

MASS SPECTROMETRY TARGETED PROTEOMICS

Eleonora

Epi-Omics Journal Club

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OUTLINE

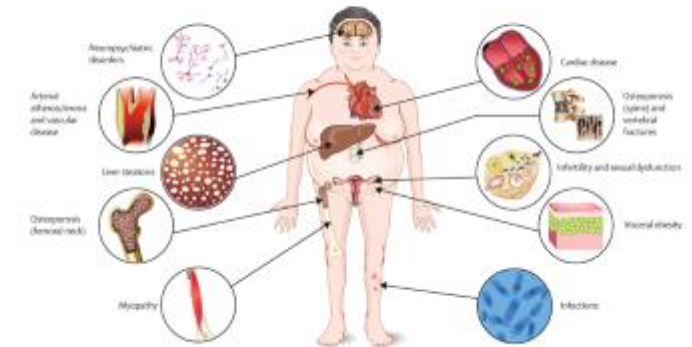
MASS SPECTROMETRY-BASED TARGETED PROTEOMICS

Relatively novel method to quantitate proteins in plasma



- High level of multiplexation (1-500 proteins)
- Requires only minimal amount of plasma (5µL)

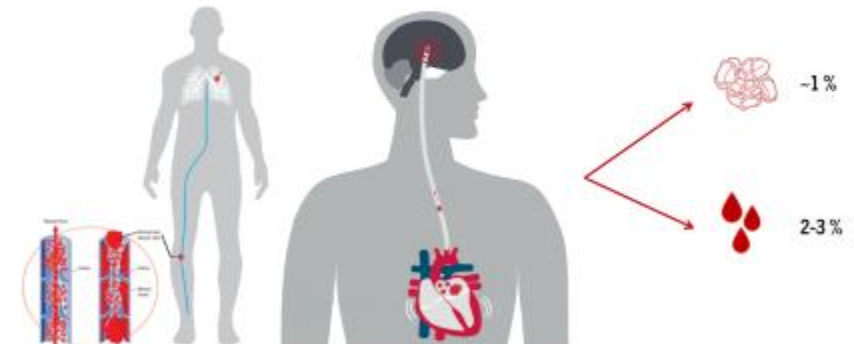
(1) CUSHING DISEASE



Piccinelli R. et al. The Lancet Diabetes & endocrinology 2016

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(2) BLEEDING AND THROMBOSIS DURING ANTICOAGULANT TREATMENT



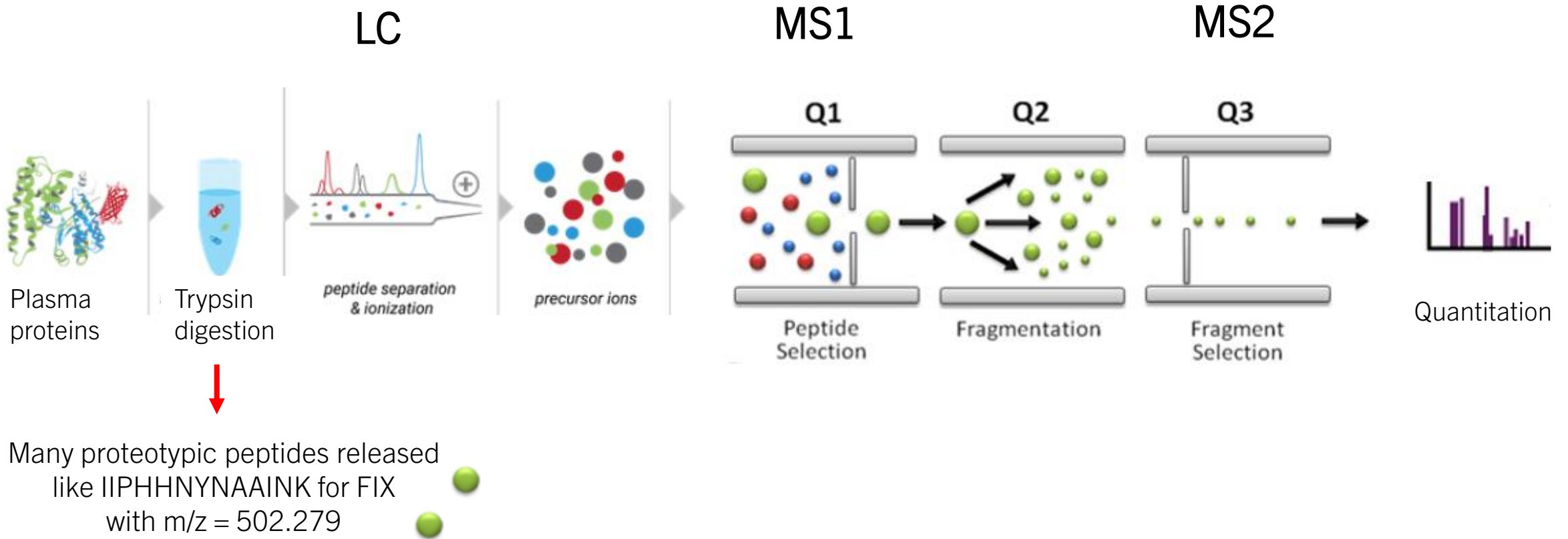
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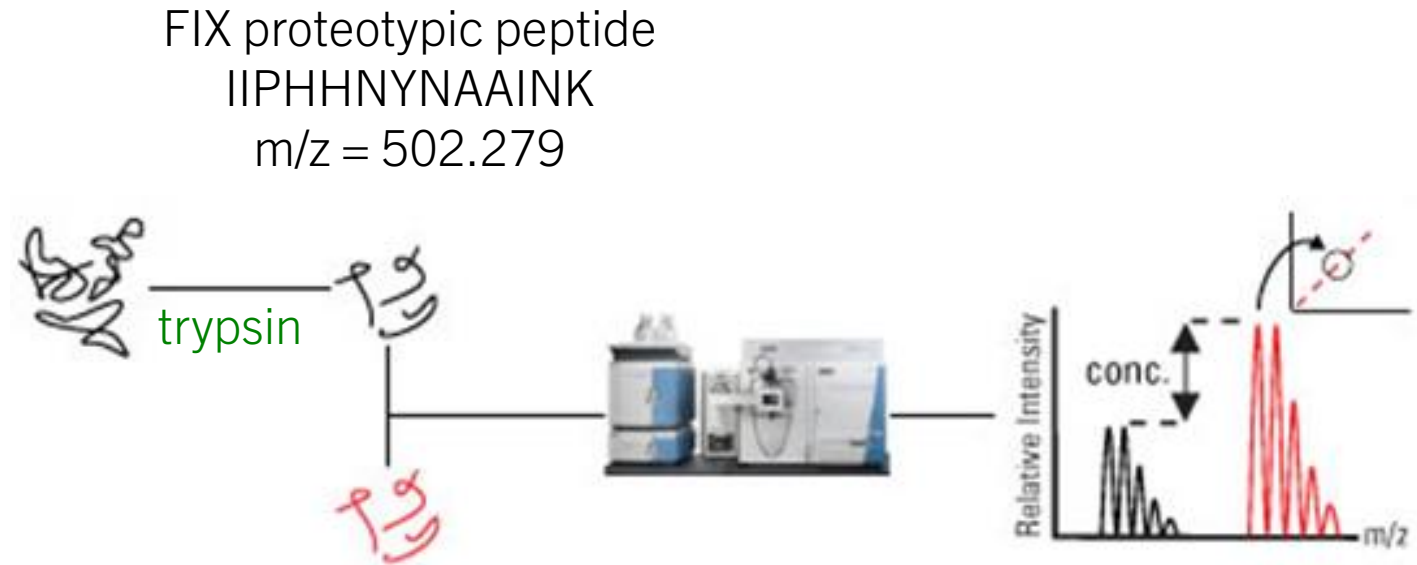
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HOW DOES IT WORK? (1)



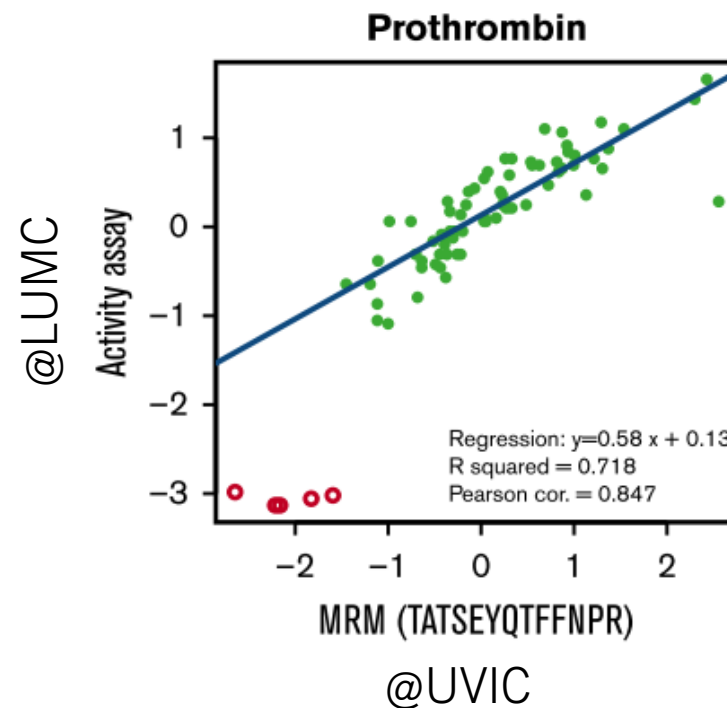
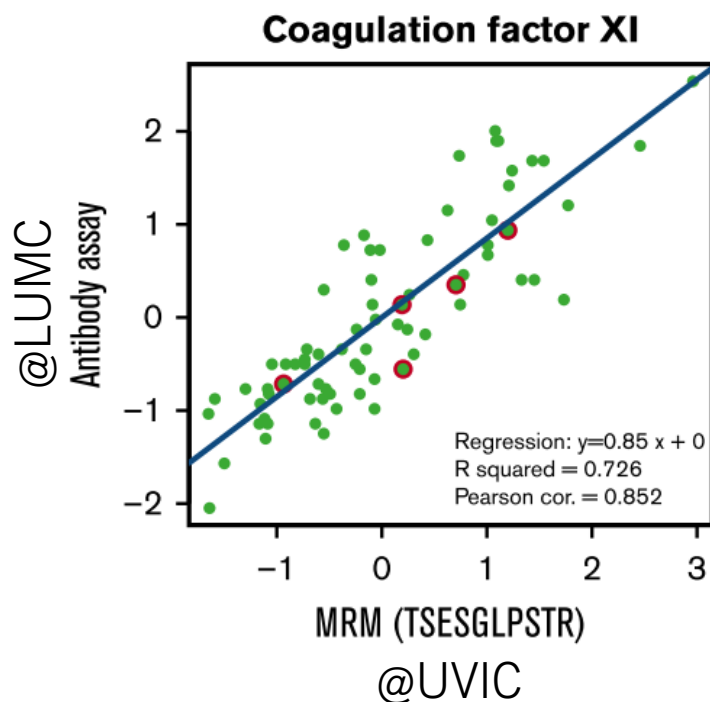
HOW DOES IT WORK? (2)

Example: FIX in plasma



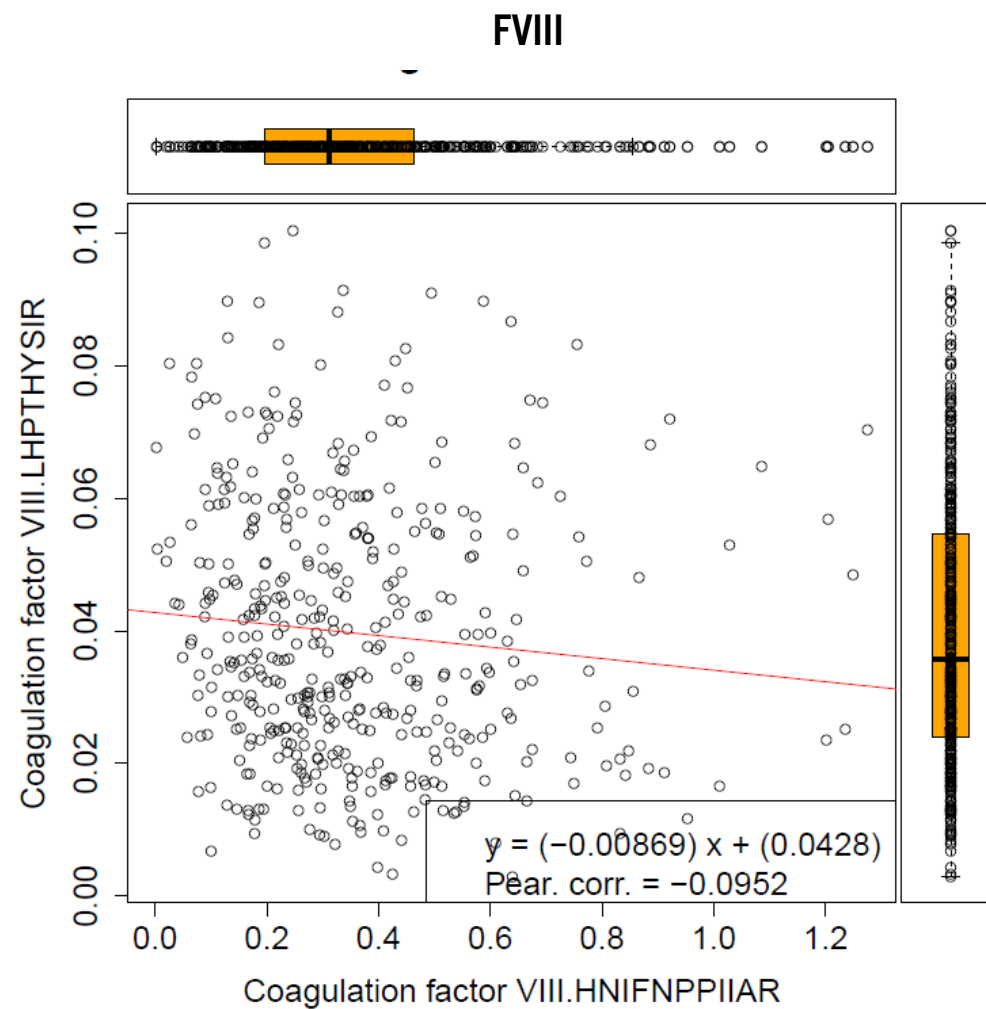
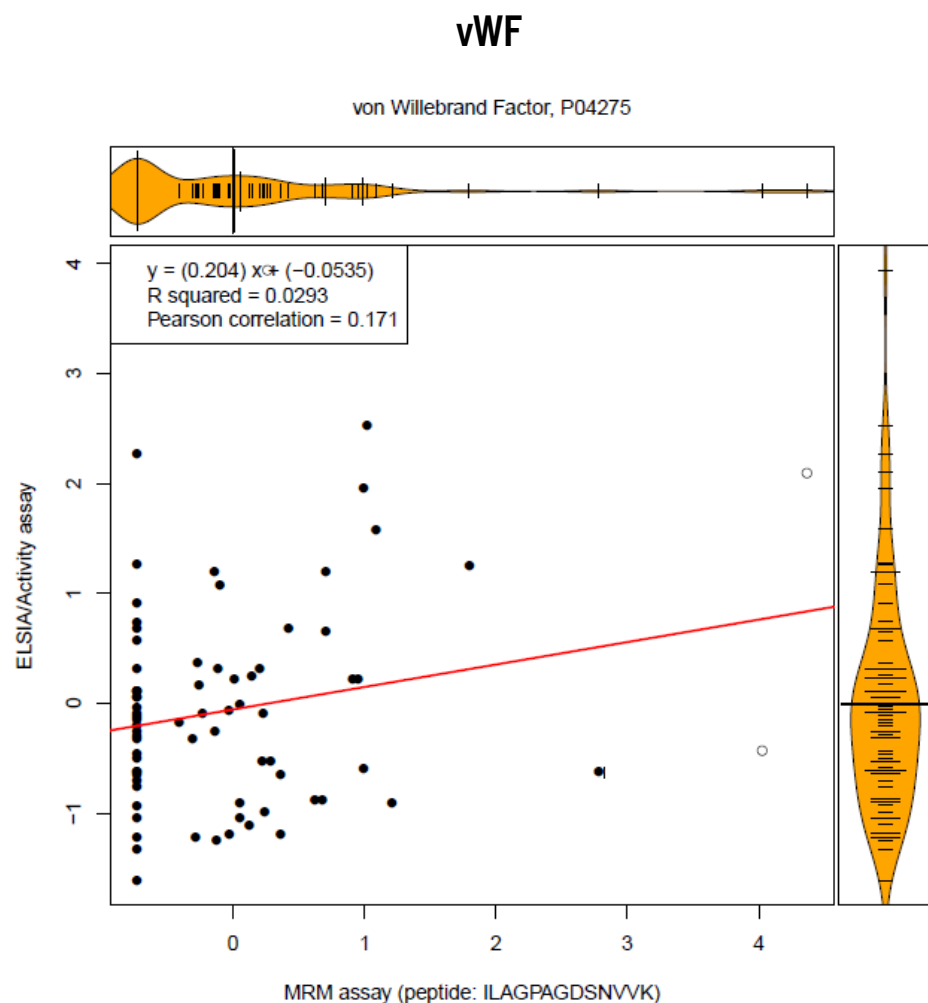
Synthetic IIPHHNYNAAINK-
[**¹³C] $m/z = 504.279$
spiked in exact amount**

MS-QTP in collaboration with Christoph Borchers group at University of Victoria (UViC)



MS-QTP successfully determined plasma levels of
31 coagulation (-related) factors in multiplex in one single run

MS-QTP in collaboration with Christoph Borchers group at University of Victoria (UViC)

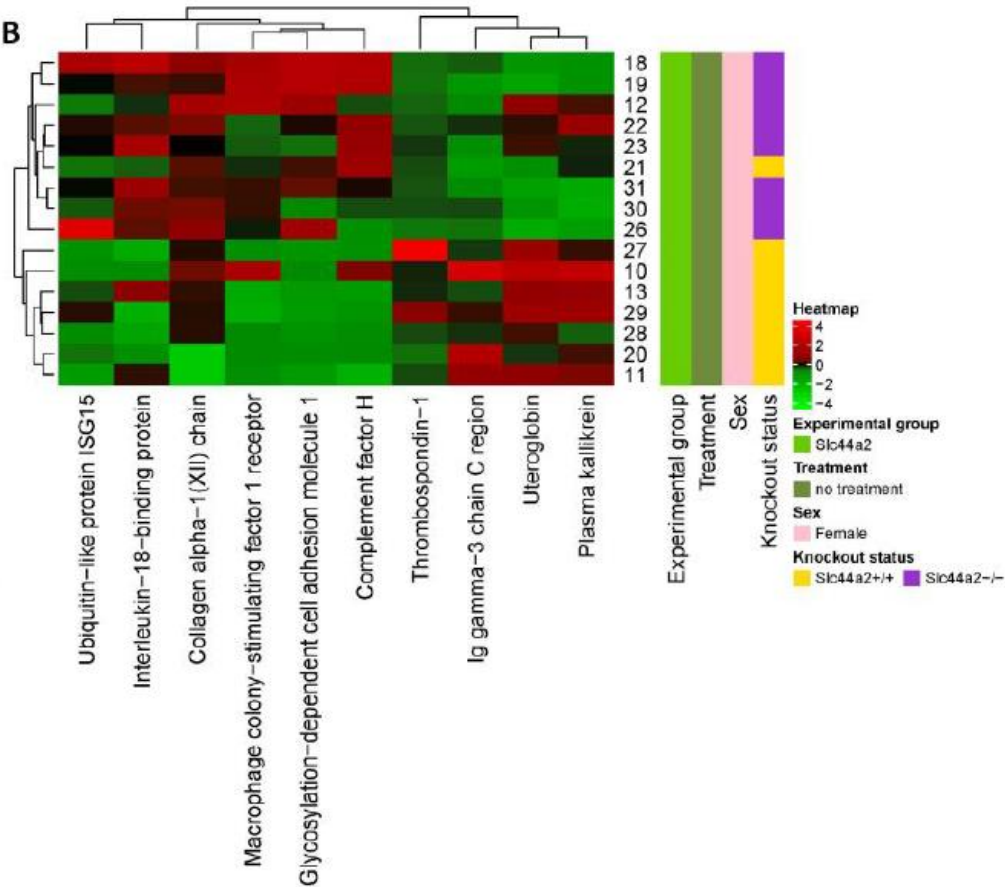
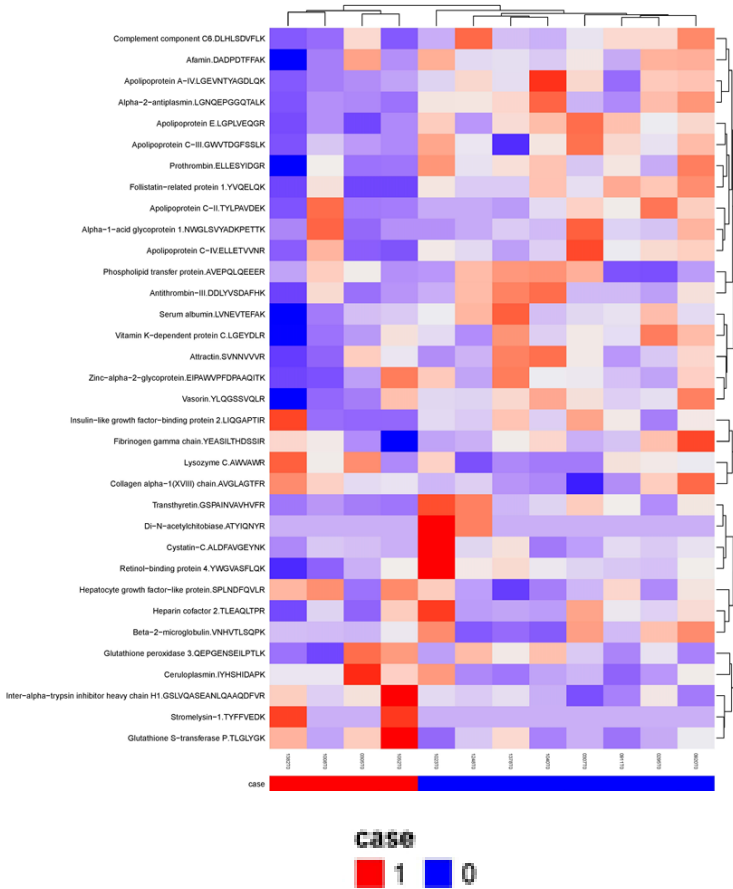


LATEST STUDIES WITH UVIC USING ‘DISCOVERY’ PANELS

Signature’ VTE in POT-(K)CAST

‘Signature’ *Slc44a2* deficiency in

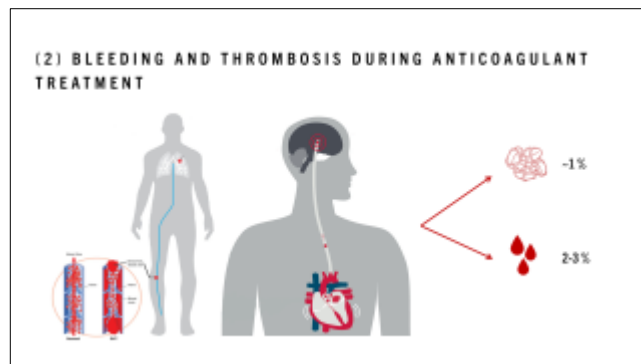
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CURRENT PROJECTS

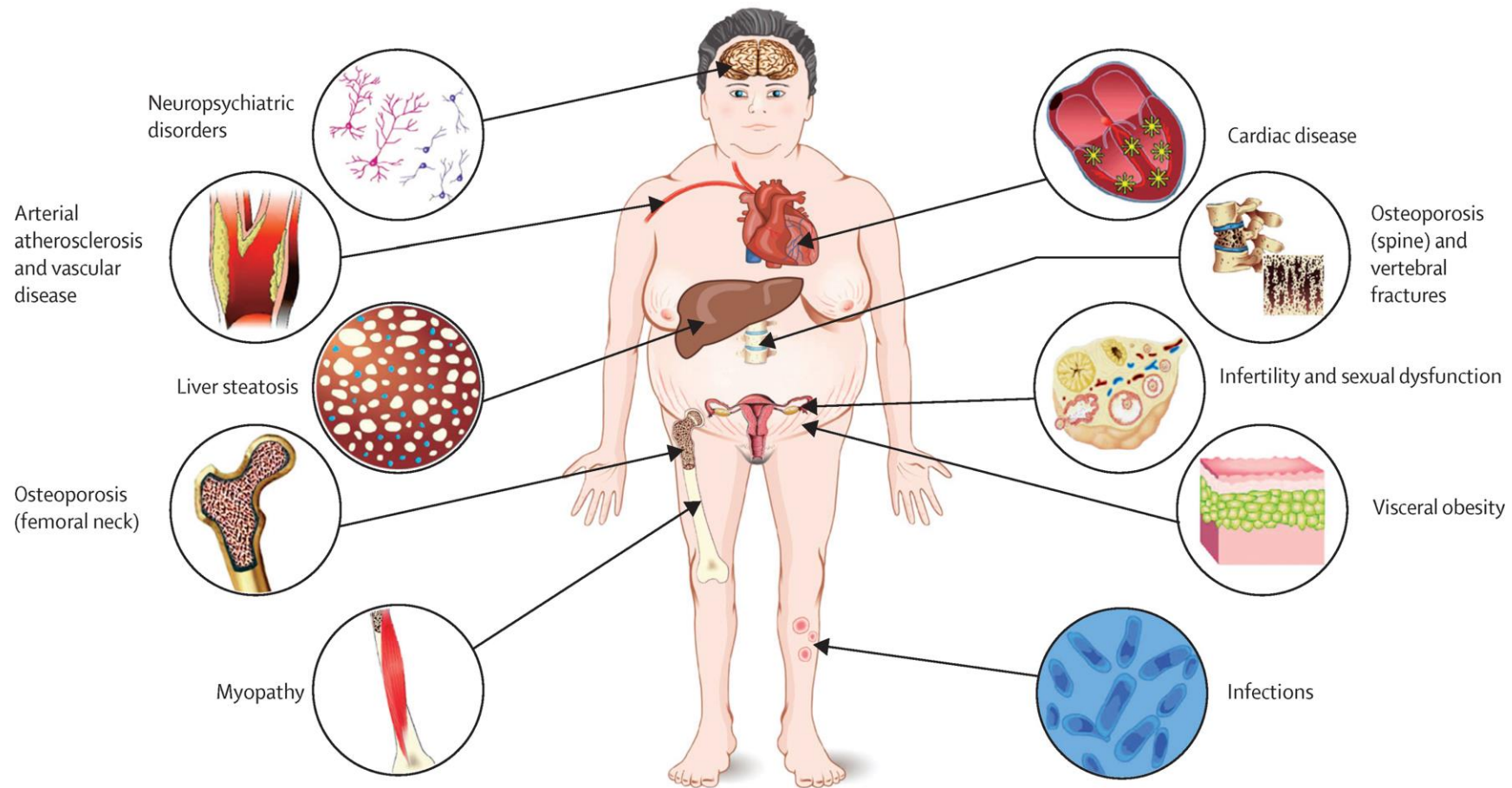


- **Plasma profiling of Cushing patients**
 - Changes before-after treatment
 - Biomarkers for remission

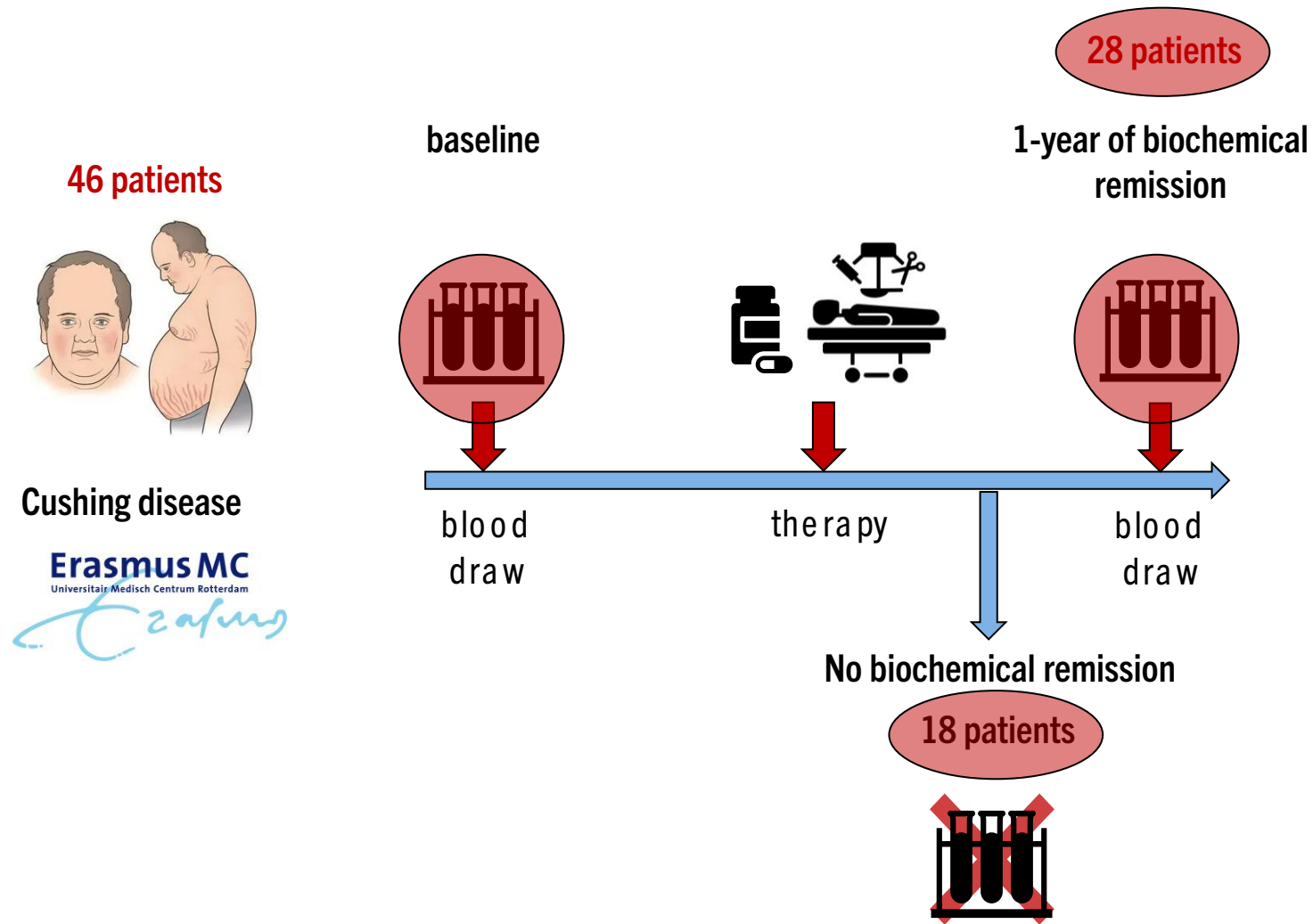


- **Plasma profiling of patients with major bleeding & thrombosis during anticoagulation**
 - Novel biomarkers for bleeding & thrombosis
 - Prediction model

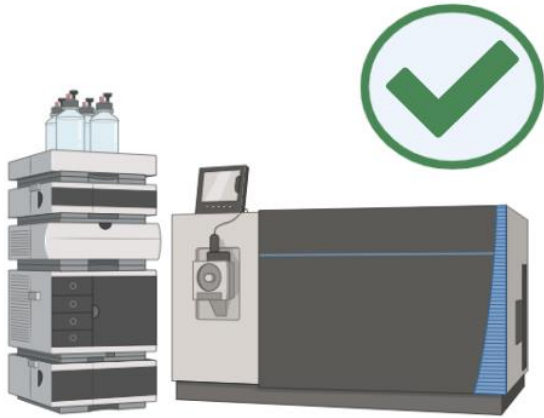
(1) CUSHING DISEASE



STUDY DESIGN AND METHODS

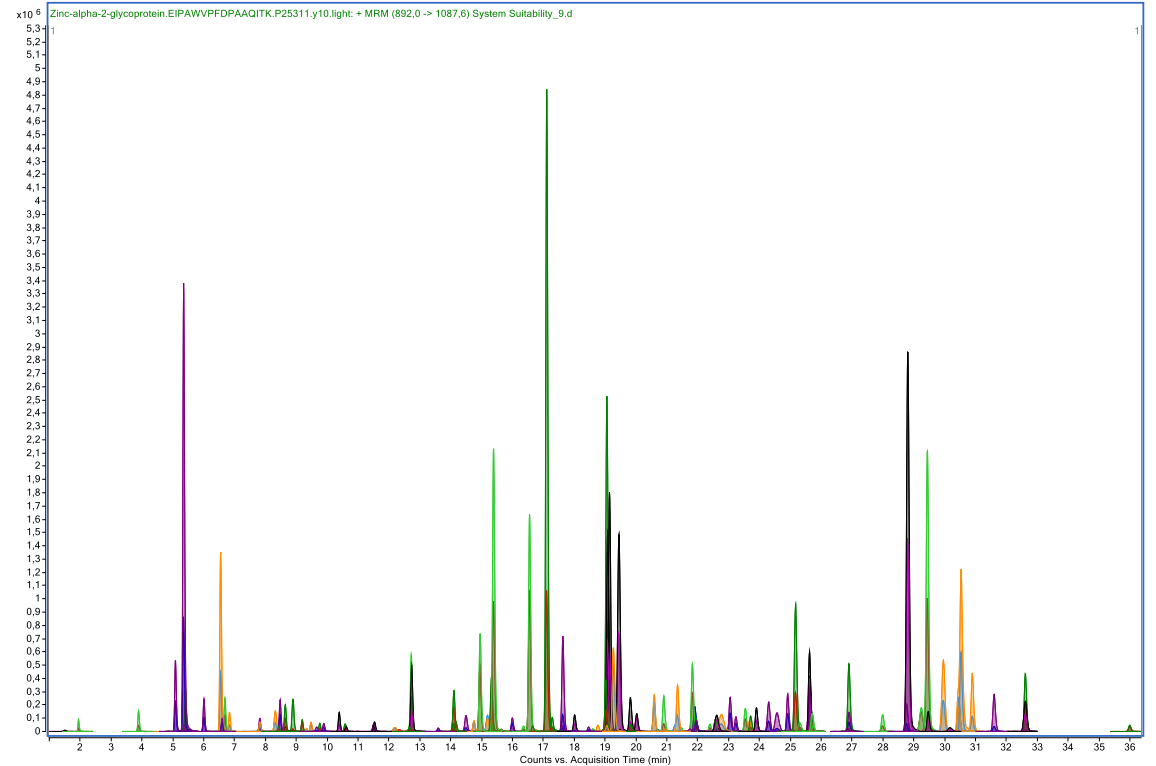


QUALITY CHECKS

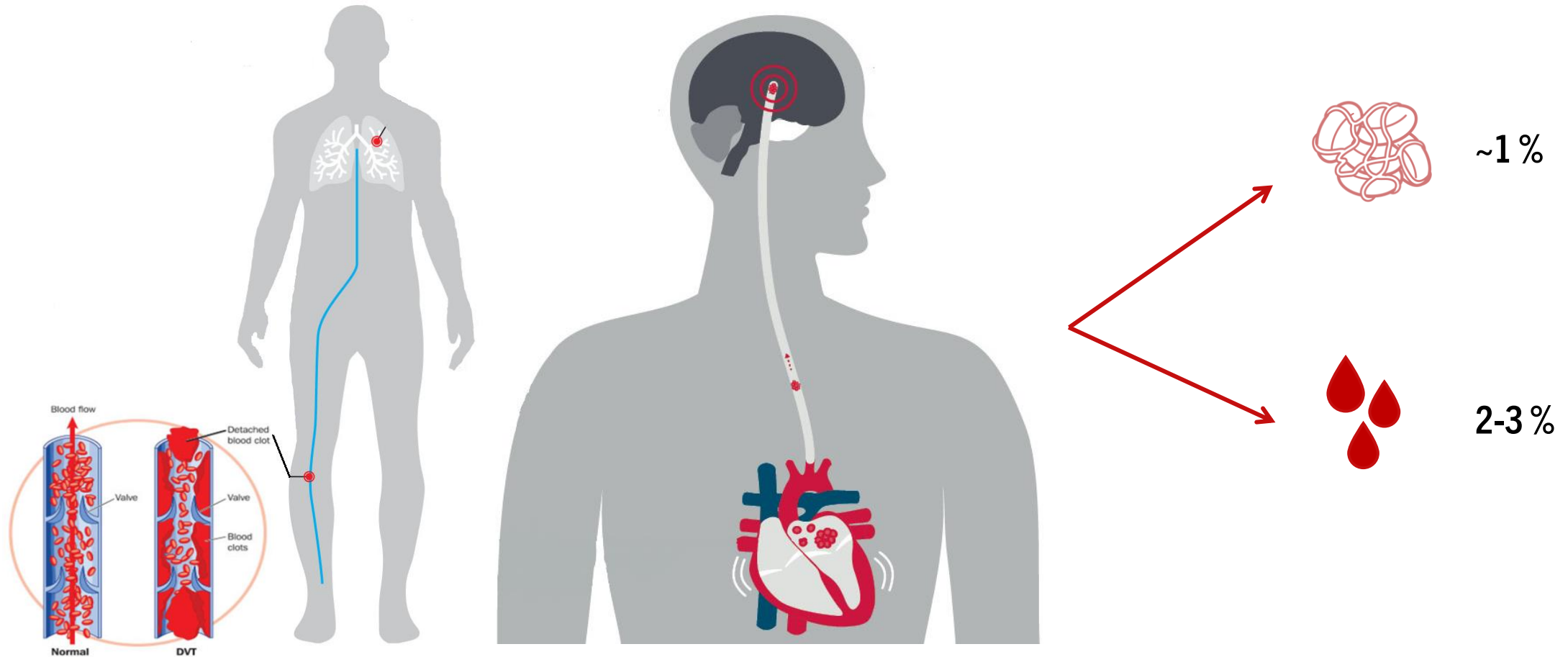


System suitability

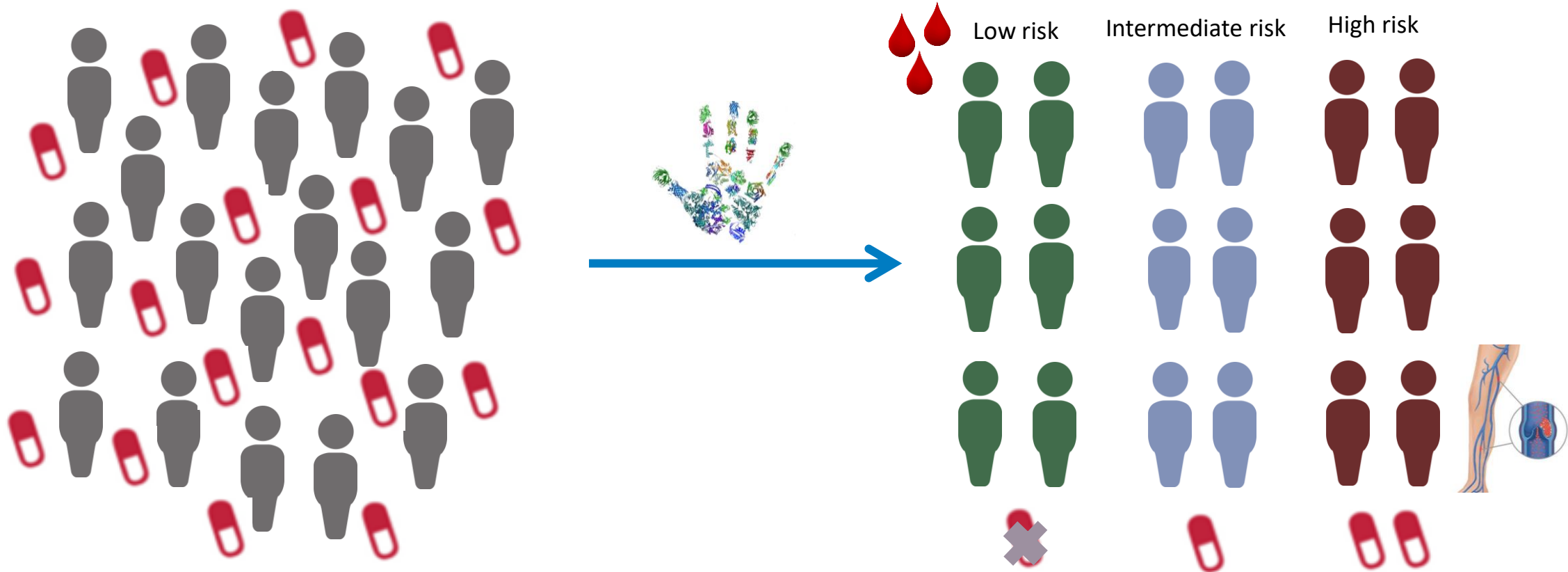
- 3 retention time check
- 3 before run
- 3 after run



(2) BLEEDING AND THROMBOSIS DURING ANTICOAGULANT TREATMENT

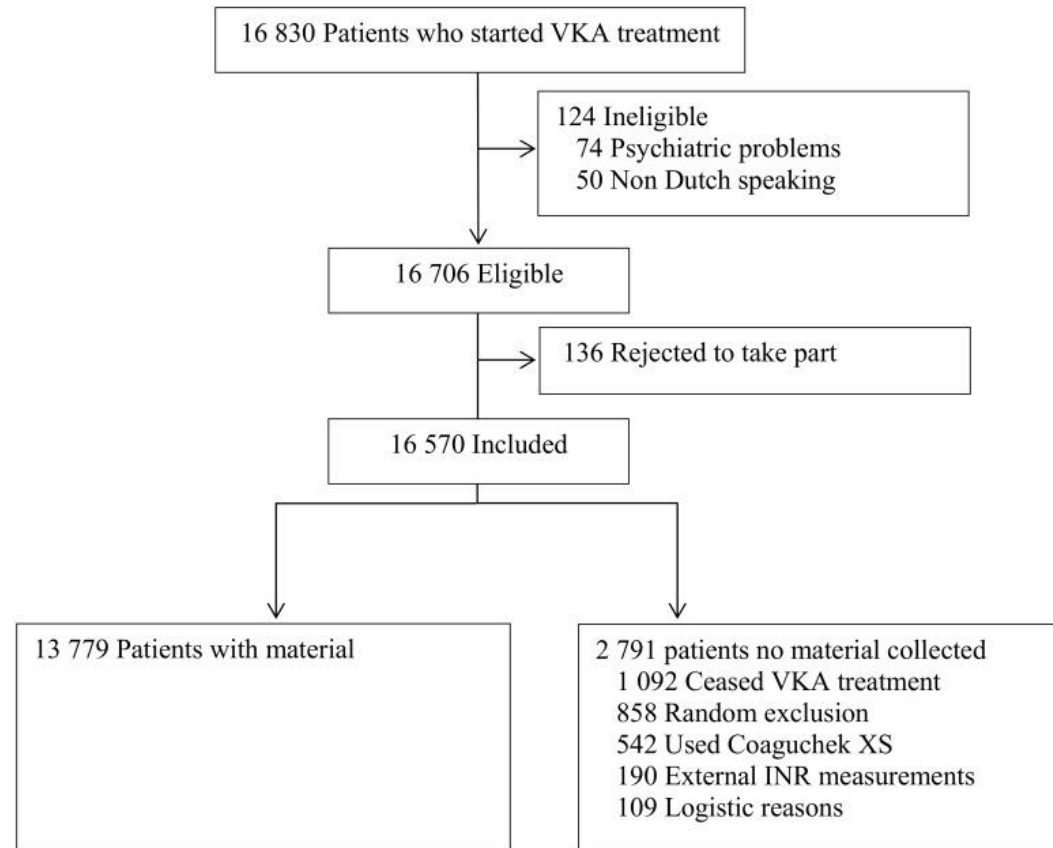


CURRENT APPROACH VS IDEAL APPROACH



BLEED STUDY

16,570 patients who started treatment with Vitamin K antagonists (2012-2014)



CASE-COHORT FROM THE BLEED STUDY

