



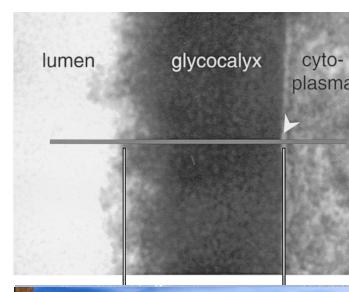
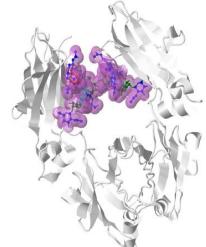
Visokoprotična glikomika u molekularnoj dijagnostici

Gordan Lauc
University of Zagreb &
Genos Glycoscience Research Laboratory

WO2014203010; US2016103137, WO2012042020; WO2011015944; WO2009044213

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Glycans are important structural component of nearly all proteins



Optical density

lumen glycocalyx cyto-plasma

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Genome does not contain templates for synthesis of glycan parts of glycoproteins

DNA ← RNA → proteins

???

glycoproteins

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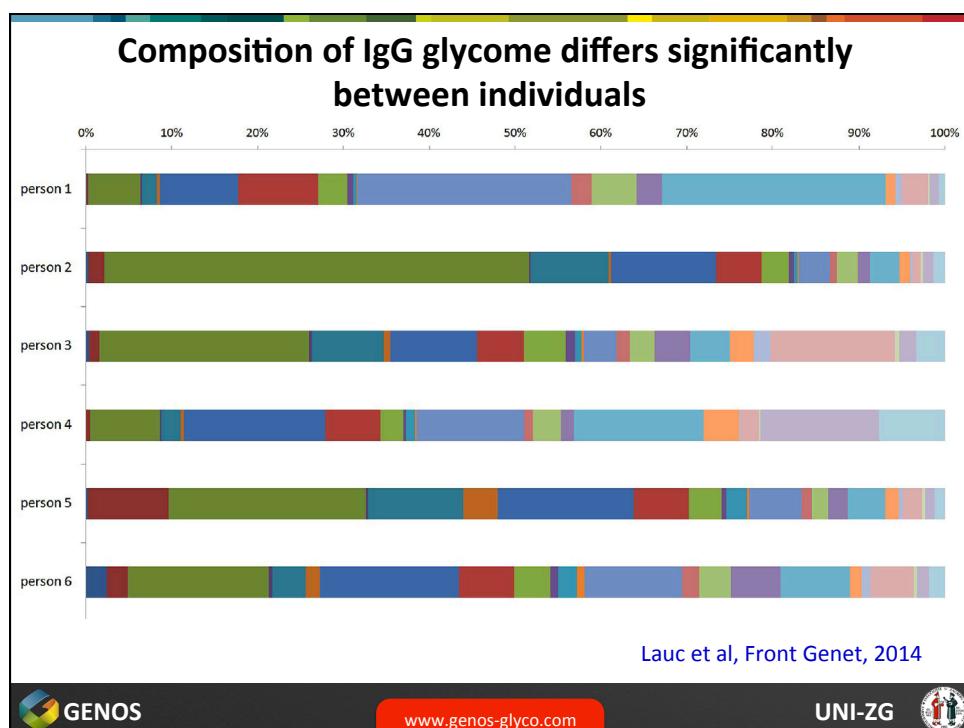
Cohort	Plasma glycome	IgG Glycome
10001 Dalmatian	2,000	4,000
Orcades	2,000*	2,000
TwinsUK	4,000	4,500
KORA	–	2,000
SABRE	2,000	–
Global population study	–	2,700
FINNRISK	–	1,200
Estonian biobank	–	1,300
China	1,000	1,000
CRC	2,000*	2,000
IBD	3,000	5,700
SLE	–	1,200
Type 1 Diabetes	1,000	1,000
Type 2 Diabetes	–	3,000
Down syndrome	–	800
PTSD	600	600
Total	17,600	33,000

* Analysed in NIBRT

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Mining the gold from big glycomics datasets

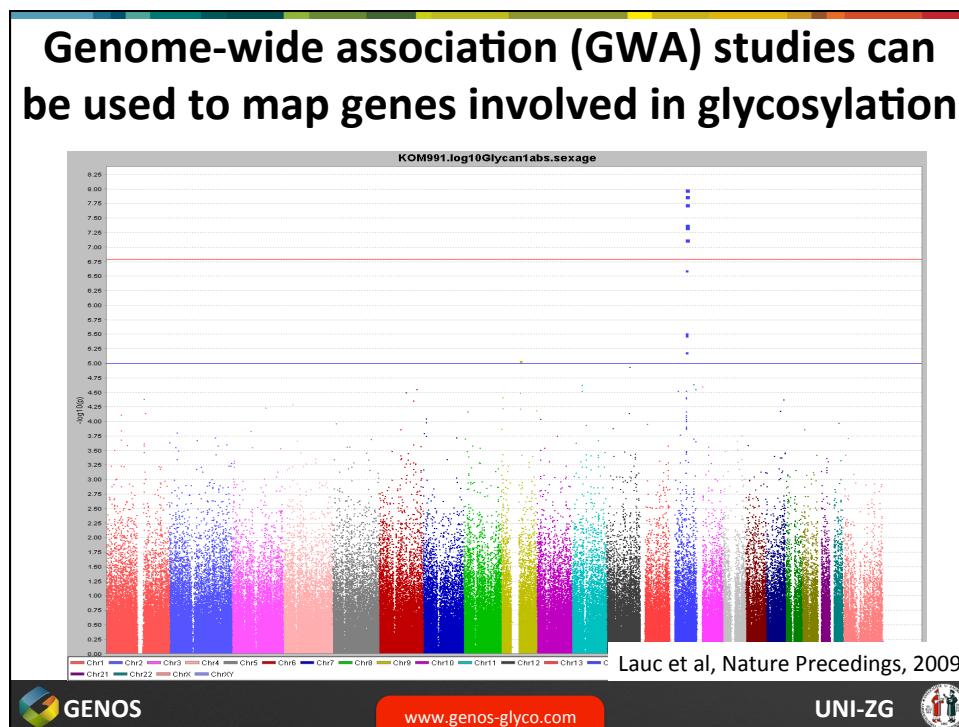
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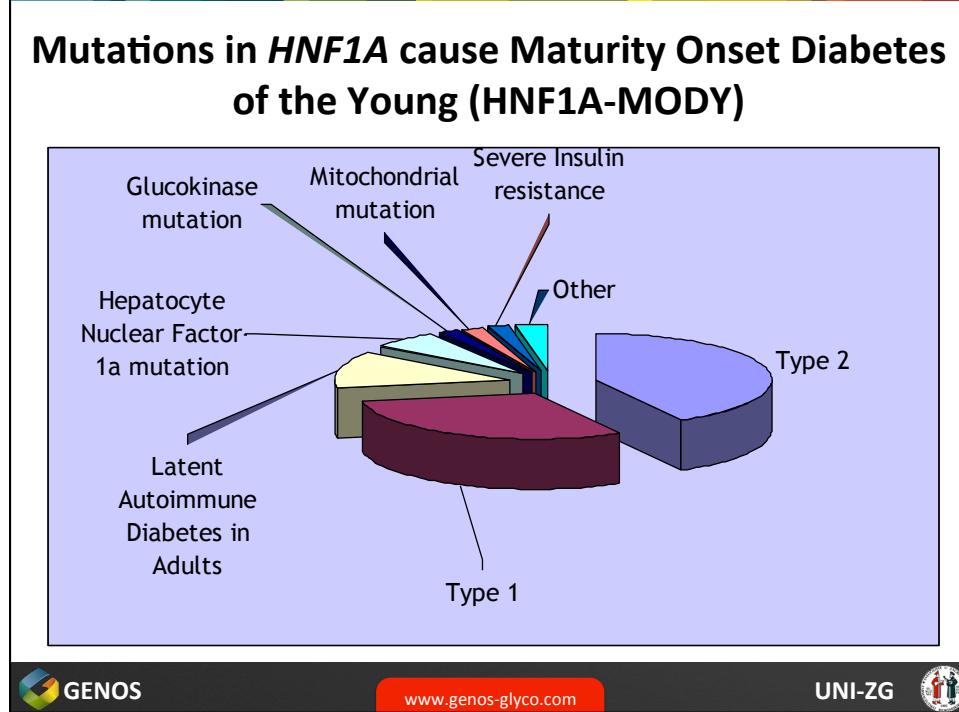
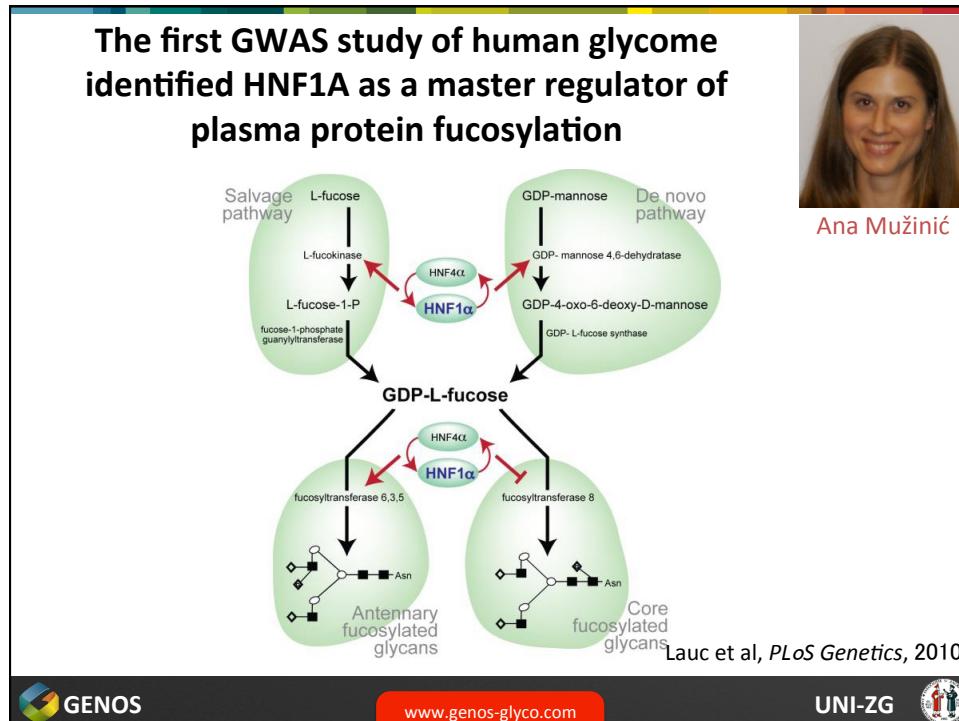


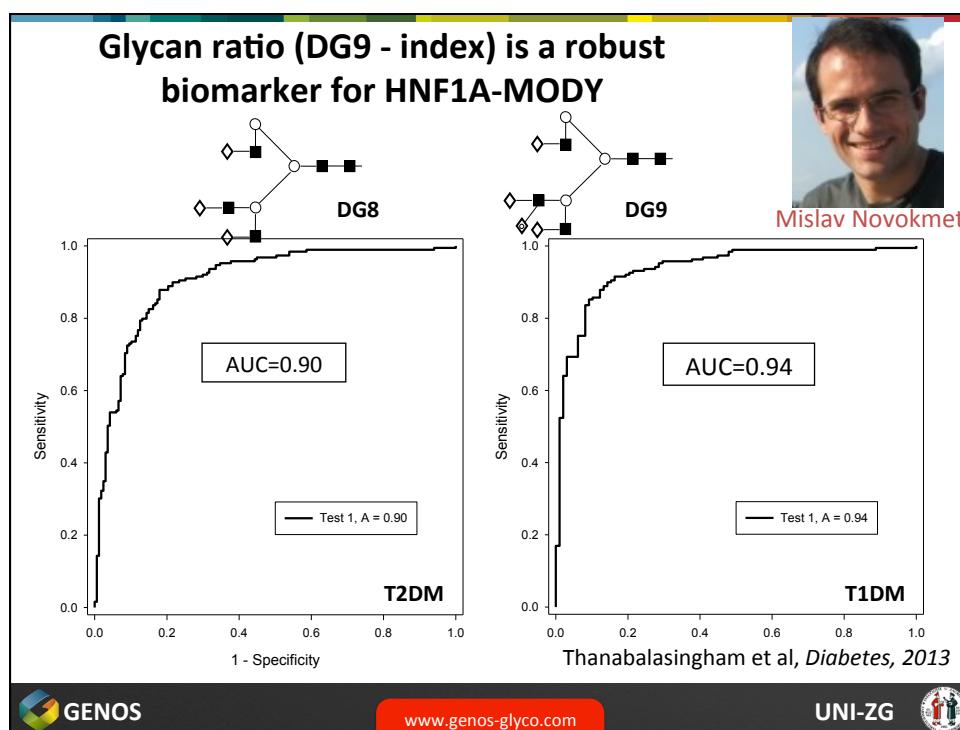
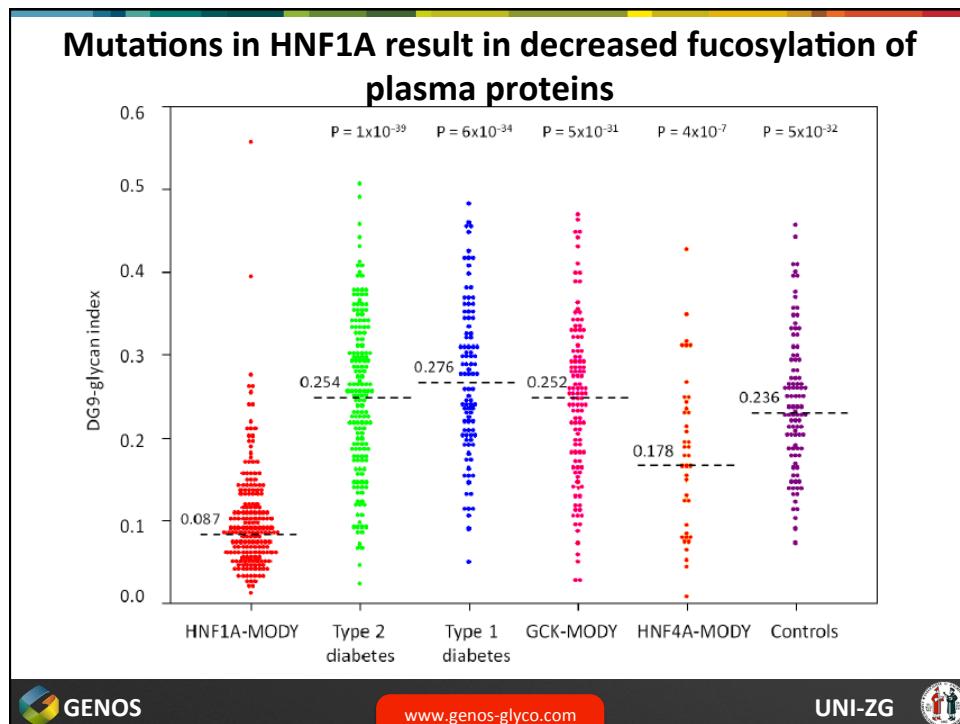
The majority of genes that affect IgG glycosylation are still not known

TF
IC
GTs
GDs
GO / TP

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Analysis in a prospective setting

- 1100 young onset diabetics recruited in Zagreb and Oxford
- Plasma glycome analysed by UPLC
- Sequencing of the entire HNF1a gene
 - 32 mutations (11 known to be pathological)
- Classification



Prof. Olga Gornik



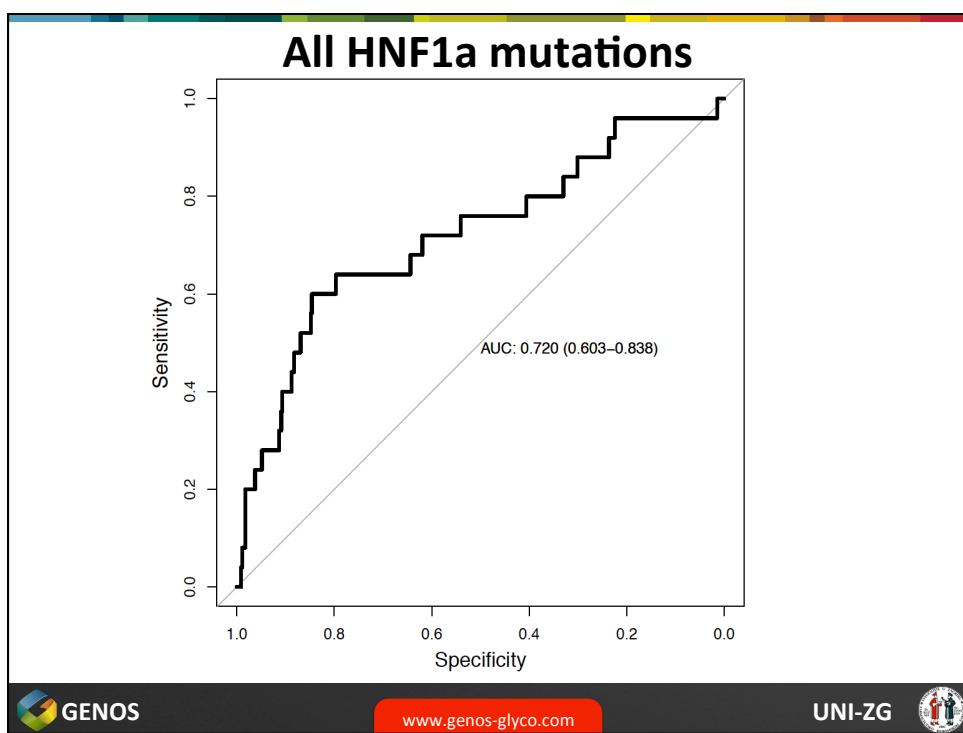
Frano Vučković

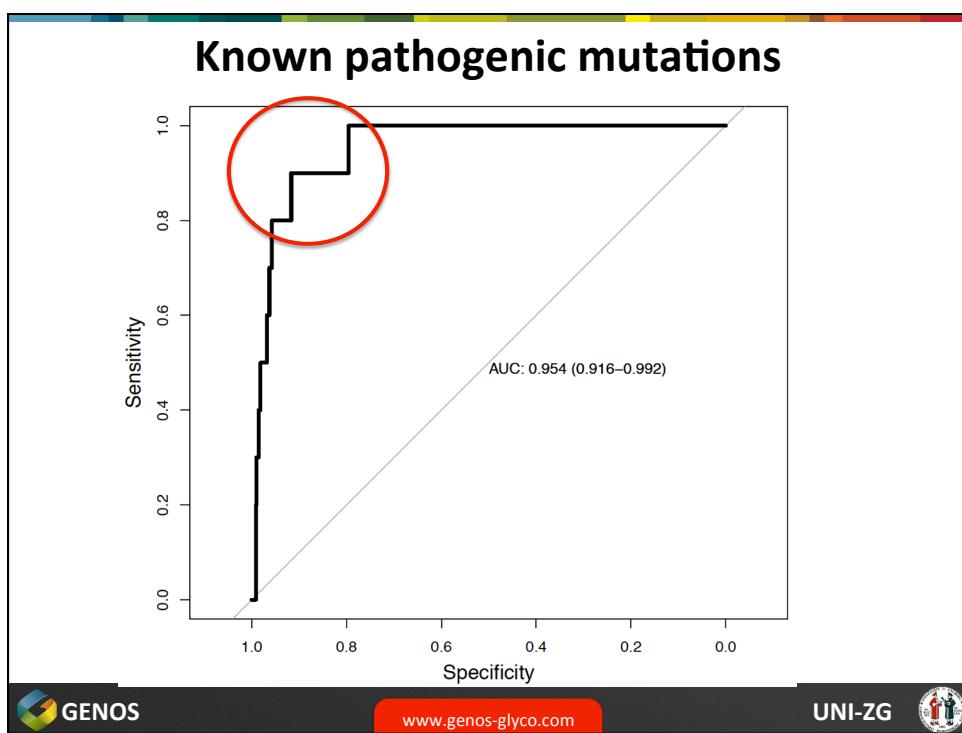
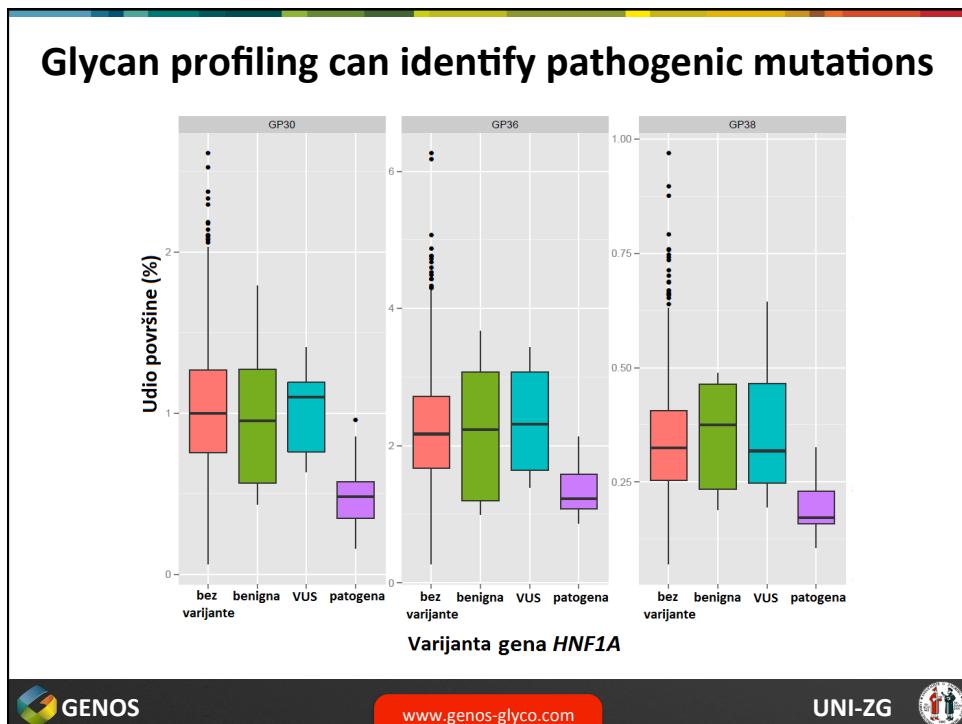


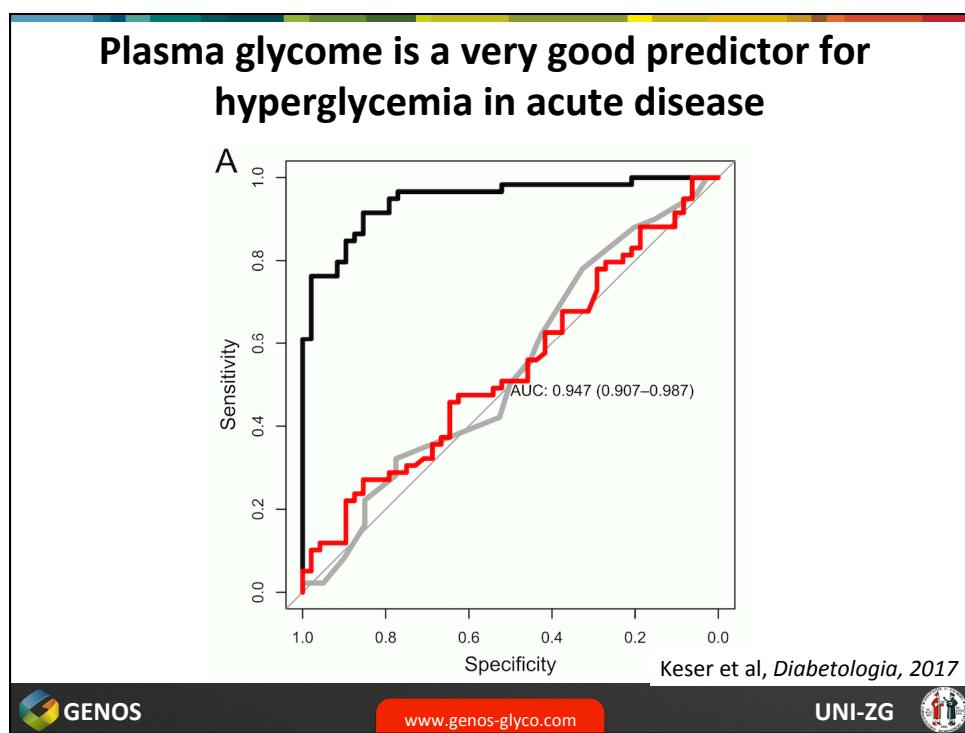
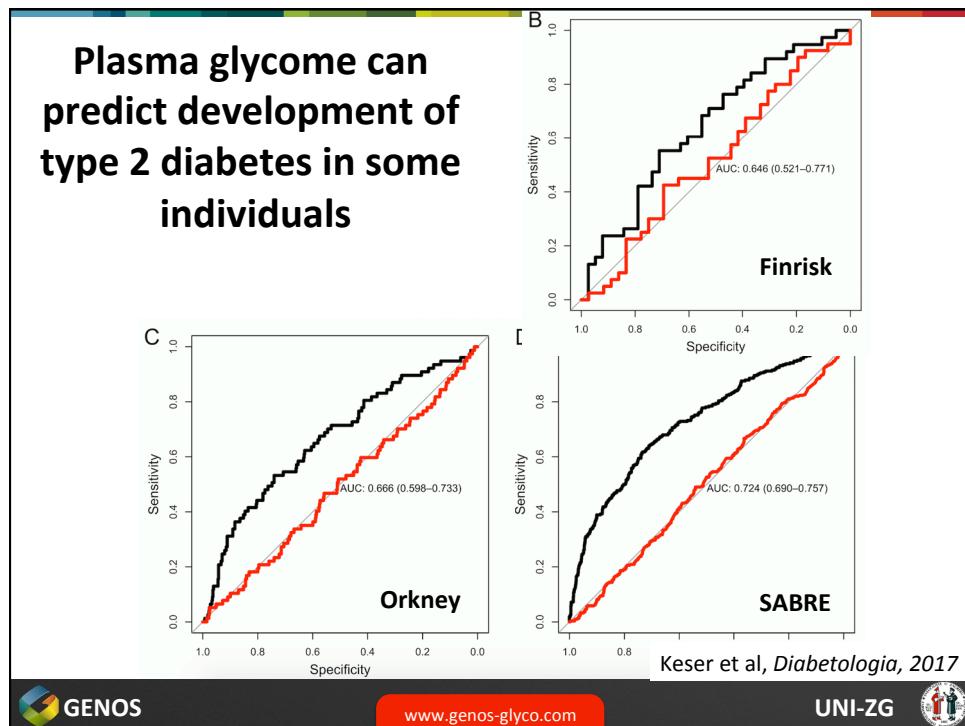
Tamara Pavić

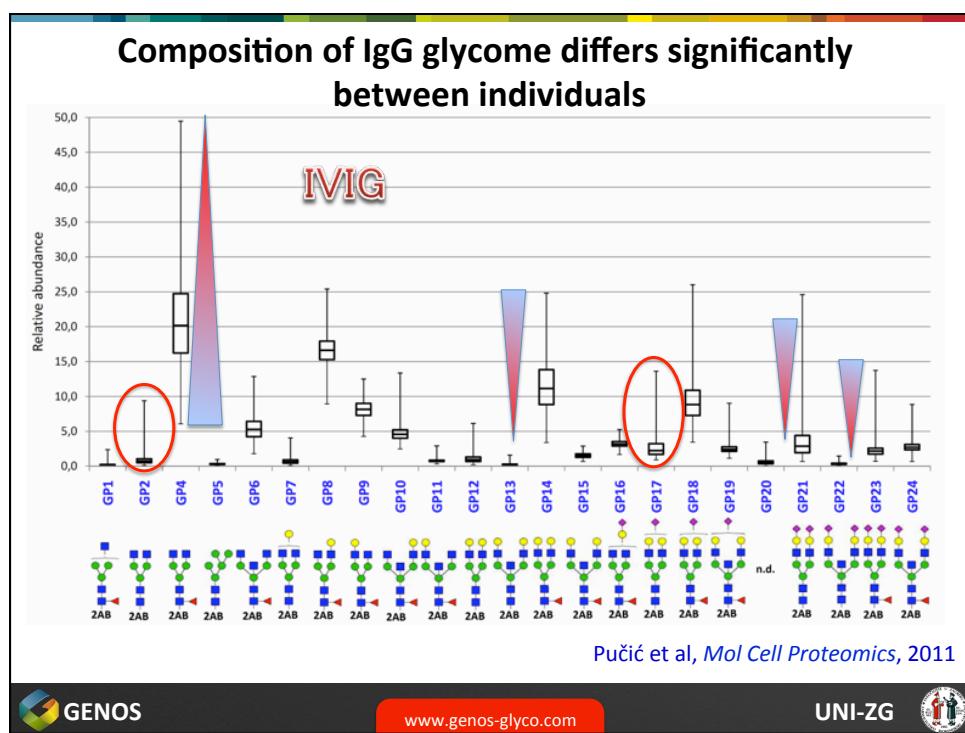
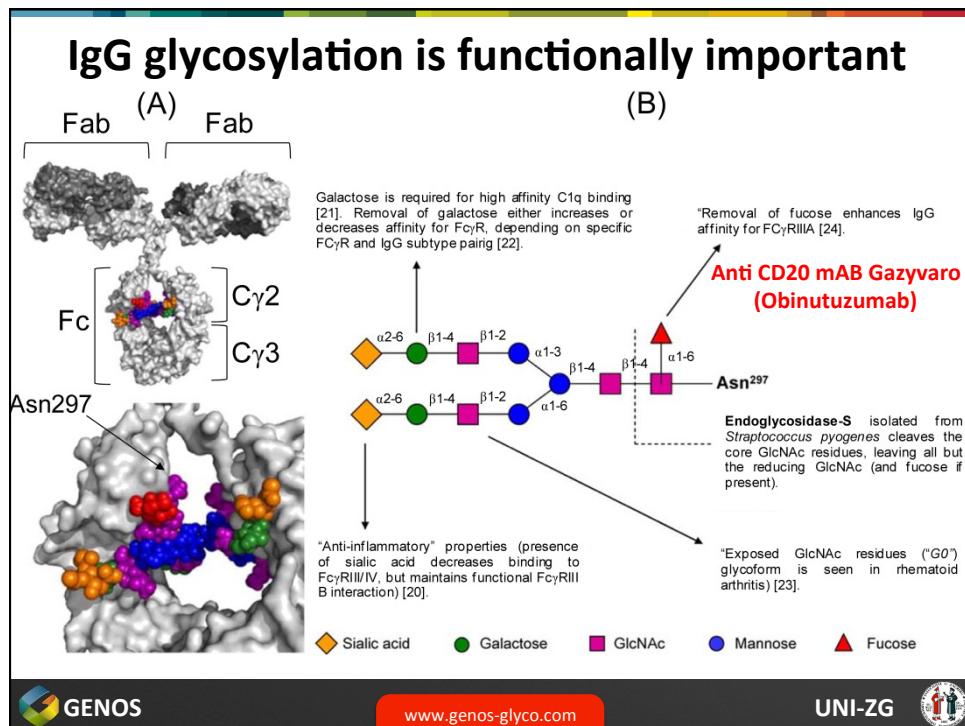
EFSD
 European Foundation for the Study of Diabetes

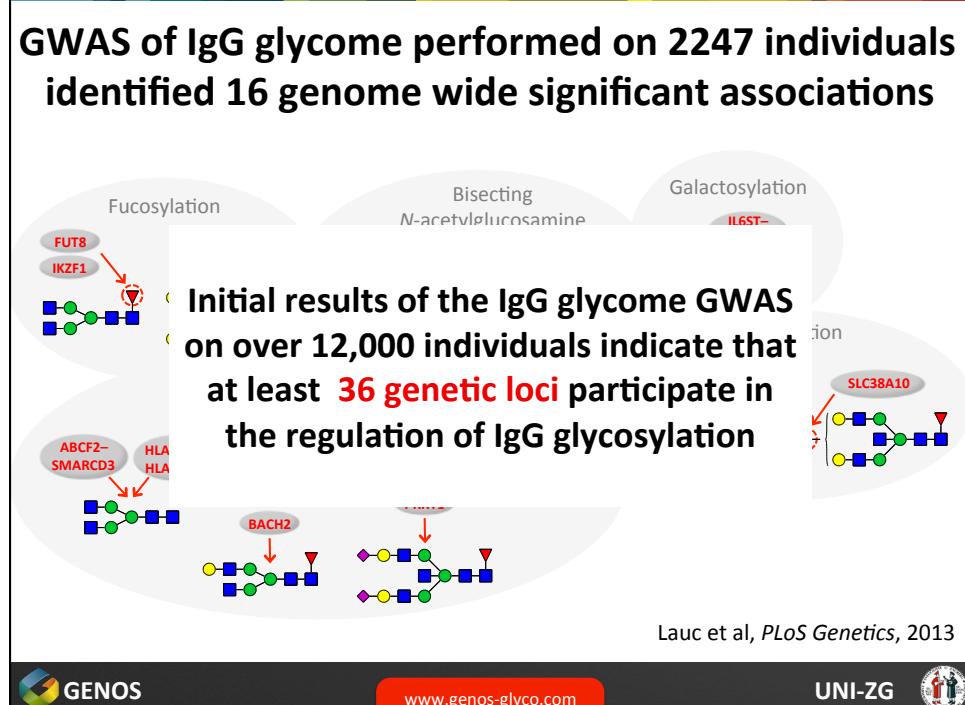
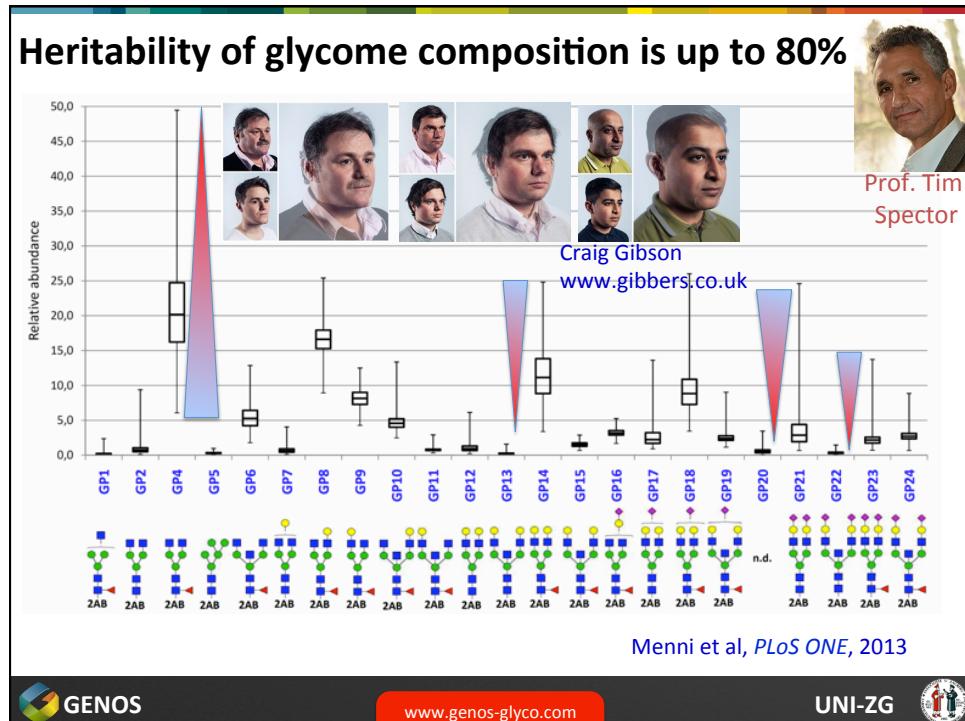
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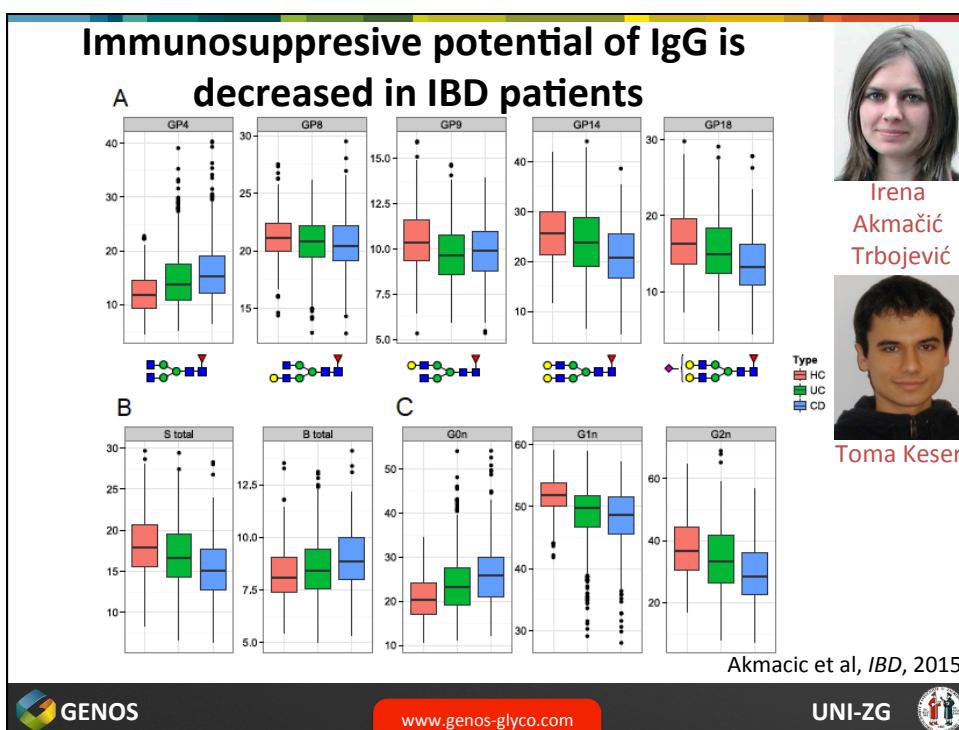
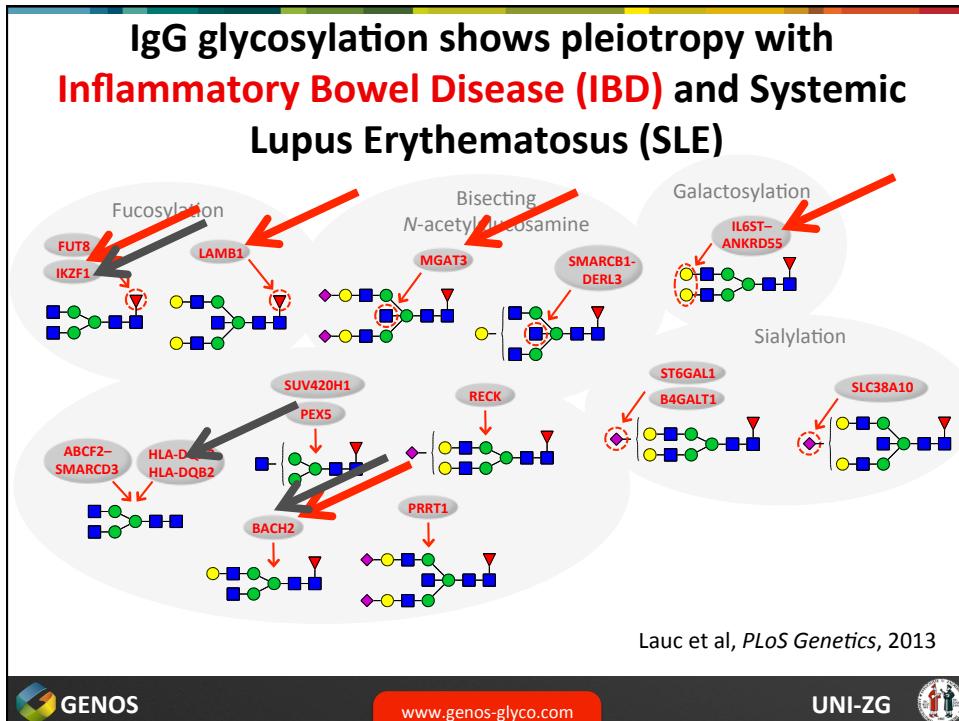




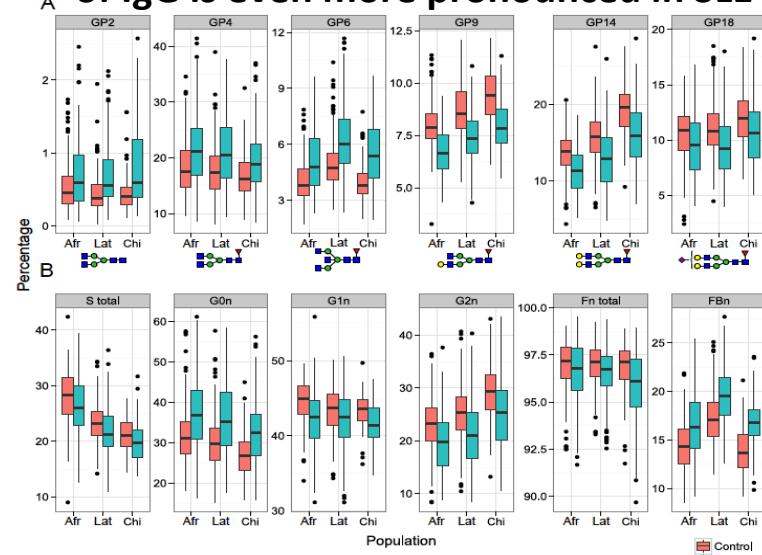








The decrease in immunosuppressive potential of IgG is even more pronounced in SLE



Frano
Vučković



Jasminka
Krištić

Vučković et al
Arthr Rheum,
2015

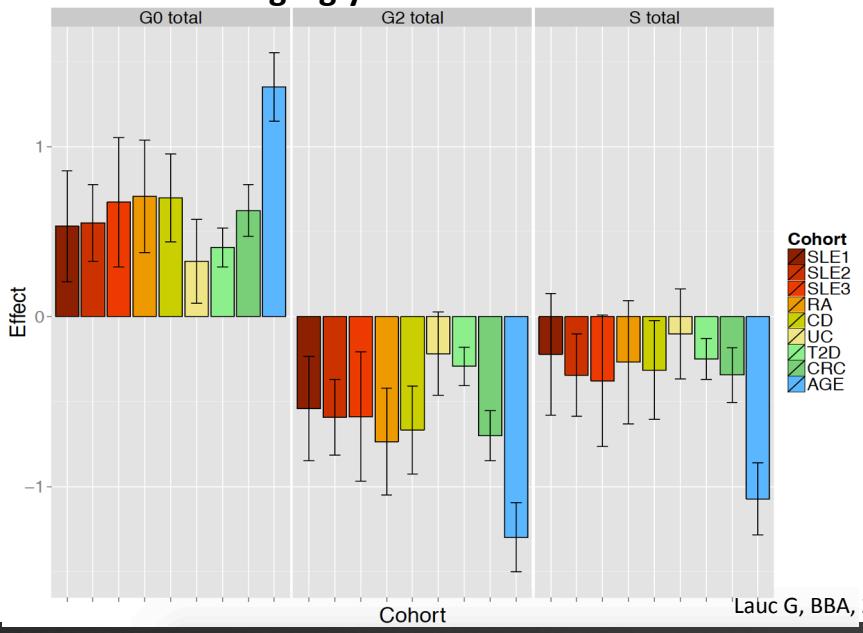


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IgG glycome in disease



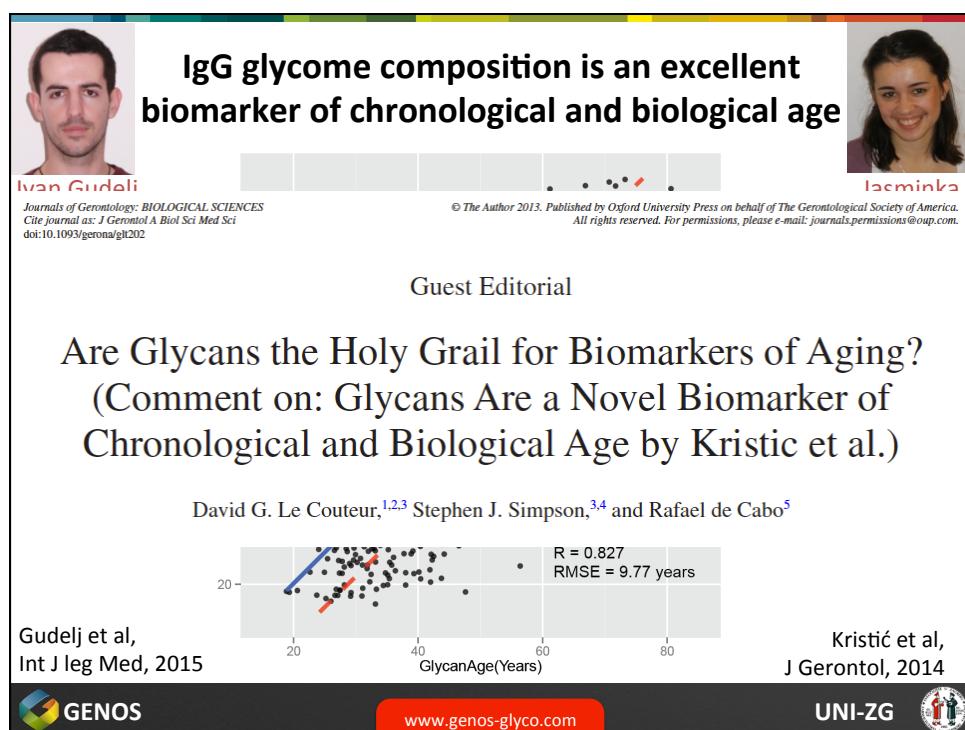
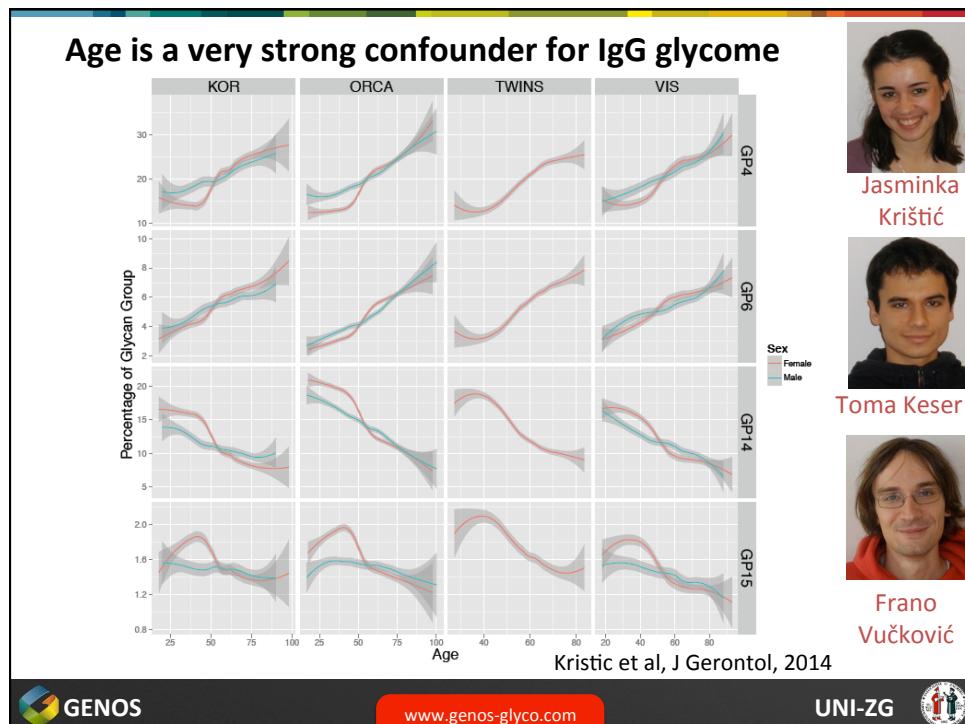
Lauc G, BBA, 2016



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After correcting for chronological age, glycan age index associates with “unhealthy” life

	Orkney		Vis and Korcula	
	Beta	p	Beta	p
Insulin	0.0755	9.22E-08	0.0402	3.50E-01
Fibrinogen	0.0157	1.98E-06	0.0167	8.83E-05
HbA1c	0.1106	2.63E-06	0.0084	3.16E-03
BMI	0.0585	1.67E-04	0.0344	1.04E-02
Triglycerides	0.0092	1.75E-04	0.0140	1.20E-04
Glucose	0.0113	2.09E-04	0.0091	4.77E-02
Waist circumference	0.1468	2.08E-04		
Calcium	0.0010	2.35E-04	0.0002	7.04E-01
D-dimer	2.9670	8.24E-04		
Cholesterol	0.0036	3.07E-01	0.0201	5.51E-08
LDL	0.0031	3.26E-01	0.0146	6.08E-06
Uric acid	1.0773	4.02E-02	0.7620	9.68E-04

Note: HbA1c = glycosylated hemoglobin; BMI = body mass index; LDL = low-density lipoprotein; p = p value; beta = regression coefficient.

Kristic et al, J Gerontol, 2014

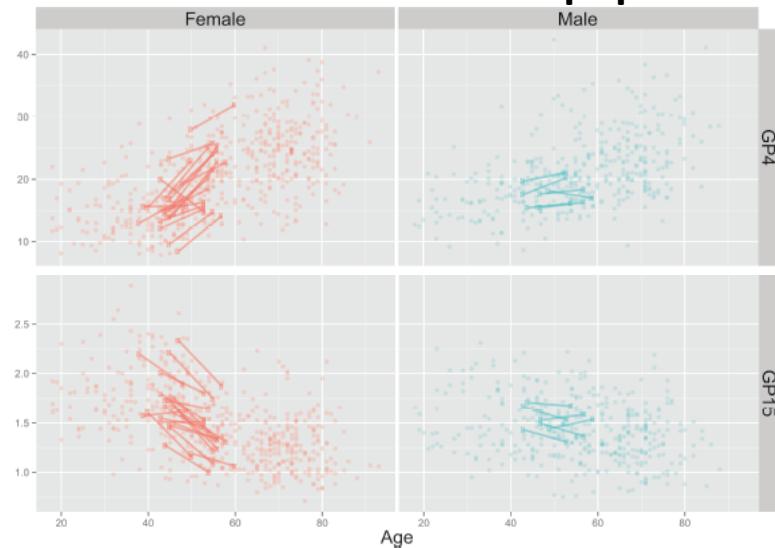


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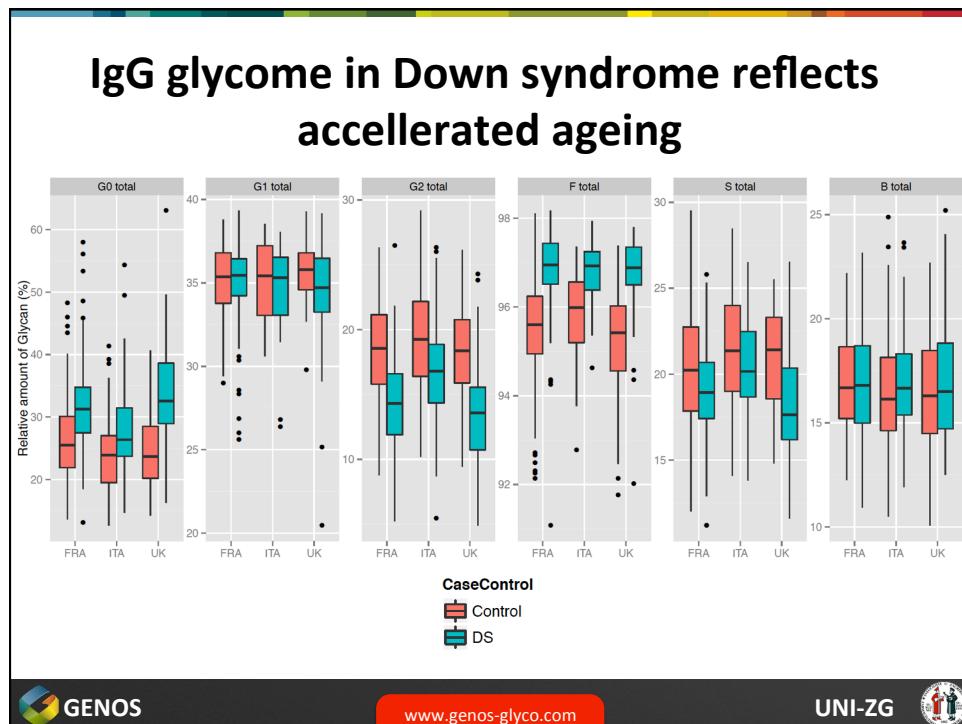
Changes within an individual generally follow trends observed in a population



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Intensive exercise makes IgG glycome more pro-inflammatory, but only transiently



Prof. Markus Perola

frontiers
in Physiology

ORIGINAL RESEARCH
published: 10 January 2017
doi: 10.3389/fphys.2016.00689



The Effects of Intensive Weight Reduction on Body Composition and Serum Hormones in Female Fitness Competitors

Juha J. Hulmi^{1,2*}, Ville Isola¹, Marianna Suonpää², Neera J. Järvinen¹, Marja Kokkonen⁴, Annika Wenneström^{5,6}, Kai Nyman⁷, Markus Perola^{8,9,10}, Juha P. Ahtiainen¹ and Keijo Häkkinen¹

 www.genos-glyco.com 

IgG glycome is better predictor of mortality, than NMR biomarkers or methylation



Prof. Ian Deary

Marioni et al. *Genome Biology* (2015) 16:25
DOI 10.1186/s13059-015-0584-6



RESEARCH Open Access

DNA methylation age of blood predicts all-cause mortality in later life

Riccardo E Marioni^{1,2,3†}, Sonia Shah^{3,4†}, Allan F McRae^{3,4†}, Brian H Chen^{5,6†}, Elena Colicino^{7†}, Sarah E Harris^{1,2}, Jude Gibson⁸, Anjali K Henders⁹, Paul Redmond¹⁰, Simon R Cox^{1,10}, Alison Pattie¹⁰, Janie Corley¹⁰, Lee Murphy⁸, Nicholas G Martin⁹, Grant W Montgomery⁹, Andrew P Feinberg^{11,12}, M Daniele Fallin^{11,13}, Michael L Multhaup¹¹, Andrew E Jaffe^{13,14}, Roby Joehanes^{5,15,16}, Joel Schwartz^{7,17}, Allan C Just⁷, Kathryn L Lunetta^{5,18}, Joanne M Murabito^{5,19}, John M Starr^{1,20}, Steve Horvath^{7,22†}, Andrea A Baccarelli^{7,17†}, Daniel Levy^{5,6†}, Peter M Visscher^{1,3,4†}, Naomi R Wray^{3,4†} and Ian J Deary^{1,10†}

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Biomarker Profiling by Nuclear Magnetic Resonance Spectroscopy for the Prediction of All-Cause Mortality: An Observational Study of 17,345 Persons

Krista Fischer^{1,9*}, Johannes Kettunen^{2,3,4*}, Peter Würz^{2,4,9*}, Toomas Haller¹, Aki S. Havulinna³, Antti J. Kangas⁴, Pasi Soininen^{4,5}, Tõnu Esko^{1,6,7,8,9,10}, Mari-Liis Tammesoo¹, Reedik Mägi¹, Steven Smit¹, Aarno Palotie^{2,6,11}, Samuli Ripatti^{2,11}, Veikko Salomaa³, Mika Ala-Korpela^{4,5,12†}, Markus Perola^{1,2†}, Andres Metspalu^{1,13†}

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