

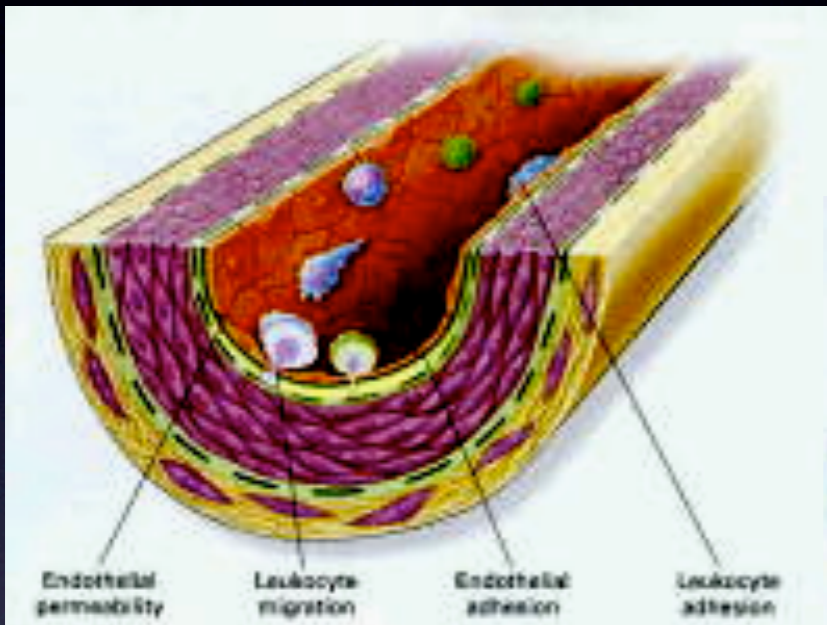
Prospective Study on Circulating MicroRNAs and Risk of Myocardial Infarction

Manuel MAYR, MD, PhD
Professor of Cardiovascular Proteomics
British Heart Foundation Centre

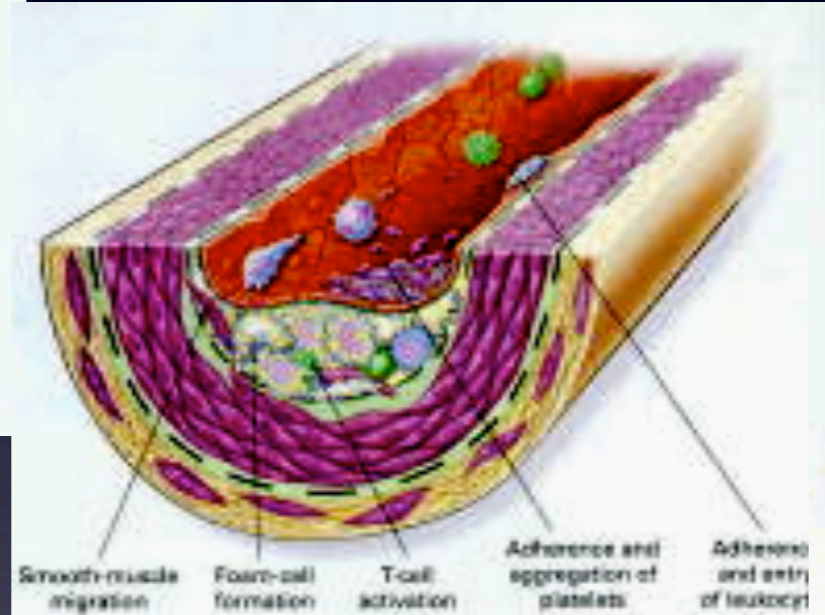


Strategies to deliver new vascular biomarkers ?

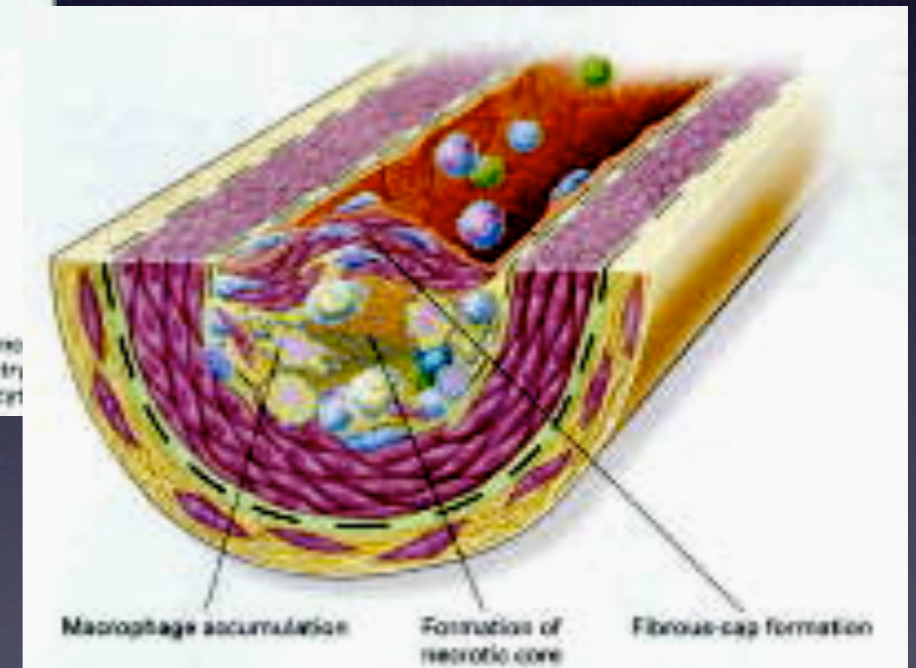
Endothelial dysfunction



Fatty streak formation



Advanced lesion



MiRNAs

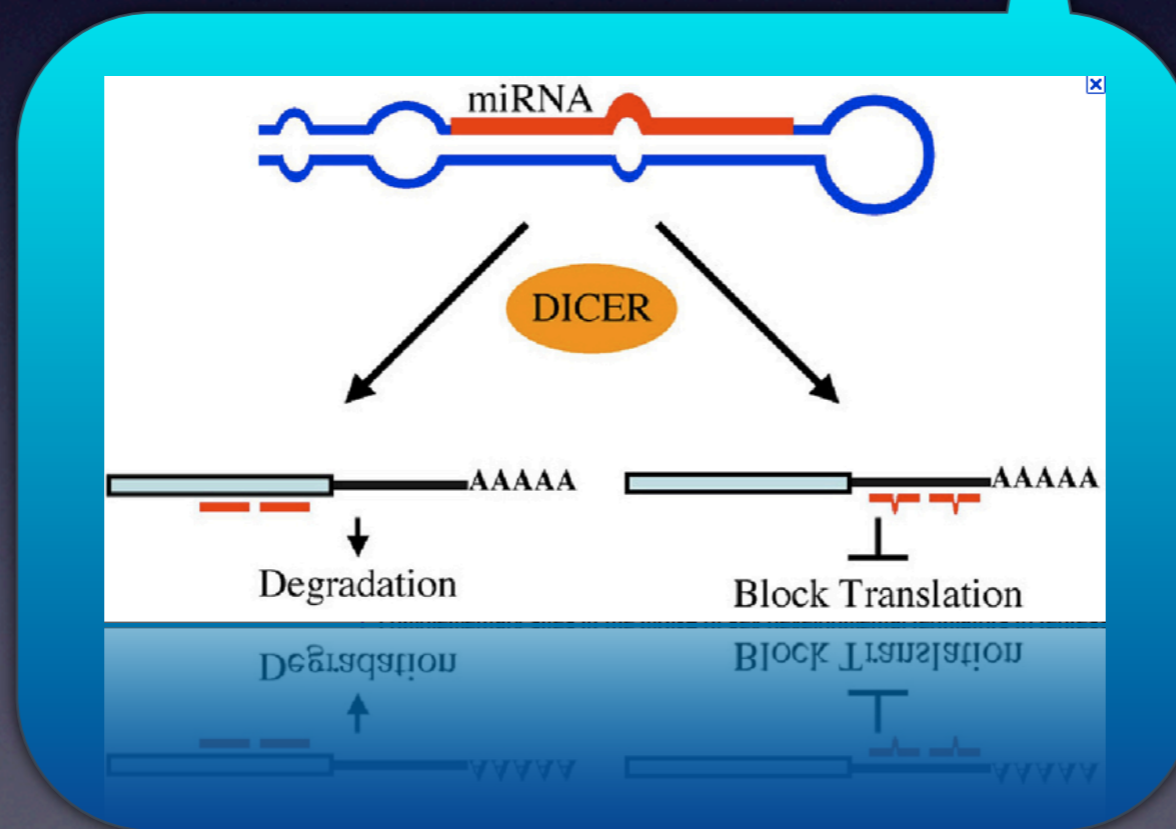
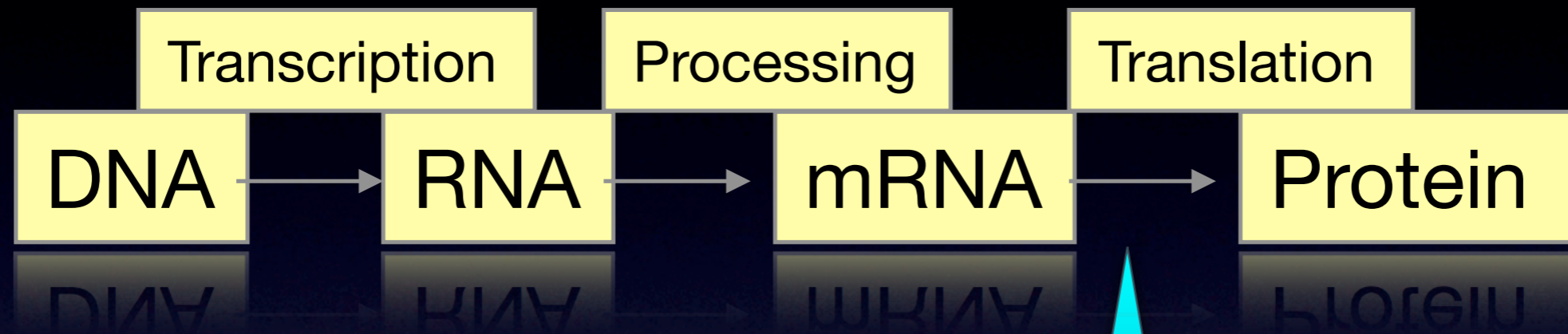
Dr. A. Zampetaki

Lipidomics

Proteomics

MicroRNAs

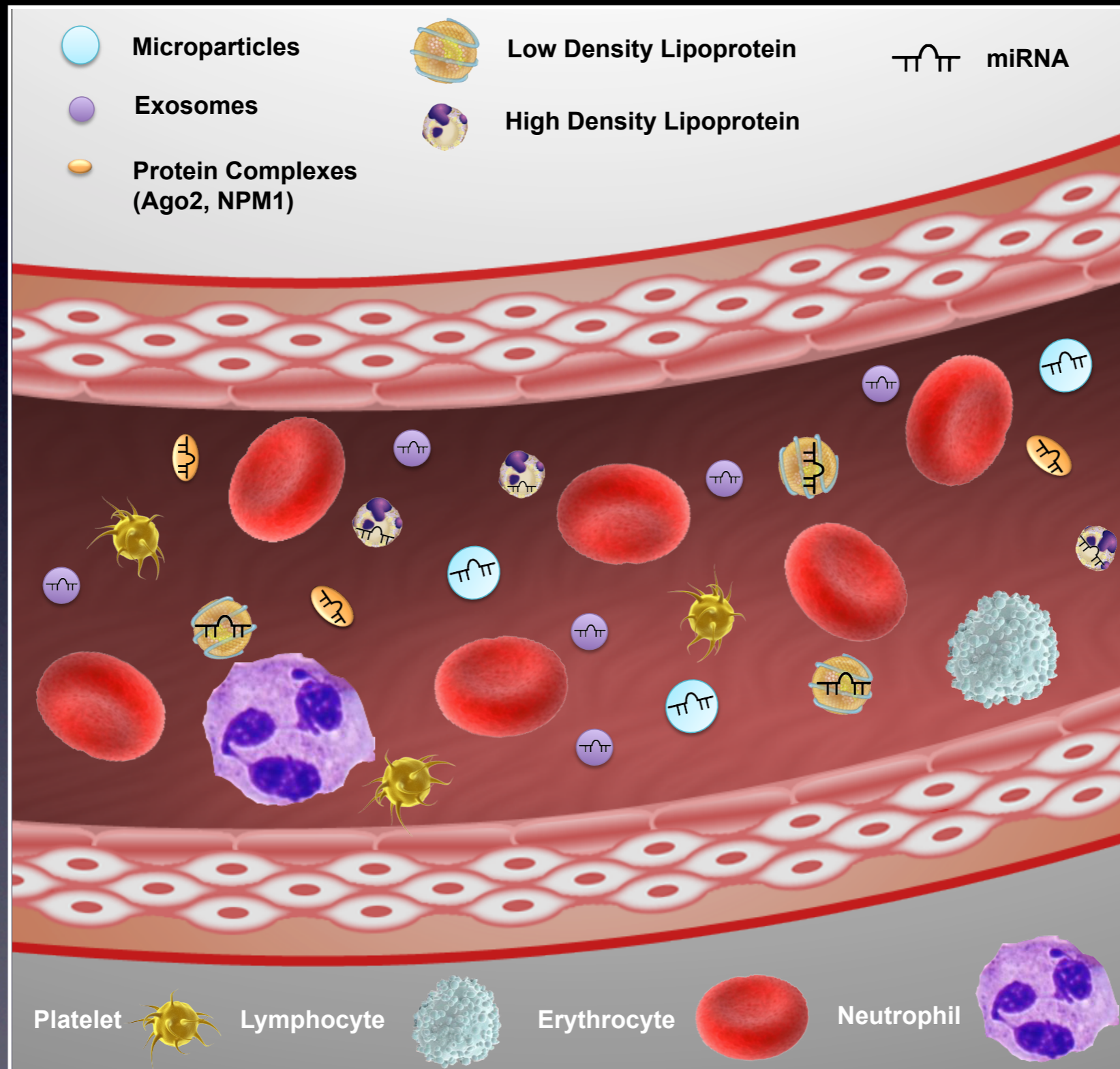
Small Non-Coding RNAs



Another layer of complexity for regulating gene expression

Circulating MicroRNAs

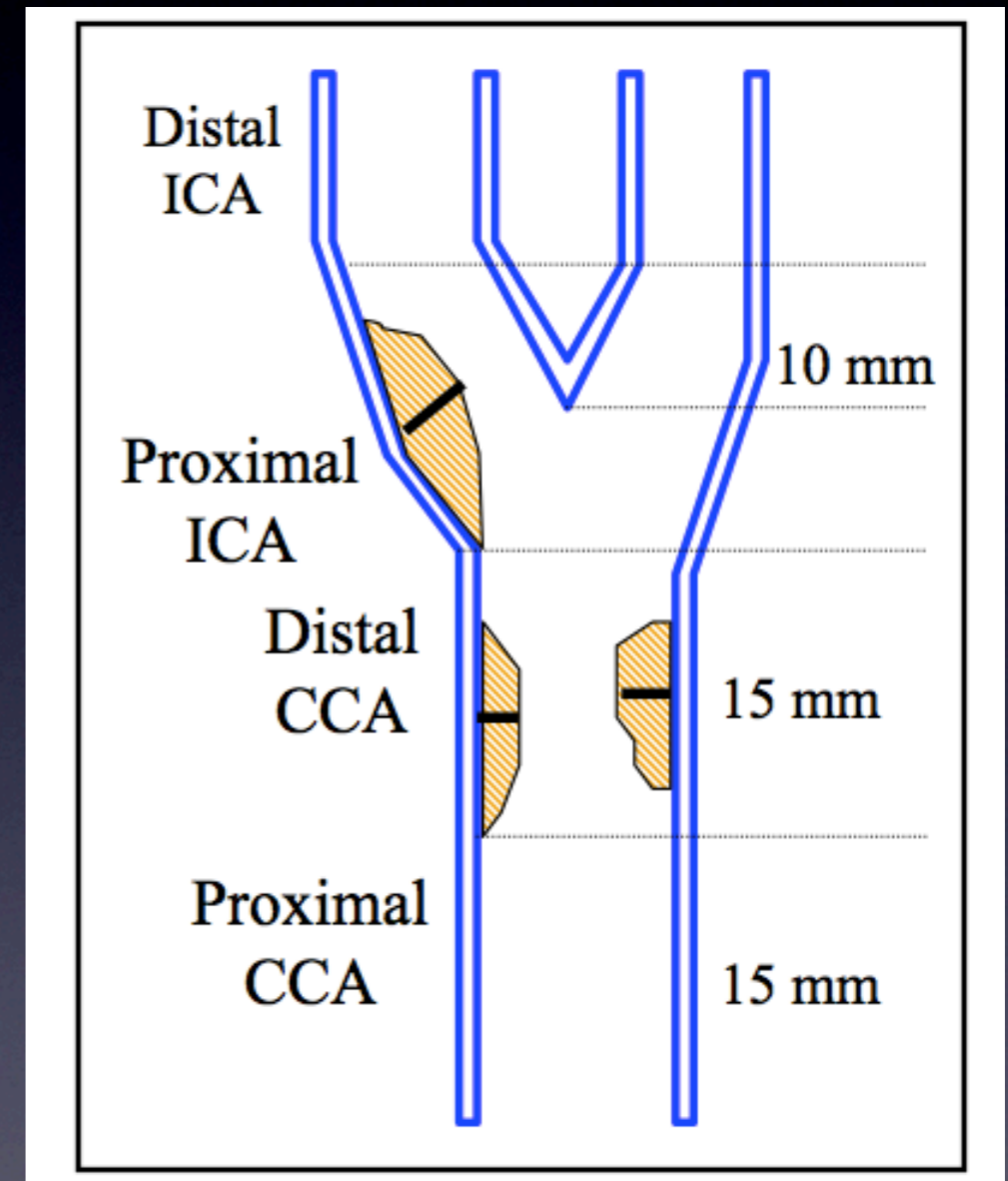
New Biomarkers for Cardiovascular Disease ?



Response to Cardiovascular Risk Factors

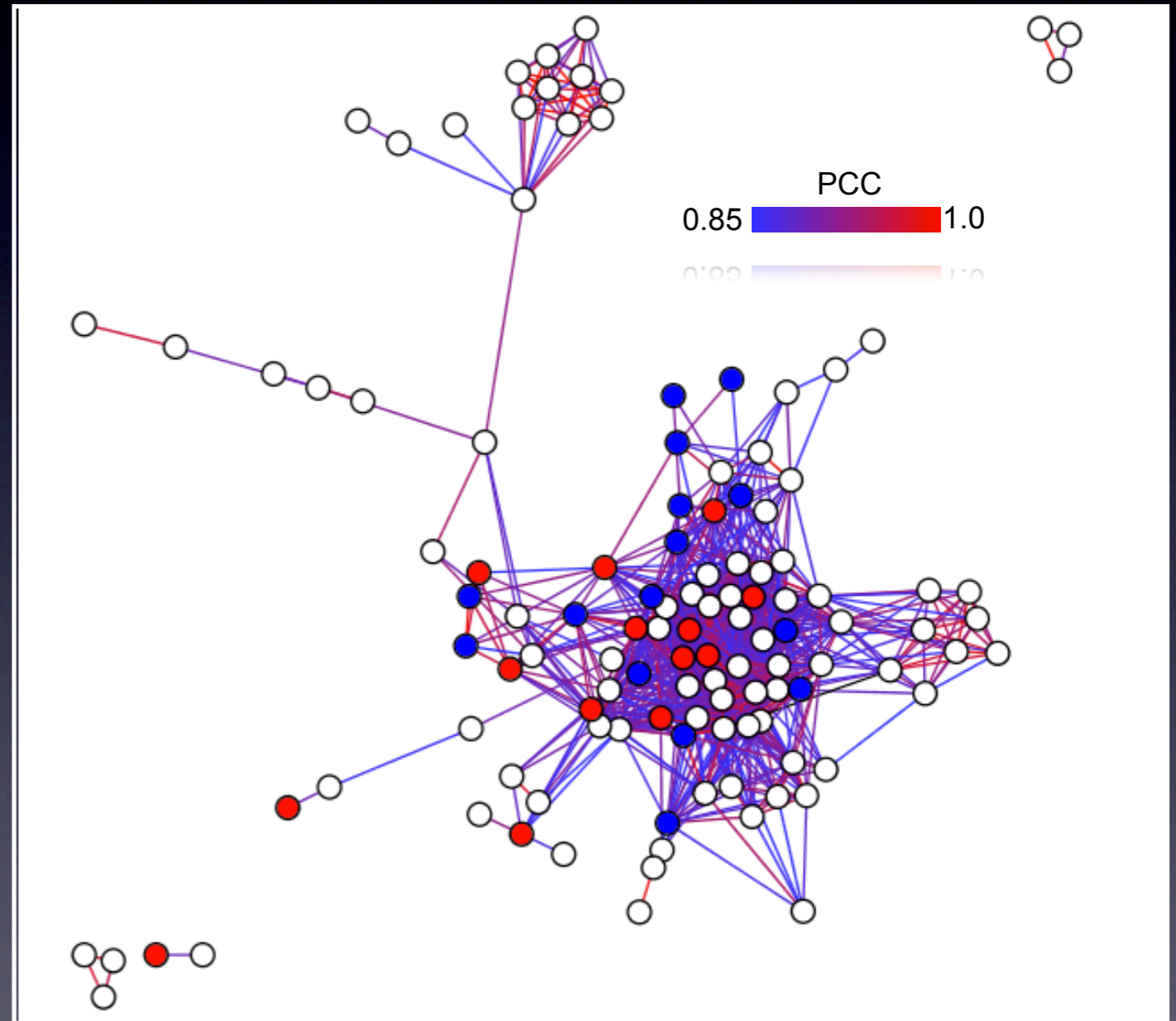
Bruneck Study

- Population-based (n=1000)
- Prospective (1990-2010)
- Assessment every 5 years
- Follow-up >90%
- Person-based progression model
- Age 40-79 years at baseline



Concepts of Network Topology

- Human Taqman miRNA arrays for 754 small non-coding RNAs
- 12 pooled samples (n=60)
- Common cardiovascular risk factors (RR, smoking, DM, LDL)
- 120 miRNAs and 1020 co-expression links

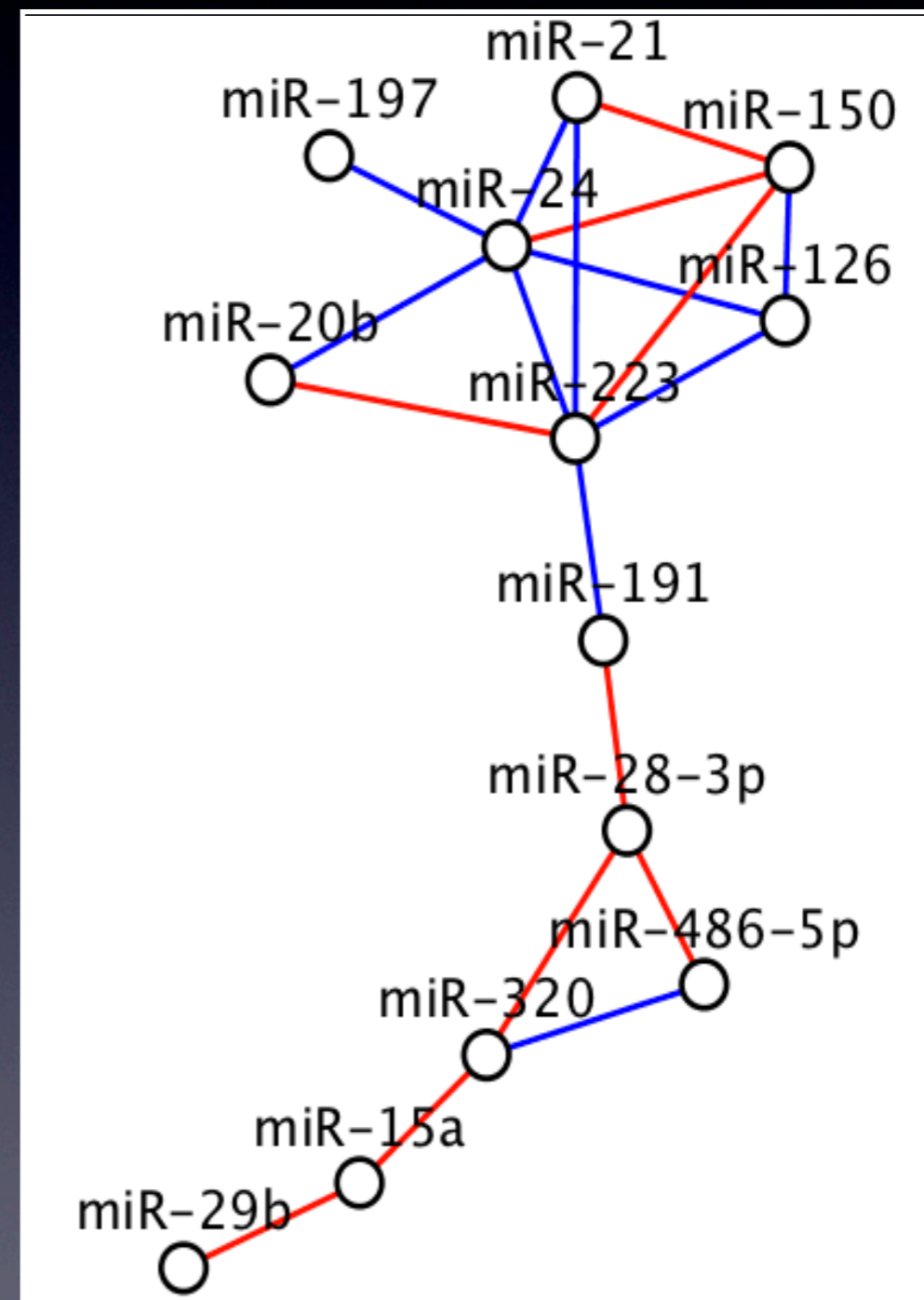
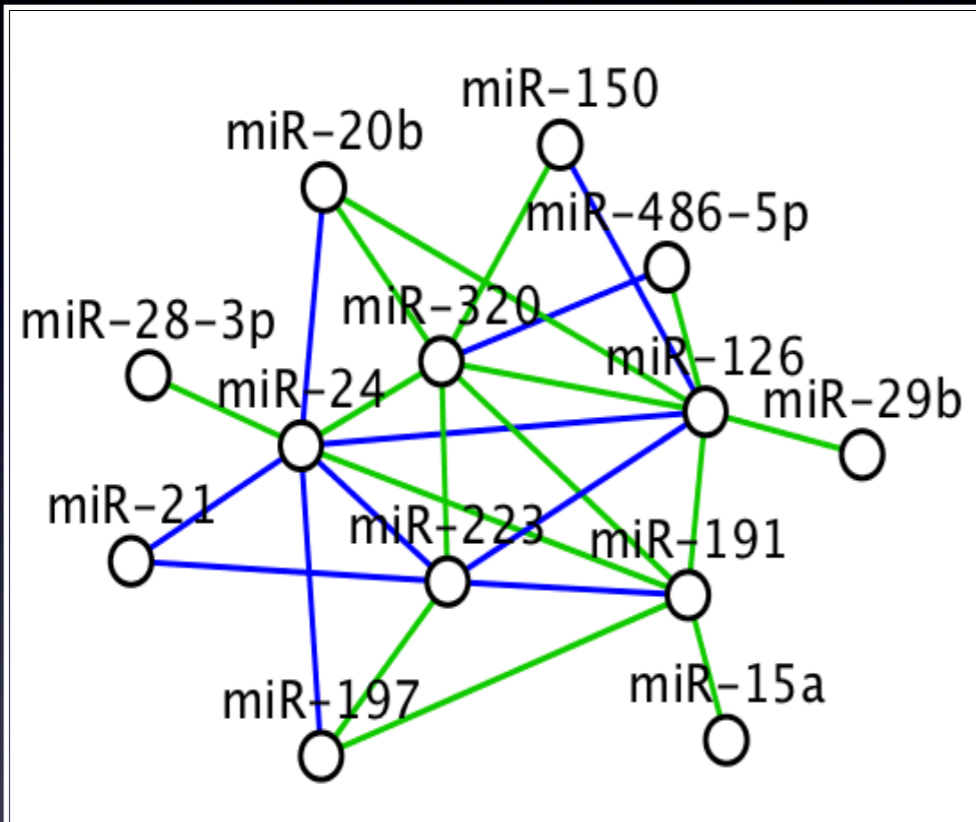


Editorial

See related article, pages 810–817

Diabetes Mellitus Reveals Its Micro-Signature

Romano Regazzi

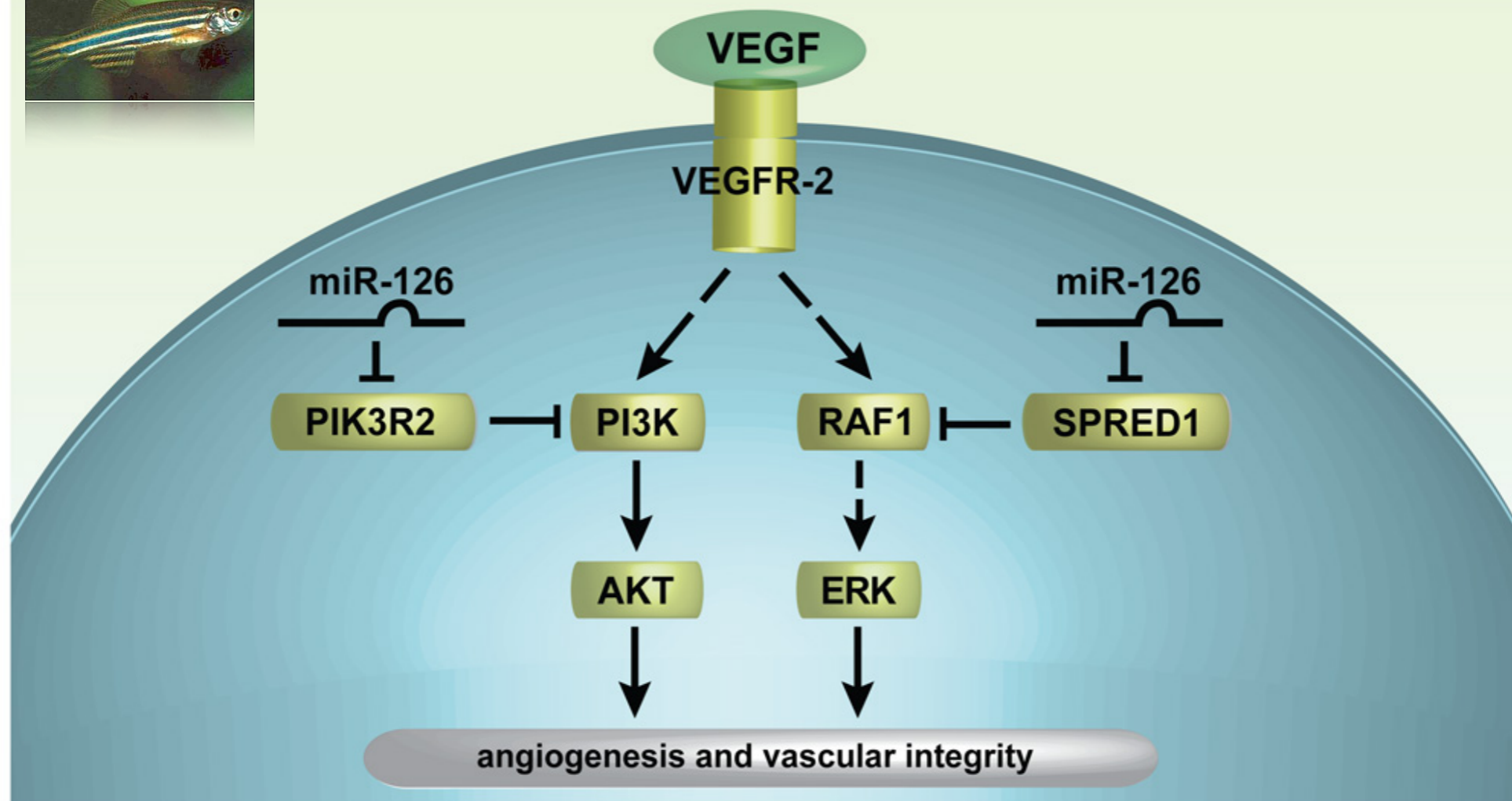


- Control network (green)
- Control & DM network (blue)
- DM network (red)

Function of MiR-126

Facilitator of VEGF Signalling

Fish et al Developmental Cell, 2008

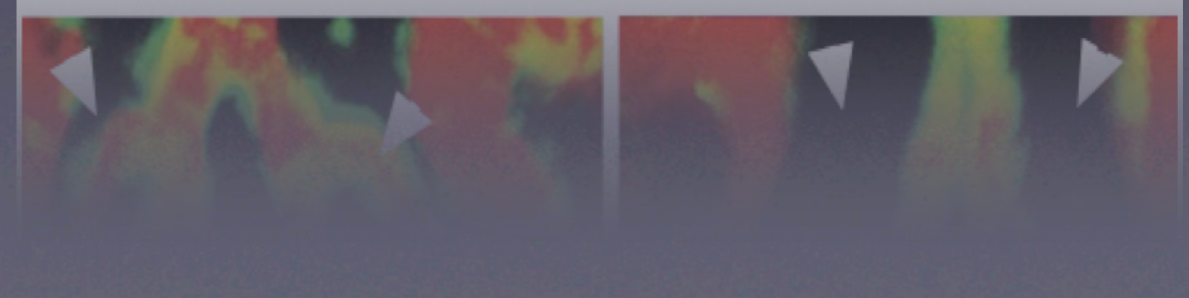
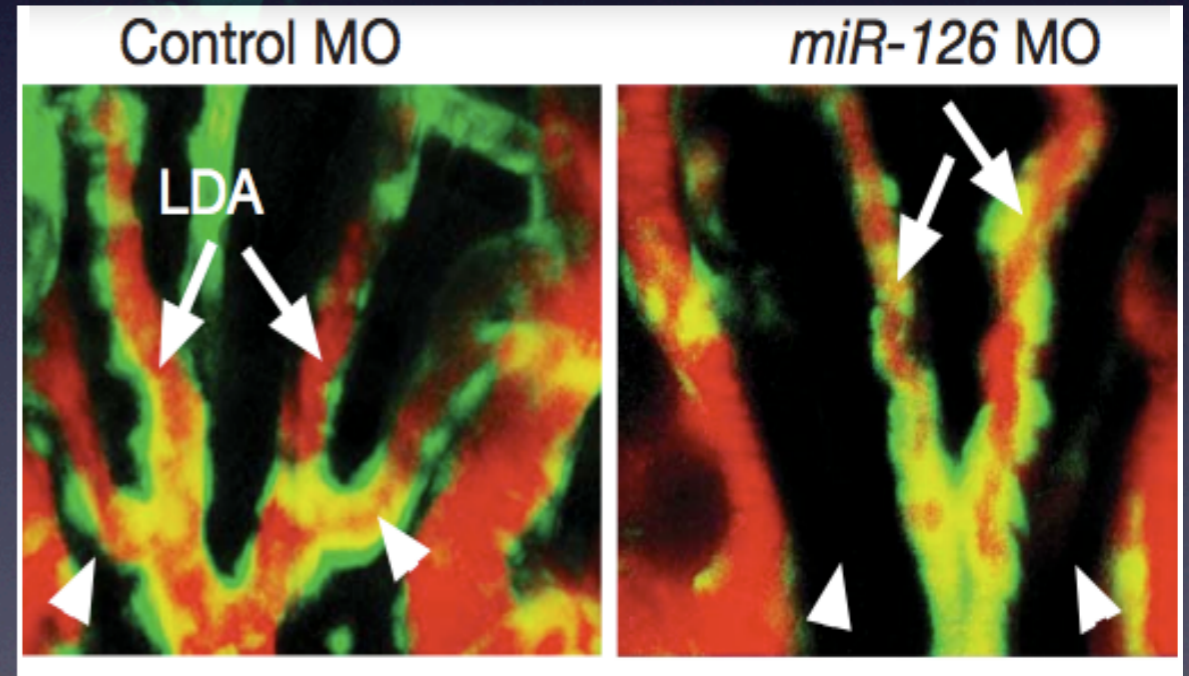
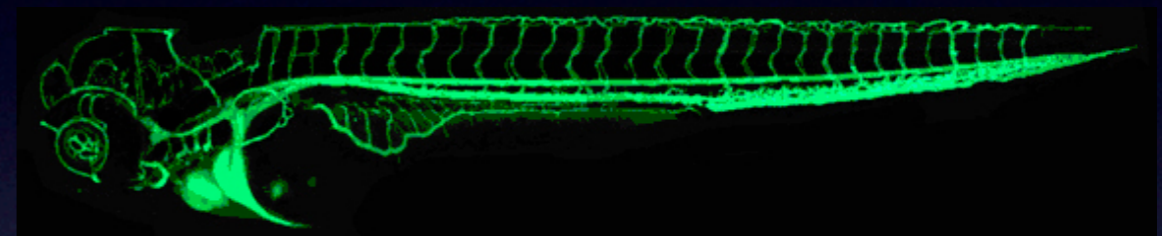
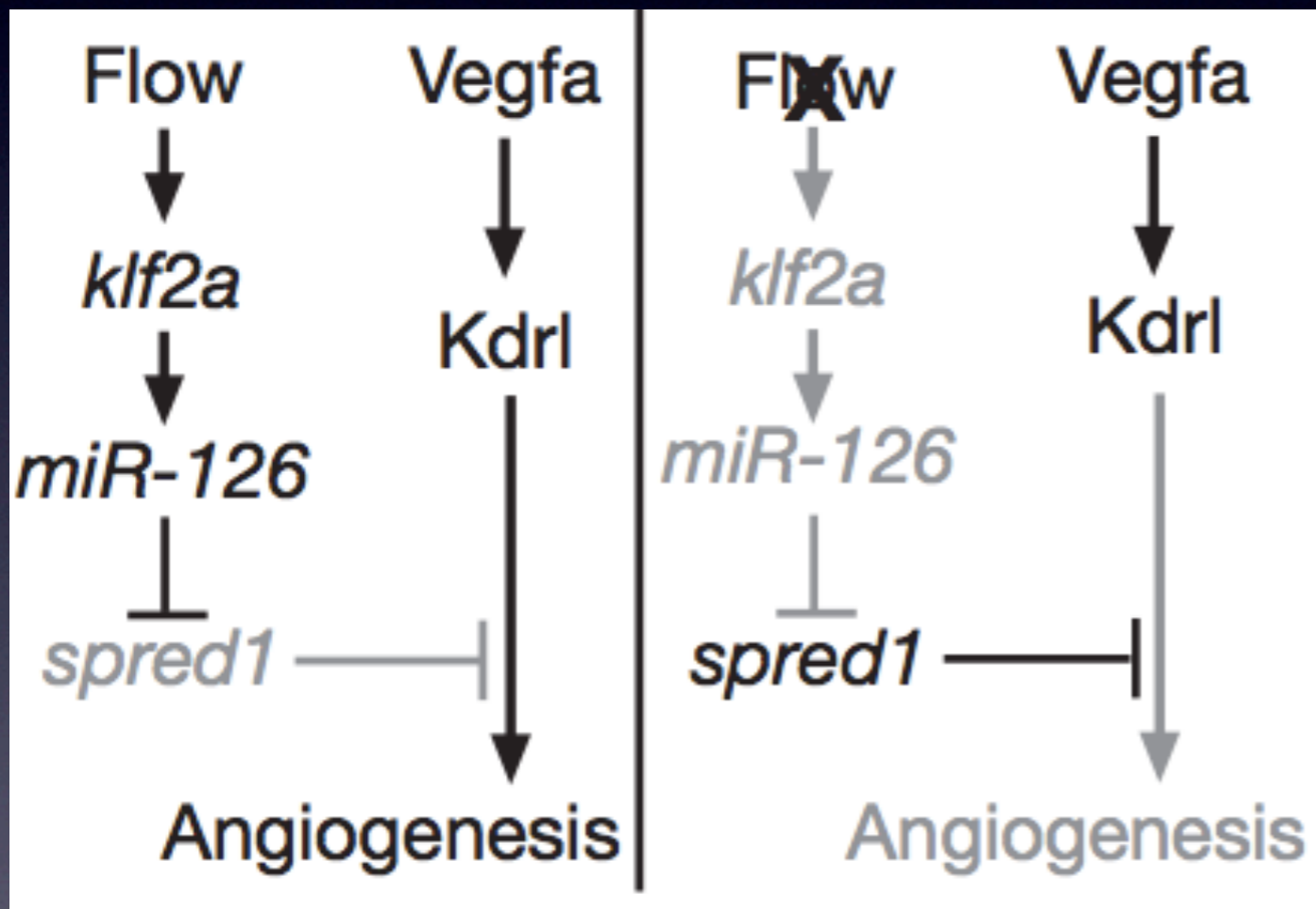


angiogenesis and vascular integrity

Function of MiR-126

Integration of Hemodynamics and VEGF Signaling

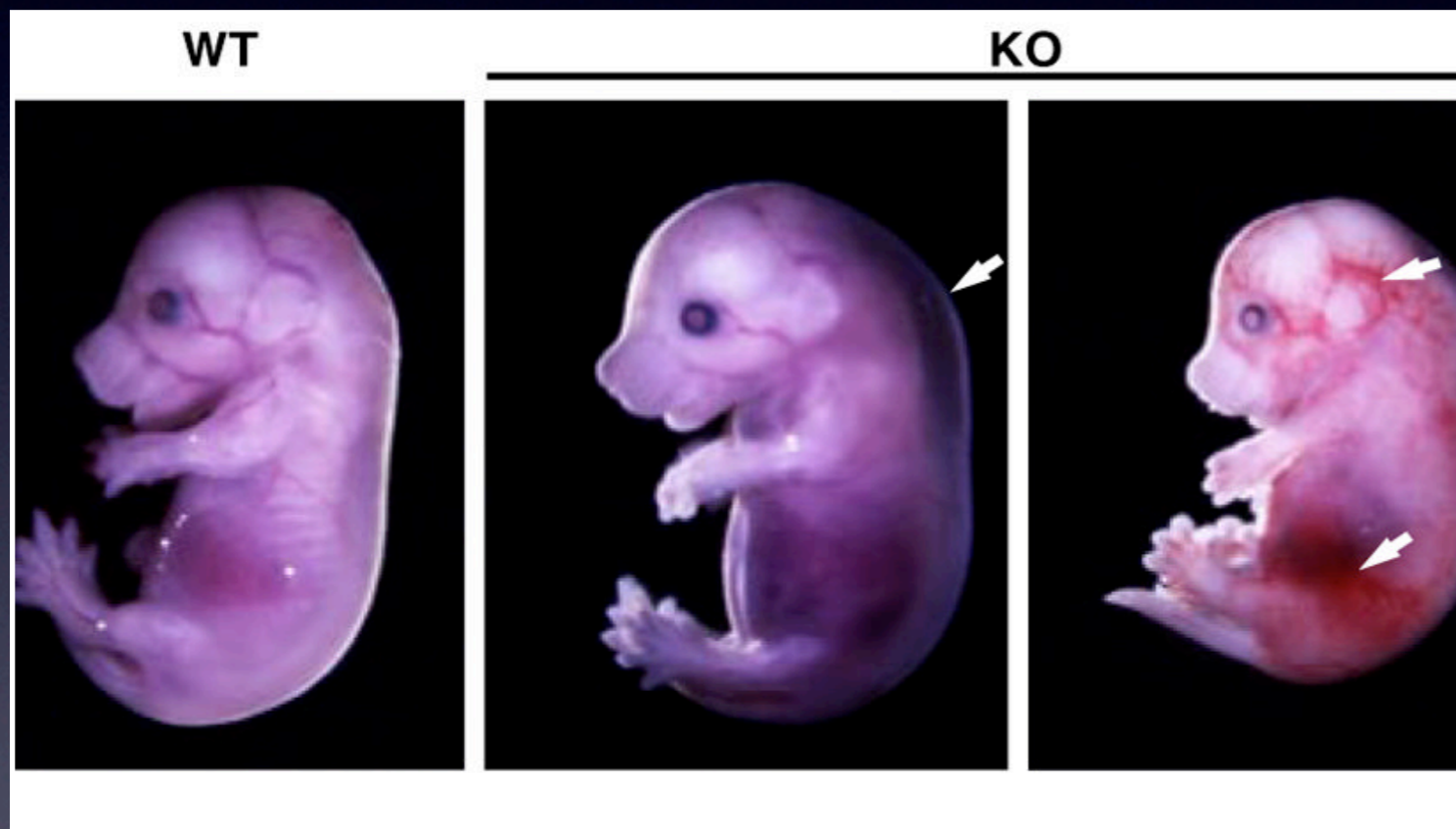
Nicoli et al, Nature, 2010



Function of MiR-126

Null Mice Prone to Vascular Leakage

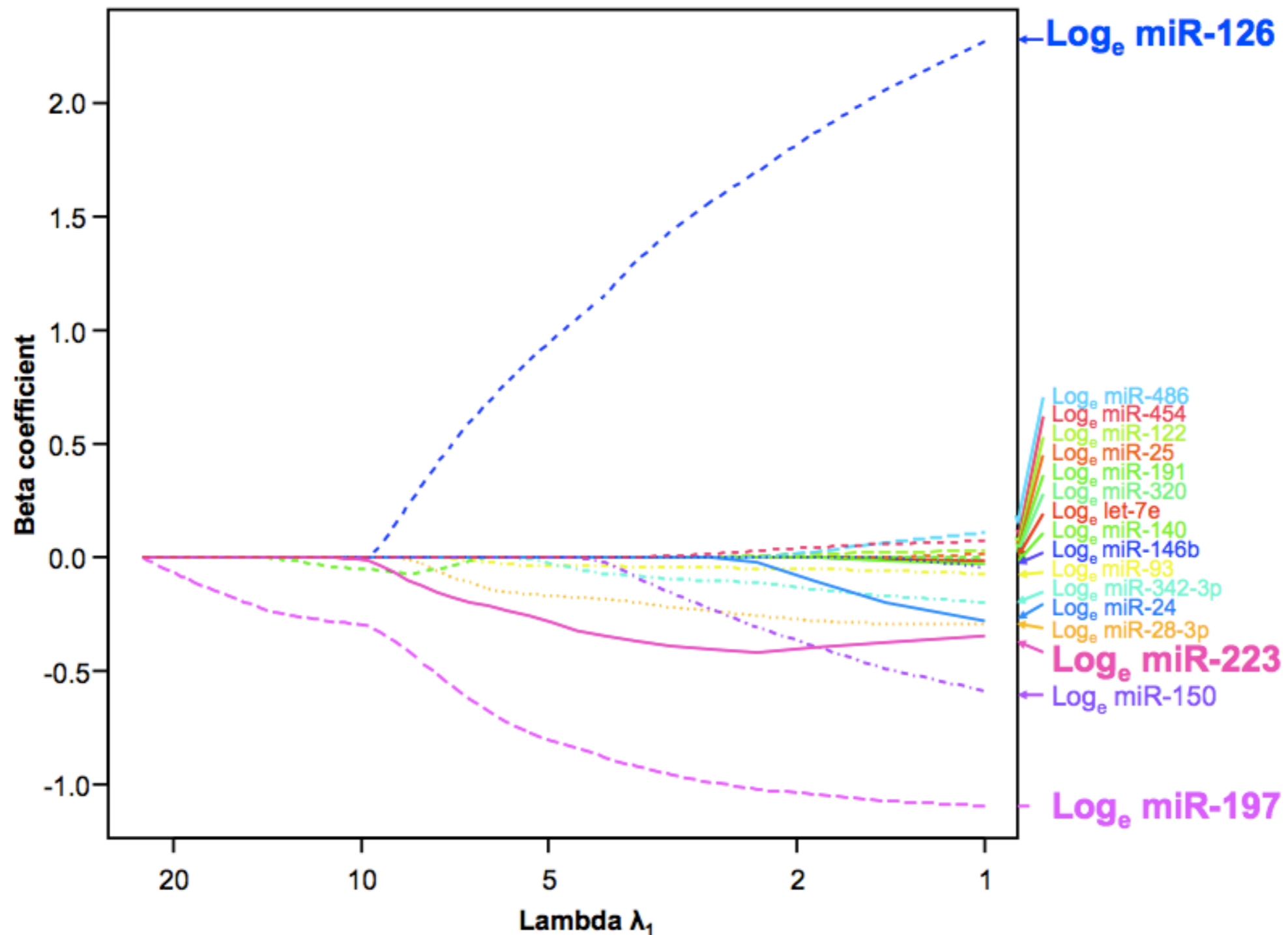
Wang et al, Developmental Cell, 2008



- 40% die during embryogenesis from vascular leakage.
- The mice that survive to adulthood are prone to vascular rupture and lethality following myocardial infarction.

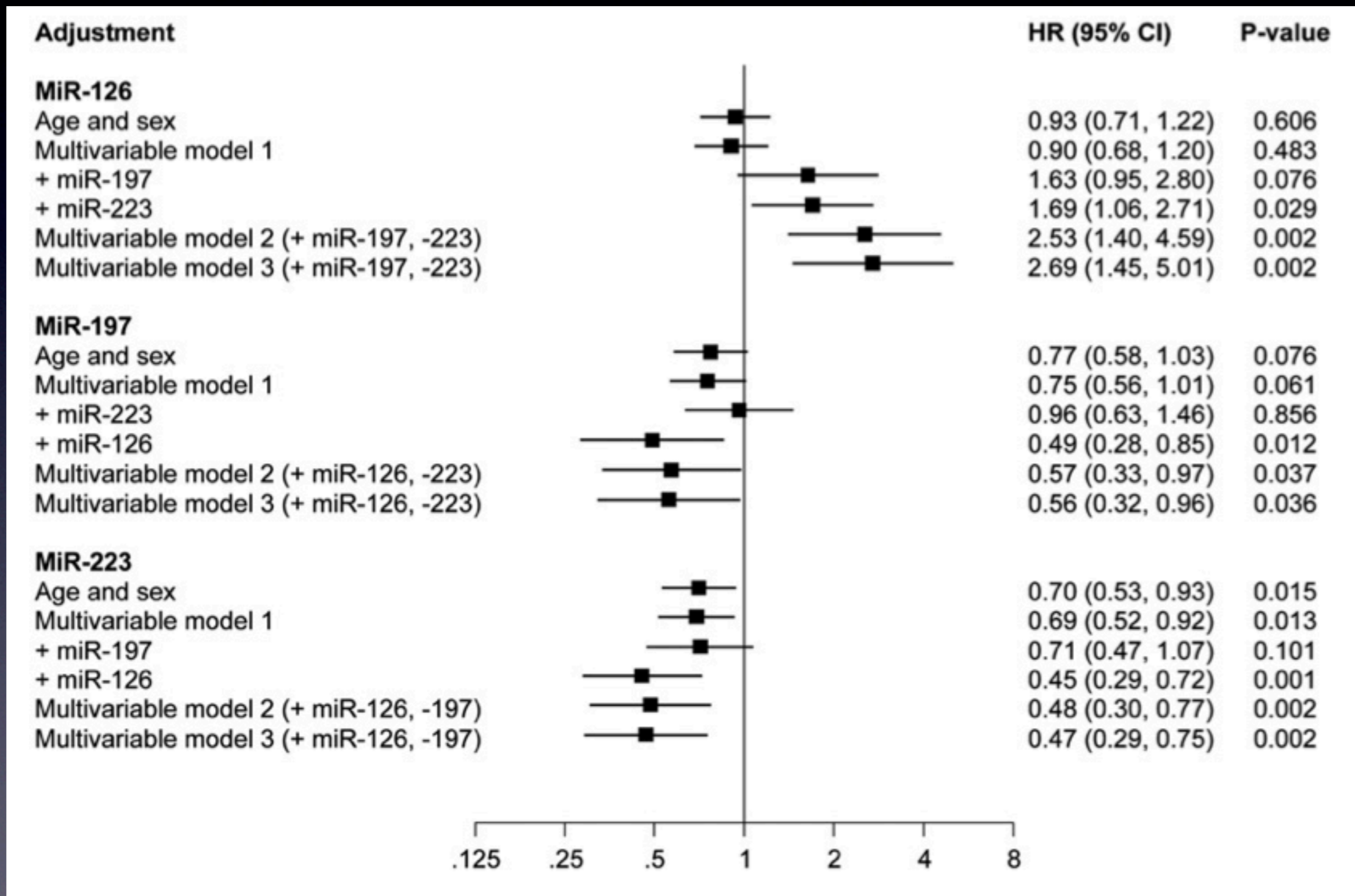
Risk of Myocardial Infarction

20 miRNAs, n=822, 10-year follow-up (1995-2005)



Risk of Myocardial Infarction

20 miRNAs, n=822, 10-year follow-up (1995-2005)



Integrated Discrimination Improvement Upon addition of miRNAs to Framingham Risk Score

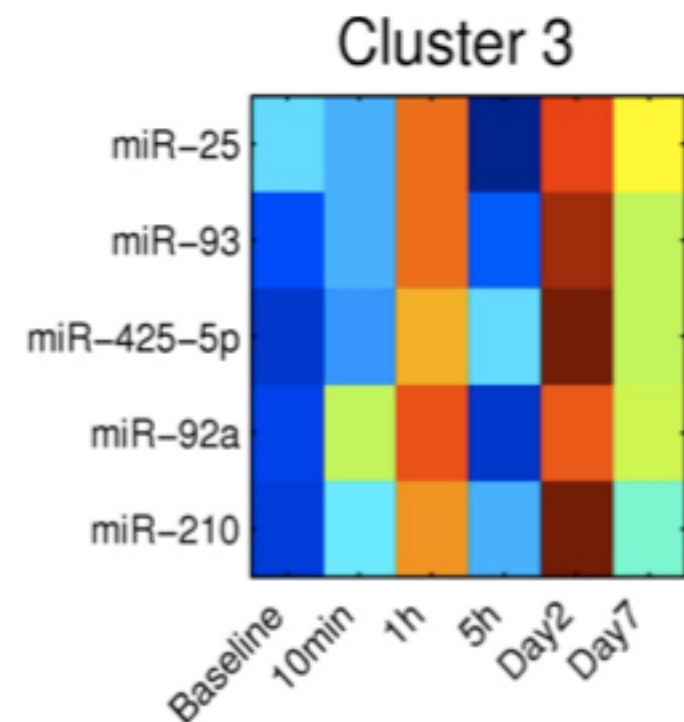
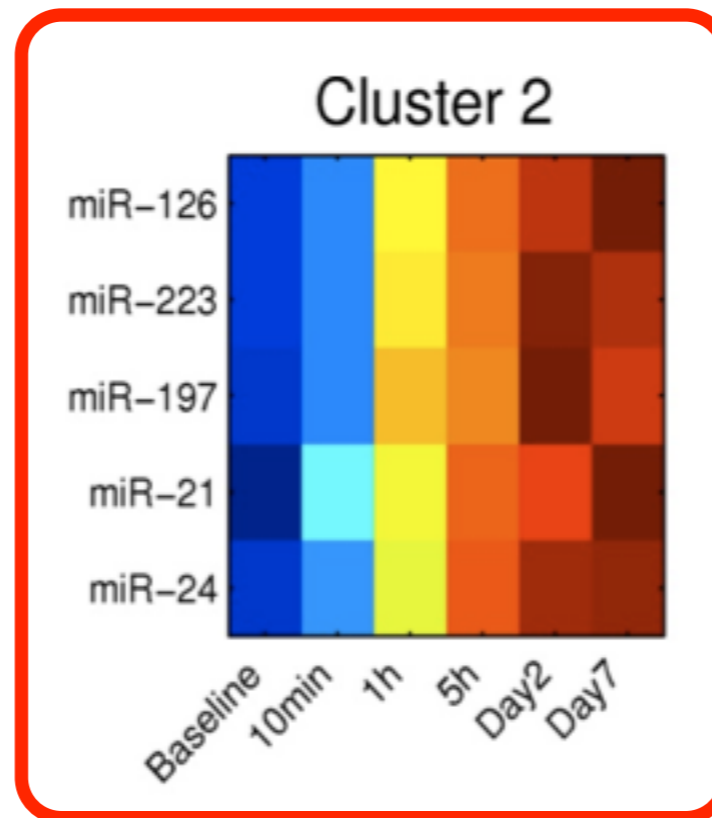
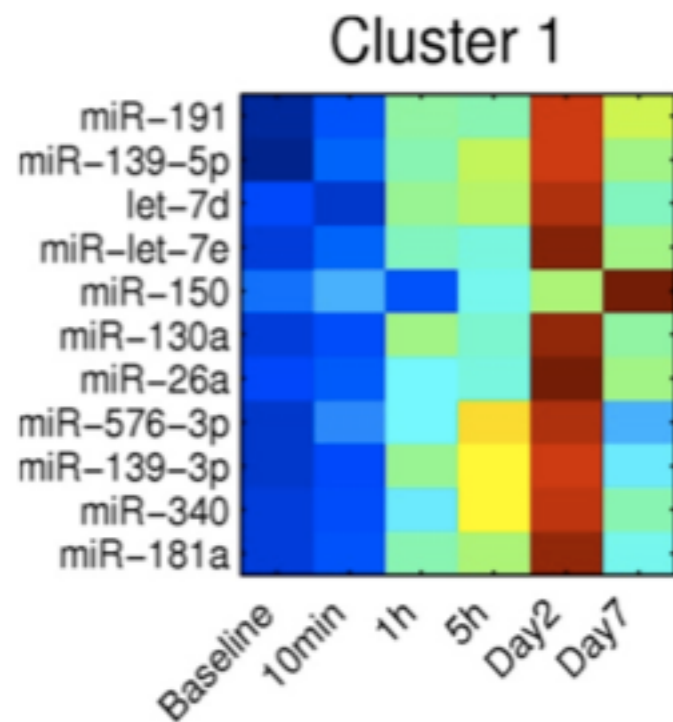
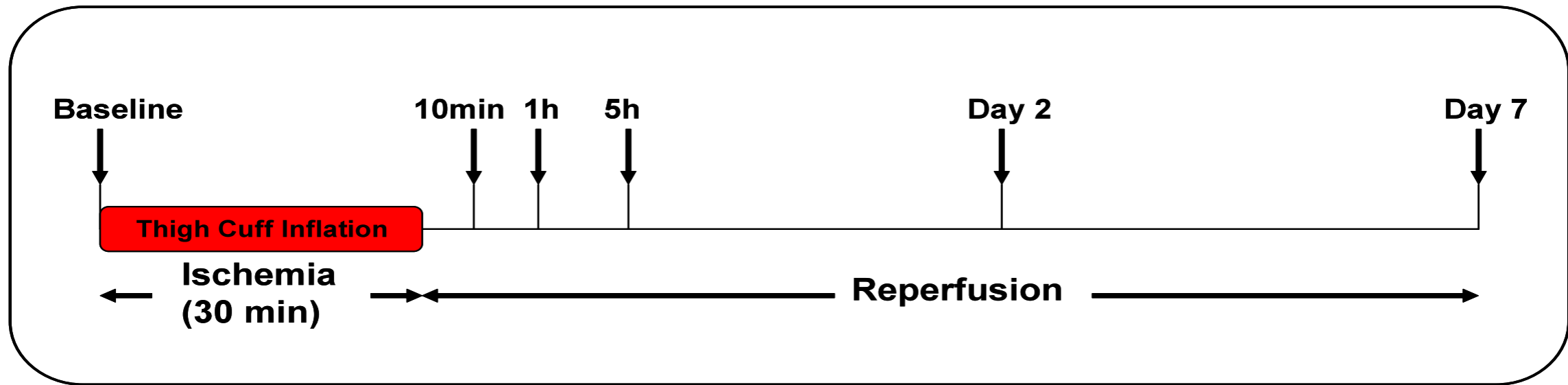
Table 2

Summary Statistics of MI Risk Reclassification by Addition of miR-126, miR-197, and miR-223 to a Model With the FRS for Hard Coronary Heart Disease

Statistic	Estimate	95% CI	p Value
Integrated discrimination improvement			
Controls	0.003331	0.000364–0.006297	0.028
Cases	0.043967	0.001742–0.086191	0.041
Overall	0.047297	0.004969–0.089626	0.029

Cellular Origin ?

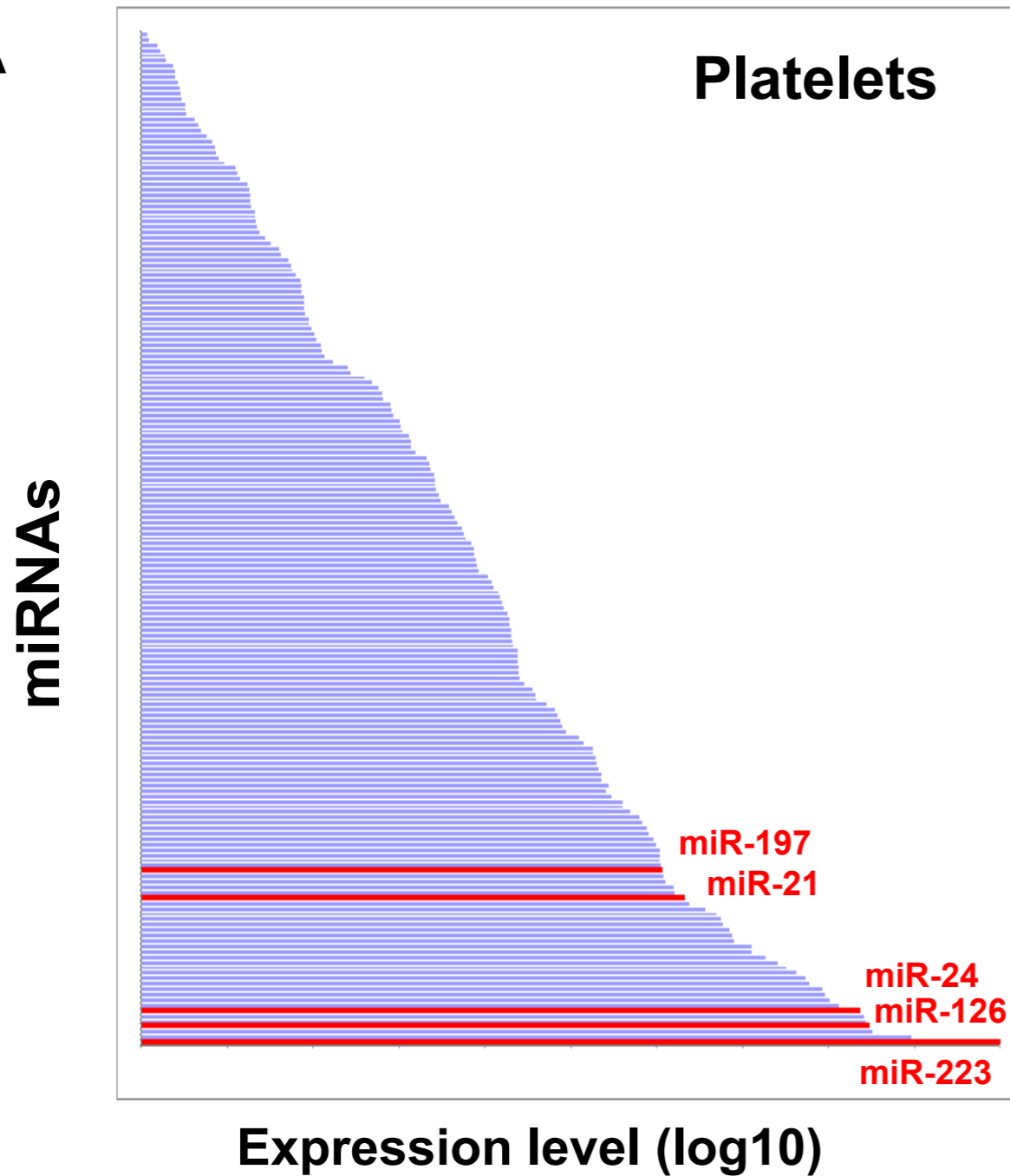
Ischemia/Reperfusion by Thigh Cuff Inflation (n=11)



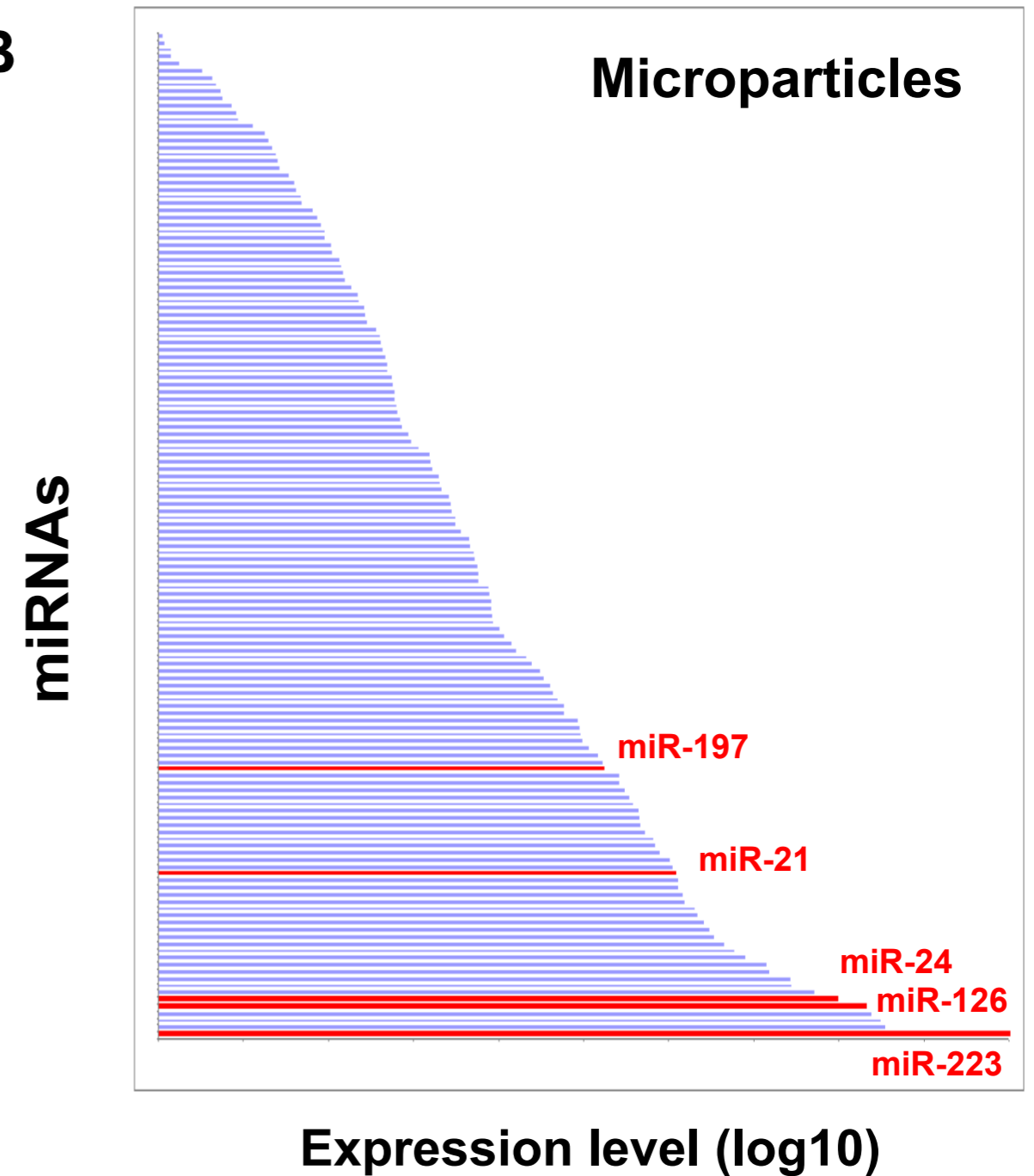
Cellular Origin ?

Presence in Platelets and Platelet Microparticles

A

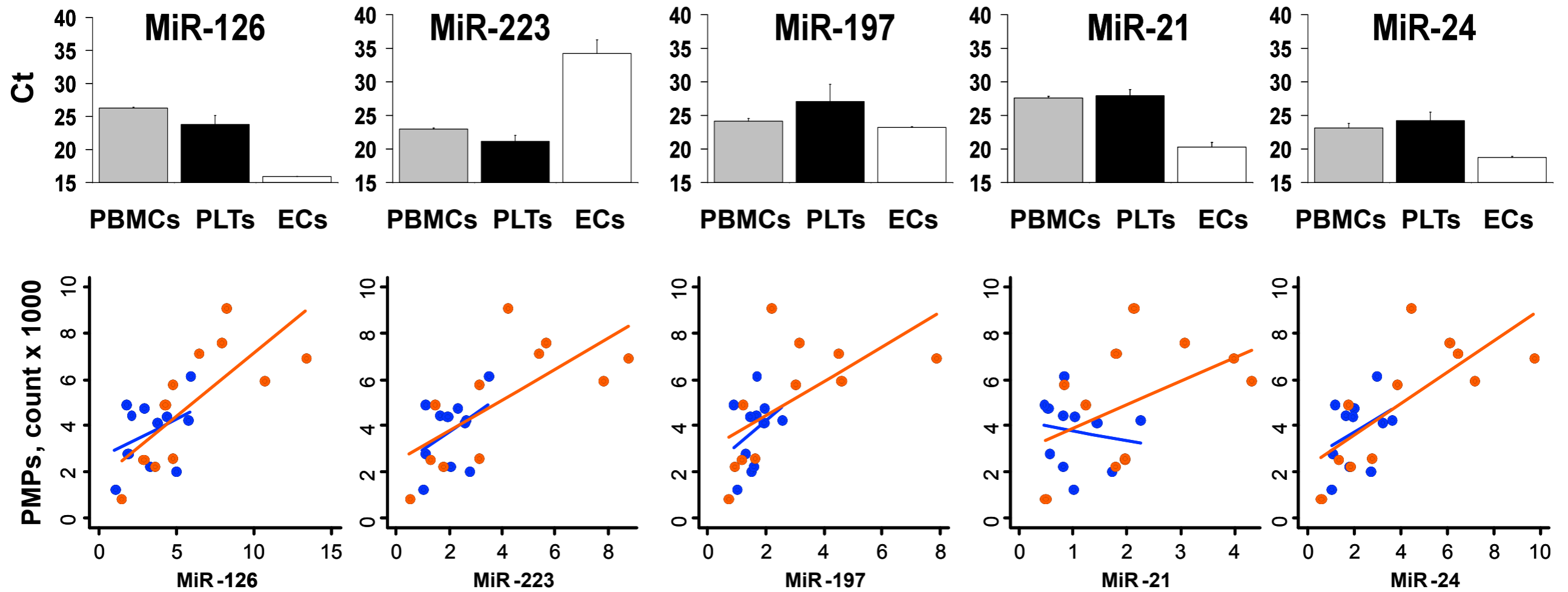


B



Platelet Contribution

Correlation of MiRNAs to Platelet Microparticles

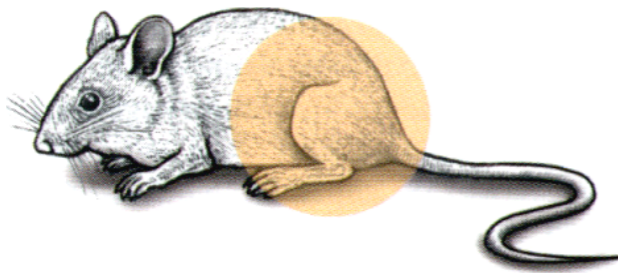


Baseline versus **Day 2** post ischemia/reperfusion

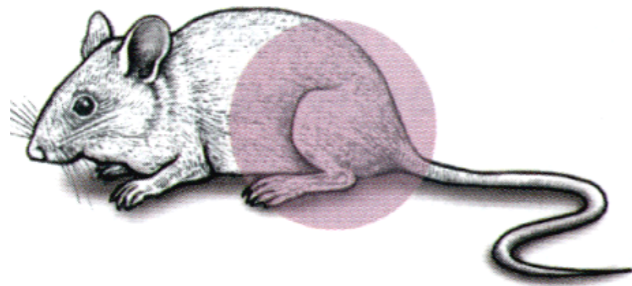
MicroRNAs in Vascular and Metabolic Disease

Anna Zampetaki, Manuel Mayr

Circulation Research 2012, 110:508-522

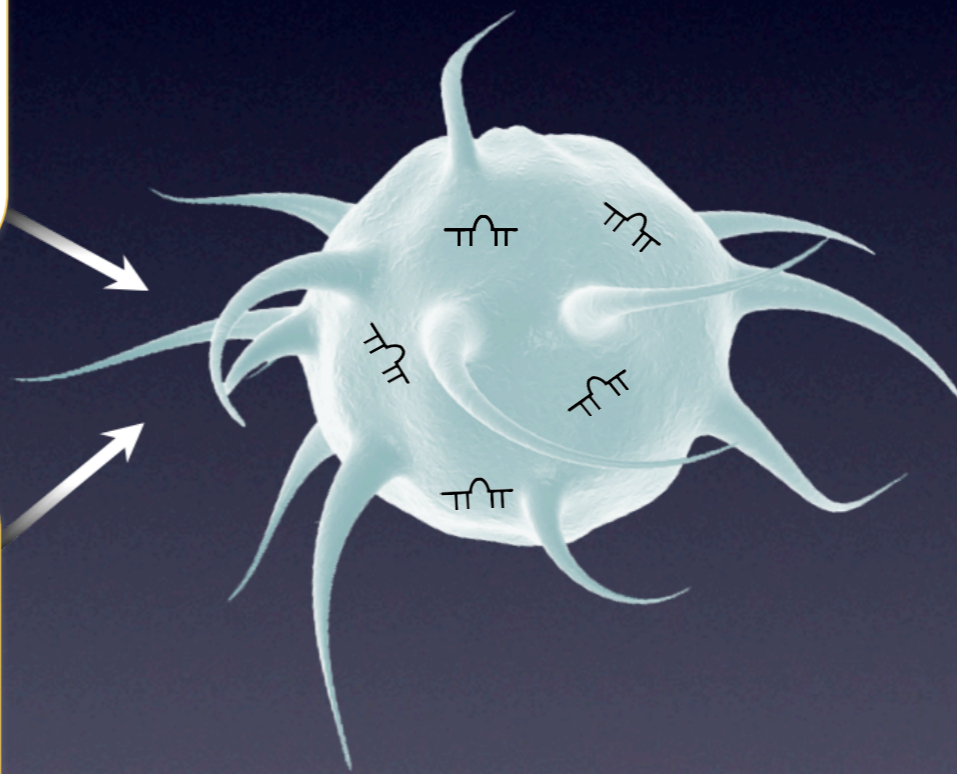


Global Knock-out



Systemic Inhibitors

Platelet Contribution ?



miR-223

miR-126

miR-103

Let-7

miR-21

miR-107

miR-24

miR-222

Conclusions

Validation in Independent Cohorts

- This is the first population-based study on circulating miRNAs.
- We identified a miRNA signature for DM and risk of MI.
- Currently, we monitor cardiovascular risk factors, but there is no good soluble biomarker to directly assess the health of blood vessels and identify “vulnerable” patients.

FOCUS ISSUE: BIOMARKERS

Editorial Comment

Small RNA Biomarkers Come of Age*

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Mr. Ignat Drozdov

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