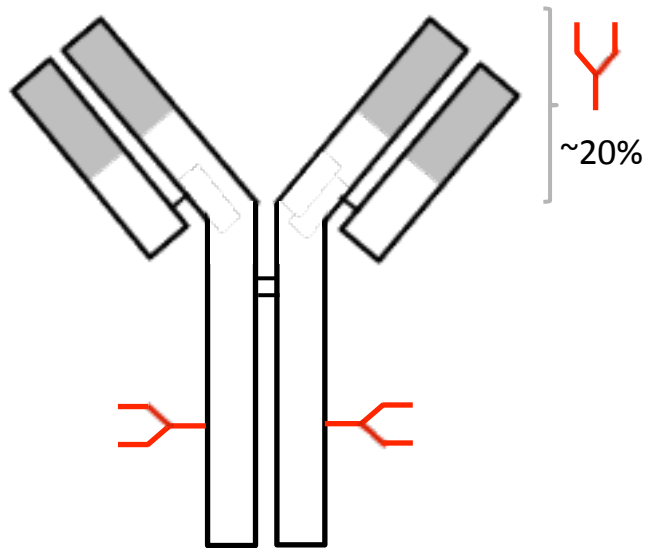SUPPLEMENTARY INFORMATION

Figure S1. Structural scheme of IgG and the location of its sites of glycosylation.

Approximately 20% of an individual's IgGs have N-glycans attached to the variable

region.

Figure S2. SDS-PAGE of purified Immunoglobulin G. Protein marker was loaded in lane 1, while immunocaptured IgG was loaded in lane 2. Clear separation was observed between the heavy chain (~49 kDa) and the light chain (~25 kDa) of IgG.
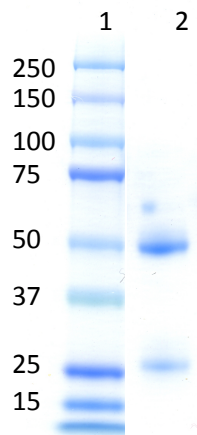
Figure S3. Typical IgG N-glycan profile obtained using nLC-PGC-chip-TOF-MS.
The thick black line represents the Extracted Glycan Chromatogram, while the inserted colored areas represent the individual glycans. Only higher abundant glycans are annotated according to the following key: blue square: N-acetyl glucosamine, green ball: mannose, yellow ball: galactose, red triangle: fucose and purple diamond: sialic acid.
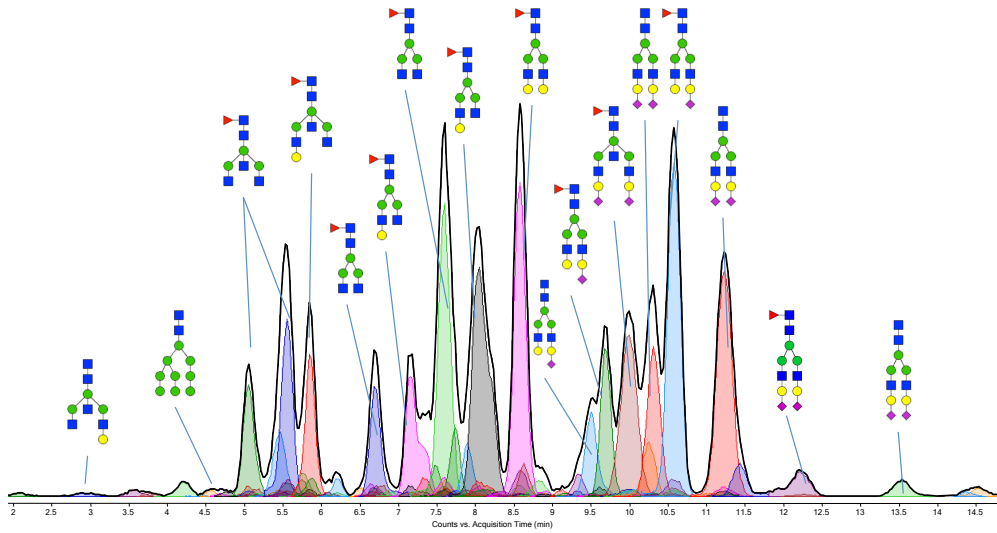
Table S4. Glycan compositions observed on IgG from patient serum. The table is ordered according to the average abundance of the individual glycan compositions in the 18 NAG cases. FDR-adjusted p-values were obtained using the three-way ANOVA for the different disease groups (NAG, DU and GC); a dash indicates a non-significant result (FDR-adjusted p-value > 0.1).

No.	Composition	Mass (calc.)	Average abundance (%)	S.D.	FDR adjusted p-value
1	$H_3N_4F_1$	1462.544	12.97	4.31	0.0026
2	$H_5N_4F_1S_1$	2077.745	12.10	3.16	0.0704
3	$H_4N_4F_1$	1624.597	11.52	2.61	0.0520
4	$H_5N_4S_2$	2222.783	10.23	5.02	-
5	$H_5N_4F_1$	1786.650	7.76	3.24	0.0757
6	$H_5N_5F_1S_2$	2571.920	6.46	1.21	-
7	$H_3N_5F_1$	1665.624	5.84	2.24	0.0656
8	$H_4N_5F_1$	1827.677	5.08	1.55	-
9	$H_5N_4S_1$	1931.688	4.09	0.95	-
10	$H_4N_4F_1S_1$	1915.693	2.62	0.66	-
11	$H_5N_5F_1S_1$	2280.825	2.55	0.66	-
12	$H_5N_4F_1S_2$	2368.841	2.42	0.87	0.0520
13	H_3N_4	1316.487	1.76	0.70	-
14	H_4N_4	1478.539	1.73	0.52	-
15	H_4N_5	1681.619	1.39	0.40	-
16	$H_5N_5F_1$	1989.729	1.29	0.60	0.0240
17	H_5N_4	1640.592	1.27	0.51	0.0738
18	H_3N_5	1519.566	1.16	0.54	0.0757
19	$H_5N_5S_2$	2425.862	1.03	0.43	-
20	$H_5N_5S_1$	2134.767	0.87	0.47	0.0240
21	$H_3N_3F_1$	1259.465	0.84	0.34	0.0902
22	H_3N_3	1113.407	0.51	0.18	-
23	$H_4N_3F_1$	1421.518	0.45	0.22	0.0240
24	$H_4N_5F_1S_1$	2118.772	0.44	0.29	0.0240
25	H_5N_5	1843.672	0.44	0.24	0.0768
26	$H_4N_4S_1$	1769.635	0.38	0.18	-
27	H_9N_2	1882.645	0.33	0.15	-
28	H_8N_2	1720.592	0.27	0.17	-
29	H_4N_3	1275.460	0.25	0.16	-
30	$H_4N_3S_1$	1566.555	0.23	0.17	-
31	$H_4N_5S_1$	1972.714	0.22	0.21	0.0181
32	$H_6N_5F_1S_1$	2442.878	0.20	0.13	-
33	$H_6N_5S_3$	2879.011	0.17	0.36	0.0240
34	$H_6N_5F_1S_3$	3025.069	0.16	0.34	-
35	H_6N_2	1396.486	0.16	0.17	-
36	H_5N_2	1234.433	0.15	0.12	-
37	$H_6N_5F_1S_2$	2733.973	0.15	0.11	0.0240

38	H_7N_2	1558.539	0.10	0.11	-
39	$H_6N_3S_1$	1890.661	0.08	0.06	-
40	$H_5N_3S_1$	1728.608	0.07	0.06	-
41	$H_4N_3F_1S_1$	1712.613	0.05	0.09	-
42	$H_5N_3F_1S_1$	1874.666	0.04	0.04	-
43	H_3N_2	910.328	0.04	0.05	-
44	H_5N_3	1437.513	0.03	0.05	0.0393
45	$H_3N_2F_1$	1056.386	0.03	0.04	-
46	$H_5N_4F_2S_1$	2223.803	0.03	0.05	-
47	$H_6N_3F_1S_1$	2036.719	0.02	0.03	-
48	H_4N_2	1072.381	0.02	0.05	-