

ERN-EuroBloodNet Topic on Focus on Inherited Platelet Function Disorders (IPFD)



webinar

HEALTH
PROFESSIONALS

Genetic testing for IPFD - Advantage, limitations and future perspectives

Kathleen Freson
KU Leuven

February 11, 2026



CRPP
Centre de Référence
Pathologies Plaquettaires

MHEMO
La Filière des maladies rares de l'hémostase



ebn
ERN | EuroBloodNet

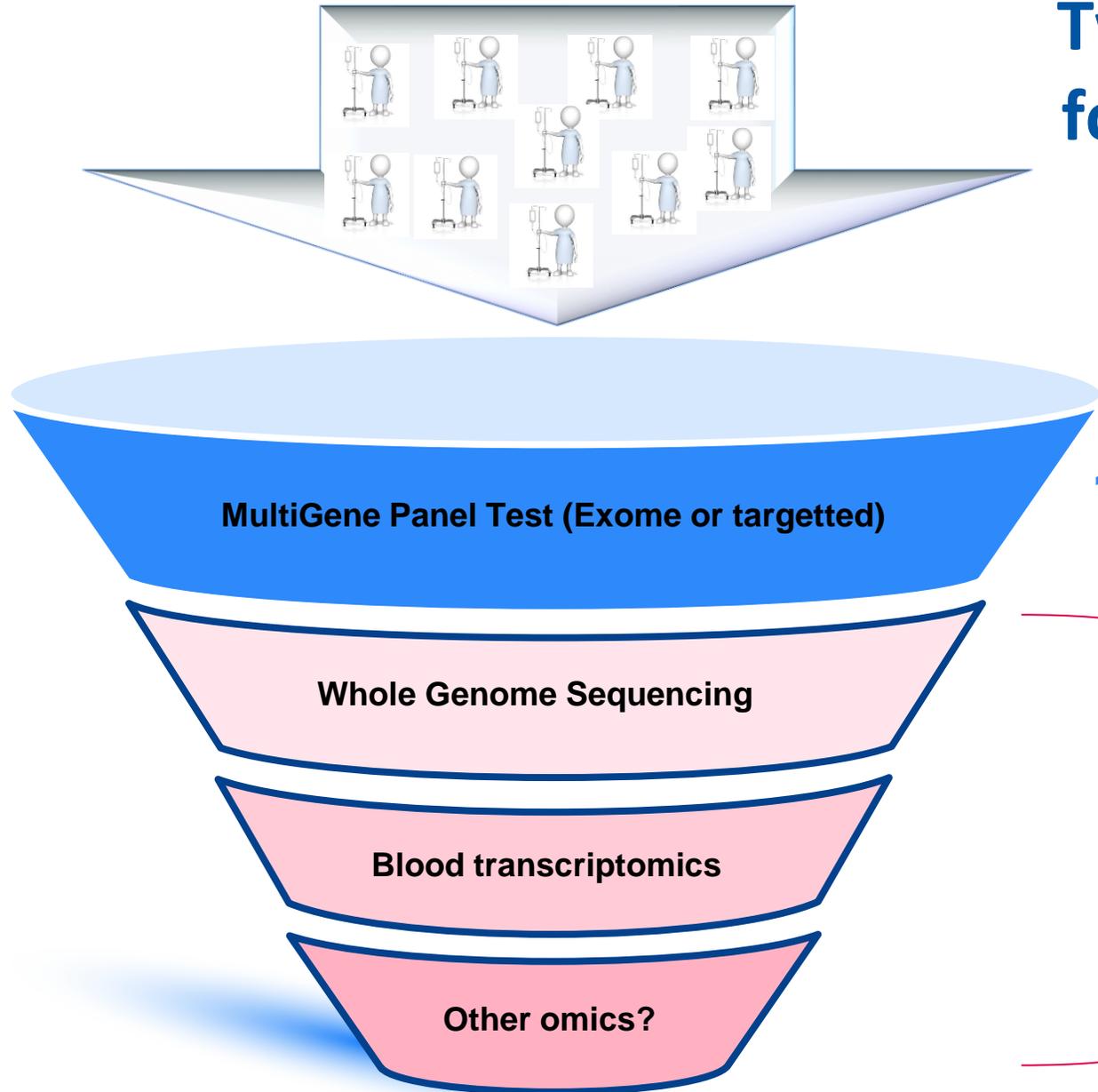


Disclosure for conflict

Research Grant

Swedish Orphan Biovitrum (SOBI)

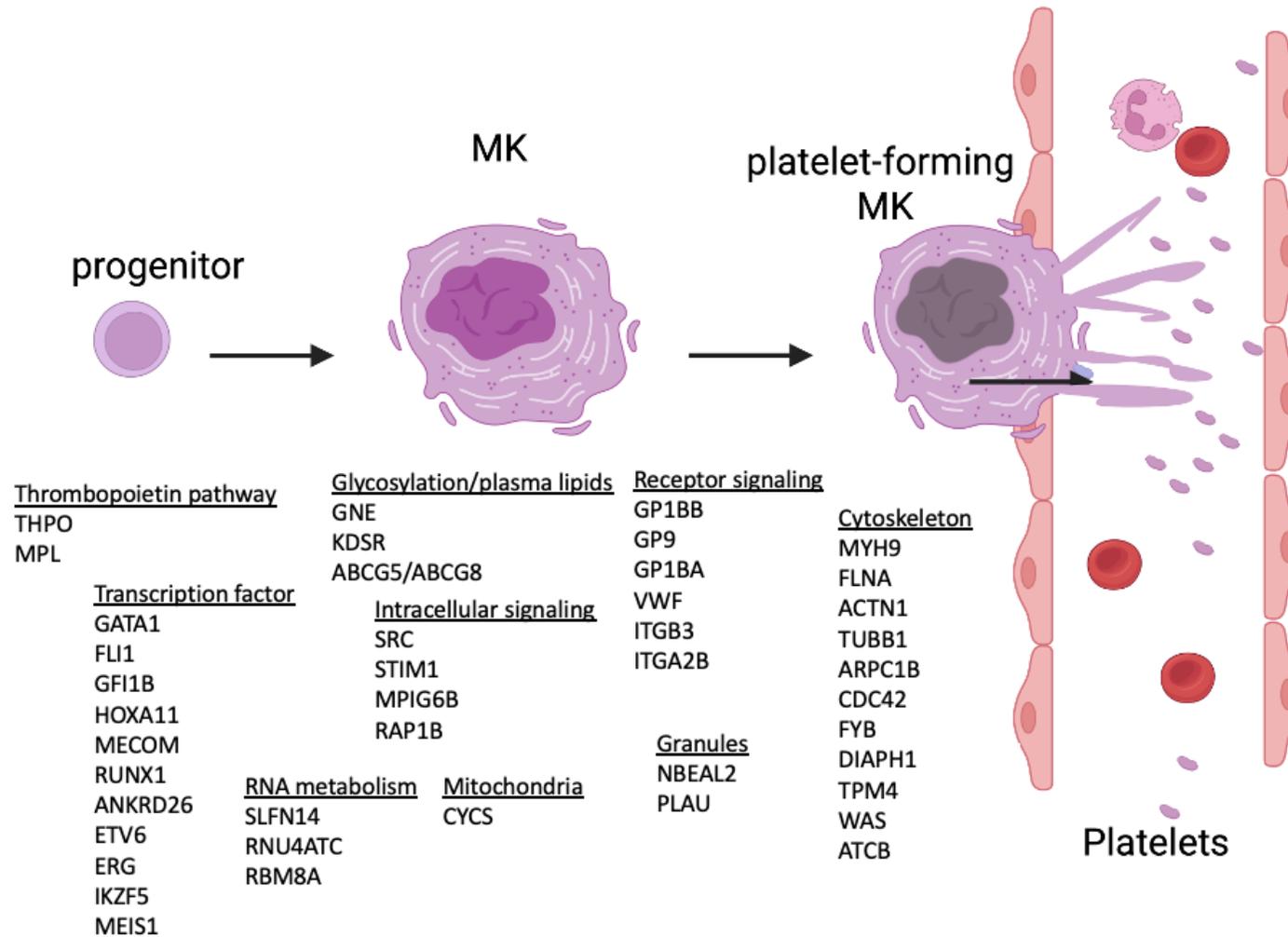
Two Genetic Testing Pathways for Inherited Platelet Function Disorders



1. Genetic testing in the clinic

2. Genetic testing in research

Inherited platelet disorders are heterogeneous (68 genes) & many are ultra rare



Receptors and Intracellular signalling

P2RY12
TBXA2R
TBXAS1
ABCC4
PTGS1
PLA2G4A
RASGRP2
FERMT3
GP6

Procoagulant activity

ANO6

Granule biogenesis secretion

HPS1, AP3B1, HPS3, HPS4, HPS5, HPS6,
DTNBP1, BLOC1S3, BLOC1S5, BLOC1S6,
AP3D1, LYST, NBEA, VPS33B, VIPAS39, STXBP2

SSC Scientific and Standardization Committee

RECOMMENDATIONS AND GUIDELINES jth

Curated disease-causing genes for bleeding, thrombotic, and platelet disorders: Communication from the SSC of the ISTH

Karyn Megy^{1,2,3} | Kate Downes^{1,2,3} | Ilenia Simeoni^{1,2,3} | Loredana Bury⁴ | Joannella Morales⁵ | Rutendo Mapeta^{1,2,3} | Daniel B. Bellissimo⁶ | Paul F. Bray⁷ | Anne C. Goodeve⁸ | Paolo Gresele⁴ | Michele Lambert^{9,10} | Pieter Reitsma¹¹ | Willem H. Ouwehand^{1,2,3} | Kathleen Freson¹² | on behalf of the Subcommittee on Genomics in Thrombosis and Hemostasis

ORIGINAL ARTICLE jth

Evaluating the clinical validity of genes related to hemostasis and thrombosis using the Clinical Genome Resource gene curation framework

Justyne E. Ross¹ | Shruthi Mohan¹ | Jing Zhang² | Mia J. Sullivan³ | Loredana Bury⁴ | Kristy Lee⁵ | Isabella Futchi¹ | Annabelle Frantz¹ | Dara McDougal¹ | Juliana Perez Botero^{1,3} | Marco Cattaneo⁶ | Nichola Cooper⁷ | Kate Downes⁸ | Paolo Gresele⁴ | Catriona Keenan⁹ | Alfred I. Lee¹⁰ | Karyn Megy¹¹ | Pierre-Emmanuel Morange^{1,14} | Neil V. Morgan^{1,9} | Harald Schulze¹⁴ | Karen Zimowski¹⁵ | Kathleen Freson¹⁶ | Michele P. Lambert^{17,18}

ClinGen Clinical Genome Resource

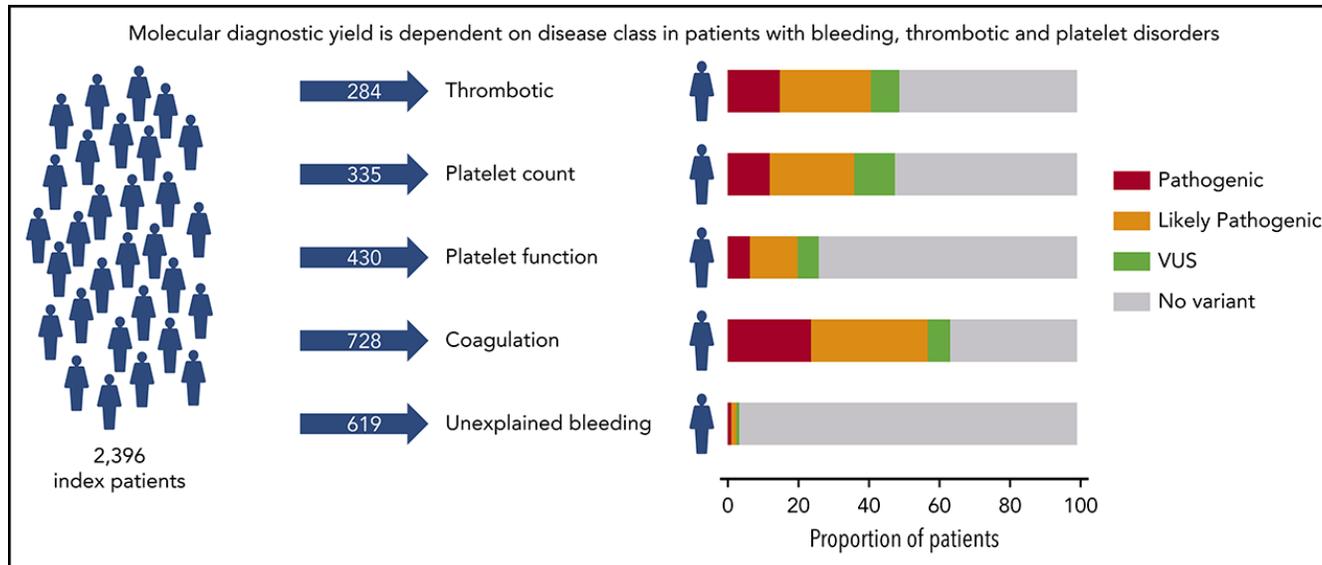
Diagnostic rates obtained in the ThromboGenomics study



THROMBOSIS AND HEMOSTASIS

Diagnostic high-throughput sequencing of 2396 patients with bleeding, thrombotic, and platelet disorders

Kate Downes, Blood 2019



Diagnostic rates for

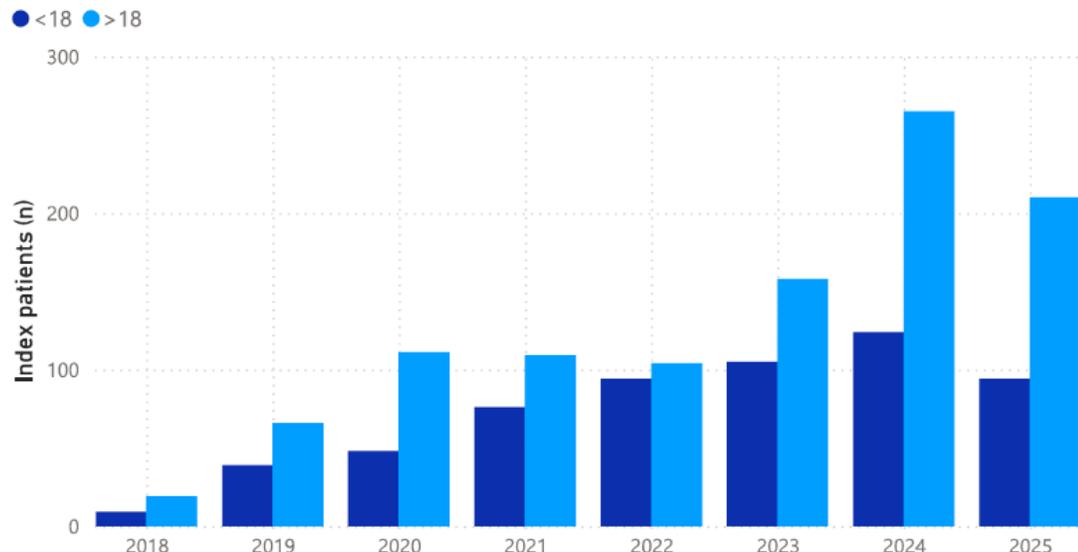
- Thrombocytopenia 50%
- Platelet function disorders 27%

WES-based panel for bleeding @UZLeuven



Christine Van Laer

Age index



- Referral center in Belgium
- Part of NHS (1200 euro/panel – 8 euro/patient), strict inclusion: **Platelet function disorders: no storage pool disease !**
- TAT 3 months
- Accredited test (100% coverage, variants are validated)

<https://doi.org/10.1016/j.jtha.2022.12.007>

J Thromb Haemost. 2023;21:887–895

BRIEF REPORT

Interim analysis

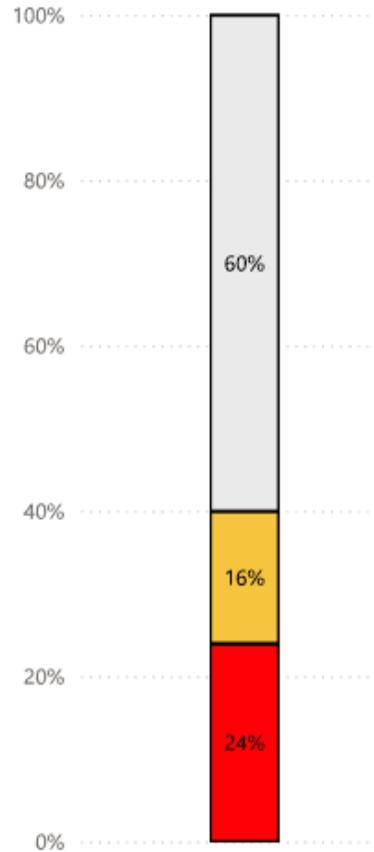
jth

Clinical application of multigene panel testing for bleeding, thrombotic, and platelet disorders: a 3-year Belgian experience

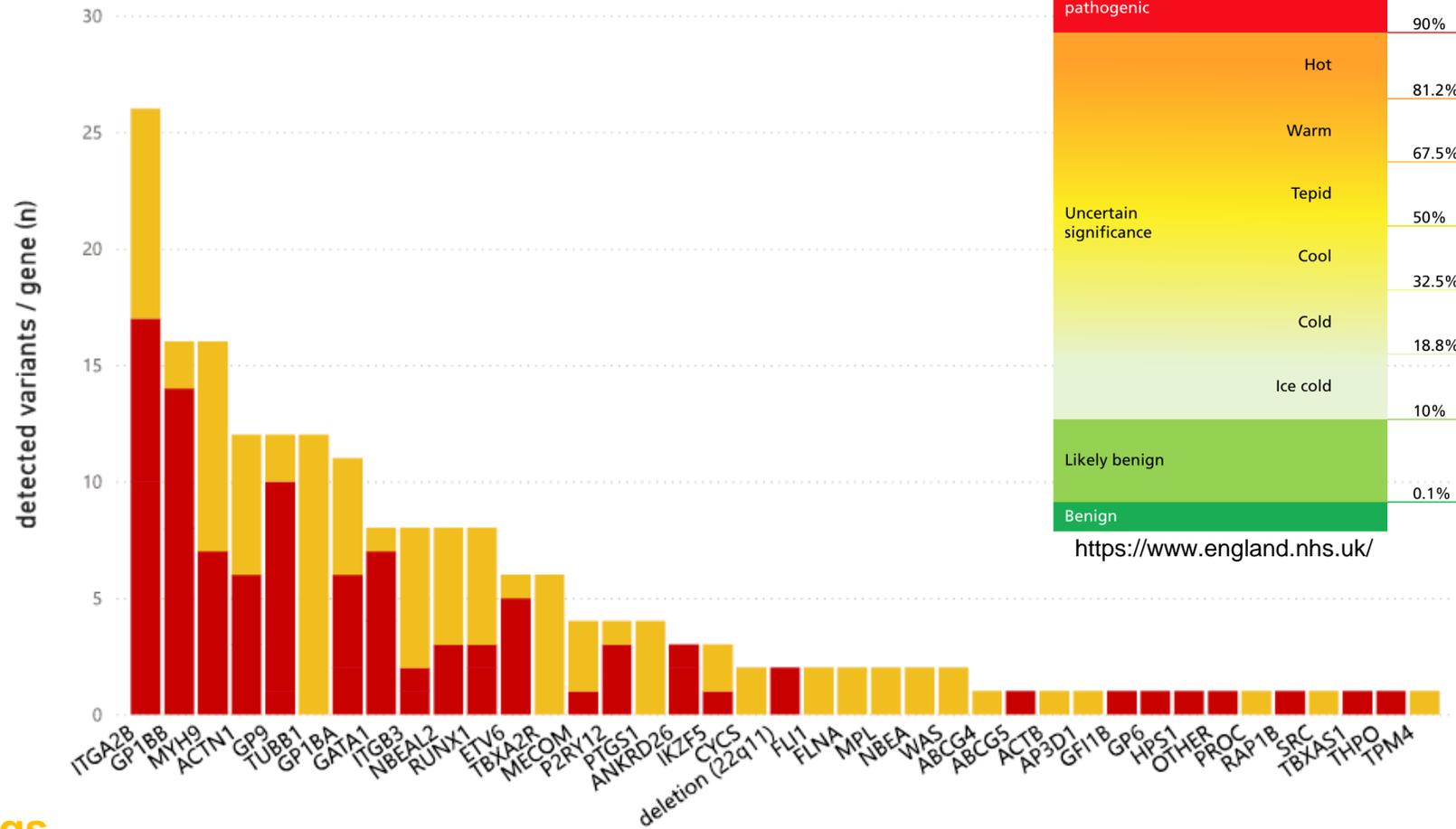
Christine Van Laer^{1,2} | Marc Jacquemin^{1,2} | Sarissa Baert³ | Veerle Labarque¹ | Chantal Thys¹ | Thomas Vanassche^{1,5} | Chris Van Geet^{1,4} | Peter Verhamme | Karen Willekens³ | Anniek Corveleyn³ | Kathelijne Peerlinck^{1,5} | Kathleen Freson¹

Platelet genes

● 1. (L)PV ● 2. VUS ○ 3. NEG



● LPV ● PV ● VUS



Variant classification	VUS temperature scale	Posterior probability
Pathogenic		99%
Likely pathogenic		90%
Uncertain significance	Hot	81.2%
	Warm	67.5%
	Tepid	50%
	Cool	32.5%
	Cold	18.8%
	Ice cold	10%
Likely benign		0.1%
Benign		

<https://www.england.nhs.uk/>

These are all “HOT” VUS findings

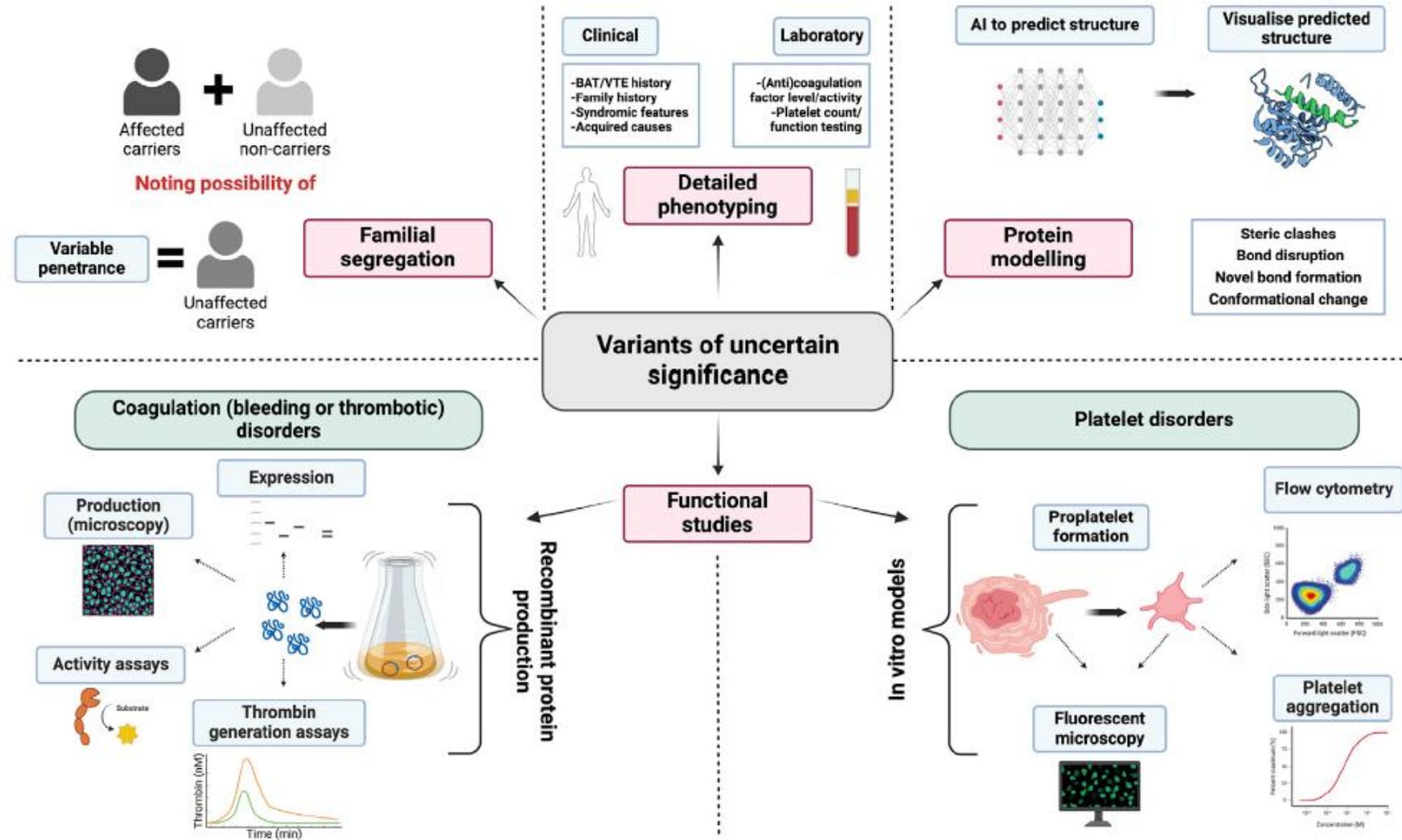
Most patients have thrombocytopenia, most common function disorders are

- Glanzmann thrombasthenia
- Dominant TBXA2R, P2RY12 and PTGS1 defects

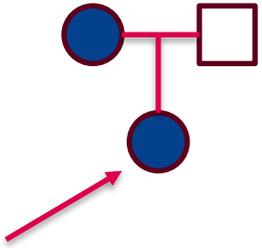
How to reclassify a VUS to LPV?

Implementation and clinical utility of multigene panels for bleeding, platelet, and thrombotic disorders

Radha Raman^{1,2,3} | Andreas Verstraete^{1,4} | Christine Van Laer^{1,5} | Kathleen Freson¹



Additional lab tests for variant reclassification



Index case, 35 y

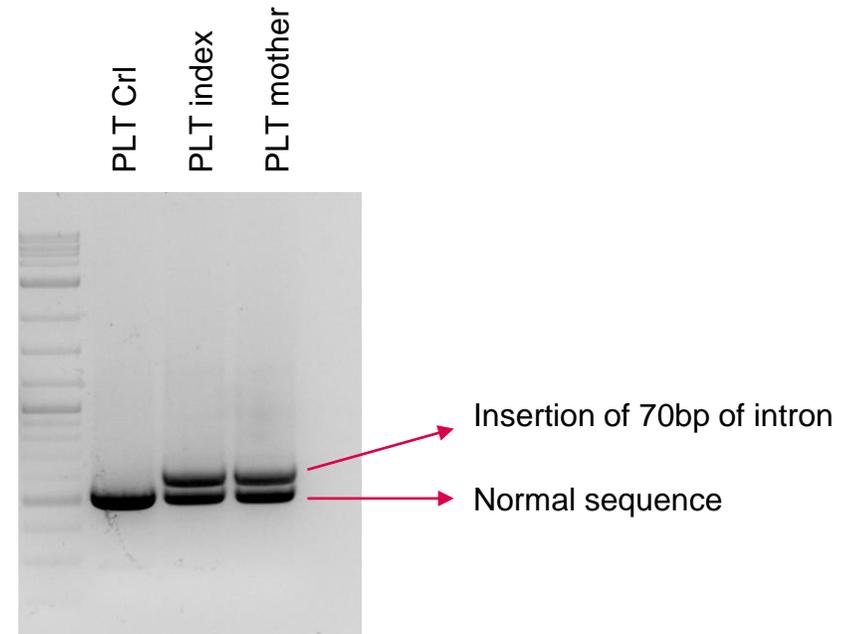
No bleeding symptoms

Platelet count 99-134 K (nl MPV)

Autosomal dominant TP

ETV6 c.1254-2A>C VUS

ETV6 c.1254-2A>C LPV



Patient with mild macrothrombocytopenia (100K, MPV 12 fL), mild bleeding, family history with dominant TP

Franklin by genoox

SEARCH
KNOWLEDGE BASE
MY CASES

All Cases > GC163145_111471630_356816_5071_single

GC163145_111471630_356816_5071_single

Assay: Internal Medicine_VCF_HG38 | Assignee: kathleen.freson@kuleuven.be | Status: Pending Review

Case Details

Analysis Results
6 Clinically relevant variants

Quality Control
All Samples Passed QC

▼ Variants
6 clinically relevant variants detected ROH | Add variant

Workbench

▼ Not in Report (4)

Variants

Waiting for assessment

Causal Variants
Variant in Table
VUS to Report

All

Coverage Report

★ **Bernard-soulier syndrome** was found to have a **Very High** connection to the case phenotypes **Thrombocytopenia, Petechiae and 2 more** ★ +2 more

	FREQUENCY	INTERNAL	COMMUNITY	CONFIDENCE	PREDICTION	INHERITANCE	CLINVAR
<input type="checkbox"/> LP	<0.01%	0%	6	High	Deleterious	AR	1 P 3 LP
	0 Hom	0 Hom	1 Hom	AB: 41.86%	Revel: 0.89	1 Conditions	P NR

Chr22:19723890-T-C | NM_000407.5 | Missense | Exon 2 Inw_single_Tier1 Inw_single_cardio_Tier1 Trombose-Hemostase_122018_GRCh38 WB

Report Preview

★ **Thrombocythemia 2 (Somatic Mutation)** was found to have a **Very High** connection to the case phenotypes **Thrombocytopenia, Petechiae a...** ★ +2 more

	FREQUENCY	INTERNAL	COMMUNITY	CONFIDENCE	PREDICTION	INHERITANCE	
<input type="checkbox"/> VUS	<0.01%	0.15%	4	High	Uncertain	AR AD +2	VUS NR
	0 Hom	0 Hom	0 Hom	AB: 62.77%	Revel: 0.41	5 Conditions	VUS NR

Chr1:43339309-G-A | NM_005373.3 | Missense | Exon 4 Inw_single_Tier1 Inw_single_cardio_Tier1 Trombose-Hemostase_122018_GRCh38 WB

Case History

💬 Volledig gecoverd

GP1BB:c.47T>C

chr22-19723890 T>C | p.Leu16Pro | NM_000407.5 | dbSNP, rs1601248210 | UCSC, gnomAD

Franklin ACMG Classification Variant Assessment Associated Conditions Pub

Suggested Classification
Likely Pathogenic

Benign Likely Benign VUS Likely Pathogenic Pathogenic

Apply Classification

EVIDENCE

Aggregated from public databases using ACMG Guidelines

Allelic Data

PM3



Pathogenic Strong:

For recessive disorders, detected in trans with a pathogenic variant, or in a homozygous or compound heterozygous state in affected cases [See Details](#)

UNMET: BP2

[See Details](#)

Population Data

PM2



Pathogenic Moderate:

Extremely low frequency in gnomAD population databases [See Details](#)

UNMET: BA1 | BS1 | BS2

[See Details](#)

In-silico Predictions

PP3



Pathogenic Moderate:

For a missense or a splicing region variant, computational prediction tools unanimously support a deleterious effect on the gene [See Details](#)

Franklin uses the latest recommendations (2022) for PP3/BP4 rules [Learn how](#)

UNMET: BP4

[See Details](#)

Functional Data

PP2



Pathogenic Supporting:

Missense variant in a gene with low rate of benign missense mutations and for which missense mutation is a common mechanism of a disease

[See Details](#)

UNMET: PM1

[See Details](#)

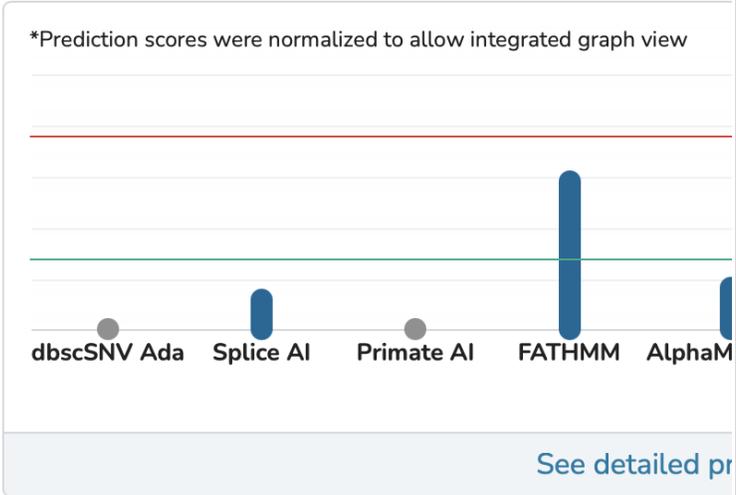
De Novo Data

Criteria unmet

UNMET: PS2 | PM6

[See Details](#)

Predictions



4 evidences

Submissions: ● LP(3) ● P(1)

[CLINVAR](#)

Franklin Community (0)

Clinvar (4)

- Clinvar Clinical Significance: **Likely pathogenic**

Thrombocytopenia

Review Status: ★☆☆☆☆ | RCV000852142 | [Clinvar](#)

Last evaluated: Feb 16, 2023 | 1 submitter
- Clinvar Clinical Significance: **Pathogenic**

Bernard Soulier Syndrome

Review Status: ★☆☆☆☆ | RCV002222630 | [Clinvar](#)

Last evaluated: Feb 16, 2023 | 1 submitter
- Clinvar Clinical Significance: **Likely pathogenic**

Not Provided

Review Status: ★☆☆☆☆ | RCV003324792 | [Clinvar](#)

Last evaluated: Feb 16, 2023 | 1 submitter
- Clinvar Clinical Significance: **Likely pathogenic**

Macrothrombocytopenia

Review Status: ☆☆☆☆☆ | RCV001003916 | [Clinvar](#)

Internal Frequency

0%

Very Rare variant in your Samples

0
Number of
Homozygote

Sample	Phenotypes	Affected status	Ethnicity	Zygoty	Depth
GC163145_1114716 30_356816_5071	Thrombocytopenia, Petechiae, Epistaxis, Menorrhagia	Affected	N/A	Het	43
GC164574_1118445 41_361920_6271	N/A	Affected	N/A	Het	52

Phenotypes

Click the tag to disable the phenotype

No Phenotype was added

[Add / Remove Phenotypes](#)

Case Comments

Phenotype: trombopenie,
verhoogde
bloedingsneiging
Voorafgaand onderzoek: /
Familiegeschiedenis:
vader milde trombopenie

[Minimize](#)

[Add / Edit](#)

Two Genetic Testing Pathways for Inherited Platelet Function Disorders

40%

MultiGene Panel Test (Exome or targeted)

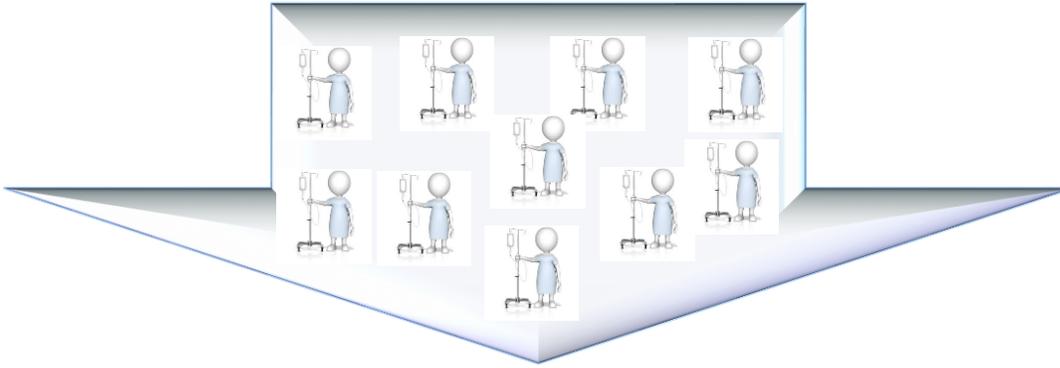
1. Genetic testing in the clinic

Whole Genome Sequencing

Blood transcriptomics

2. Genetic testing in research

Other omics?



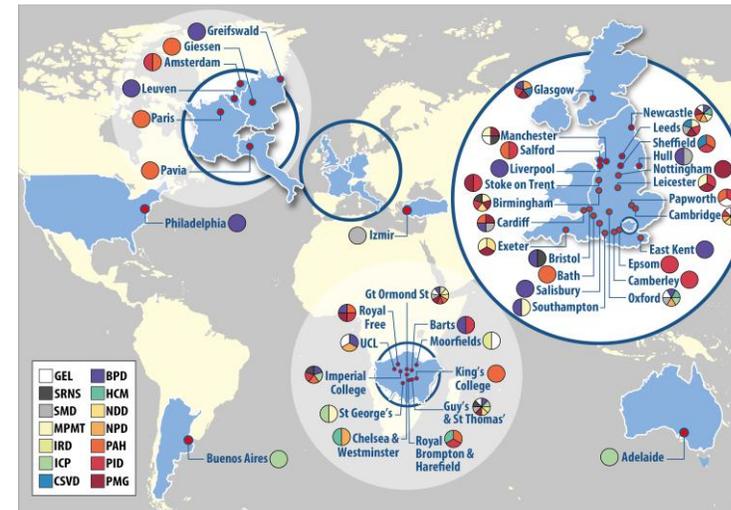
Gene discovery using WGS

 Bleeding, thrombotic and Platelet Disorders	BPD	 Multiple Primary Malignant Tumours	MPMT
 Cerebral Small Vessel Disease	CSVD	 Neurological and Developmental Disorders	NDD
 Ehler-Danlos Syndromes	EDS	 Neuropathic Pain Disorders	NPD
 Rare Diseases Pilot-II	GEL	 Pulmonary Arterial Hypertension	PAH
 Hypertrophic Cardiomyopathy	HCM	 Primary Immune Disorders	PID
 Intrahepatic Cholestasis of Pregnancy	ICP	 Primary Membranoproliferative Glomerulonephritis	PMG
 Inherited Retinal Disorders	IRD	 Stem cell and Myeloid Disorders	SMD
 Leber Hereditary Optic Neuropathy	LHON	 Steroid Resistant Nephrotic Syndrome	SRNS
			UKBio
UK Biobank – Extreme Red Cell Traits			

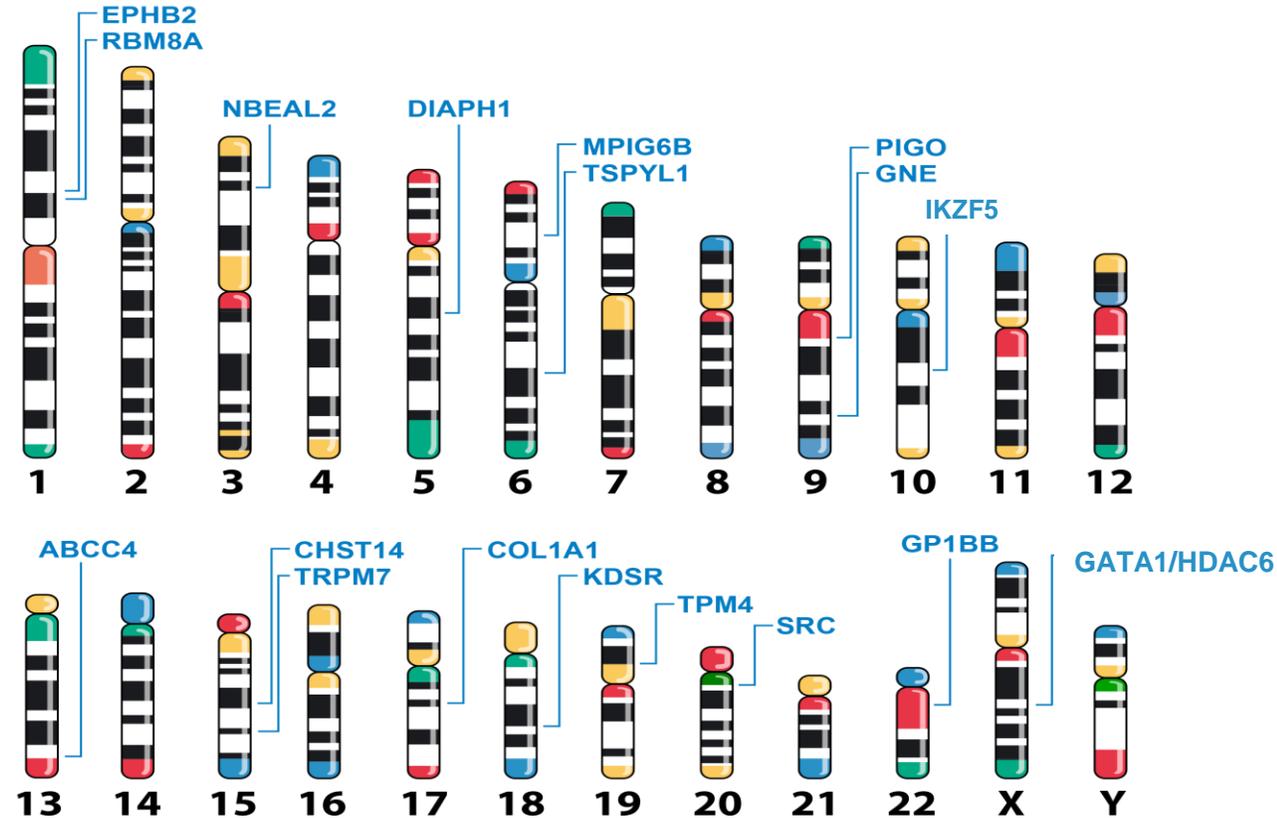
- **57 NHS Hospitals and 26 non-UK Hospitals**

(Bleeding & Platelet Disorders 1916 patients)

- **13,037 index patients**



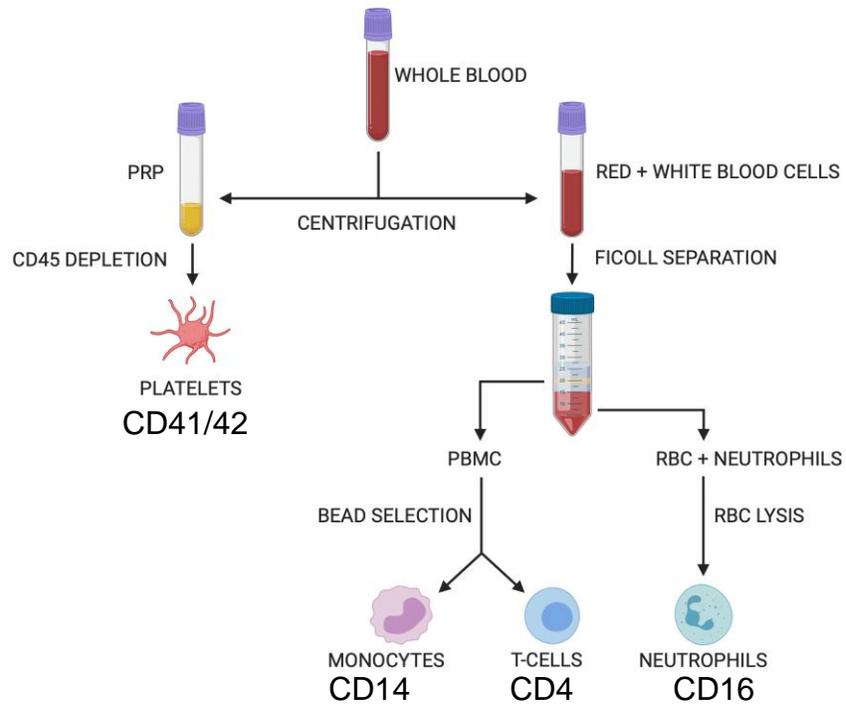
2011-2020: 18 new genes for bleeding & platelet disorders



UZLeuven (543 patients):
Only 10% diagnostic rate

Albers *et al*, Nat Genetics 2011; Albers *et al*, Nat Genetics 2012; Cvejic *et al*, Nat Genetics 2013; Chen *et al*, Science 2014; Westbury *et al*, Genome Medicine 2015; Green *et al*, AJHG 2016; Stritt *et al*, Nat Comm 2016; Turro *et al*, Science Transl Med 2016; Stritt *et al*, Blood 2016; Simeoni *et al*, Blood 2016; Lentaingne *et al*, Blood 2016; Poggi *et al*, Haematologica 2016; Bariana *et al*, BJH 2017; Siva-palaratnam *et al*, Blood 2017; Pleines *et al*, JCI 2017; Greene *et al*, AJHG 2017; Westbury *et al*, Blood 2017; Sivapalaratnam *et al*, BJH 2017; Morren *et al*, Orphanet 2017; Freson *et al*, JTH 2017; Sowerby *et al*, JCI 2017; Mayer *et al*, Blood 2018; Revel-Vilk *et al*, Blood 2018; Berrou *et al*, Blood 2018; Hofman *et al*, Blood 2018; Bariana *et al*, Haematologica 2018; Westbury *et al*, Blood Adv 2018; Lentaingne *et al*, Blood 2019; Buyse *et al*, HMG 2021

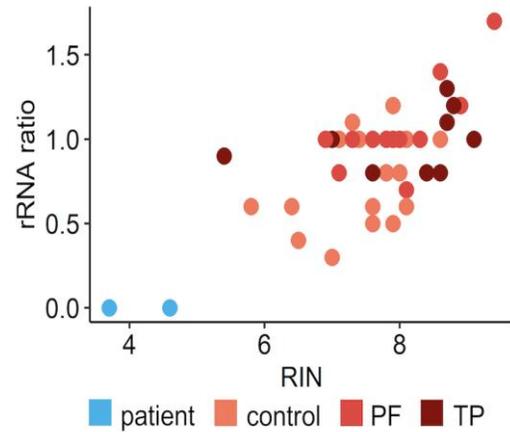
Added value of (blood cell) transcriptomics?



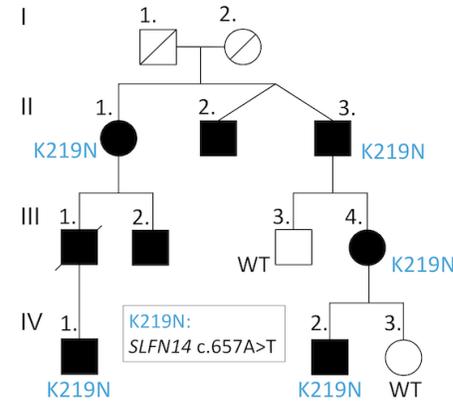
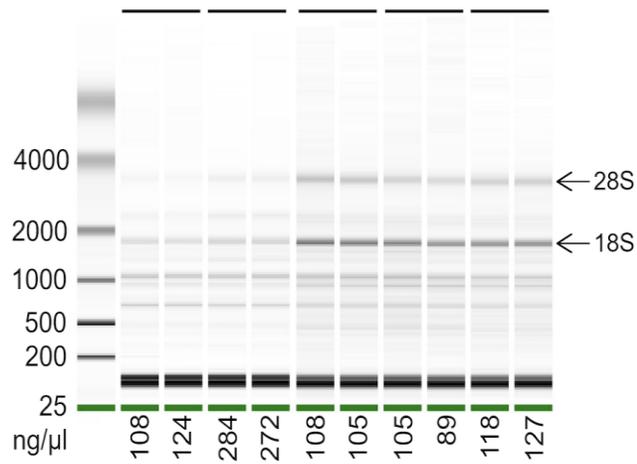
Information about gene expression and splicing outliers
using ML-based approaches
OUTRIDER and FRASER

Brechtmann et al OUTRIDER: A statistical method for detecting aberrantly expressed genes in RNA sequencing data; *AJHG*, 2018
Scheller et al Improved detection of aberrant splicing with FRASER 2.0 and the intron Jaccard index. *AJHG*, 2023

Transcriptomics for understanding of disease mechanism



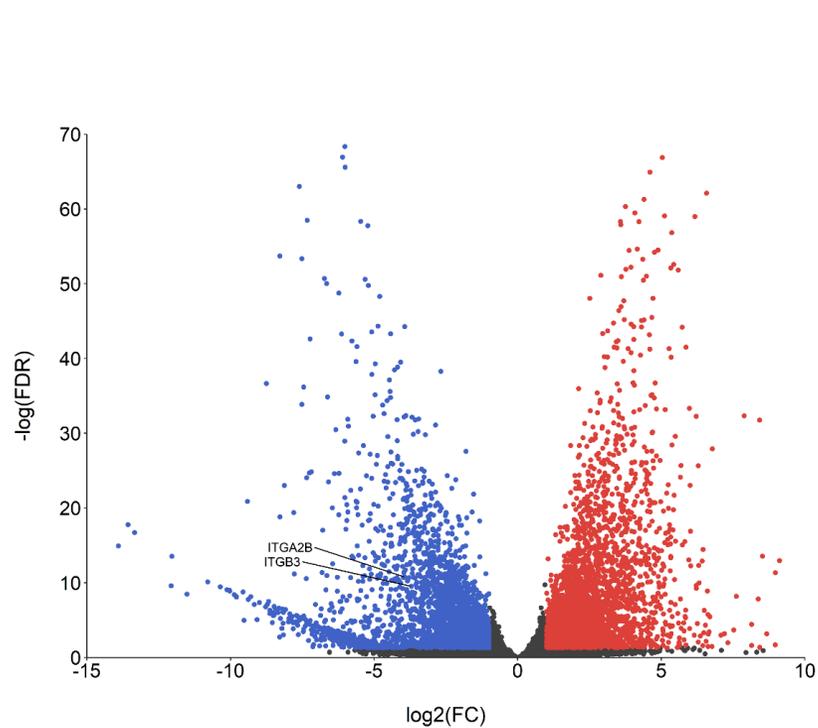
L IV.2 III.4 C1 C2 C3



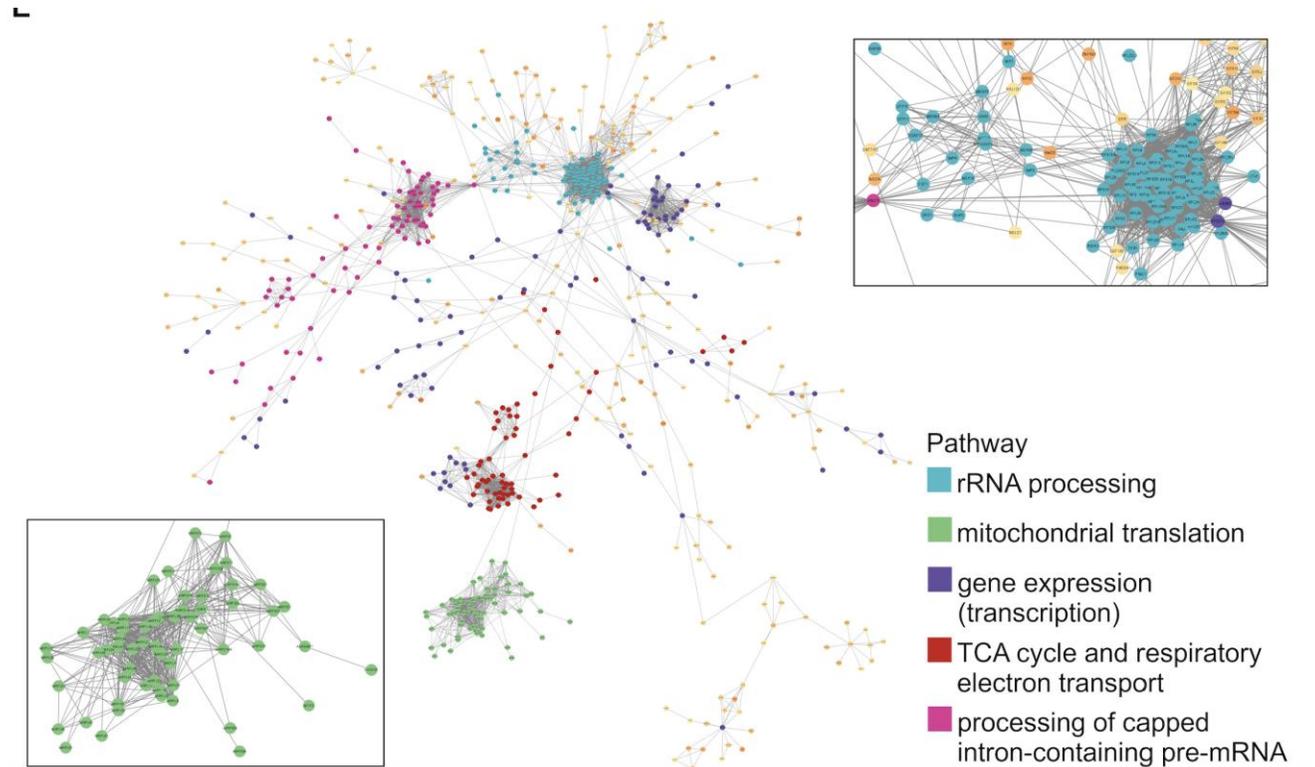
SLFN14 –K219N (endoribonuclease with an unknown role in blood)

Mild thrombocytopenia + Mild PLT dysfunction + “Obvious bleeding”

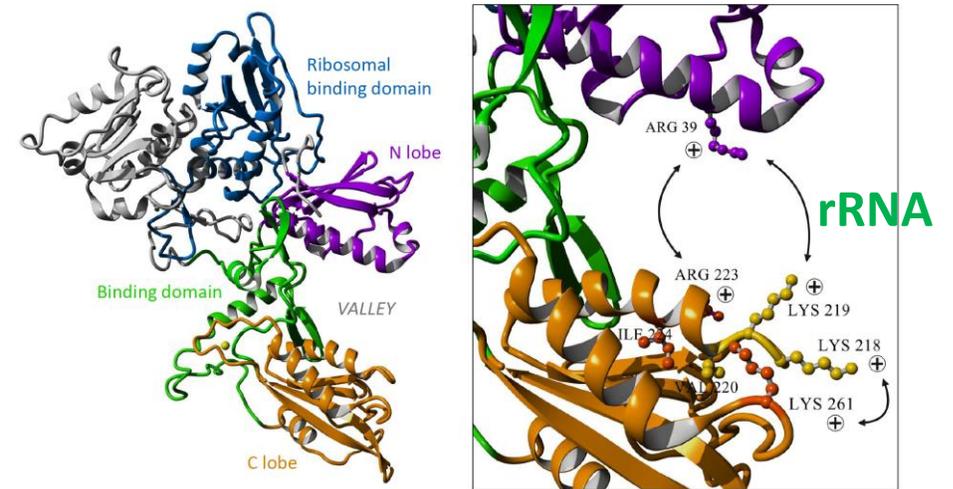
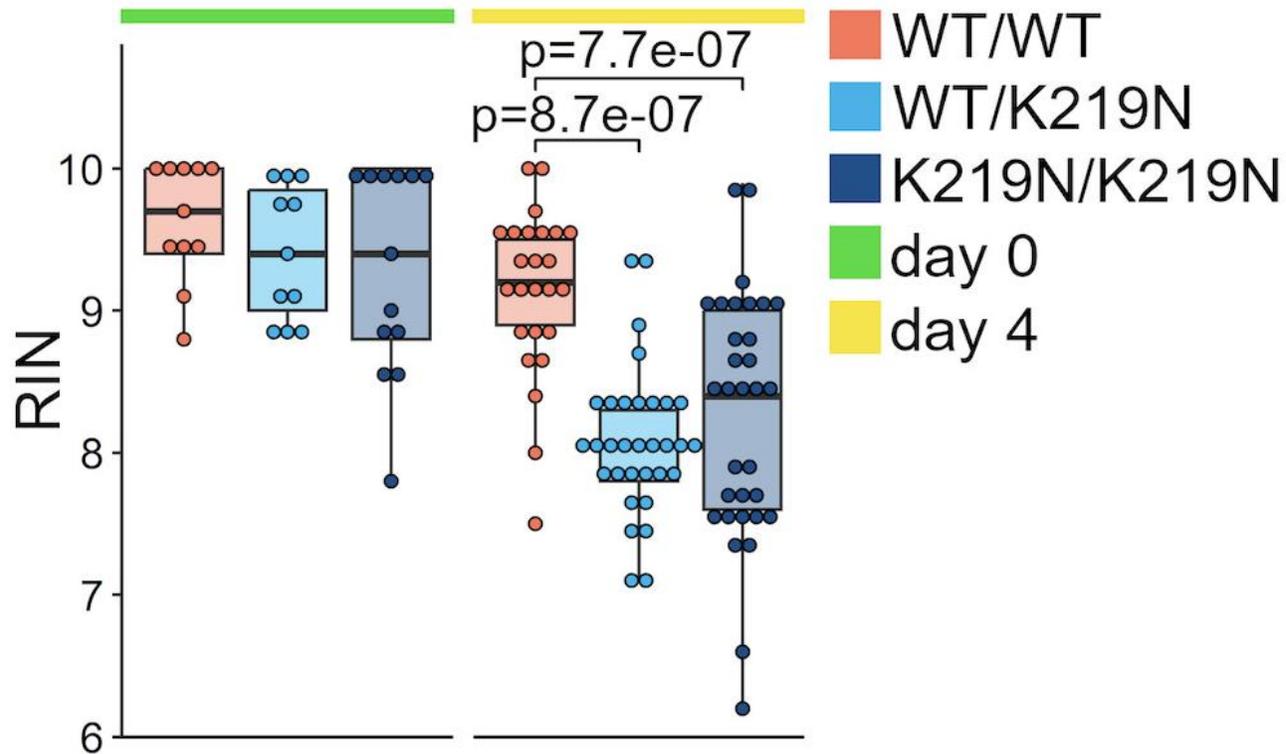
Extensive RNA dysregulation in SLFN14 defective platelets



2888 DOWN & 2999 UP
($|\log_2\text{FC}| > 1, \text{FDR} < 0.05$)



Cell model for the disease : rRNA degradation in SLFN14 defective megakaryocytes



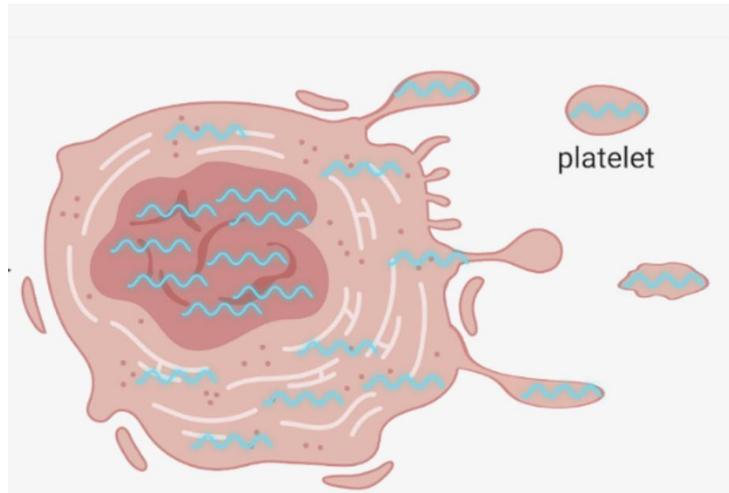
SLFN14 structure

Can platelet transcriptomes (no nucleus) be used ?

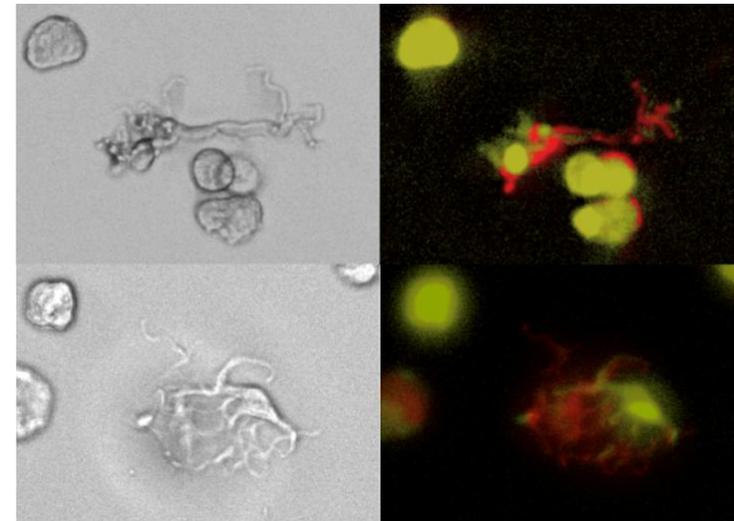
What will happen in case of thrombocytopenia?



Koen De Wispelaere



De Wispelaere et al, IJMC, 2022



StrandBrite RNA
SiR-Actin

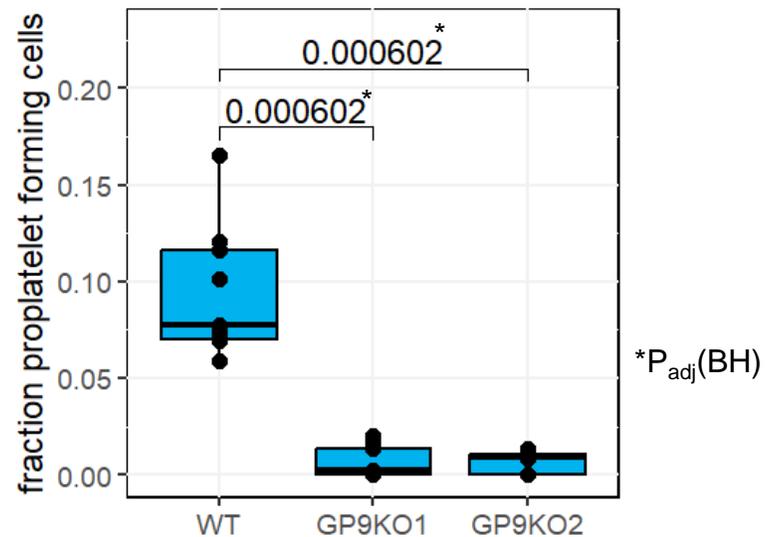
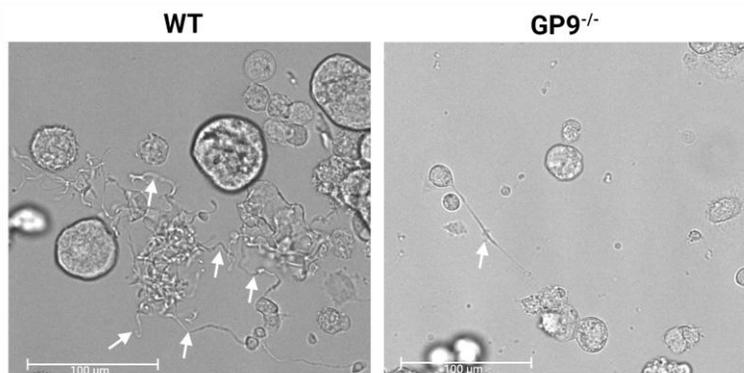
De Wispelaere et al, HemaSphere, 2025

imMKCL disease models for BSS and IKZF5-related thrombocytopenia

Bernard Soulier Syndrome GP9^{-/-}

VWF receptor

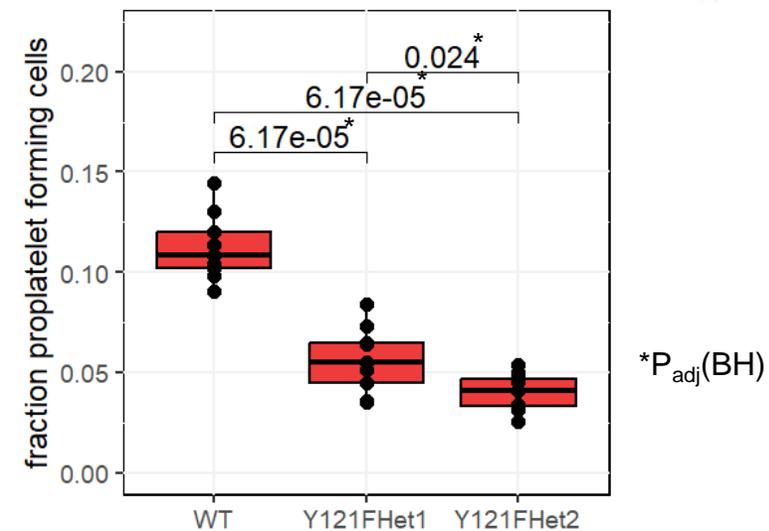
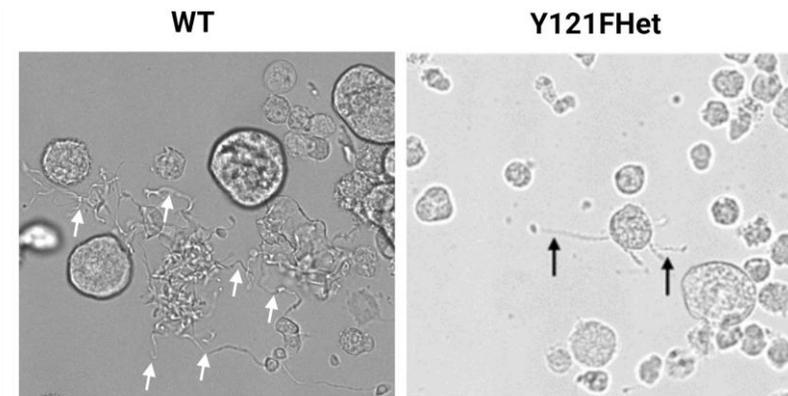
day 4



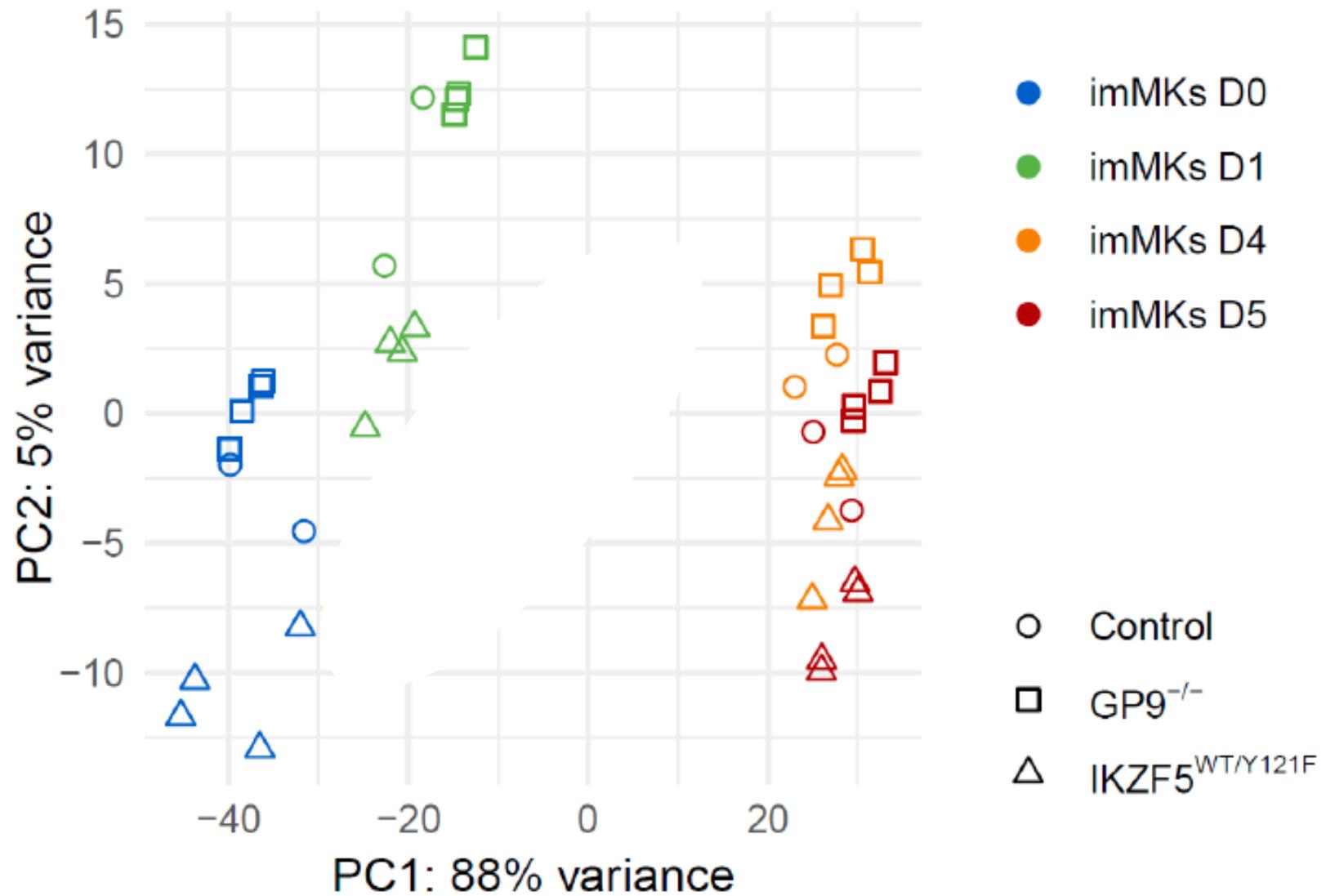
IKZF5-related thrombocytopenie IKZF5^{Y121F/WT}

Transcription factor

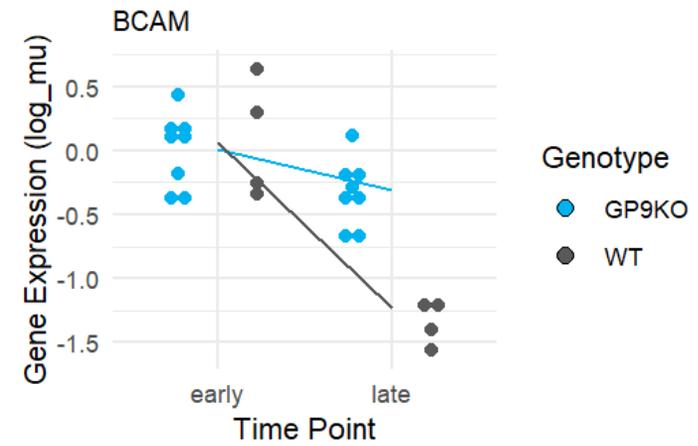
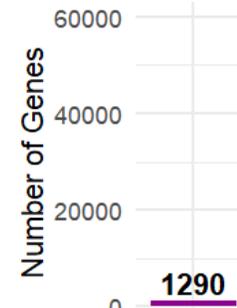
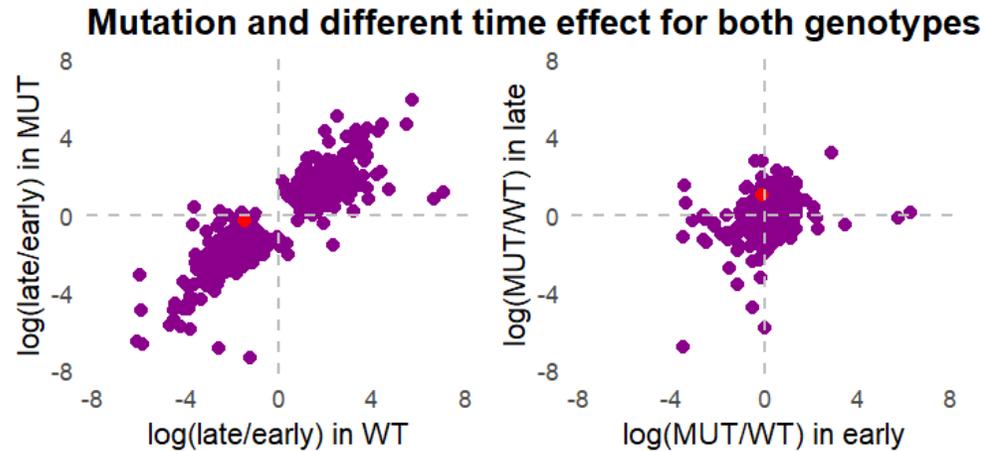
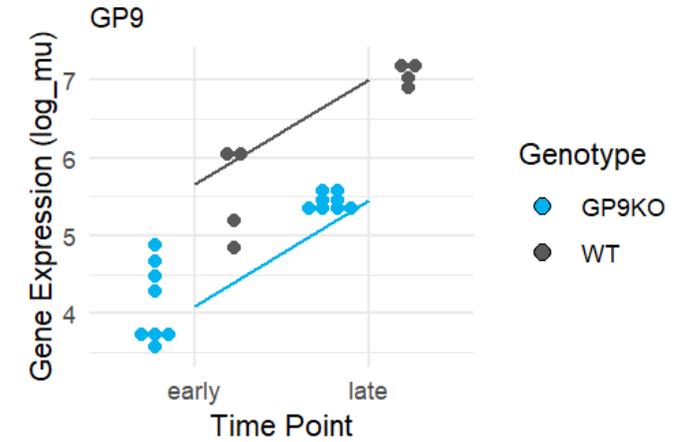
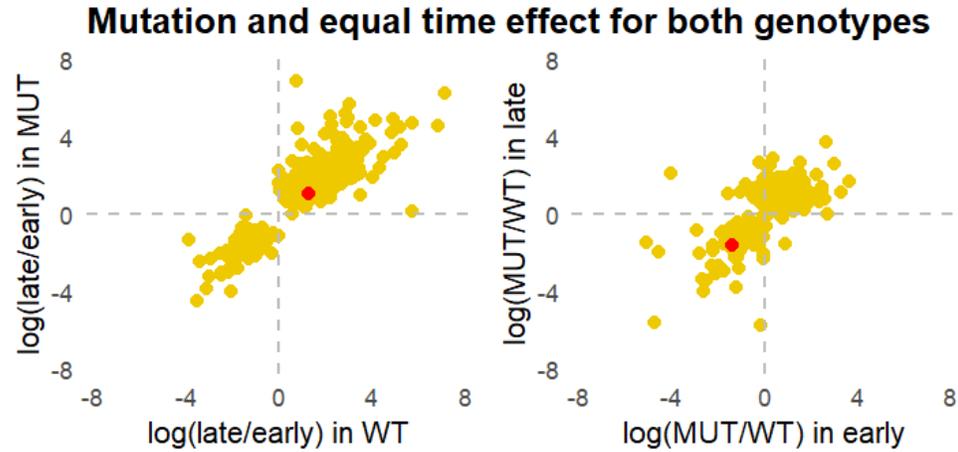
day 4



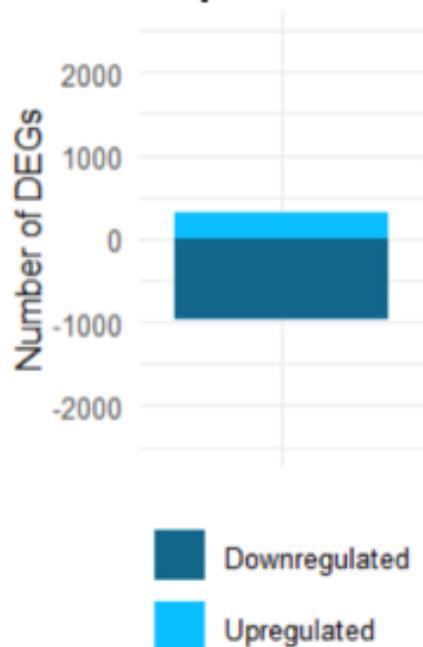
Transcriptome analysis of GP9^{-/-} and IKZF5^{Y121F/WT} deficient MKs (in vitro) and platelets (patients)



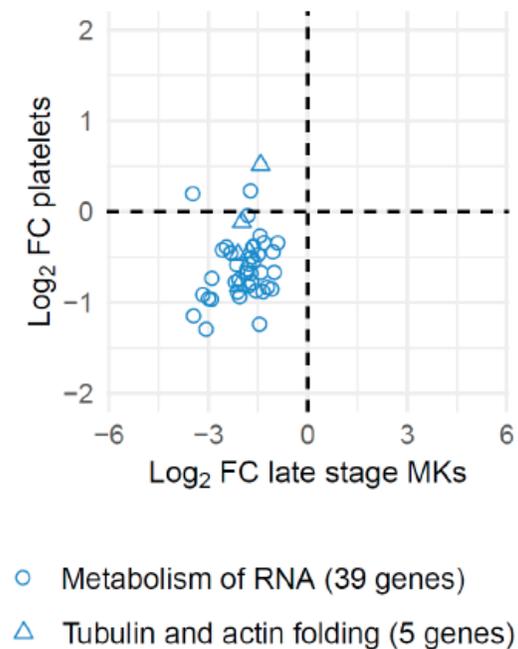
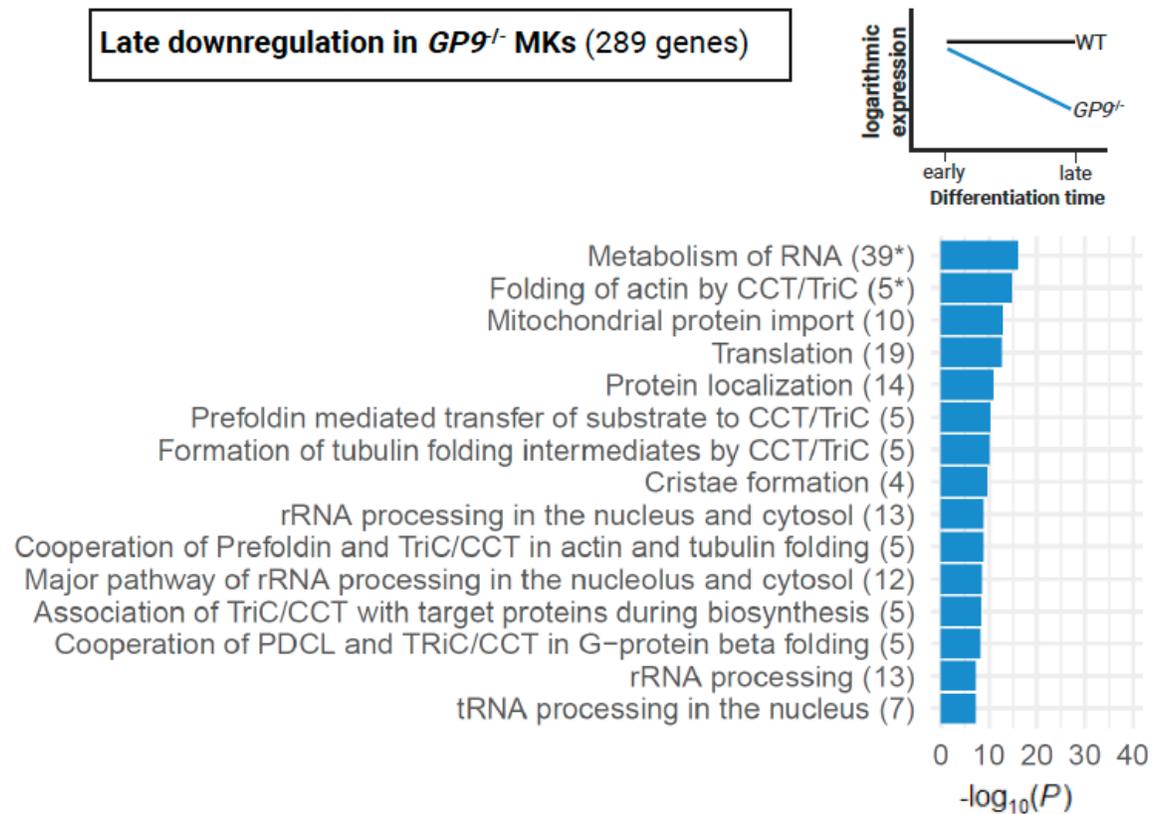
Longitudinal gene expression during MK differentiation



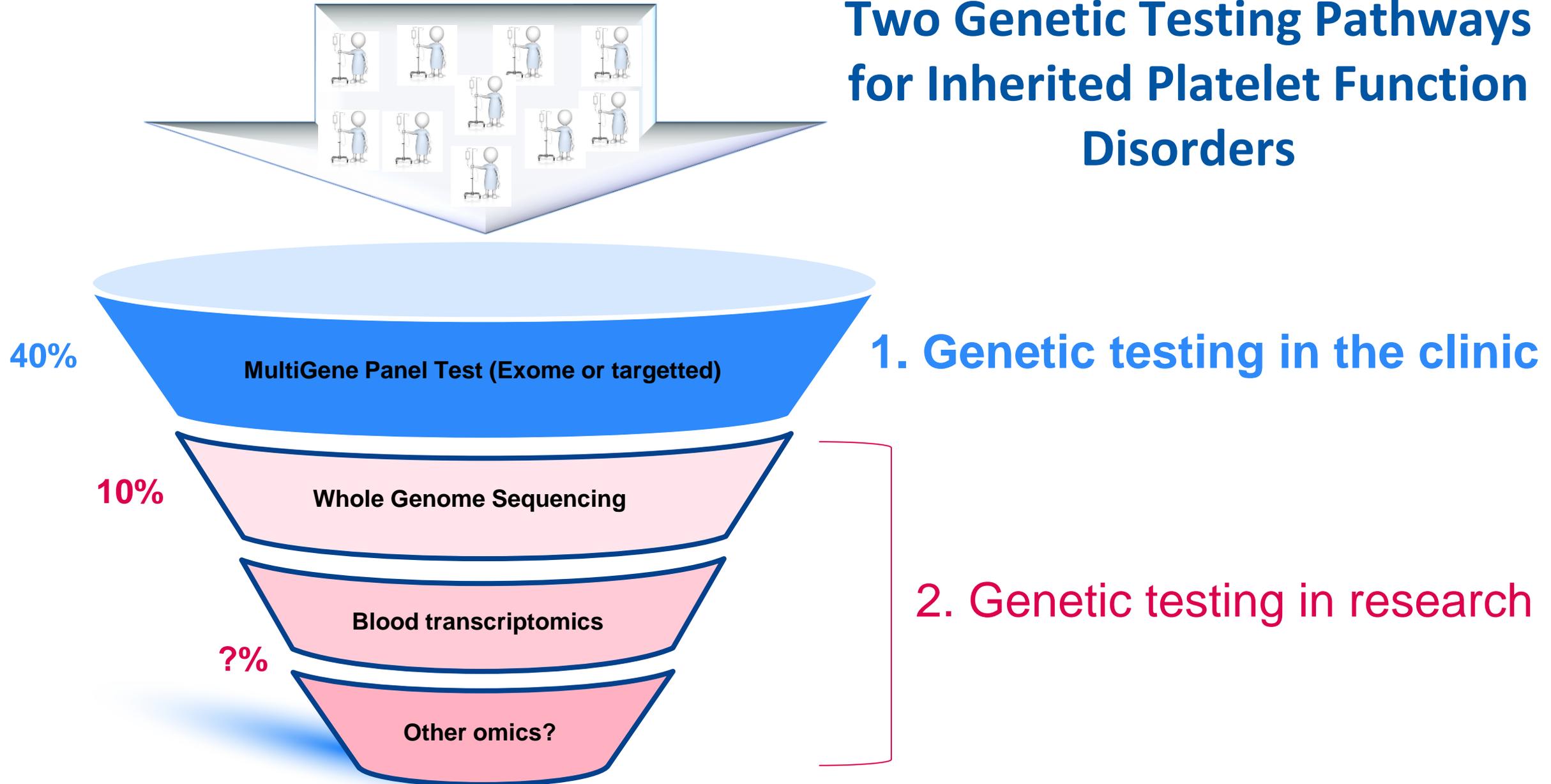
GP9 patient platelets



Late downregulation in *GP9*^{-/-} MKs (289 genes)



Two Genetic Testing Pathways for Inherited Platelet Function Disorders



Take home messages

- NGS for clinical purposes: use of a multigene panel results in 30 (function disorders) - 60% (thrombocytopenia) diagnostic rate
- Whole genomes are useful for gene discovery, but it feels like finding a needle in the haystack at the single patient level
- Transcriptomes can contribute to disease understanding but their added value for gene discovery is not yet clear

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Peter Verhamme
Thomas Vanassche
Quentin Van Thillo
Marc Jacquemin

Collaborators

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Daniel Greene (Cambridge - NY)
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Willem Ouwehand (Cambridge)
Koji Eto (Kyoto)
Alan Nurden (Bordeaux)
Alessandra Balduini (Pavia)

Human Genetics

Anniek Corverleyn
Sarissa Baert
Cyrille Kint
Sarah Willemsens



THANK YOU



CRPP
Centre de Référence
Pathologies Plaquettaires

MHEMO
La Filière des maladies rares de l'hémostase



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<https://maladies-plaquettes.fr/>



<https://x.com/crpp12>



<https://www.linkedin.com/company/fili%C3%A8re-de-sant%C3%A9-maladies-rares-mhemo/>



<https://mhemo.fr/>



<https://x.com/filiereMHEMO>



<https://www.linkedin.com/company/fili%C3%A8re-de-sant%C3%A9-maladies-rares-mhemo/>



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www.eurobloodnet.eu



@ERNEuroBloodNet



eurobloodnet-european-reference-network-on-rare-hematological-diseases



Eurobloodnet - European Reference Network on Rare Hematological Diseases



ERN-EuroBloodNet's EDUcational Youtube channel



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