

Supplementary Materials

IgG N-glycosylation is altered in coronary artery disease

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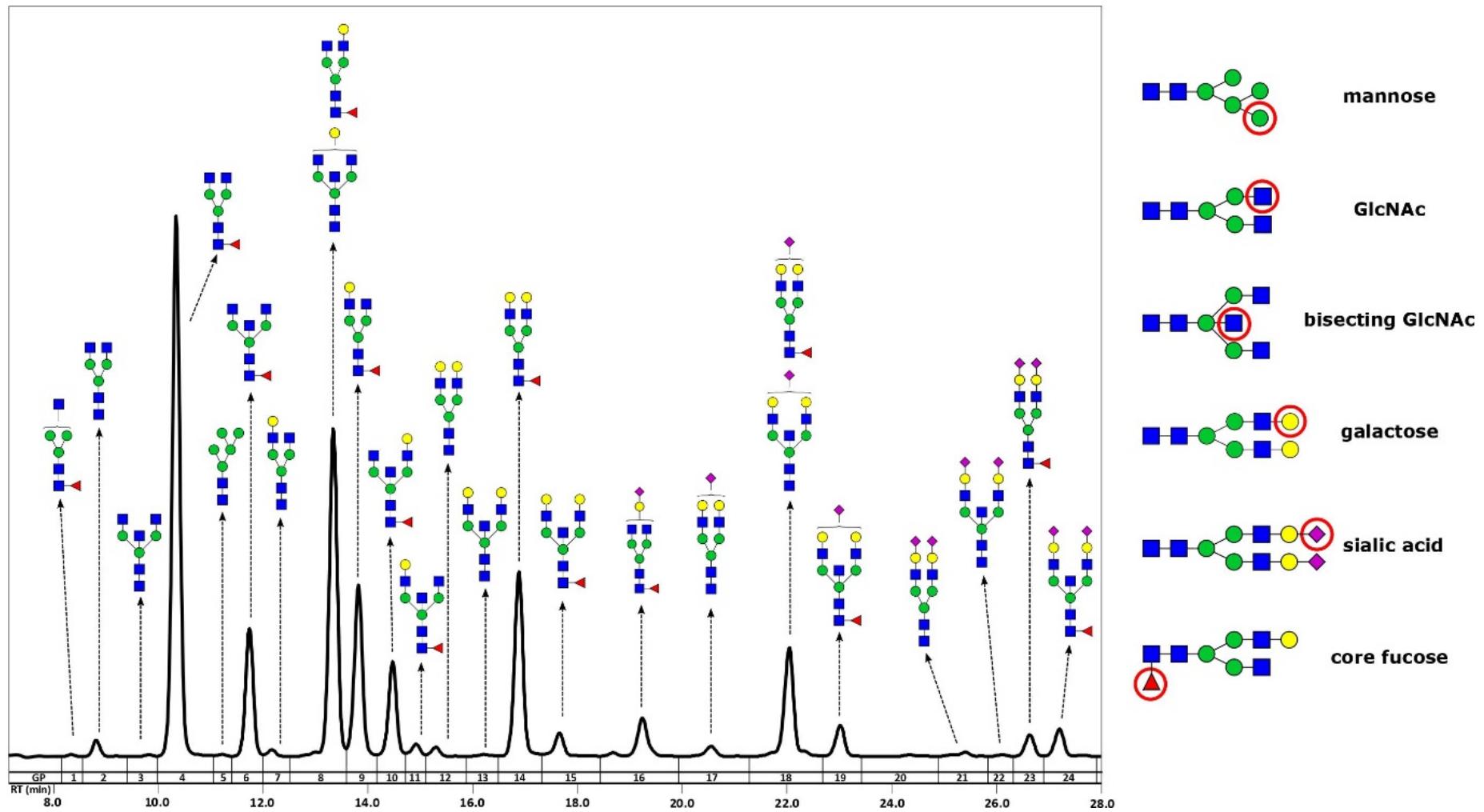


Figure S1. Representative chromatogram of 2-AB labelled IgG N-glycans separated by HILIC-UHPLC-FLR. The integration areas, together with a major structure presented in each glycan peak are given. Glycan peaks are numbered as used in the paper

Table S1. IgG derived N-glycan traits calculated out of 24 directly measured IgG N-glycan peaks

Derived trait	Formula
Agalactosylation G0	$\text{SUM}(\text{GP1} + \text{GP2} + \text{GP3} + \text{GP4} + \text{GP6}) / \text{GP}_{\text{total}} * 100$
Monogalactosylation G1	$\text{SUM}(\text{GP7} + \text{GP8} + \text{GP9} + \text{GP10} + \text{GP11}) / \text{GP}_{\text{total}} * 100$
Digalactosylation G2	$\text{SUM}(\text{GP12} + \text{GP13} + \text{GP14} + \text{GP15}) / \text{GP}_{\text{total}} * 100$
Sialylation S	$\text{SUM}(\text{GP16} + \text{GP17} + \text{GP18} + \text{GP19} + \text{GP20} + \text{GP21} + \text{GP22} + \text{GP23} + \text{GP24}) / \text{GP}_{\text{total}} * 100$
Core fucosylation CF	$\text{SUM}(\text{GP1} + \text{GP4} + \text{GP6} + \text{GP8} + \text{GP9} + \text{GP10} + \text{GP11} + \text{GP14} + \text{GP15} + \text{GP16} + \text{GP18} + \text{GP19} + \text{GP23} + \text{GP24}) / \text{GP}_{\text{total}} * 100$
Bisecting GlcNAc B	$\text{SUM}(\text{GP3} + \text{GP6} + \text{GP10} + \text{GP11} + \text{GP13} + \text{GP15} + \text{GP19} + \text{GP22} + \text{GP24}) / \text{GP}_{\text{total}} * 100$
Bisecting GlcNAc in all fucosylated monosialylated structures FBS1/(FS1+FBS1)	$\text{GP19} / \text{SUM}(\text{GP16} + \text{GP18} + \text{GP19})$
Core fucosylated monosialylated with and without bisecting GlcNAc FBS1/FS1	$\text{GP19} / \text{SUM}(\text{GP16} + \text{GP18})$
Sialylated glycans of all fucosylated structures without bisecting GlcNAc FGS/(F+FG+FGS)	$\text{SUM}(\text{GP16} + \text{GP18} + \text{GP23}) / \text{SUM}(\text{GP16} + \text{GP18} + \text{GP23} + \text{GP4} + \text{GP8} + \text{GP9} + \text{GP14}) * 100$

Table S2. Statistical analysis of associations between IgG glycosylation traits (24 directly measured and six derived) and coronary artery disease at the inclusion point and during the two-year follow up period, after adjustment for age and sex

Glycan trait	Inclusion point				Two-year follow up point			
	Effect	SE	p-value	p ^{adj} -value*	Effect	SE	p-value	p ^{adj} -value*
GP1	0	0.1035	9.92E-01	9.92E-01	0.02	0.0597	7.74E-01	8.60E-01
GP2	0.06	0.1094	5.67E-01	7.09E-01	-0.1	0.0523	6.52E-02	4.89E-01
GP3	0.11	0.101	2.69E-01	5.04E-01	-0.01	0.0724	8.99E-01	8.99E-01
GP4	0.12	0.0988	2.27E-01	4.55E-01	-0.05	0.0484	2.76E-01	7.94E-01
GP5	-0.1	0.1073	3.29E-01	5.48E-01	-0.14	0.0969	1.45E-01	7.26E-01
GP6	0.21	0.1011	3.99E-02	4.25E-01	0.03	0.0409	4.56E-01	7.94E-01
GP7	0.01	0.1099	9.47E-01	9.88E-01	-0.05	0.0492	3.18E-01	7.94E-01
GP8	-0.11	0.1082	3.05E-01	5.37E-01	-0.03	0.0559	5.78E-01	7.94E-01
GP9	-0.19	0.108	8.04E-02	4.25E-01	-0.11	0.05	2.39E-02	3.59E-01
GP10	0.14	0.1095	1.88E-01	4.33E-01	0.11	0.0474	1.83E-02	3.59E-01
GP11	0.08	0.1082	4.78E-01	7.09E-01	0.02	0.0416	6.55E-01	7.94E-01
GP12	0.03	0.1065	7.83E-01	9.40E-01	-0.02	0.0494	6.62E-01	7.94E-01
GP13	-0.17	0.1062	1.03E-01	4.25E-01	0.07	0.0559	2.33E-01	7.94E-01
GP14	-0.14	0.0955	1.39E-01	4.25E-01	0.04	0.0489	4.67E-01	7.94E-01
GP15	-0.06	0.1061	5.66E-01	7.09E-01	0.09	0.0538	1.01E-01	6.04E-01
GP16	-0.09	0.1089	4.16E-01	6.56E-01	-0.01	0.0425	8.13E-01	8.71E-01
GP17	-0.02	0.1096	8.56E-01	9.51E-01	-0.07	0.0723	3.20E-01	7.94E-01
GP18	-0.15	0.1003	1.35E-01	4.25E-01	0.03	0.0497	5.73E-01	7.94E-01
GP19	-0.14	0.1091	2.08E-01	4.45E-01	0.02	0.05	7.07E-01	8.16E-01
GP20	-0.14	0.1073	1.82E-01	4.33E-01	-0.09	0.1096	4.12E-01	7.94E-01
GP21	-0.07	0.1089	5.12E-01	7.09E-01	0.02	0.1181	8.75E-01	8.99E-01
GP22	0.06	0.1096	5.60E-01	7.09E-01	0.06	0.0683	4.16E-01	7.94E-01
GP23	-0.25	0.1064	1.98E-02	4.25E-01	0.02	0.0534	6.57E-01	7.94E-01
GP24	-0.01	0.1092	9.55E-01	9.88E-01	0.04	0.0612	5.59E-01	7.94E-01
G0 total	0.15	0.0974	1.16E-01	4.25E-01	-0.04	0.0494	3.94E-01	7.94E-01
G1 total	-0.14	0.1085	1.81E-01	4.33E-01	-0.03	0.0637	5.89E-01	7.94E-01

G2 total	-0.14	0.0955	1.41E-01	4.25E-01	0.04	0.0492	3.98E-01	7.94E-01
S total	-0.18	0.104	8.91E-02	4.25E-01	0.03	0.0486	5.37E-01	7.94E-01
F total	-0.02	0.1093	8.25E-01	9.51E-01	0.06	0.0566	2.74E-01	7.94E-01
B total	0.15	0.1057	1.42E-01	4.25E-01	0.1	0.0487	4.67E-02	4.67E-01

*False discovery rate was controlled using Benjamini–Hochberg method

Table S3. Interaction analysis for IgG glycosylation traits (24 directly measured and 9 calculated derived) and CAD by sex

Glycan trait	p-value	p _{adj} -value*
GP1	3.75E-02	9.10E-02
GP2	4.85E-02	1.05E-01
GP3	1.07E-02	3.51E-02
GP4	1.24E-02	3.51E-02
GP5	6.93E-01	7.85E-01
GP6	1.20E-02	3.51E-02
GP7	6.40E-01	7.50E-01
GP8	9.35E-01	9.35E-01
GP9	7.84E-01	8.58E-01
GP10	2.55E-01	4.13E-01
GP11	2.16E-01	3.67E-01
GP12	5.79E-01	7.29E-01
GP13	6.23E-01	7.50E-01
GP14	5.25E-02	1.05E-01
GP15	2.76E-01	4.26E-01
GP16	1.02E-02	3.51E-02
GP17	1.19E-02	3.51E-02
GP18	4.58E-04	3.11E-03
GP19	1.90E-02	4.96E-02
GP20	1.81E-01	3.24E-01
GP21	6.73E-03	3.27E-02
GP22	1.80E-01	3.24E-01
GP23	2.87E-04	2.44E-03
GP24	2.51E-05	3.98E-04
S total	3.81E-06	1.29E-04
B total	3.78E-01	5.58E-01

F total	8.07E-01	8.58E-01
G0 total	3.31E-03	1.87E-02
G1 total	4.25E-01	6.02E-01
G2 total	5.00E-02	1.05E-01

*False discovery rate was controlled using Benjamini–Hochberg method

