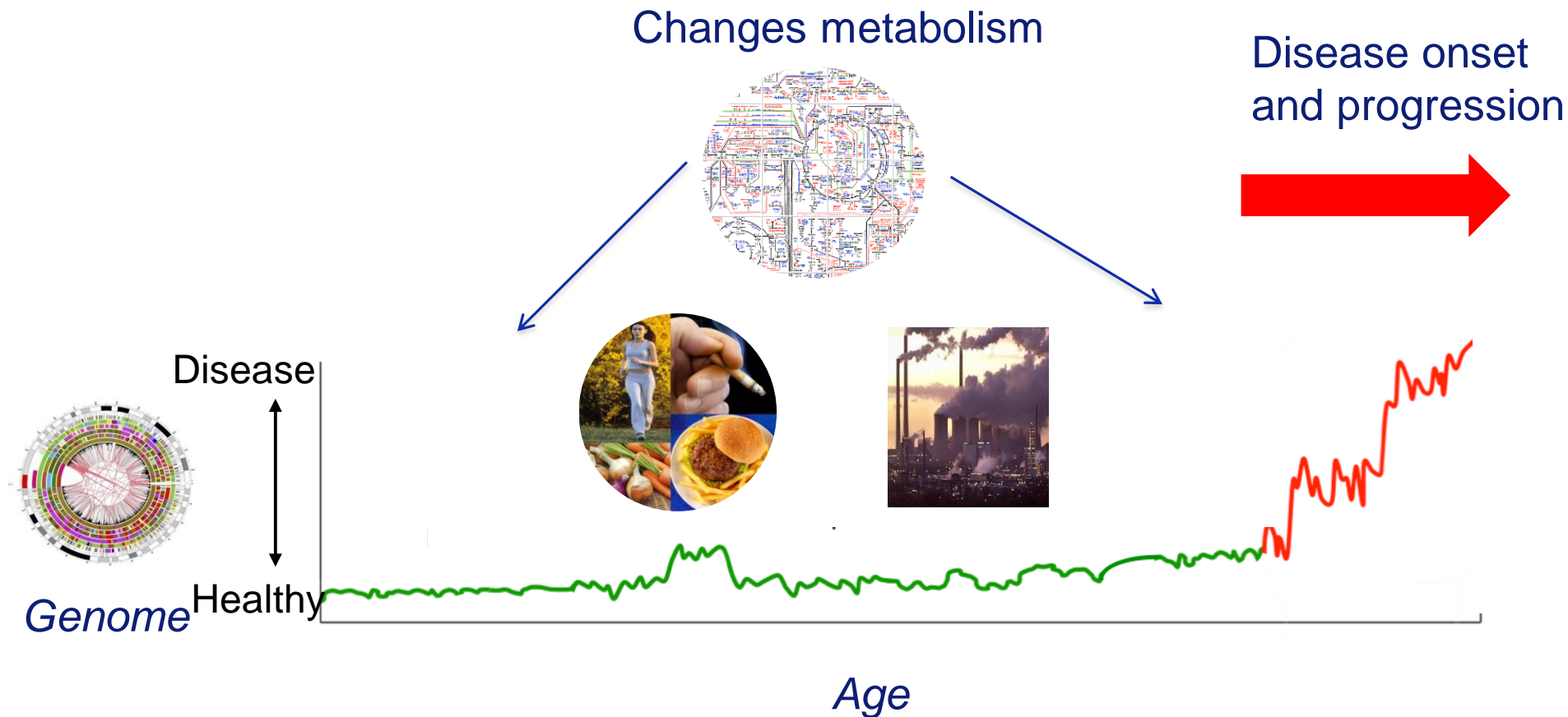
We accelerate
the application of metabolomics

in biomedical research
&
clinical application

for personalized health
&
precision medicine

Why Metabolomics?

Metabolomics allows the science-based measurement of your health state: it captures the interaction of the genome and environment (exposome)



Especially in elderly genome is less predictive!

Aim of Metabolomics XL field lab

We will develop novel products/ services together with SME's in strategic alliances to realize:

- Better and more specific prognosis and diagnosis of chronic diseases
- Patient stratification for more personalized therapeutics and prevention
- Identify new targets and to develop novel stratification strategies, including repurposing of drugs
- Novel prevention strategies
- Clinical assays with higher specificity

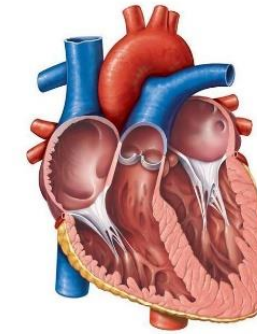
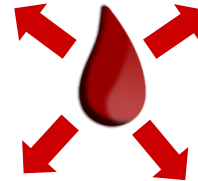


Examples of metabolic biomarkers of early disease pathways (pathways we have to modulate)



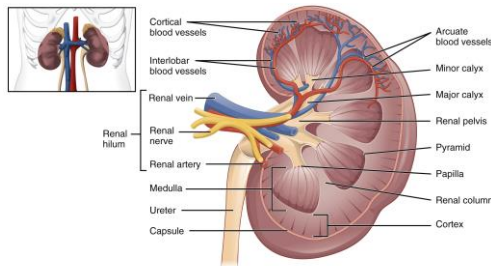
Early prediction of dementia

*Van der Lee et al (2018)
Alzheimers Dement. 14: 707 ff*



Prediction of sudden cardiac death

*Zhang YY et al, PLoS One
(2016) 11:e0157035*



Prediction of kidney failure

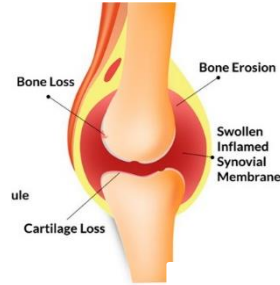
*Van der Kloet F et al (2012)
Metabolomics 8: 109ff*



Prediction of healthy aging

*Gonzalez-Covarrubias et al,
Aging Cell, 2013*

Metabolic biomarkers of prediction of treatment outcome (do drugs or nutrition modulate the right pathways?)

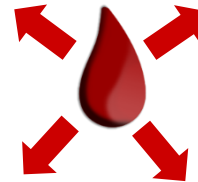


Prediction of response to rheumatoid arthritis drugs

Teitsma XM et al, Arthritis Res Ther (2018) 20: 230

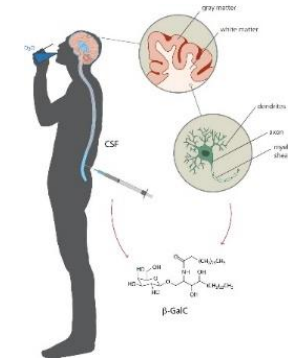
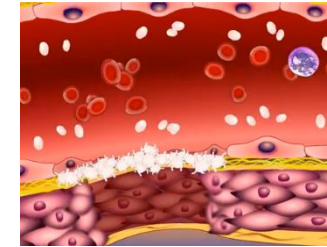


Prediction of responders/non-responders to breast cancer treatment



Prediction of anti-platelet effect

Yerges-Armstrong LM et al, CPT (2018) 94: 952



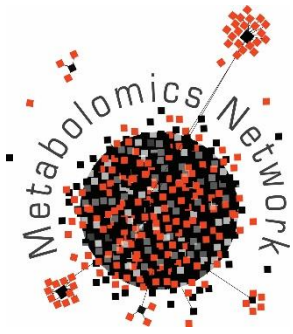
Determine myelin turnover for multiple sclerosis drugs

Kanhai KMS et al. 2016. Clinical and Translational Sciences. 9: 321ff

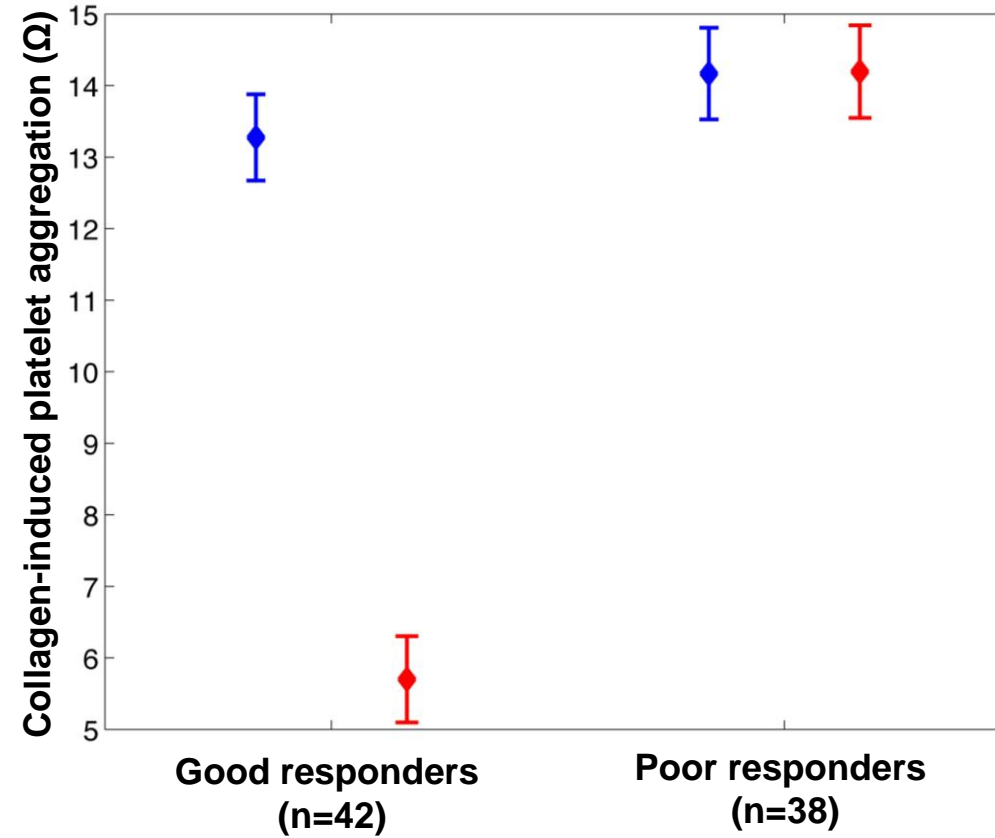
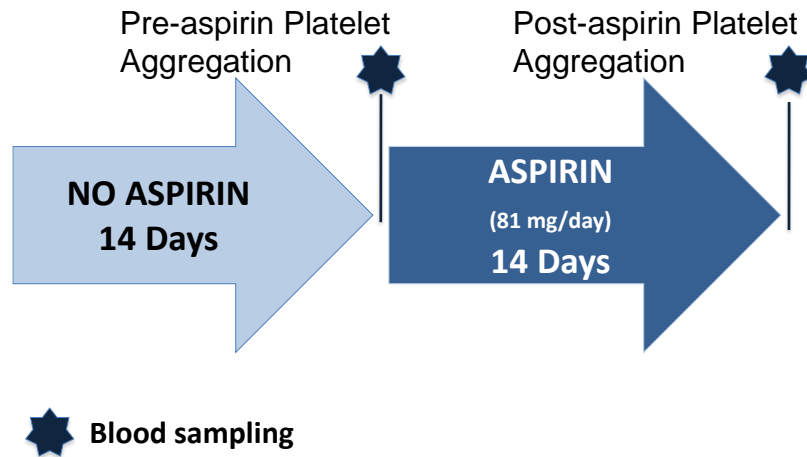


Prediction of weight loss by diet intervention (Diogenes Study)

Vogelzangs N, Int. J. Obesity, in press



The Heredity And Phenotype Intervention (HAPI) heart study^{1,2}



Data represent mean ± 95% CI before or after aspirin.

Collaborators

Duke University School of Medicine
Rima Kaddurah-Daouk, Deepak Voora, Geoffrey Ginsburg
 University of Maryland School of Medicine
Alan Shuldiner, Joshua Lewis, Laura Yerges
 University of California Davis
Oliver Fiehn

Signature of aspirin exposure



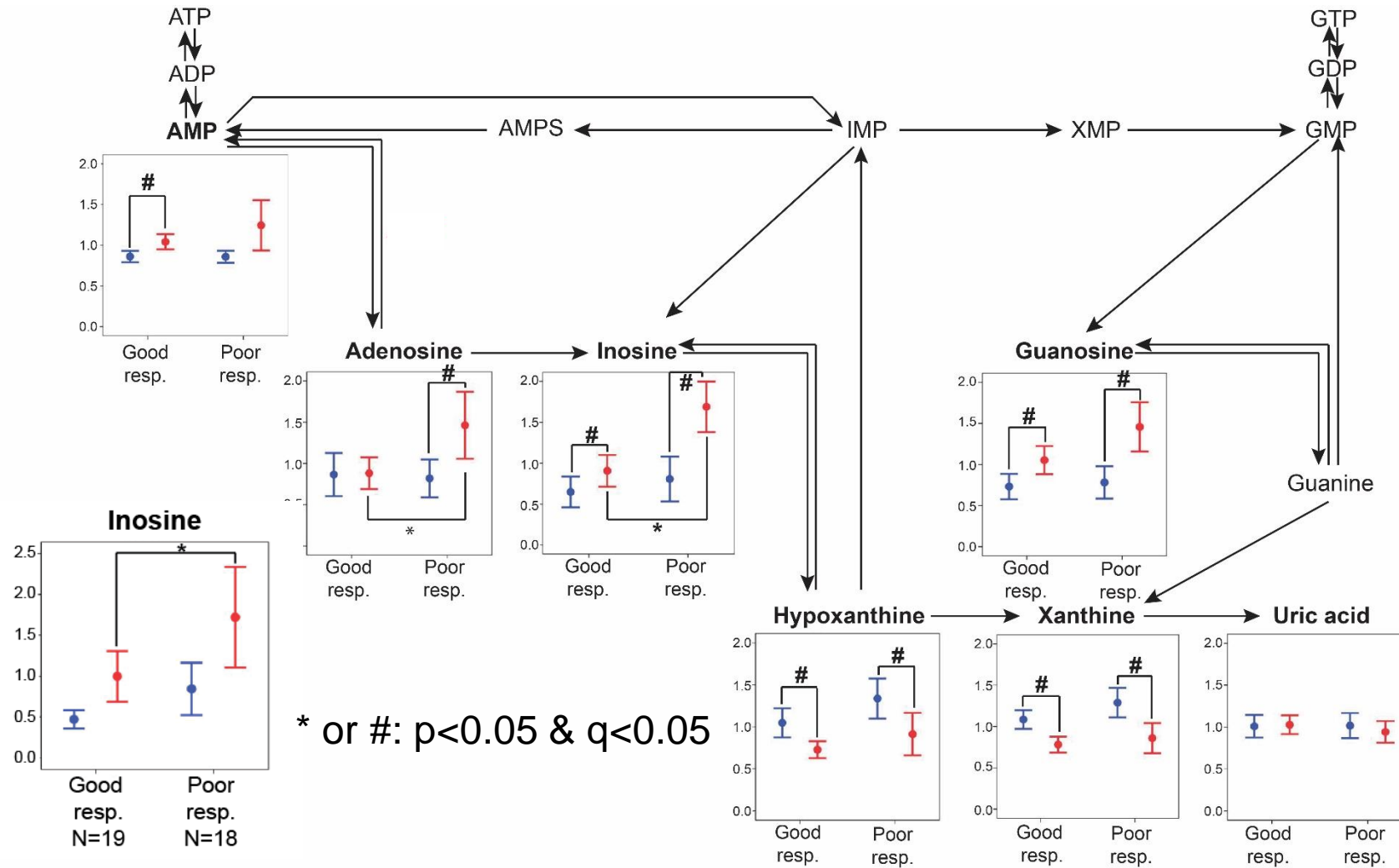
Sandrine Ellero

Pathway	Metabolites	
Aspirin and xenobiotic metabolism	↑ salicylic acid	↑ 2-hydroxyhippuric acid
Purine pathway	↑ inosine ↑ guanosine ↓ xanthine	↑ AMP ↑ adenosine ↓ hypoxanthine
Fatty acids	↓ oleic acid	↓ arachidonic acid
	↓ palmitoleic acid ↓ linoleic acid	↓ azelaic acid
Amino acids and related	↓ L-aspartic acid ↓ L-glutamic acid ↓ L-leucine ↓ L-phenylalanine ↓ L-serine ↓ cystine ↓ L-asparagine ↓ L-valine ↓ Beta-alanine ↓ L-glutamine	↓ glycine ↓ ethanolamine ↓ glycylglycine ↑ o-phosphoethanolamine ↓ ornithine ↑ serotonin ↓ taurine ↓ L-tyrosine ↓ L-lysine ↓ L-histidine
Others	↓ shikimic acid ↓ ribose	↓ 3-phosphoglycerate ↑ 2,5-furandicarboxylic acid

Metabolites significantly changed post- vs. pre-aspirin in all subjects (N=80) are displayed (p<0.05, q<0.05).

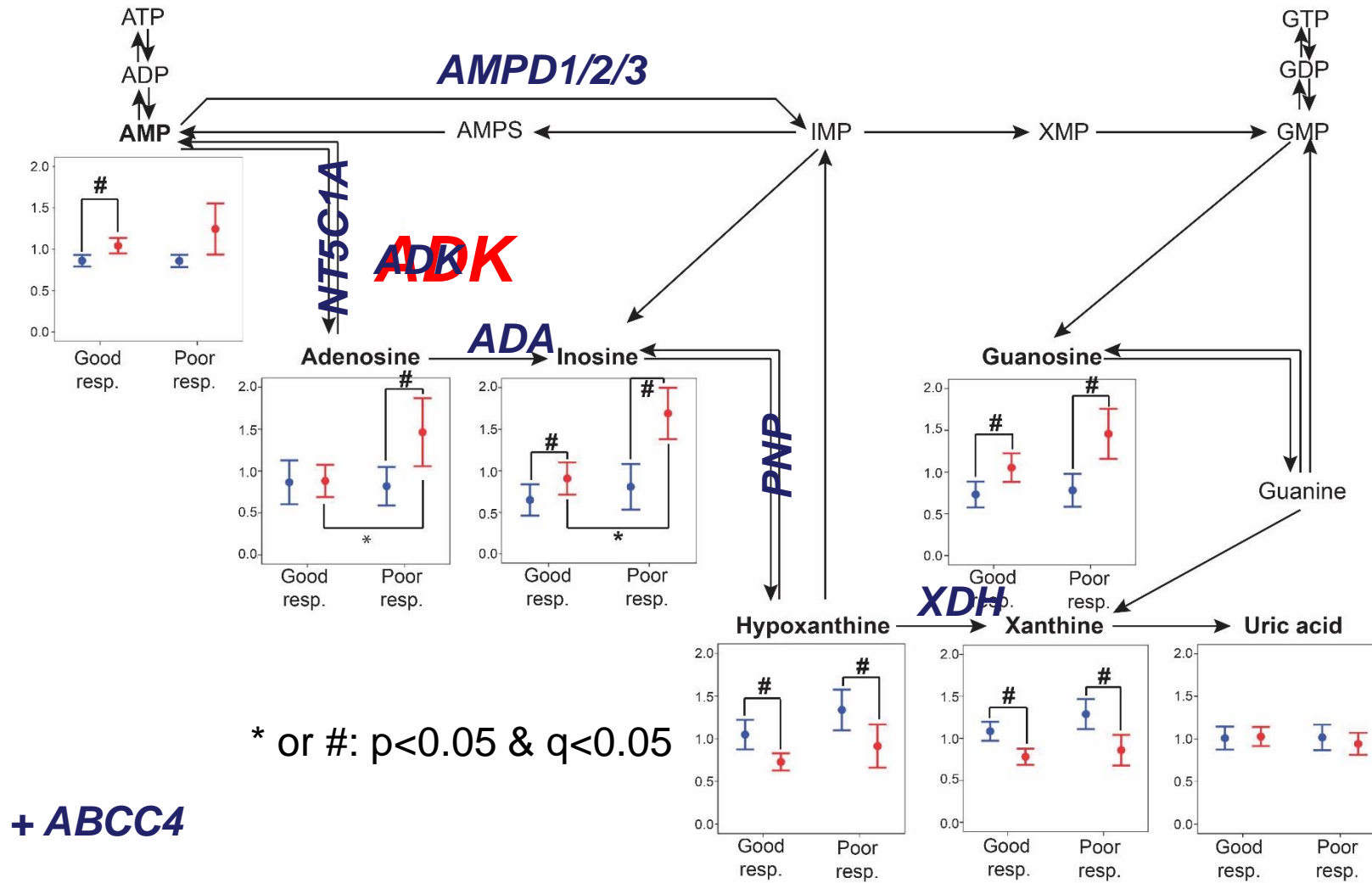
□ Measured by GC-MS; ◻ Measured by LC-MS; ▣ Measured by LC- and GC-MS.

Purine pathway in relation to variation in aspirin response



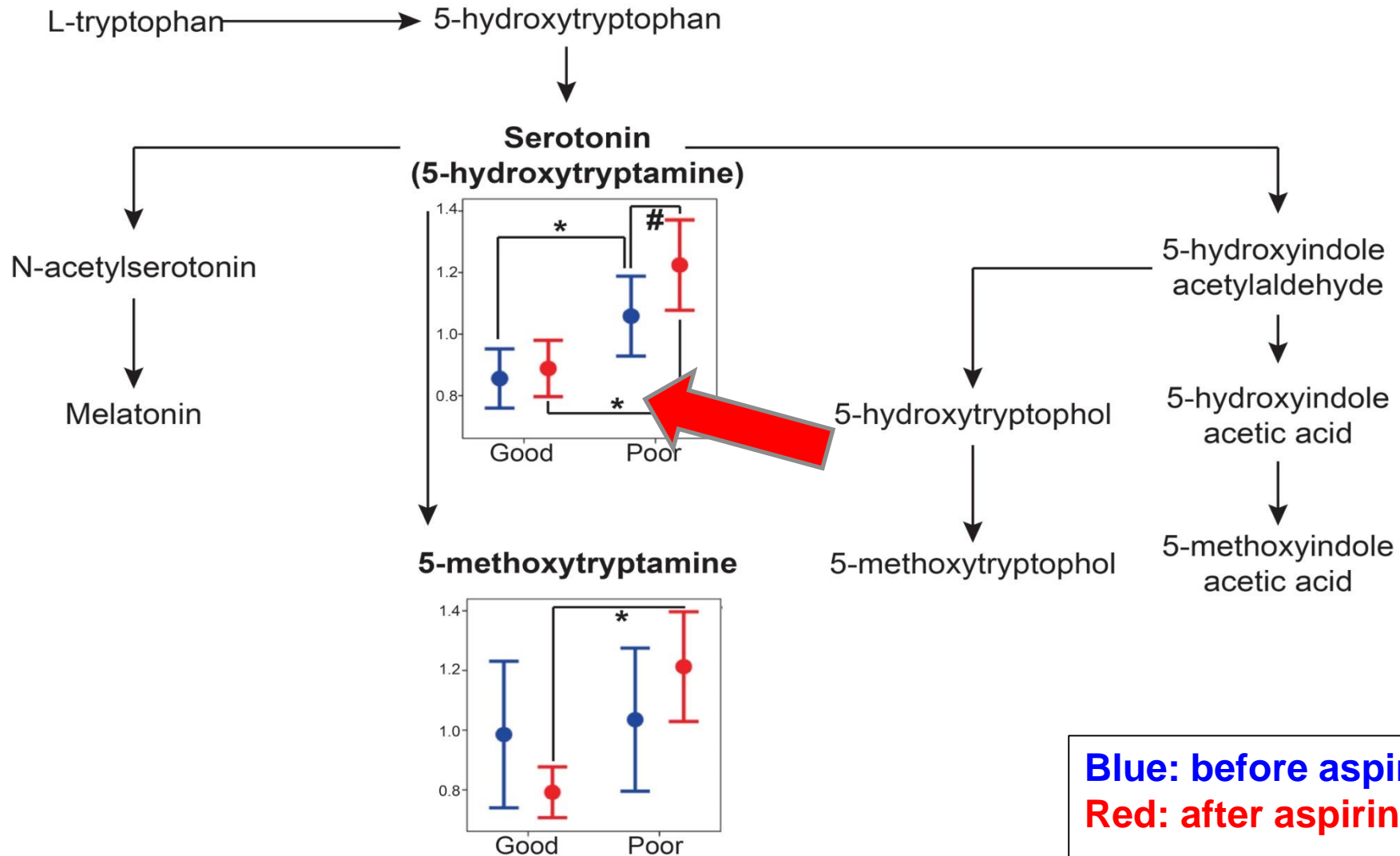
Data represent mean ± 95% CI of metabolite level, before or after aspirin

Purine pathway in relation to variation in aspirin response



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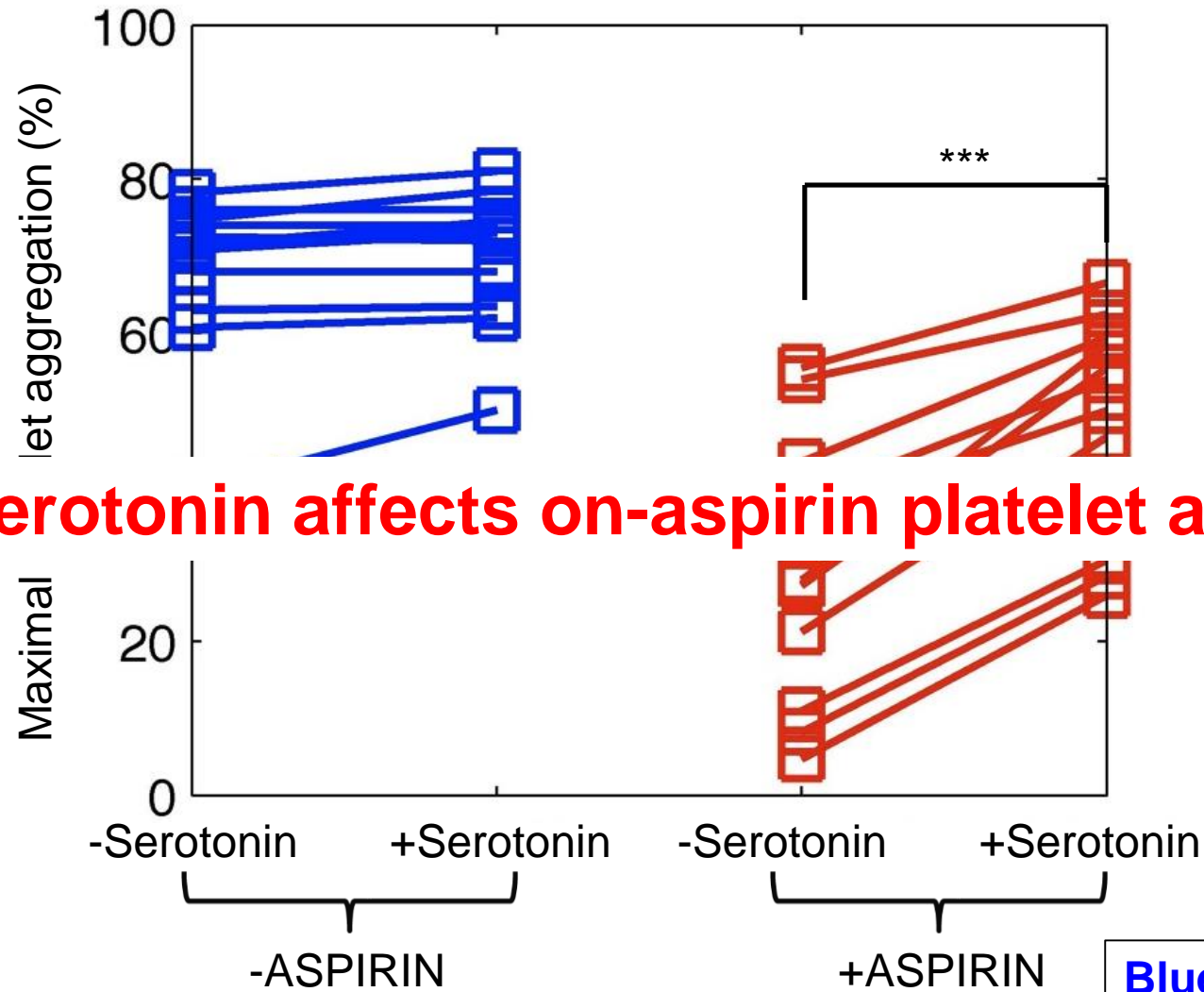
Differences between good and poor responders: The serotonin pathway



Blue: before aspirin
Red: after aspirin

***: P<0.05**

Validation of biochemistry: functional studies



⇒ **Serotonin affects on-aspirin platelet aggregation**

Blue: before aspirin
Red: after aspirin

***: $P < 0.001$

Our unique approach to Metabolomics for biobanks & clinical studies

We combine **powerful technologies** with **proven methodologies** and **patented analytics** to deliver quantitative measurements of the metabolome using targeted and global platforms.

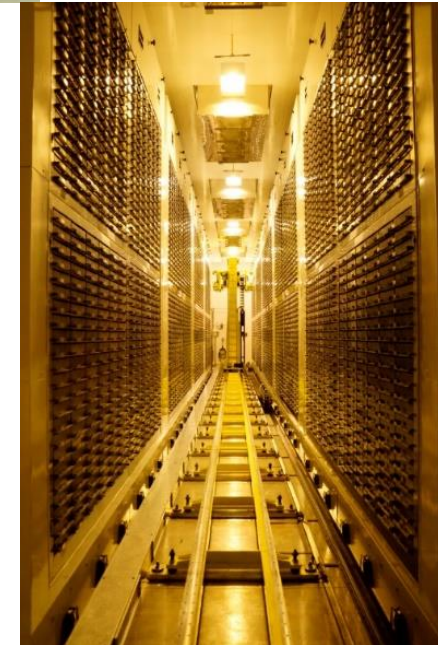


For this we formed a strategic alliance with Imperial College London.

Our new metabolomics platform will be:

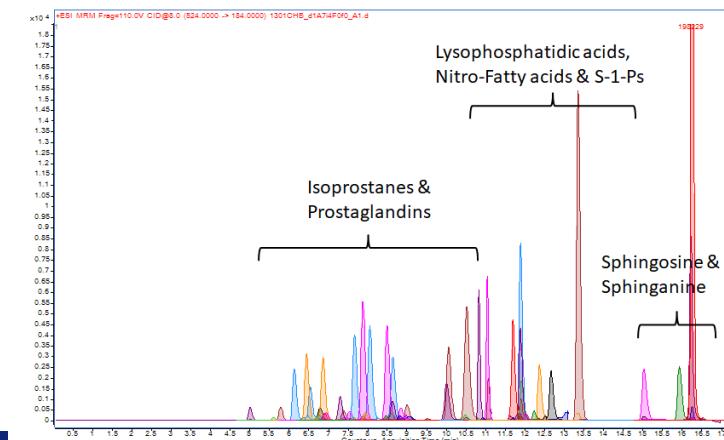


- ✓ **Robust**
- ✓ **Scalable**
- ✓ **Quantitative**
- ✓ **Quality controlled**
- ✓ **More than 2000 metabolites & lipids**



Oxidative stress & signaling platform

- Unique platform with > 250 markers that inform you about the status of inflammation and oxidative stress, fully quantitative.
- About 100 special targets that you don't find in other platforms (Metabolon, Biocrates, Nightingale);
 - Pro & anti inflammatory metabolites;
 - Oxidative stress; oxidative signalling, anti-oxidants;
 - Immune response
 - Endocannabinoid
 - Bile acids
 - Vascular function



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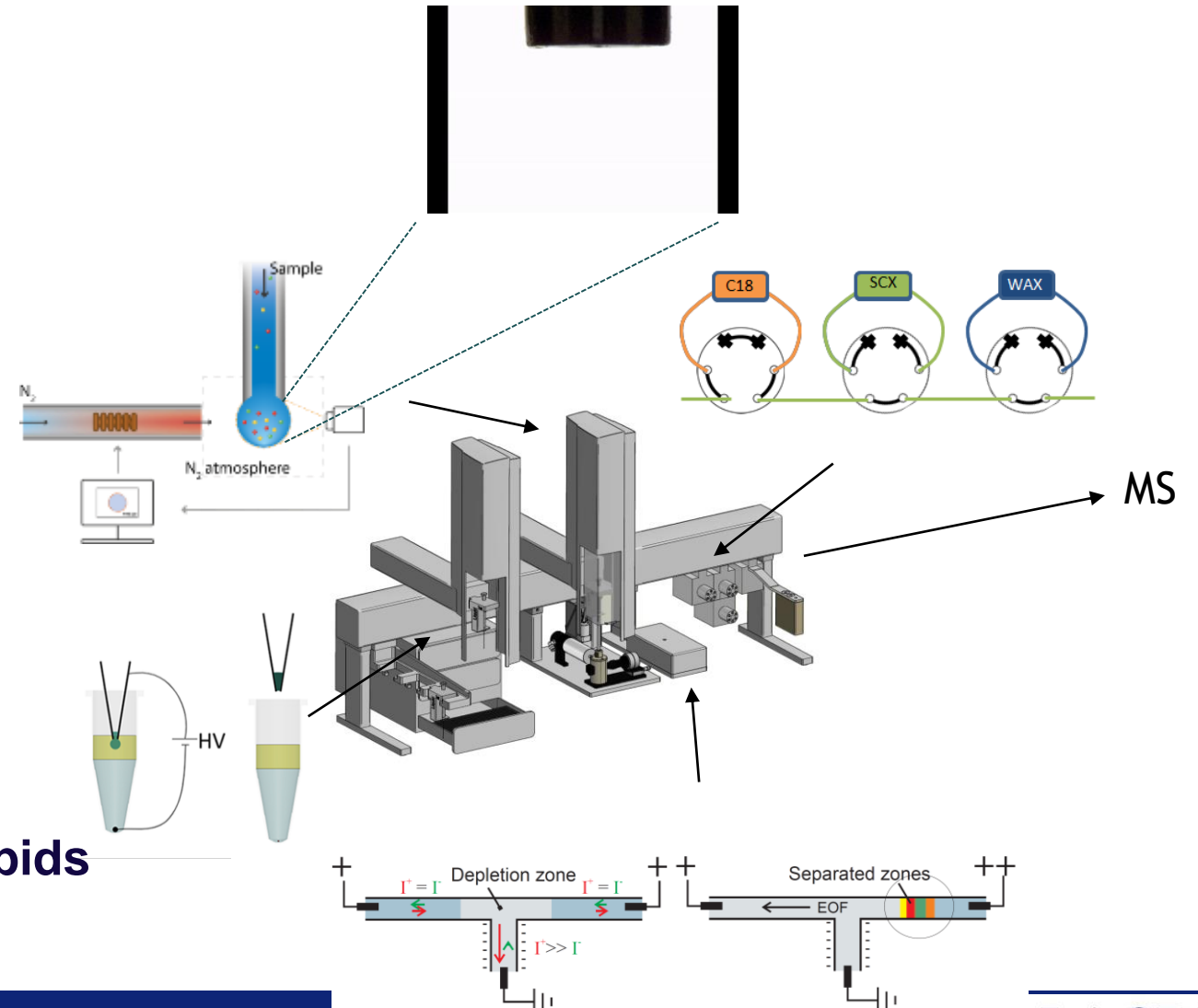
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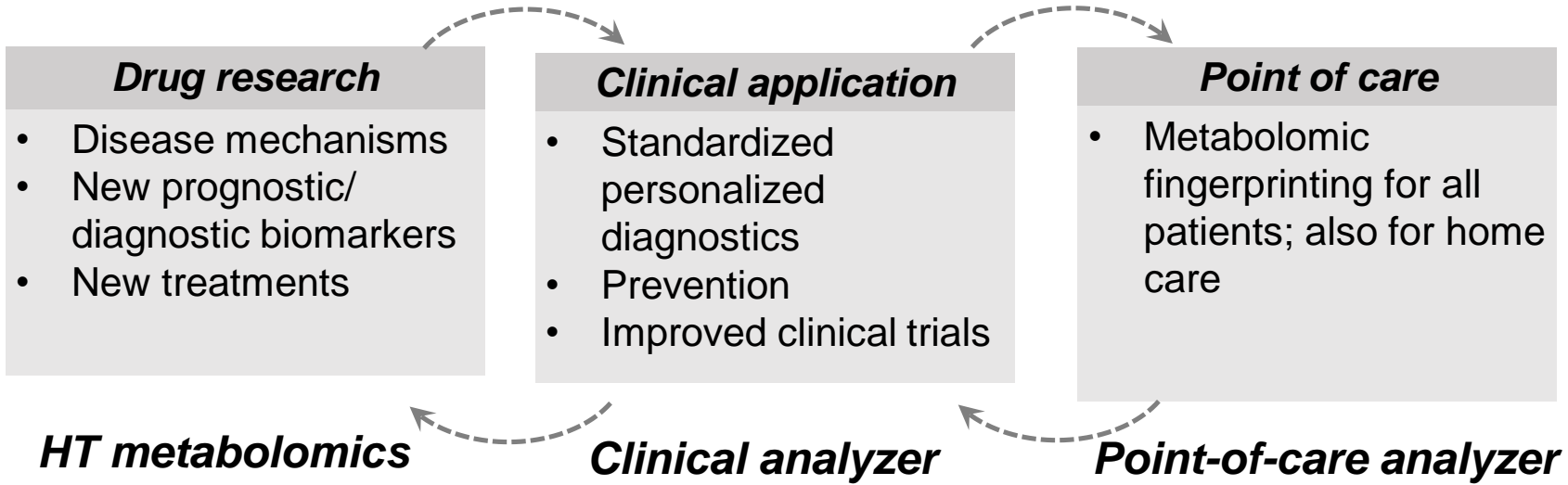


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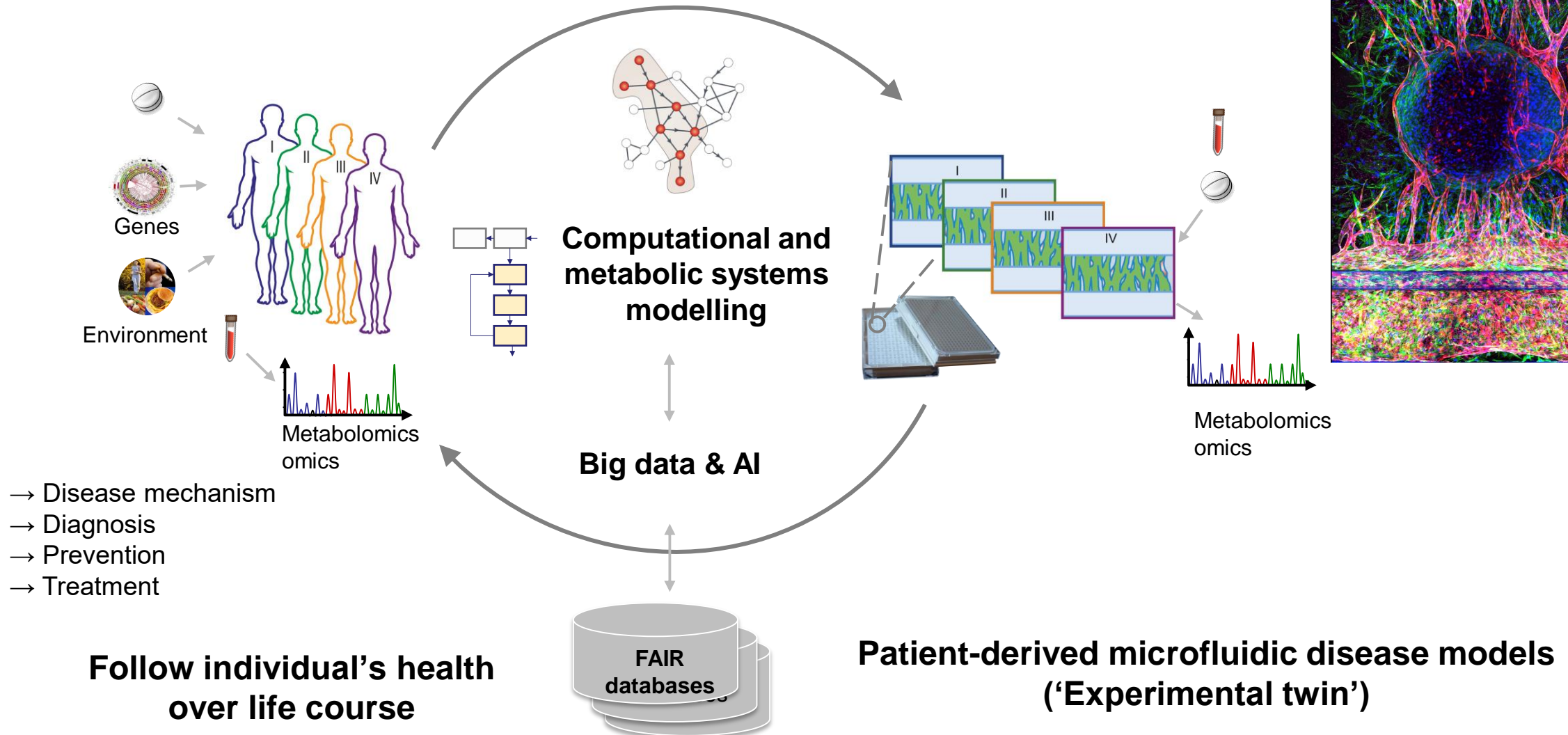


Fieldlab MXL: SME's developing novel products and services for pharma, biotech, agrofood, biobankspartners

Technology development



Metabolomics for novel diagnostic and individualized prevention & treatment strategies



What metabolomics will deliver

- **Pharma:** Improved clinical trials to predict outcome, on-target/off-target effects (companion diagnostics) and to identify new drug targets and new therapeutic opportunities based on novel early disease pathways. Drug rescue using metabolomics for 'failed' trials.
- **Health care/clinics:** new generation diagnostic tests allowing earlier diagnosis and predict treatment outcome
- **Nutrition and prevention:** New opportunities to promote health with optimized personalized diets and life style advise.
- **Academia and biobanks:** affordable quantitative metabolomics data will improve scientific discoveries
- **Population:** metabolic health monitoring integrated with genomics, wearables, AI will allow personalized health promotion and prevention (MyMetabolome)



Great opportunities for pharma and biotech!

Metabolomics XL to accelerate clinical, biomedical and drug research in academia and industry

