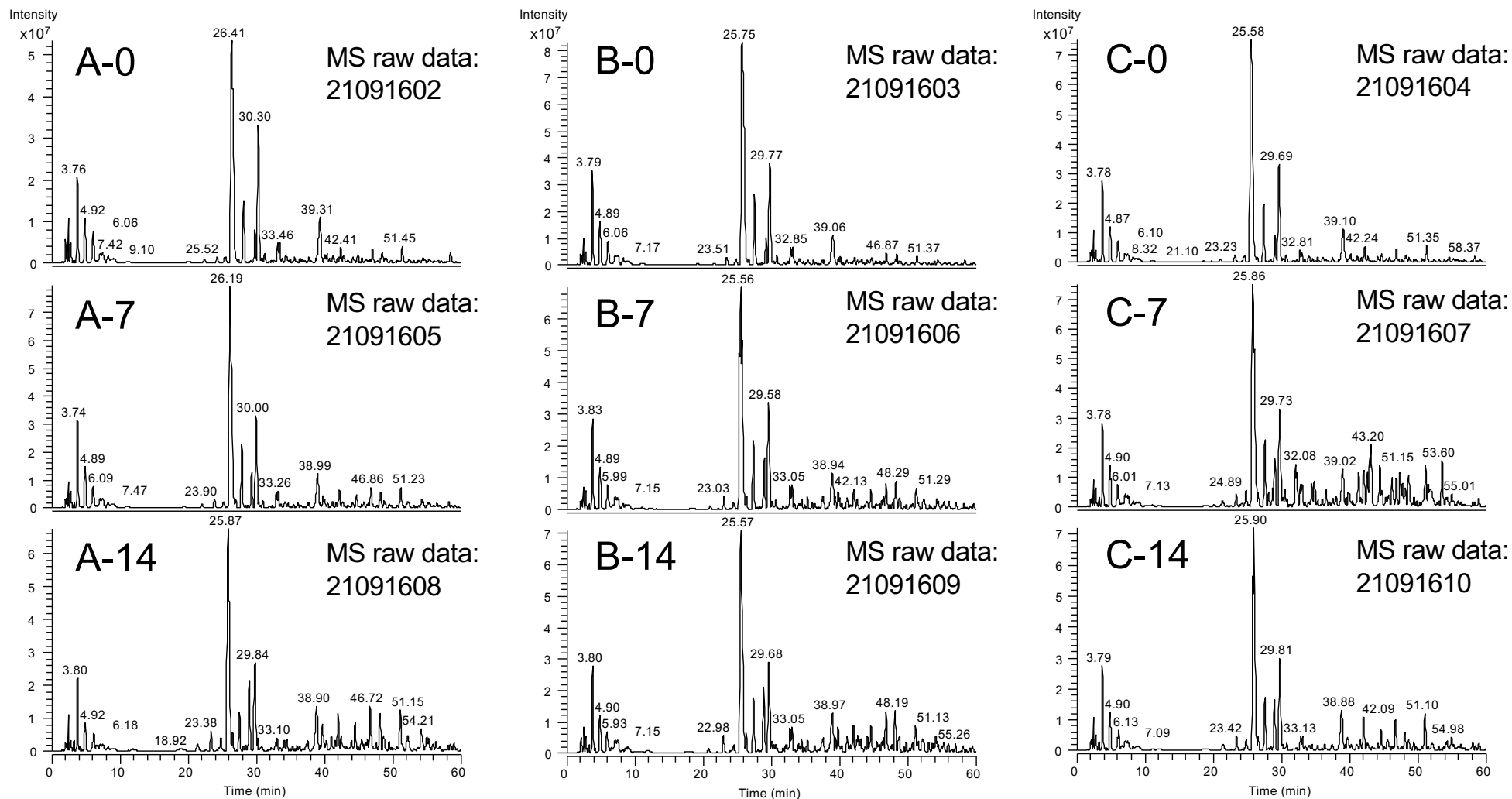


Supplemental Fig. 1

Base Peak Chromatogram (BPC) in MS

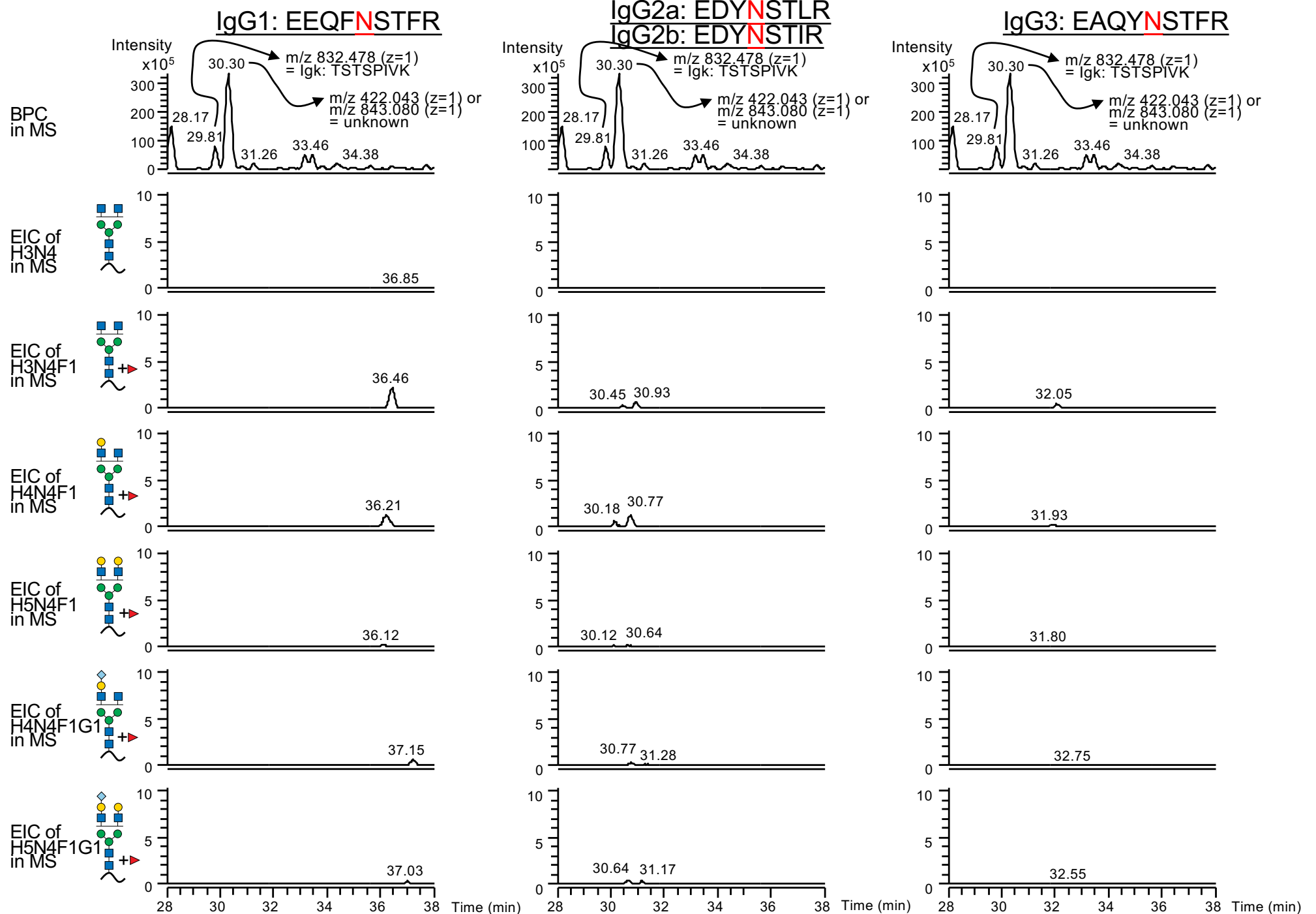


These glycoproteomic raw MS data and the identification result file for analysis of glycan structures on peptides have been deposited to the GlycoPOST (announced ID: GPST000407).

Supplemental Fig. 2

A-0: before treatment with 0.15 mg/g/day L-fucose (0th day)

MS raw data: 21091602

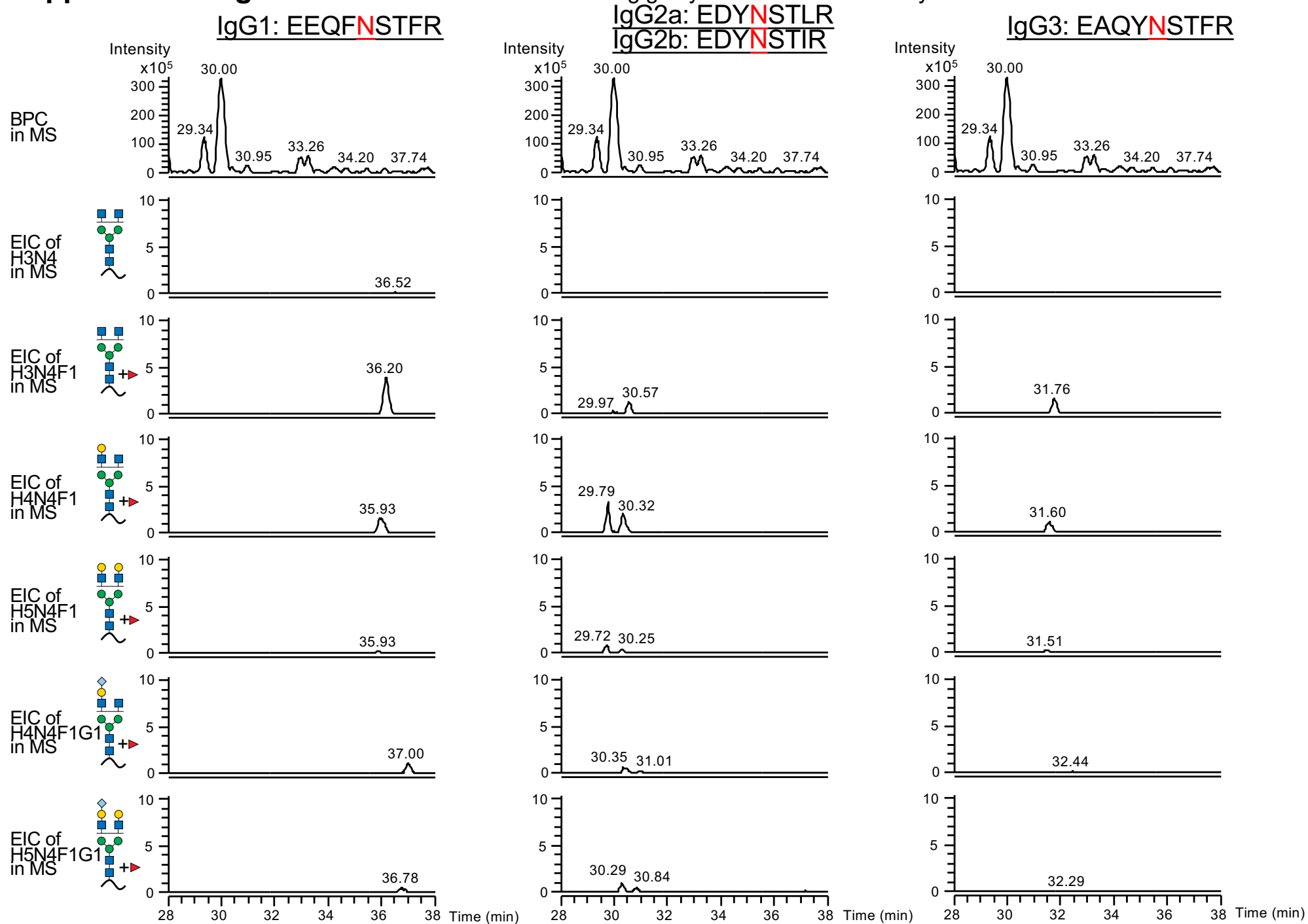


LC-MS analysis of N-glycans on IgGs obtained from *Fut8*^{-/-} mice before treatment with 0.15 mg/g/day L-fucose_0th day (A-0).

Supplemental Fig. 3

A-7: treatment with 0.15 mg/g/day L-fucose on the 7th day

MS raw data: 21091605

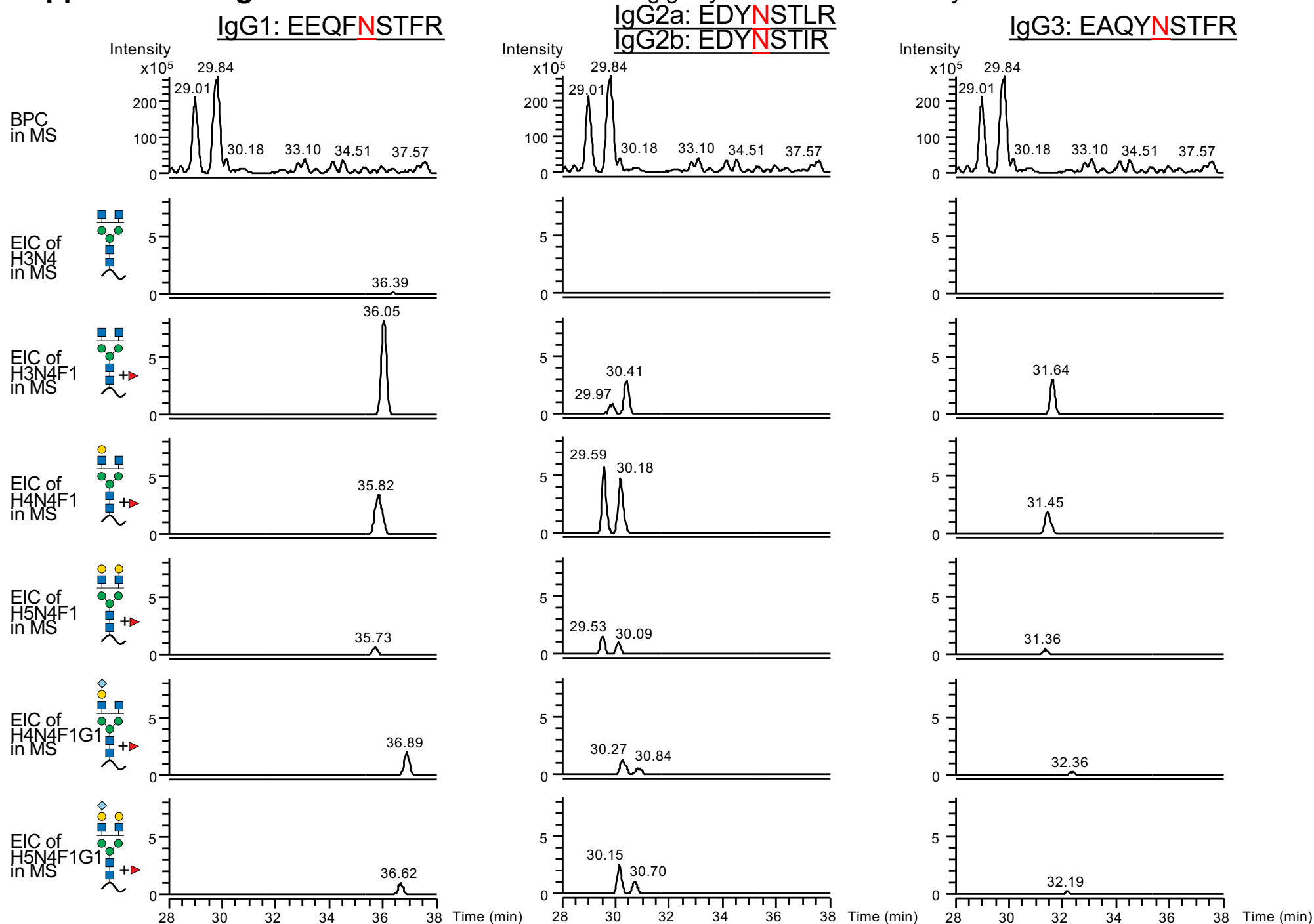


LC-MS analysis of N-glycans on IgGs obtained from *Fut8*^{+/-} mice treated with 0.15 mg/g/day L-fucose on the 7th day (A-7).

Supplemental Fig. 4

A-14: treatment with 0.15 mg/g/day L-fucose on the 14th day

MS raw data: 21091608

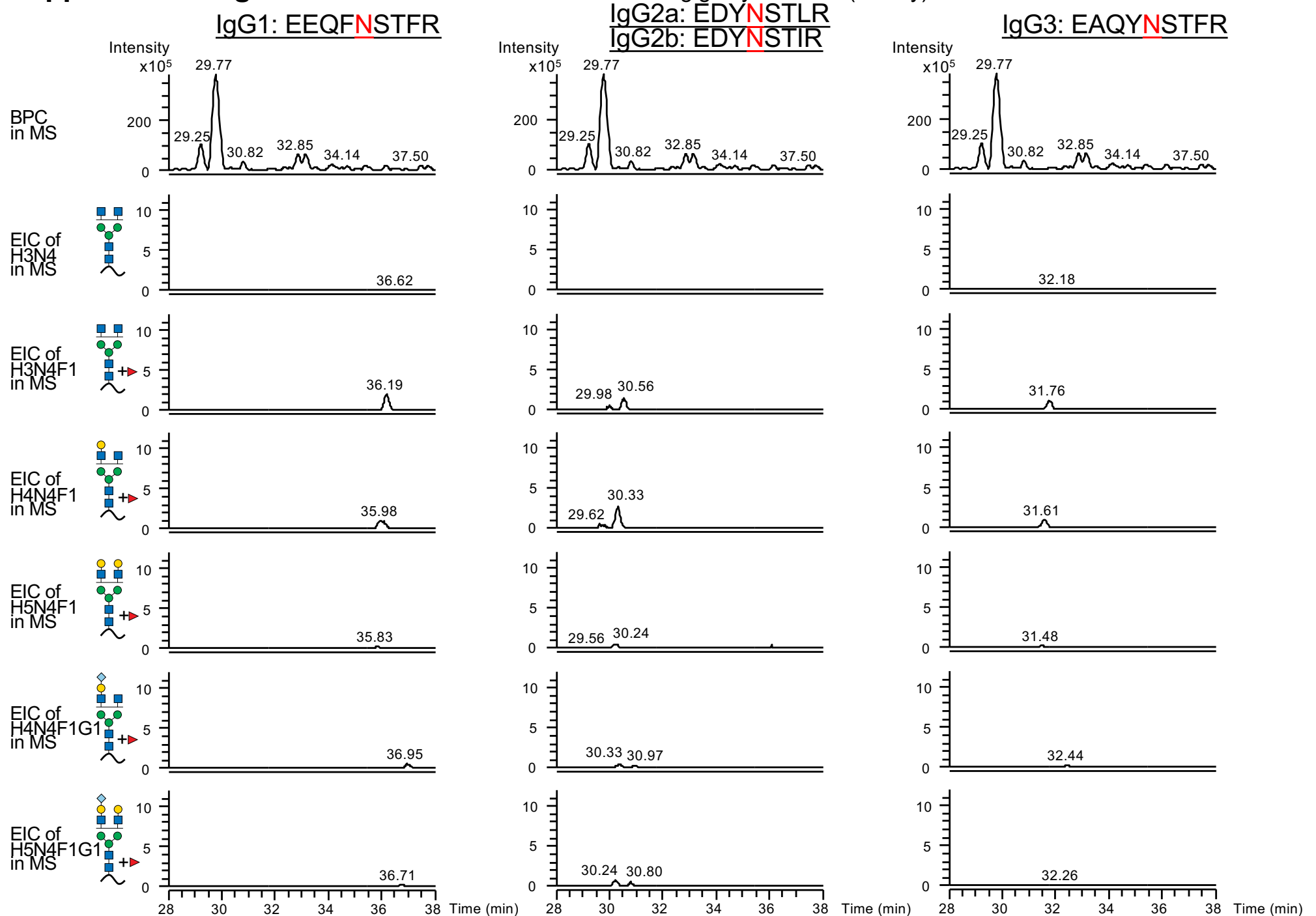


LC-MS analysis of N-glycans on IgGs obtained from *Fut8*^{+/-} mice treated with 0.15 mg/g/day L-fucose on the 14th day (A-14).

Supplemental Fig. 5

B-0: before treatment with 0.4 mg/g/day L-fucose (0th day)

MS raw data: 21091603

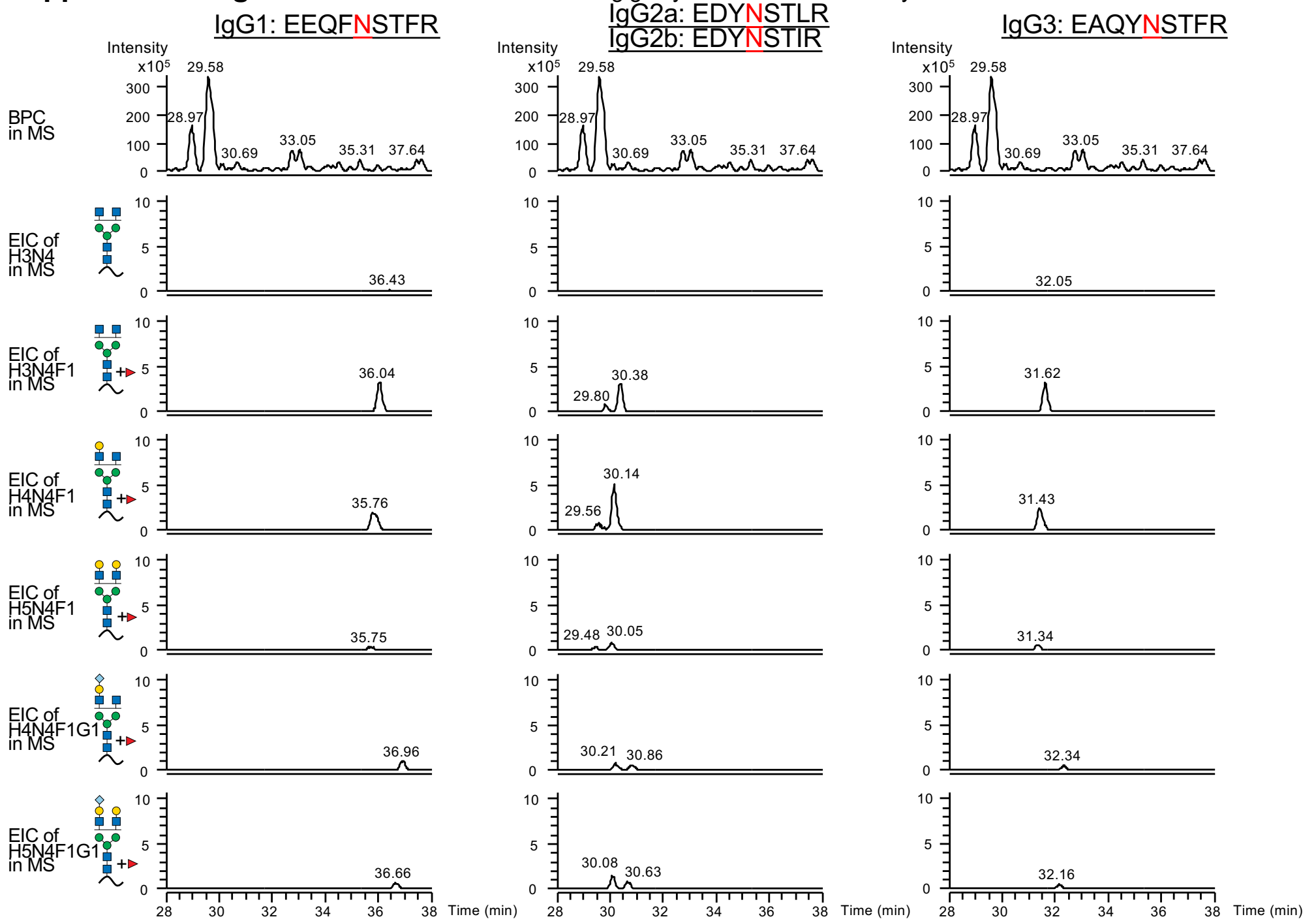


LC-MS analysis of N-glycans on IgGs obtained from *Fut8*^{+/-} mice before treatment with 0.4 mg/g/day L-fucose_0th day (B-0).

Supplemental Fig. 6

B-7: treatment with 0.4 mg/g/day L-fucose on the 7th day

MS raw data: 21091606

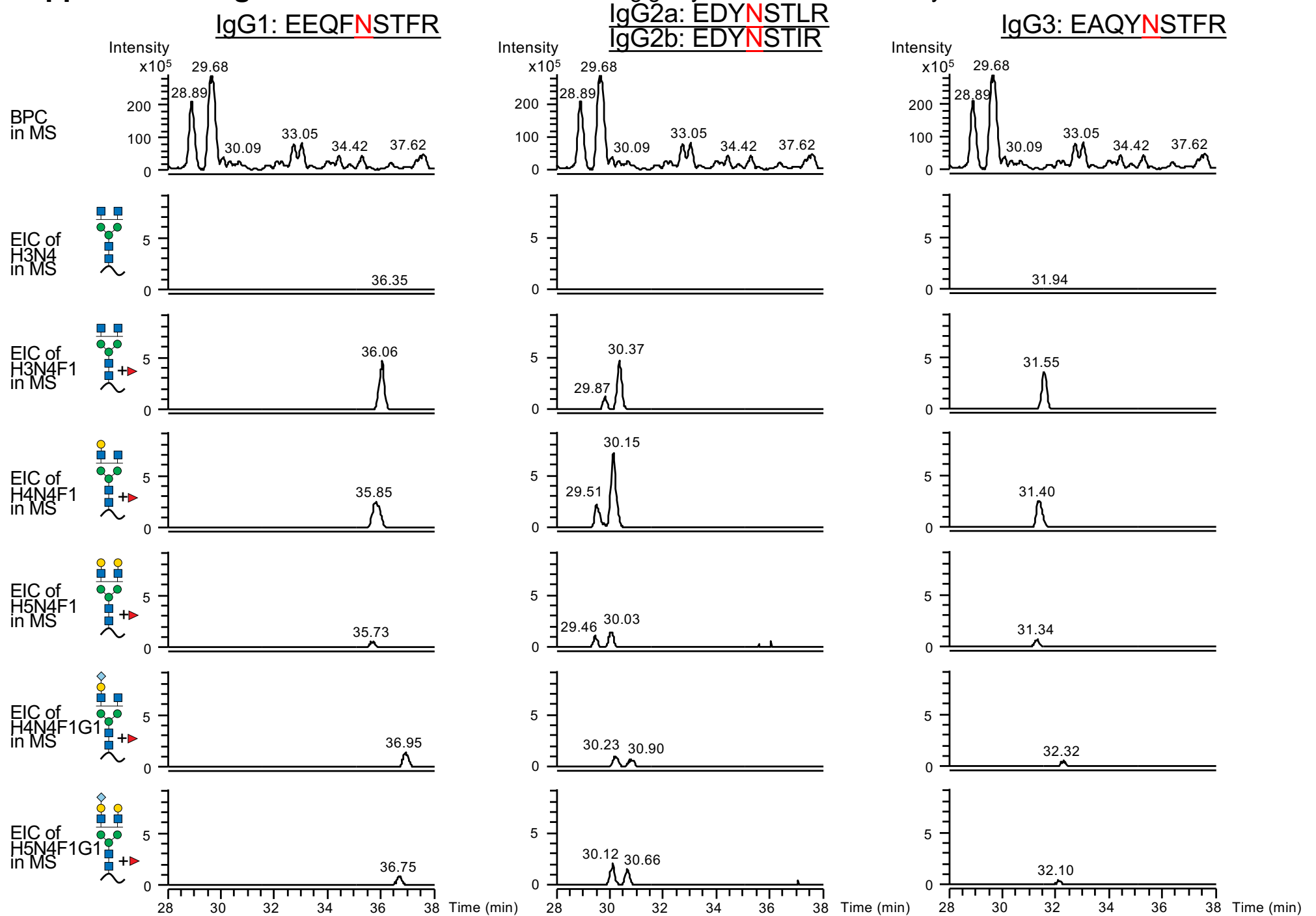


LC-MS analysis of N-glycans on IgGs obtained from *Fut8*^{+/-} mice treated with 0.4 mg/g/day L-fucose on the 7th day (B-7).

Supplemental Fig. 7

B-14: treatment with 0.4 mg/g/day L-fucose on the 14th day

MS raw data: 21091609

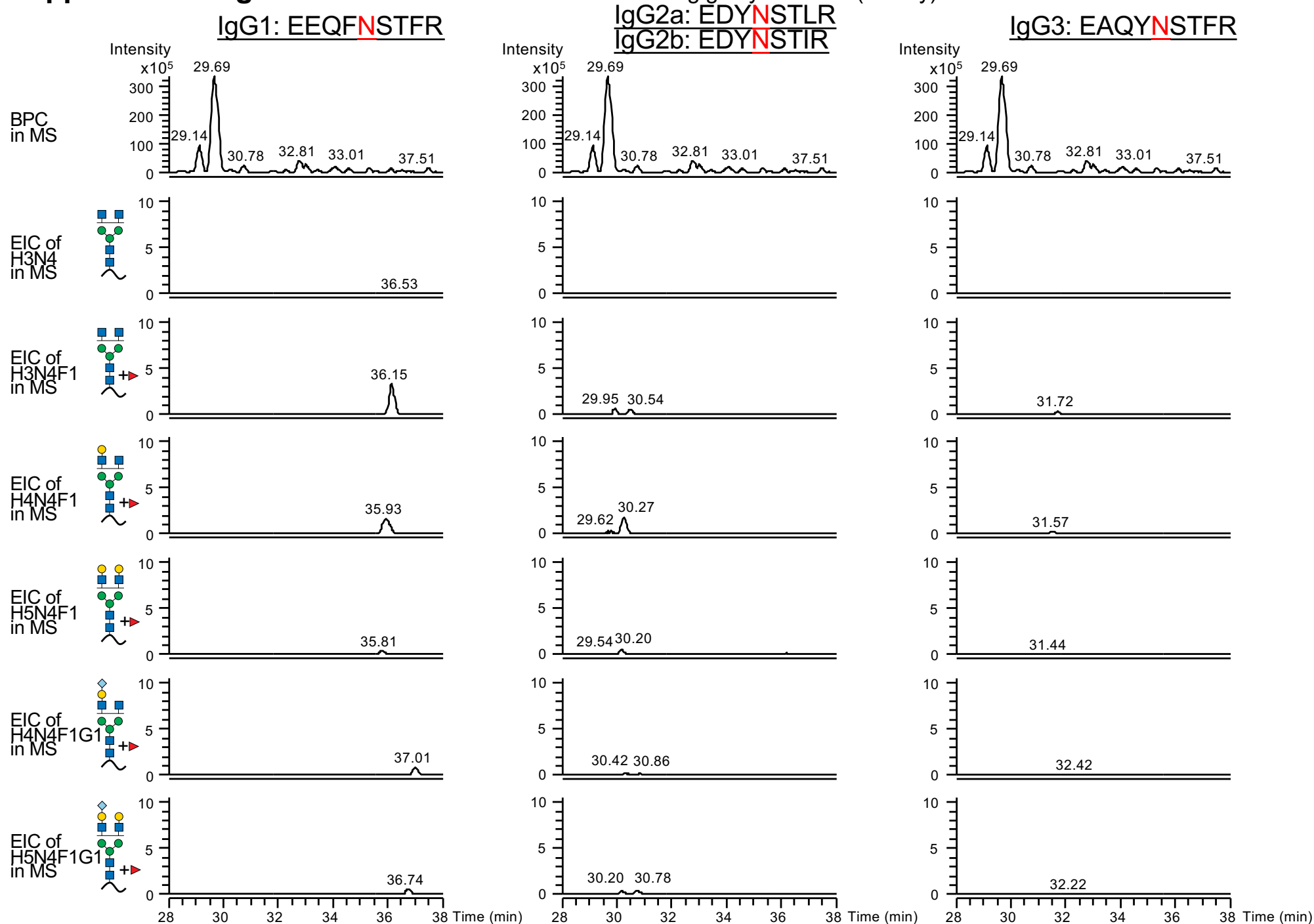


LC-MS analysis of N-glycans on IgGs obtained from *Fut8*^{-/-} mice treated with 0.4 mg/g/day L-fucose on the 14th day (B-14).

Supplemental Fig. 8

C-0: before treatment with 1.2 mg/g/day L-fucose (0th day)

MS raw data: 21091604

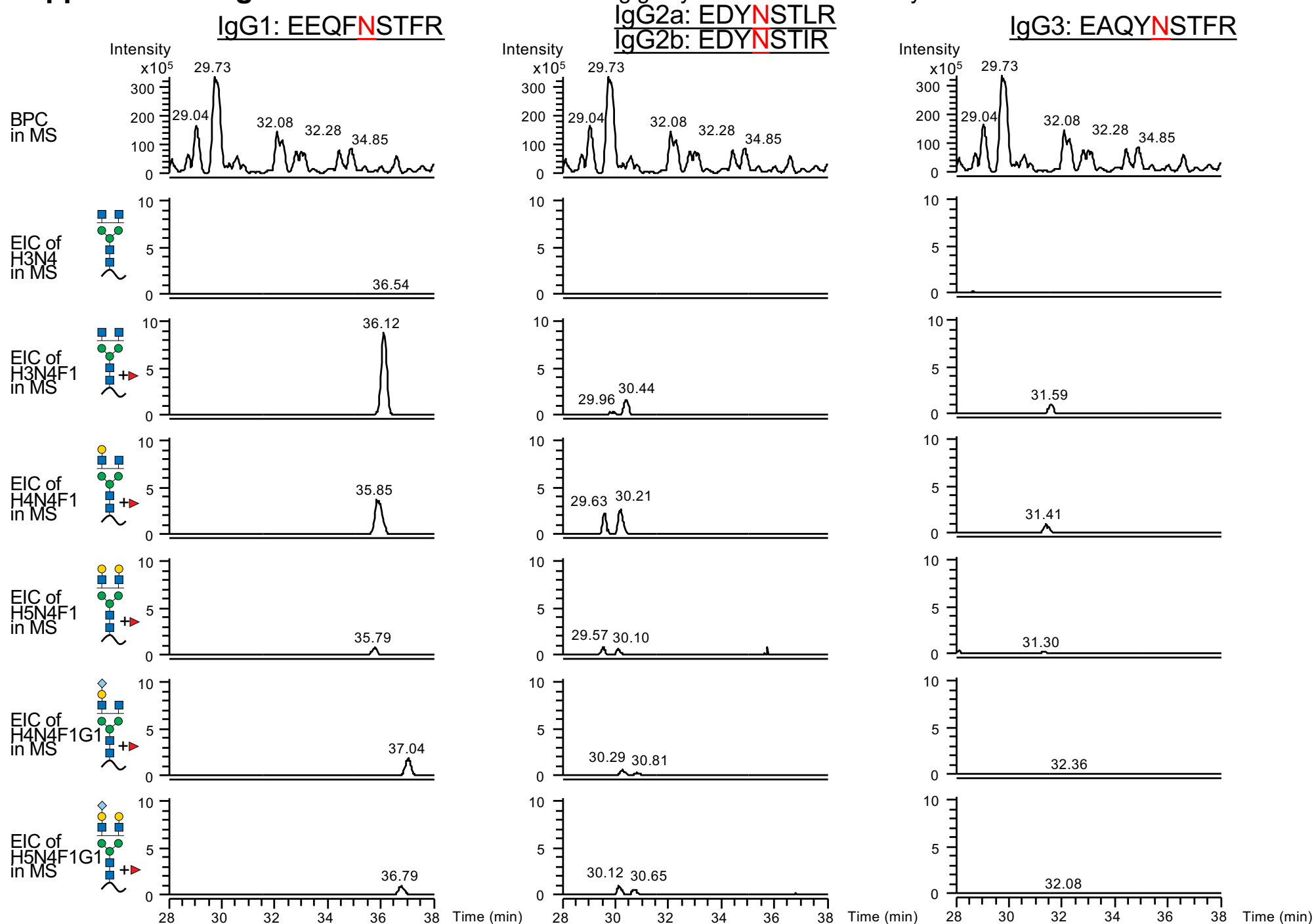


LC-MS analysis of N-glycans on IgGs obtained from *Fut8*^{+/-} mice before treatment with 1.2 mg/g/day L-fucose_0th day (C-0).

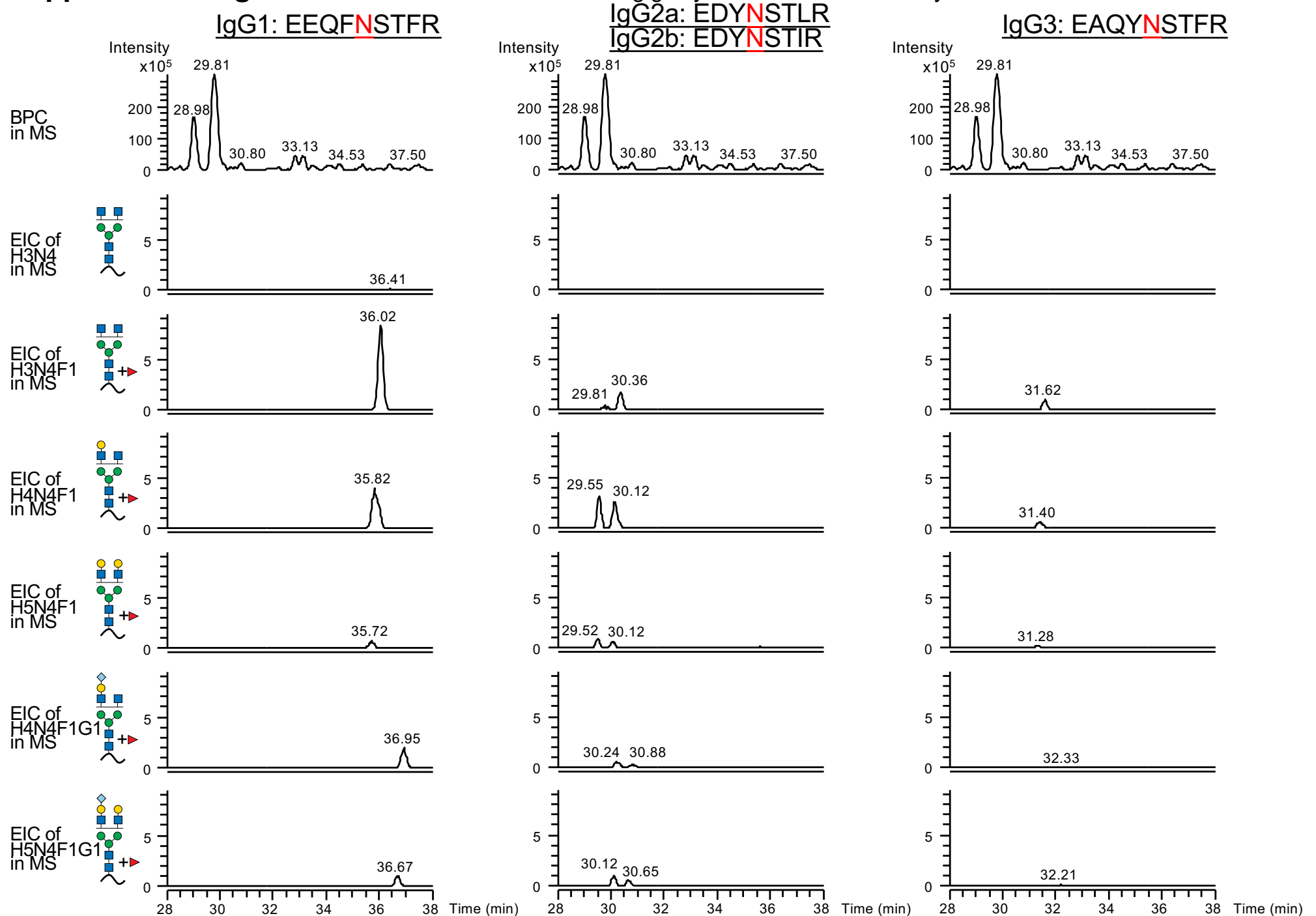
Supplemental Fig. 9

C-7: treatment with 1.2 mg/g/day L-fucose on the 7th day

MS raw data: 21091607



LC-MS analysis of N-glycans on IgGs obtained from *Fut8*^{+/-} mice treated with 1.2 mg/g/day L-fucose on the 7th day (C-7).



LC-MS analysis of N-glycans on IgGs obtained from *Fut8*^{-/-} mice treated with 1.2 mg/g/day L-fucose on the 14th day (C-14).

Supplemental Fig. 11

Identification of the linkage of fucose (Core or Lewis) based on the retention time

Mouse IgG1

~ EEQF**N**STFR

MS raw data: 21091608

A-14

Human Haptoglobin Site2

~ NLFL**N**HSE

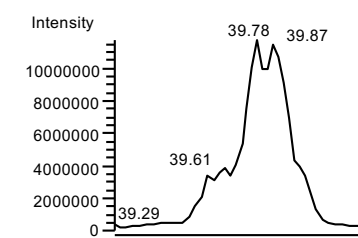
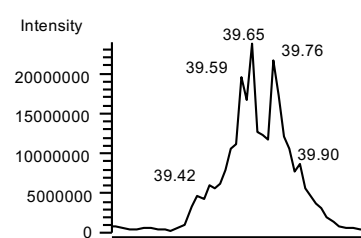
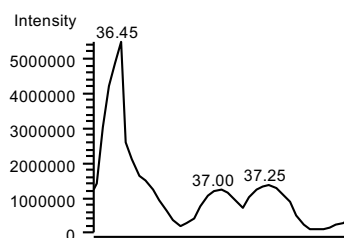
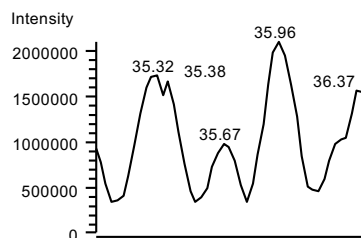
Ref. 67: Takahashi, S. *et al* (2016) *Glycoconj. J.* **33**, 471-482, Fig. 1, 2, 3, 5 and Sfig. 2, 6

Normal Volunteer
(NV pool)

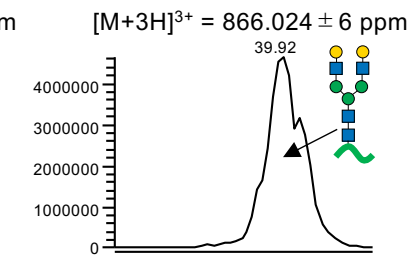
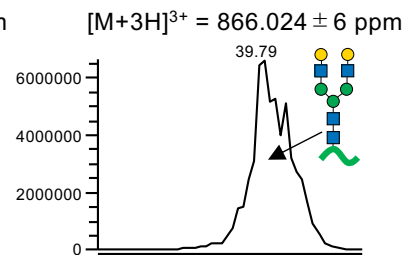
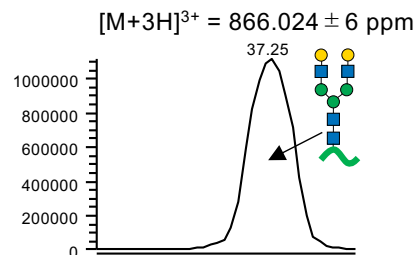
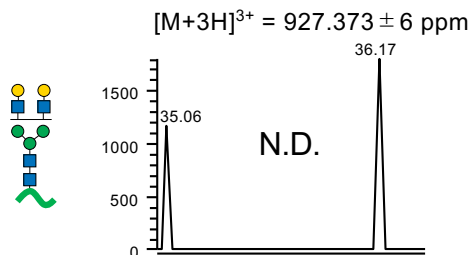
Prostate Cancer
(Pro #18)

Prostate Cancer
(Pro #14, Meta)

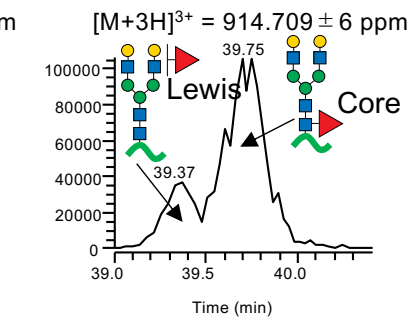
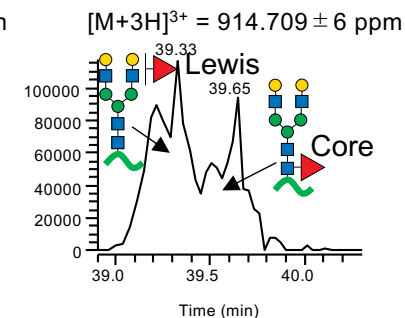
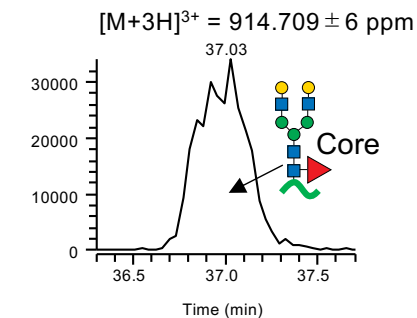
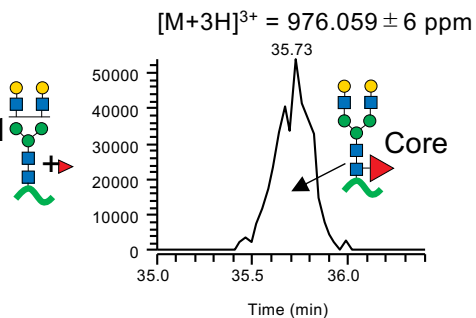
BPC
in MS



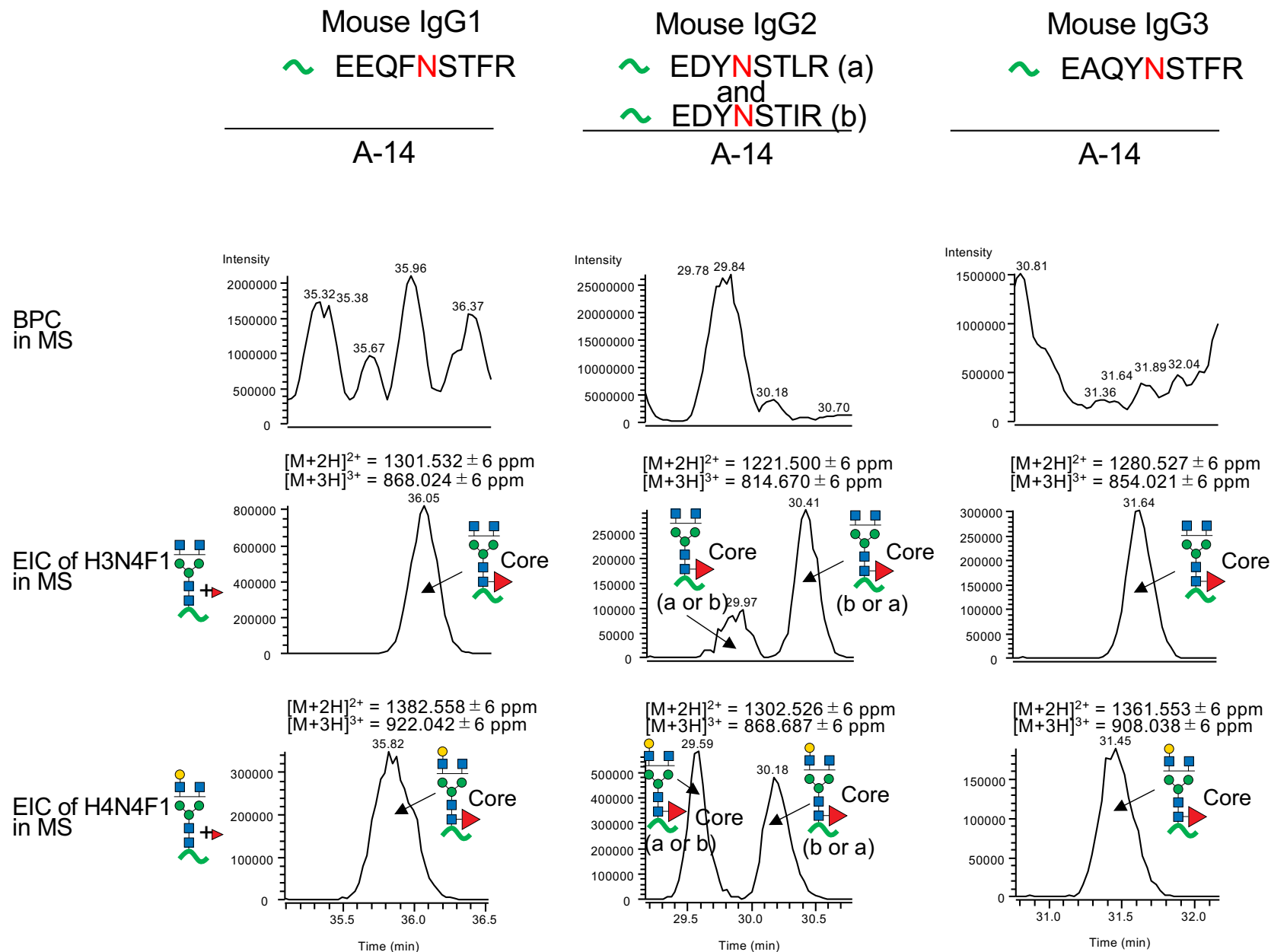
EIC of H5N4
in MS



EIC of H5N4F1
in MS



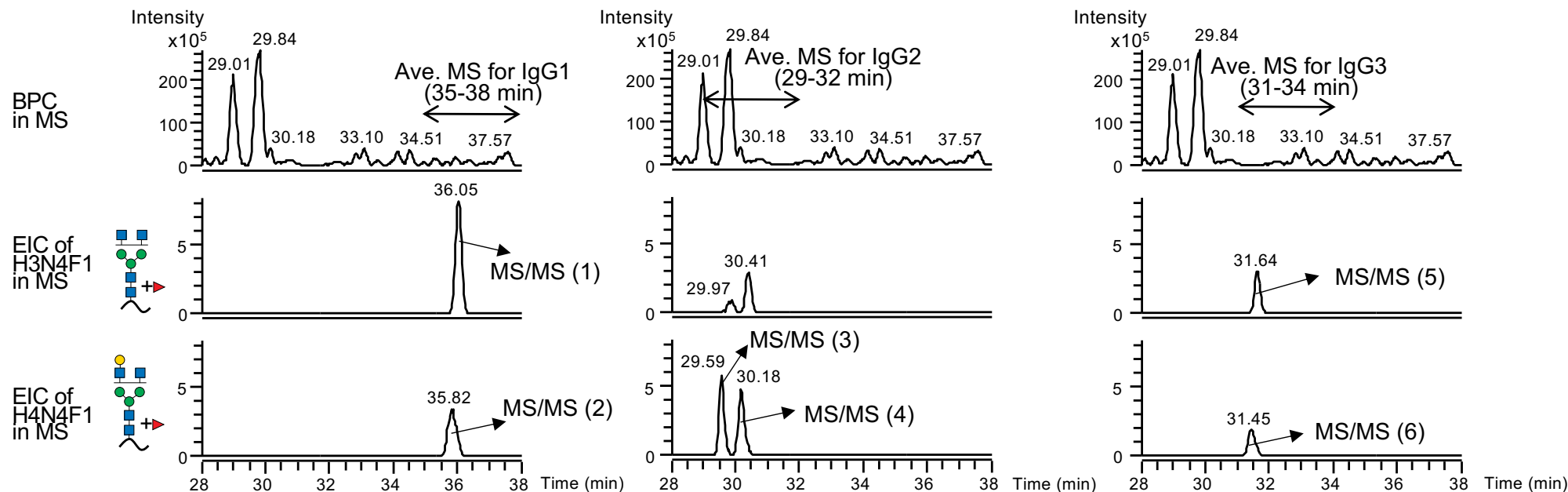
Identification of the linkage of fucose (Core or Lewis) based on the retention time



IgG1: EEQFNSTFR

IgG2a: EDYNSTLR
IgG2b: EDYNSTIR

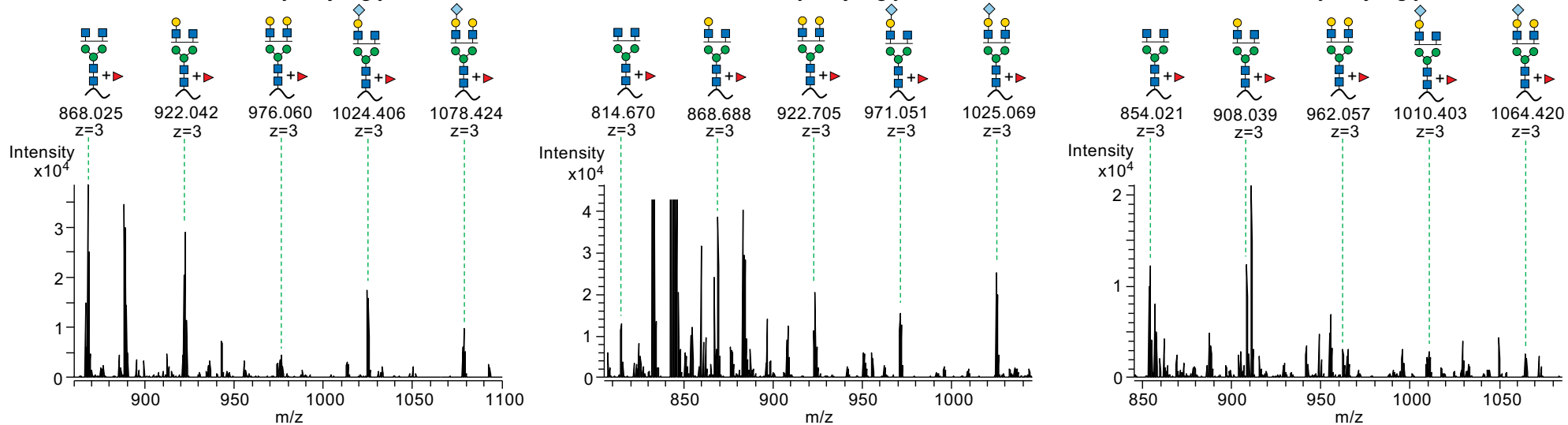
IgG3: EAQYNSTFR



Ave. MS for IgG1 (35-38 min)
shown only major glycans

Ave. MS for IgG2 (29-32 min)
shown only major glycans

Ave. MS for IgG3 (31-34 min)
shown only major glycans



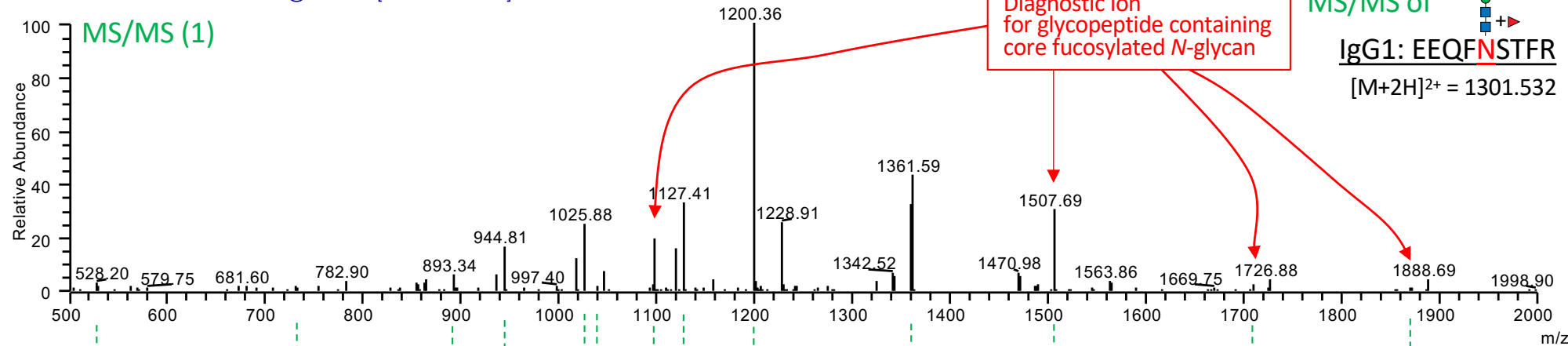
Supplemental Fig. 14

MS raw data: 21091608

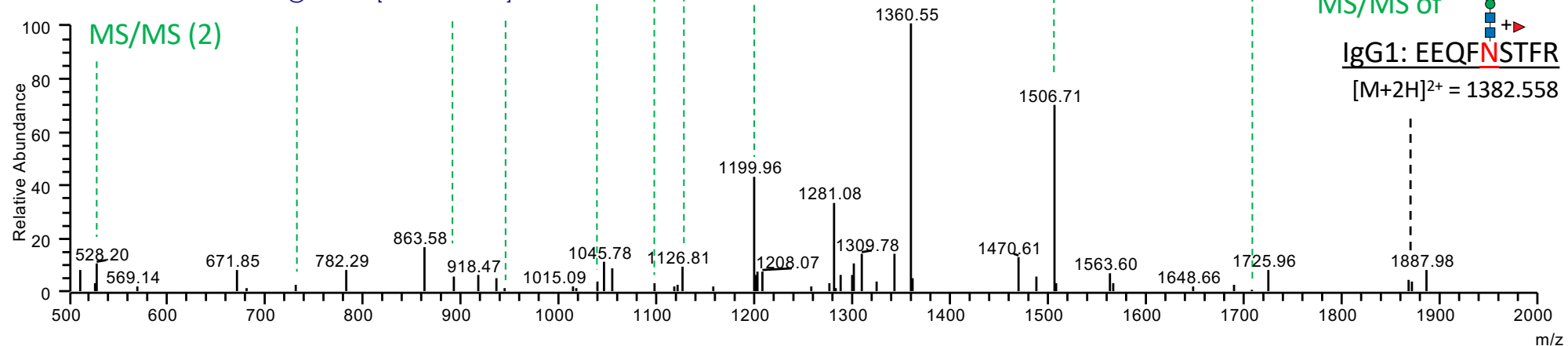
A-14

Identification of the linkage of fucose (Core or Lewis) based on MS/MS fragmentation

21091608_mouse_IgG_A14#4571 RT: 36.04 AV: 1 NL: 2.14E3
T: ITMS + c ESI d Full ms2 1302.54@cid35.00 [345.00-2000.00]



21091608_mouse_IgG_A14#4534 RT: 35.78 AV: 1 NL: 3.10E2
T: ITMS + c ESI d Full ms2 1383.06@cid35.00 [370.00-2000.00]



MS/MS spectrum of glycopeptide of IgG1 represented [M+2H]²⁺ of 1301.532 m/z (MS/MS (1)) and [M+2H]²⁺ of 1382.558 m/z (MS/MS (2)). These diagnostic ions revealed that these two glycopeptides contain core fucosylated N-glycans.

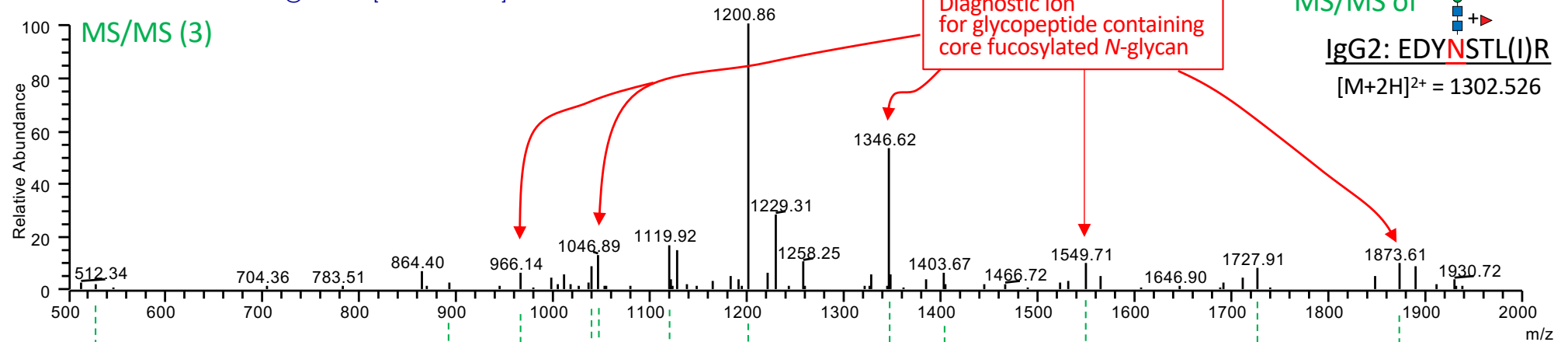
Supplemental Fig. 15

MS raw data: 21091608

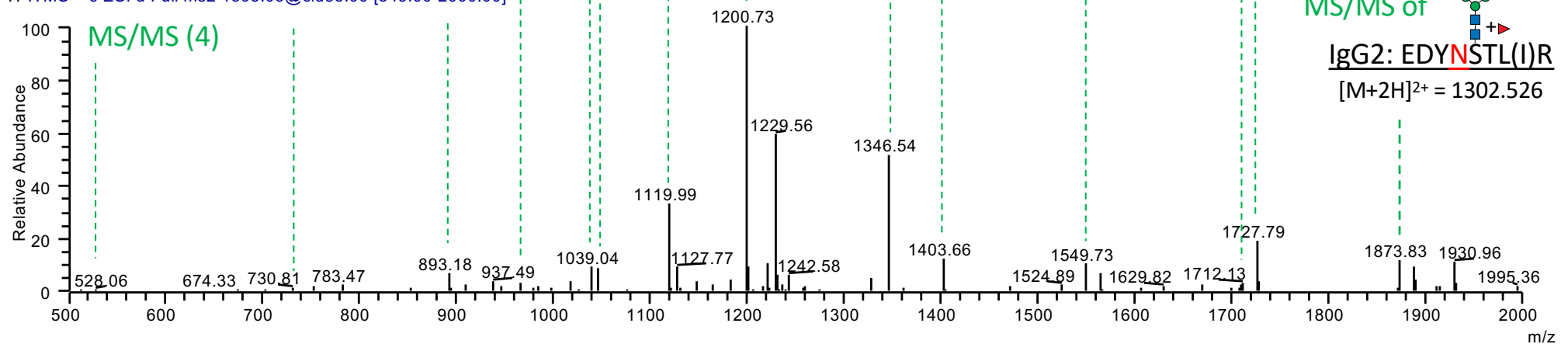
A-14

Identification of the linkage of fucose (Core or Lewis) based on MS/MS fragmentation

21091608_mouse_IgG_A14#3669 RT: 29.51 AV: 1 NL: 6.01E2
T: ITMS + c ESI d Full ms2 1303.03@cid35.00 [345.00-2000.00]



21091608_mouse_IgG_A14#3762 RT: 30.16 AV: 1 NL: 7.10E2
T: ITMS + c ESI d Full ms2 1303.03@cid35.00 [345.00-2000.00]



MS/MS spectrum of glycopeptide of IgG2 represented [M+2H]²⁺ of 1302.526 m/z (MS/MS (3), retention time 29.51 min) and [M+2H]²⁺ of 1302.526 m/z (MS/MS (4), retention time 30.16 min). These diagnostic ions revealed that these two glycopeptides contain core fucosylated *N*-glycans.

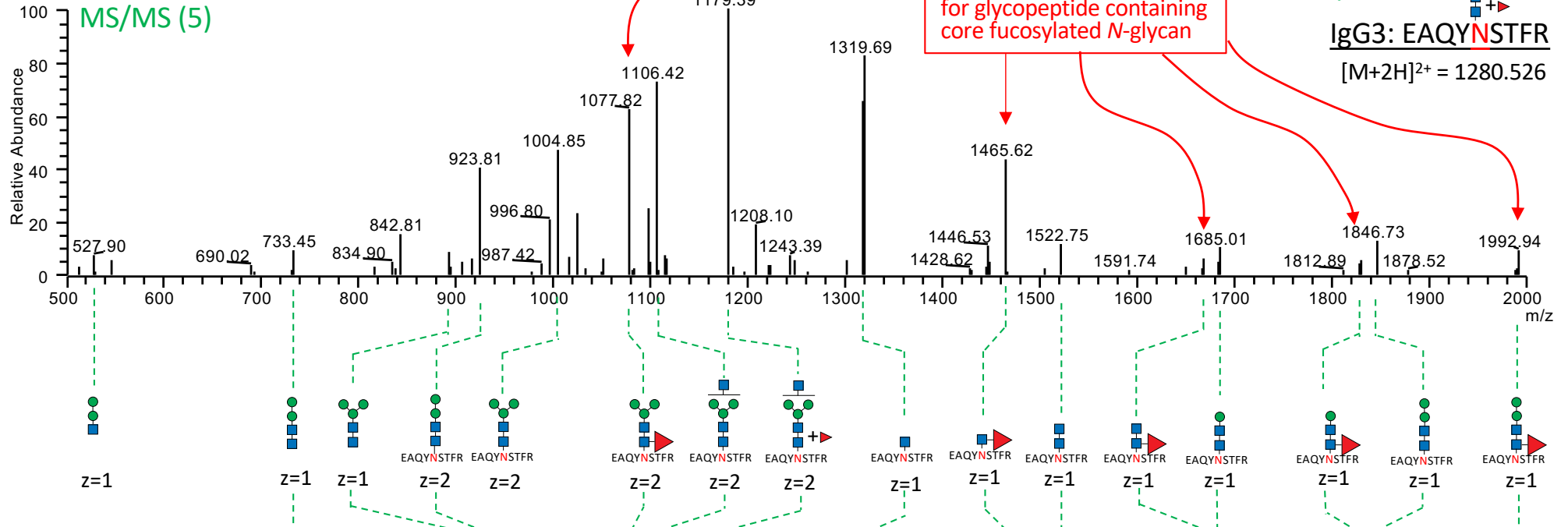
Supplemental Fig. 16

MS raw data: 21091608

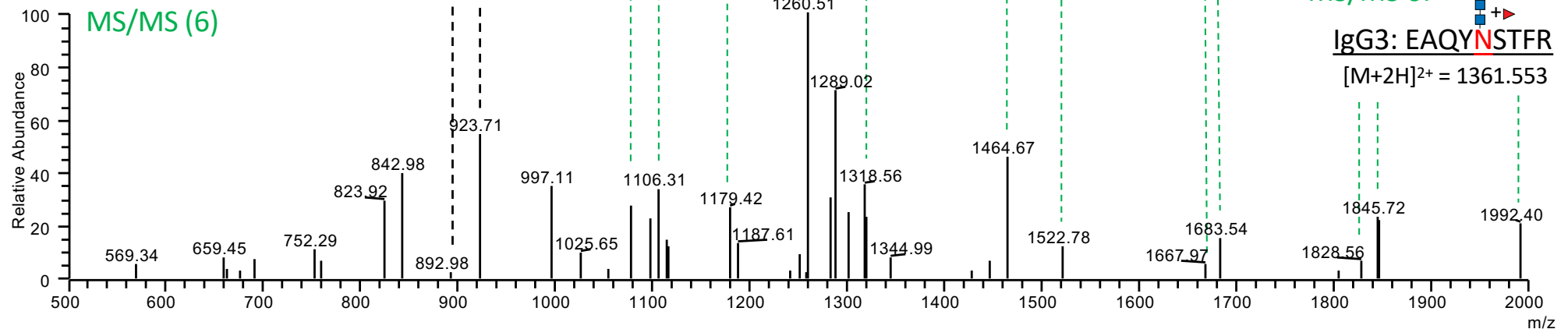
A-14

Identification of the linkage of fucose (Core or Lewis) based on MS/MS fragmentation

21091608_mouse_IgG_A14#3966 RT: 31.69 AV: 1 NL: 3.75E2
T: ITMS + c ESI d Full ms2 1281.53@cid35.00 [340.00-2000.00]

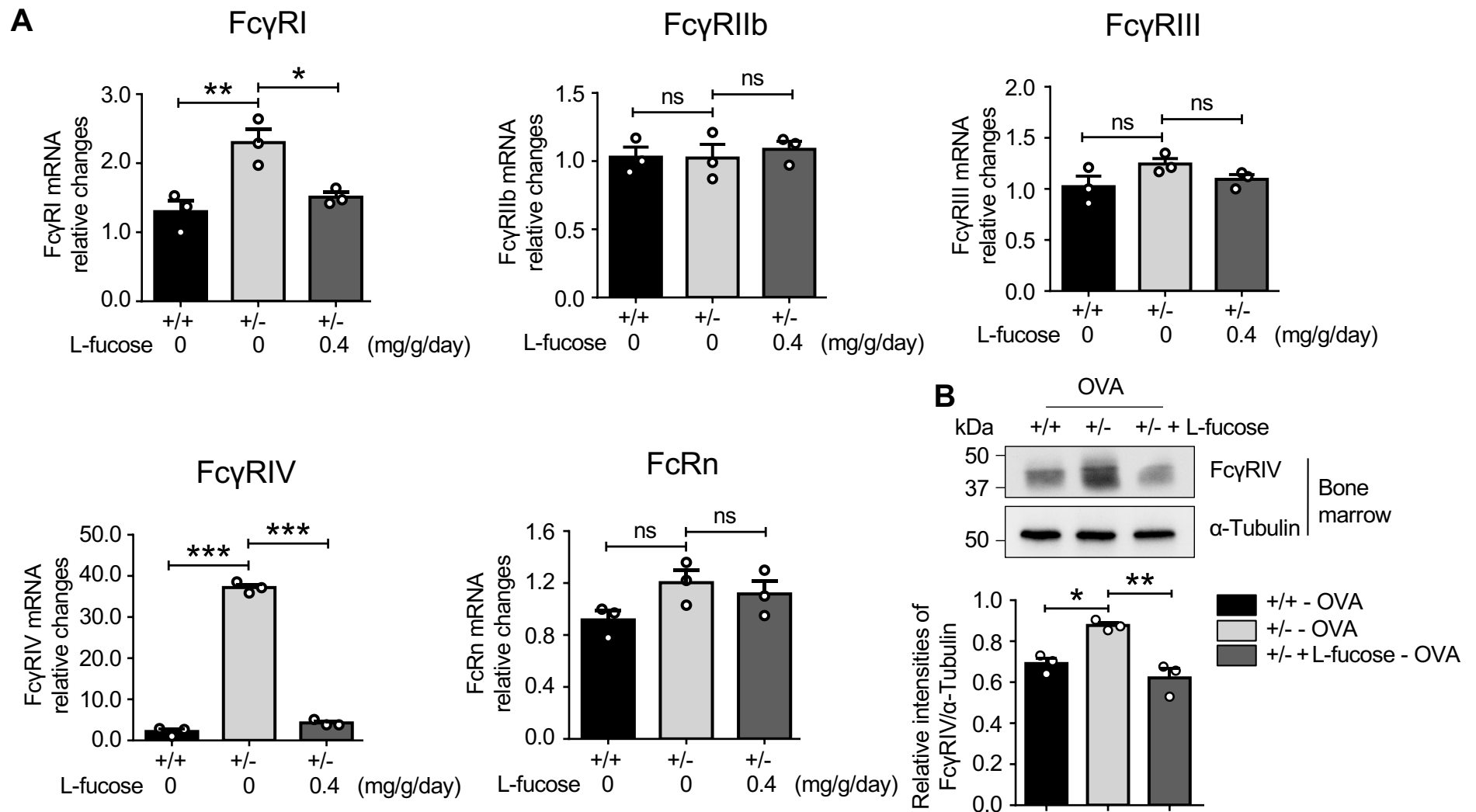


21091608_mouse_IgG_A14#3943 RT: 31.51 AV: 1 NL: 1.21E2
T: ITMS + c ESI d Full ms2 1362.56@cid35.00 [365.00-2000.00]



MS/MS spectrum of glycopeptide of IgG3 represented [M+2H]²⁺ of 1280.526 m/z (MS/MS (5)) and [M+2H]²⁺ of 1361.553 m/z (MS/MS (4)). These diagnostic ions revealed that these two glycopeptides contain core fucosylated N-glycans.

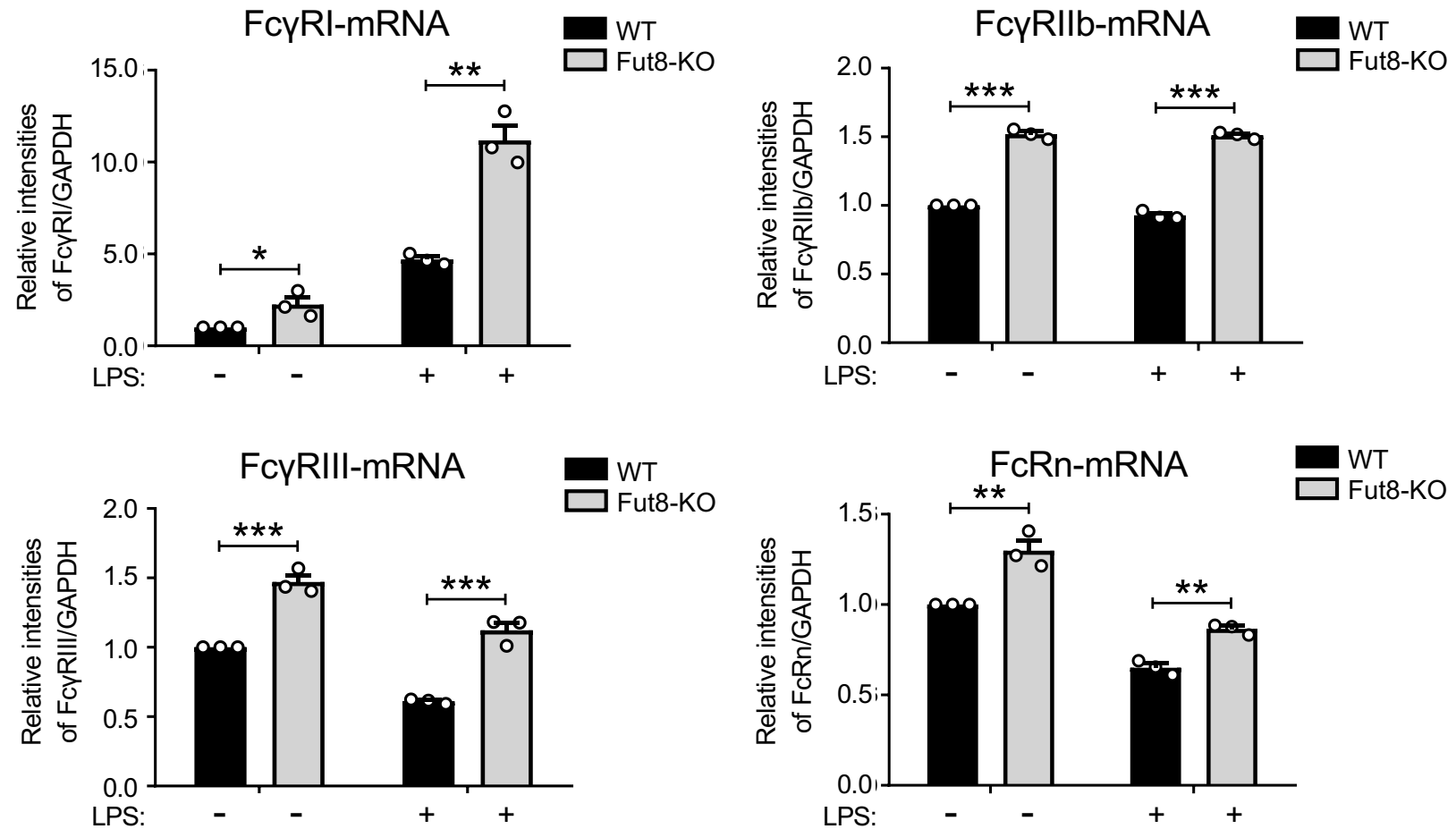
Supplemental Fig. 17



sFig.17. Effects of exogenous L-fucose on FcγRs levels after immunizing with OVA.

(A) After being immunized for the 7th week, the bone marrows were collected, and the mRNA levels of FcγRs in bone marrows were compared among *Fut8*^{+/+}, *Fut8*^{+/-}, and *Fut8*^{-/-} mice treated with L-fucose at 0.4 mg/g/day. GAPDH was used as an internal control. The data was obtained from three mice, and the data in *Fut8*^{+/+} mice was set as 1.0, which was analyzed by one-way ANOVA with Tukey's *post hoc* analysis as the mean ± SEM. **p* < 0.05; ***p* < 0.01; ****p* < 0.001. (B) The expression levels of FcγRIV in the same protein amounts of marrow tissues were detected using Western blot. α-Tubulin was used as a loading control. Data were shown as relative intensities of FcγRIV/α-tubulin, obtained from three mice. The data were qualified by one-way ANOVA with Tukey's *post hoc* analysis as the mean ± SEM. **p* < 0.05, ***p* < 0.01.

Supplemental Fig. 18



sFig.18. Effects of core fucosylation on the mRNA expression of FcγRs and FcRn.

The WT and Fut8-KO BV2 cells were cultured with or without LPS in a final concentration at 250 ng/ml for 4 h. Real-time PCR was employed to detect the mRNA expression levels of other FcγRs, including FcγRI, FcγRIIb, and FcγRIII, and FcRn. GAPDH was used as an internal control. The value representing relative intensities of FcγRs or FcRn versus GAPDH in WT cells cultured without LPS was set as 1.0. The data were obtained from three independent experiments and subjected to qualification by an unpaired Student *t*-test as the mean ± SEM. **p* < 0.05, ***p* < 0.01, ****p* < 0.001.