**IgG glycome in colorectal cancer**

Frano Vučković1,\*, Evropi Theodoratou2,3,\*, Kujtim Thaçi1,\*, Maria Timofeeva3, Aleksandar Vojta4, Jerko Štambuk1, Maja Pučić-Baković1, Pauline Rudd5, Annika Wennerström6, Susan M Farrington3, Markus Perola6, Yurii Aulchenko7, Malcolm G Dunlop3, Harry Campbell2,3,\*, Gordan Lauc1,8,\*

**1** Genos Glycoscience Research Laboratory, Zagreb, Croatia

**2** Centre for Population Health Sciences, University of Edinburgh, Edinburgh, UK

**3** Colon Cancer Genetics Group, Institute of Genetics and Molecular Medicine, University of Edinburgh and Medical Research Council Human Genetics Unit, Edinburgh, UK

**4** University of Zagreb Faculty of Science, Zagreb, Croatia

**5** National institute for bioprocessing research & training, Dublin, Ireland

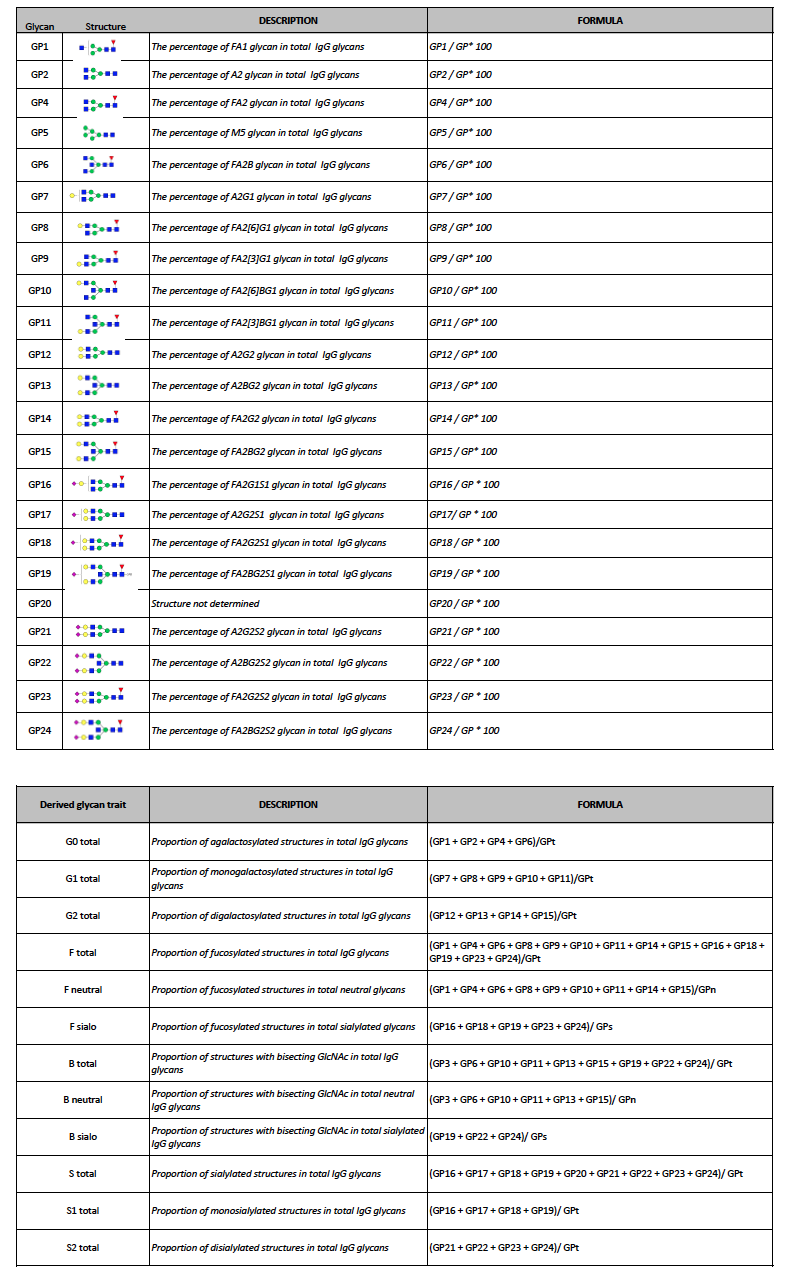
**6** Department of Health, THL, Finland

**7** Polyomica, Groningen, The Netherlands

**8** University of Zagreb Faculty of Pharmacy and Biochemistry, Zagreb, Croatia

\*These authors contributed equally

**Supplementary Table 1. Directly measured glycans and derived glycan traits**



**Supplementary Table 2. IgG glycome composition in CRC patients and controls**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Glycan** | **Description** | **Control (median[IQR])** | | **Patient (median[IQR])** | | **OddsRatio** | **95%ConfInt** | **p.value** | **p.adjusted** |
| GP1 | The percentage of FA1 glycan in total IgG glycans | 0,12 | (0,08-0,22) | 0,15 | (0,10-0,26) | 1,28 | (1,11 - 1,48) | 5,20E-04 | 1,17E-03 |
| GP2 | The percentage of A2 glycan in total IgG glycans | 0,49 | (0,34-0,71) | 0,54 | (0,36-0,79) | 1,18 | (1,03 - 1,37) | 2,10E-02 | 3,15E-02 |
| GP3 | The percentage of A2B glycan in total IgG glycans | 0,37 | (0,29-0,52) | 0,46 | (0,34-0,65) | 1,5 | (1,29 - 1,74) | 4,79E-08 | 1,72E-07 |
| GP4 | The percentage of FA2 glycan in total IgG glycans | 18,68 | (15,42-21,98) | 22,34 | (18,34-26,87) | 2,33 | (1,94 - 2,79) | 1,83E-23 | 2,20E-22 |
| GP5 | The percentage of M5 glycan in total IgG glycans | 0,29 | (0,24-0,37) | 0,32 | (0,26-0,41) | 1,26 | (1,09 - 1,46) | 1,30E-03 | 2,47E-03 |
| GP6 | The percentage of FA2B glycan in total IgG glycans | 4,97 | (4,02-6,01) | 5,39 | (4,53-6,45) | 1,44 | (1,23 - 1,69) | 4,13E-06 | 1,24E-05 |
| GP7 | The percentage of A2G1 glycan in total IgG glycans | 0,57 | (0,43-0,75) | 0,54 | (0,39-0,76) | 0,88 | (0,77 - 1,02) | 8,42E-02 | 1,05E-01 |
| GP8 | The percentage of FA2[6]G1 glycan in total IgG glycans | 18,9 | (17,73-20,18) | 18,82 | (17,59-19,97) | 0,85 | (0,74 - 0,98) | 2,43E-02 | 3,51E-02 |
| GP9 | The percentage of FA2[3]G1 glycan in total IgG glycans | 9,87 | (8,89-11,04) | 9,66 | (8,80-10,54) | 0,78 | (0,68 - 0,90) | 5,52E-04 | 1,17E-03 |
| GP10 | The percentage of FA2[6]BG1 glycan in total IgG glycans | 5,62 | (4,95-6,43) | 5,37 | (4,66-6,27) | 0,72 | (0,62 - 0,83) | 4,65E-06 | 1,29E-05 |
| GP11 | The percentage of FA2[3]BG1 glycan in total IgG glycans | 0,82 | (0,72-0,95) | 0,8 | (0,70-0,91) | 0,78 | (0,68 - 0,91) | 8,05E-04 | 1,61E-03 |
| GP12 | The percentage of A2G2 glycan in total IgG glycans | 0,68 | (0,50-0,93) | 0,55 | (0,37-0,77) | 0,6 | (0,51 - 0,70) | 9,93E-12 | 5,11E-11 |
| GP13 | The percentage of A2BG2 glycan in total IgG glycans | 0,45 | (0,36-0,57) | 0,4 | (0,31-0,53) | 0,68 | (0,58 - 0,78) | 1,09E-07 | 3,55E-07 |
| GP14 | The percentage of FA2G2 glycan in total IgG glycans | 13,59 | (11,57-15,90) | 11,45 | (9,40-13,80) | 0,37 | (0,30 - 0,45) | 4,21E-29 | 7,57E-28 |
| GP15 | The percentage of FA2BG2 glycan in total IgG glycans | 1,73 | (1,47-2,06) | 1,47 | (1,20-1,82) | 0,49 | (0,41 - 0,57) | 6,94E-20 | 5,00E-19 |
| GP16 | The percentage of FA2G1S1 glycan in total IgG glycans | 3,27 | (2,95-3,65) | 3,37 | (2,99-3,76) | 1,17 | (1,02 - 1,34) | 2,65E-02 | 3,67E-02 |
| GP17 | The percentage of A2G2S1 glycan in total IgG glycans | 0,94 | (0,82-1,08) | 0,92 | (0,80-1,07) | 0,92 | (0,79 - 1,06) | 2,39E-01 | 2,60E-01 |
| GP18 | The percentage of FA2G2S1 glycan in total IgG glycans | 9,52 | (8,09-11,43) | 8,47 | (6,98-9,99) | 0,56 | (0,47 - 0,66) | 8,05E-13 | 4,83E-12 |
| GP19 | The percentage of FA2BG2S1 glycan in total IgG glycans | 1,88 | (1,65-2,15) | 1,81 | (1,61-2,07) | 0,82 | (0,72 - 0,95) | 5,63E-03 | 9,64E-03 |
| GP20 | Structure not determined | 0,36 | (0,25-0,51) | 0,38 | (0,27-0,52) | 1,12 | (0,96 - 1,30) | 1,41E-01 | 1,64E-01 |
| GP21 | The percentage of A2G2S2 glycan in total IgG glycans | 0,89 | (0,74-1,06) | 0,92 | (0,77-1,10) | 1,11 | (0,96 - 1,28) | 1,71E-01 | 1,93E-01 |
| GP22 | The percentage of A2BG2S2 glycan in total IgG glycans | 0,16 | (0,11-0,24) | 0,15 | (0,10-0,21) | 0,84 | (0,73 - 0,97) | 1,62E-02 | 2,66E-02 |
| GP23 | The percentage of FA2G2S2 glycan in total IgG glycans | 1,45 | (1,14-1,85) | 1,4 | (1,11-1,72) | 0,96 | (0,84 - 1,11) | 5,96E-01 | 6,03E-01 |
| GP24 | The percentage of FA2BG2S2 glycan in total IgG glycans | 1,78 | (1,48-2,13) | 1,74 | (1,43-2,08) | 0,95 | (0,82 - 1,09) | 4,44E-01 | 4,71E-01 |

**Supplementary Table 3. Pleiotropic effects of top glycan SNPs relevant for fucosylation on CRC**. SNPs with strongest associations with IgG fucosylation in our recent IgG glycome GWAS (Lauc et al, Plos Genet, 2013) were selected and their associations with CRC in the SOCCS cohort are presented here. Genetic associations are based on 939 cases and 945 controls from phase 1 initial GWAS from SOCCS (as described in Dunlop et al., Nat Genet, 2012; Al-Tassan et al., Sci Rep, 2015) imputed to 1000 Genome data (phase 1, v3).

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **SNP** | **CHR** | **Position (bp)** | **Effect allele** | **Gene** | **SNP location** | **Glycan[[1]](#endnote-1)** | **Beta glycans** | **P glycans** | **Effect Direction in Glycans Analysis** | **OR for CRC analysis** | **P for CRC analysis** | **Effect Direction in CRC risk analysis** | **FDR corrected p value for CRC analysis** |
| rs3742597 | 14 | 66200177 | G | FUT8 | intron\_variant | FG0n total/G0n | -0.290 | 6.05E-17 | Negative | 0.914 | 0.248 | Negative | 0.636 |
| rs1950557 | 14 | 66201757 | C | FUT8 | intron\_variant | FG0n total/G0n | 0.290 | 6.37E-17 | Positive | 1.097 | 0.234 | Positive | 0.605 |
| rs2268962 | 14 | 66147273 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | 0.251 | 3.56E-16 | Positive | 1.163 | 0.021 | Positive | 0.101 |
| rs11627067 | 14 | 66182953 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | 0.251 | 3.59E-16 | Positive | 1.156 | 0.027 | Positive | 0.101 |
| rs8018278 | 14 | 66180088 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | 0.251 | 3.60E-16 | Positive | 1.168 | 0.018 | Positive | 0.101 |
| rs2411351 | 14 | 66171541 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | 0.251 | 3.61E-16 | Positive | 1.164 | 0.020 | Positive | 0.101 |
| rs2268961 | 14 | 66146765 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | 0.251 | 3.65E-16 | Positive | 1.163 | 0.021 | Positive | 0.101 |
| rs11628765 | 14 | 66168449 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | 0.251 | 3.74E-16 | Positive | 1.164 | 0.020 | Positive | 0.101 |
| rs12588838 | 14 | 66162638 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | -0.250 | 4.00E-16 | Negative | 0.860 | 0.021 | Negative | 0.101 |
| rs2064694 | 14 | 66148246 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | -0.250 | 4.18E-16 | Negative | 0.860 | 0.021 | Negative | 0.101 |
| rs1998036 | 14 | 66138199 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | 0.250 | 4.54E-16 | Positive | 1.157 | 0.026 | Positive | 0.101 |
| rs7142651 | 14 | 66132721 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant, upstream\_gene\_variant | FG0n total/G0n | -0.250 | 4.77E-16 | Negative | 0.861 | 0.022 | Negative | 0.101 |
| rs11627185 | 14 | 66121492 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | 0.249 | 5.40E-16 | Positive | 1.161 | 0.023 | Positive | 0.101 |
| rs11627184 | 14 | 66121443 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | -0.249 | 5.66E-16 | Negative | 0.862 | 0.023 | Negative | 0.101 |
| rs2300865 | 14 | 66120015 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | 0.249 | 6.06E-16 | Positive | 1.161 | 0.023 | Positive | 0.101 |
| rs11622829 | 14 | 66191782 | T | FUT8 | intron\_variant, downstream\_gene\_variant | FG0n total/G0n | -0.249 | 6.13E-16 | Negative | 0.856 | 0.018 | Negative | 0.101 |
| rs12890902 | 14 | 66116622 | T | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | -0.249 | 6.17E-16 | Negative | 0.863 | 0.025 | Negative | 0.101 |
| rs8012278 | 14 | 66082573 | G | FUT8 | intron\_variant | FG0n total/G0n | 0.248 | 8.28E-16 | Positive | 1.161 | 0.023 | Positive | 0.101 |
| rs11624104 | 14 | 66196137 | G | FUT8 | intron\_variant | FG0n total/G0n | 0.248 | 9.61E-16 | Positive | 1.153 | 0.029 | Positive | 0.103 |
| rs1535173 | 14 | 66199139 | C | FUT8 | intron\_variant | FG0n total/G0n | -0.247 | 1.01E-15 | Negative | 0.865 | 0.027 | Negative | 0.101 |
| rs927004 | 14 | 66200911 | C | FUT8 | intron\_variant | FG0n total/G0n | 0.247 | 1.16E-15 | Positive | 1.157 | 0.025 | Positive | 0.101 |
| rs8010876 | 14 | 66206976 | G | FUT8 | intron\_variant | FG0n total/G0n | 0.247 | 1.17E-15 | Positive | 1.157 | 0.025 | Positive | 0.101 |
| rs12887134 | 14 | 66045543 | C | FUT8 | intron\_variant | FG0n total/G0n | 0.247 | 1.31E-15 | Positive | 1.155 | 0.027 | Positive | 0.101 |
| rs7155541 | 14 | 66046242 | C | FUT8 | intron\_variant | FG0n total/G0n | 0.247 | 1.32E-15 | Positive | 1.156 | 0.026 | Positive | 0.101 |
| rs2149841 | 14 | 66010319 | C | FUT8 | intron\_variant | FG0n total/G0n | -0.247 | 1.40E-15 | Negative | 0.868 | 0.030 | Negative | 0.106 |
| rs3825640 | 14 | 65961204 | C | FUT8 | intron\_variant | FG0n total/G0n | -0.246 | 1.51E-15 | Negative | 0.871 | 0.034 | Negative | 0.109 |
| rs11158601 | 14 | 66025363 | G | FUT8 | intron\_variant | FG0n total/G0n | 0.244 | 2.30E-15 | Positive | 1.158 | 0.025 | Positive | 0.101 |
| rs12589698 | 14 | 65920435 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | -0.246 | 2.33E-15 | Negative | 0.843 | 0.009 | Negative | 0.101 |
| rs1958561 | 14 | 66036761 | G | FUT8 | intron\_variant | FG0n total/G0n | 0.244 | 2.43E-15 | Positive | 1.161 | 0.023 | Positive | 0.101 |
| rs7161123 | 14 | 66052901 | G | FUT8 | intron\_variant | FG0n total/G0n | -0.244 | 2.45E-15 | Negative | 0.866 | 0.028 | Negative | 0.103 |
| rs4581615 | 14 | 66055943 | C | FUT8 | intron\_variant | FG0n total/G0n | -0.244 | 2.45E-15 | Negative | 0.863 | 0.025 | Negative | 0.101 |
| rs3783709 | 14 | 66058664 | T | FUT8 | intron\_variant | FG0n total/G0n | -0.244 | 2.46E-15 | Negative | 0.864 | 0.025 | Negative | 0.101 |
| rs12889002 | 14 | 66063582 | C | FUT8 | intron\_variant | FG0n total/G0n | -0.244 | 2.46E-15 | Negative | 0.862 | 0.024 | Negative | 0.101 |
| rs743085 | 14 | 66068133 | G | FUT8 | intron\_variant | FG0n total/G0n | 0.244 | 2.46E-15 | Positive | 1.158 | 0.024 | Positive | 0.101 |
| rs11627084 | 14 | 65978836 | G | FUT8 | intron\_variant | FG0n total/G0n | 0.244 | 2.85E-15 | Positive | 1.154 | 0.029 | Positive | 0.103 |
| rs2184603 | 14 | 65930670 | C | FUT8, RPL21P8 | intron\_variant, downstream\_gene\_variant | FG0n total/G0n | 0.244 | 3.54E-15 | Positive | 1.149 | 0.033 | Positive | 0.109 |
| rs4899179 | 14 | 65926748 | G | FUT8 | intron\_variant, downstream\_gene\_variant | FG0n total/G0n | 0.244 | 3.68E-15 | Positive | 1.191 | 0.008 | Positive | 0.101 |
| rs11621680 | 14 | 66014681 | G | FUT8 | intron\_variant | FG0n total/G0n | 0.240 | 7.18E-15 | Positive | 1.148 | 0.035 | Positive | 0.110 |
| rs10483780 | 14 | 65980170 | C | FUT8 | intron\_variant | FG0n total/G0n | 0.240 | 8.49E-15 | Positive | 1.151 | 0.032 | Positive | 0.109 |
| rs12892058 | 14 | 65903441 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | 0.239 | 1.29E-14 | Positive | 1.193 | 0.007 | Positive | 0.101 |
| rs1953416 | 14 | 65878807 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant, upstream\_gene\_variant | FG0n total/G0n | -0.235 | 2.49E-14 | Negative | 0.841 | 0.008 | Negative | 0.101 |
| rs883081 | 14 | 65880621 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | -0.235 | 2.57E-14 | Negative | 0.871 | 0.034 | Negative | 0.109 |
| rs12879971 | 14 | 65901604 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | -0.235 | 2.93E-14 | Negative | 0.837 | 0.007 | Negative | 0.101 |
| rs2411822 | 14 | 65878395 | G | FUT8 | upstream\_gene\_variant, 5\_prime\_UTR\_variant | FG0n total/G0n | 0.232 | 4.82E-14 | Positive | 1.195 | 0.007 | Positive | 0.101 |
| rs883082 | 14 | 65880940 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | 0.232 | 5.02E-14 | Positive | 1.148 | 0.034 | Positive | 0.109 |
| rs867972 | 14 | 65895761 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG0n total/G0n | 0.232 | 1.07E-13 | Positive | 1.190 | 0.008 | Positive | 0.101 |
| rs3742597 | 14 | 66200177 | G | FUT8 | intron\_variant | Fn total | -0.244 | 1.34E-12 | Negative | 0.914 | 0.248 | Negative | 0.636 |
| rs1950557 | 14 | 66201757 | C | FUT8 | intron\_variant | Fn total | 0.244 | 1.39E-12 | Positive | 1.097 | 0.234 | Positive | 0.605 |
| rs2268962 | 14 | 66147273 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG2n total/G2n | 0.216 | 1.57E-12 | Positive | 1.163 | 0.021 | Positive | 0.101 |
| rs11627185 | 14 | 66121492 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG2n total/G2n | 0.216 | 1.59E-12 | Positive | 1.161 | 0.023 | Positive | 0.101 |
| rs2268961 | 14 | 66146765 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG2n total/G2n | 0.216 | 1.59E-12 | Positive | 1.163 | 0.021 | Positive | 0.101 |
| rs11627184 | 14 | 66121443 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG2n total/G2n | -0.216 | 1.63E-12 | Negative | 0.862 | 0.023 | Negative | 0.101 |
| rs2300865 | 14 | 66120015 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG2n total/G2n | 0.215 | 1.68E-12 | Positive | 1.161 | 0.023 | Positive | 0.101 |
| rs12890902 | 14 | 66116622 | T | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG2n total/G2n | -0.215 | 1.68E-12 | Negative | 0.863 | 0.025 | Negative | 0.101 |
| rs1054218 | 14 | 66209190 | C | FUT8 | 3\_prime\_UTR\_variant | FG0n total/G0n | -0.224 | 1.75E-12 | Negative | 0.954 | 0.484 | Negative | 0.701 |
| rs761830 | 14 | 66212986 | G | FUT8 | downstream\_gene\_variant | FG0n total/G0n | -0.224 | 1.76E-12 | Negative | 0.958 | 0.528 | Negative | 0.701 |
| rs1998036 | 14 | 66138199 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG2n total/G2n | 0.216 | 1.76E-12 | Positive | 1.157 | 0.026 | Positive | 0.101 |
| rs7142651 | 14 | 66132721 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant, upstream\_gene\_variant | FG2n total/G2n | -0.215 | 1.78E-12 | Negative | 0.861 | 0.022 | Negative | 0.101 |
| rs8012278 | 14 | 66082573 | G | FUT8 | intron\_variant | FG2n total/G2n | 0.215 | 1.86E-12 | Positive | 1.161 | 0.023 | Positive | 0.101 |
| rs11627185 | 14 | 66121492 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | Fn total | 0.215 | 2.24E-12 | Positive | 1.161 | 0.023 | Positive | 0.101 |
| rs11627184 | 14 | 66121443 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | Fn total | -0.215 | 2.26E-12 | Negative | 0.862 | 0.023 | Negative | 0.101 |
| rs12890902 | 14 | 66116622 | T | FUT8 | intron\_variant, non\_coding\_transcript\_variant | Fn total | -0.215 | 2.27E-12 | Negative | 0.863 | 0.025 | Negative | 0.101 |
| rs2300865 | 14 | 66120015 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | Fn total | 0.215 | 2.28E-12 | Positive | 1.161 | 0.023 | Positive | 0.101 |
| rs8012278 | 14 | 66082573 | G | FUT8 | intron\_variant | Fn total | 0.215 | 2.39E-12 | Positive | 1.161 | 0.023 | Positive | 0.101 |
| rs11628765 | 14 | 66168449 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG2n total/G2n | 0.214 | 2.48E-12 | Positive | 1.164 | 0.020 | Positive | 0.101 |
| rs2411351 | 14 | 66171541 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG2n total/G2n | 0.214 | 2.49E-12 | Positive | 1.164 | 0.020 | Positive | 0.101 |
| rs8018278 | 14 | 66180088 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG2n total/G2n | 0.214 | 2.53E-12 | Positive | 1.168 | 0.018 | Positive | 0.101 |
| rs12588838 | 14 | 66162638 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG2n total/G2n | -0.214 | 2.54E-12 | Negative | 0.860 | 0.021 | Negative | 0.101 |
| rs2064694 | 14 | 66148246 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG2n total/G2n | -0.214 | 2.57E-12 | Negative | 0.860 | 0.021 | Negative | 0.101 |
| rs11627067 | 14 | 66182953 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG2n total/G2n | 0.214 | 2.57E-12 | Positive | 1.156 | 0.027 | Positive | 0.101 |
| rs11627084 | 14 | 65978836 | G | FUT8 | intron\_variant | FG2n total/G2n | 0.214 | 2.70E-12 | Positive | 1.154 | 0.029 | Positive | 0.103 |
| rs2184603 | 14 | 65930670 | C | FUT8, RPL21P8 | intron\_variant, downstream\_gene\_variant | FG2n total/G2n | 0.215 | 2.75E-12 | Positive | 1.149 | 0.033 | Positive | 0.109 |
| rs4899179 | 14 | 65926748 | G | FUT8 | intron\_variant, downstream\_gene\_variant | FG2n total/G2n | 0.215 | 2.82E-12 | Positive | 1.191 | 0.008 | Positive | 0.101 |
| rs7142651 | 14 | 66132721 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant, upstream\_gene\_variant | Fn total | -0.214 | 3.00E-12 | Negative | 0.861 | 0.022 | Negative | 0.101 |
| rs2268962 | 14 | 66147273 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | Fn total | 0.214 | 3.00E-12 | Positive | 1.163 | 0.021 | Positive | 0.101 |
| rs2268961 | 14 | 66146765 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | Fn total | 0.214 | 3.01E-12 | Positive | 1.163 | 0.021 | Positive | 0.101 |
| rs1998036 | 14 | 66138199 | C | FUT8 | intron\_variant, non\_coding\_transcript\_variant | Fn total | 0.214 | 3.06E-12 | Positive | 1.157 | 0.026 | Positive | 0.101 |
| rs11158601 | 14 | 66025363 | G | FUT8 | intron\_variant | FG2n total/G2n | 0.213 | 3.23E-12 | Positive | 1.158 | 0.025 | Positive | 0.101 |
| rs1958561 | 14 | 66036761 | G | FUT8 | intron\_variant | FG2n total/G2n | 0.213 | 3.38E-12 | Positive | 1.161 | 0.023 | Positive | 0.101 |
| rs4581615 | 14 | 66055943 | C | FUT8 | intron\_variant | FG2n total/G2n | -0.212 | 3.77E-12 | Negative | 0.863 | 0.025 | Negative | 0.101 |
| rs7161123 | 14 | 66052901 | G | FUT8 | intron\_variant | FG2n total/G2n | -0.212 | 3.77E-12 | Negative | 0.866 | 0.028 | Negative | 0.103 |
| rs3783709 | 14 | 66058664 | T | FUT8 | intron\_variant | FG2n total/G2n | -0.212 | 3.77E-12 | Negative | 0.864 | 0.025 | Negative | 0.101 |
| rs12889002 | 14 | 66063582 | C | FUT8 | intron\_variant | FG2n total/G2n | -0.212 | 3.77E-12 | Negative | 0.862 | 0.024 | Negative | 0.101 |
| rs743085 | 14 | 66068133 | G | FUT8 | intron\_variant | FG2n total/G2n | 0.212 | 3.77E-12 | Positive | 1.158 | 0.024 | Positive | 0.101 |
| rs11627084 | 14 | 65978836 | G | FUT8 | intron\_variant | Fn total | 0.213 | 4.00E-12 | Positive | 1.154 | 0.029 | Positive | 0.103 |
| rs3825640 | 14 | 65961204 | C | FUT8 | intron\_variant | FG2n total/G2n | -0.212 | 4.34E-12 | Negative | 0.871 | 0.034 | Negative | 0.109 |
| rs3825640 | 14 | 65961204 | C | FUT8 | intron\_variant | Fn total | -0.213 | 4.46E-12 | Negative | 0.871 | 0.034 | Negative | 0.109 |
| rs2149841 | 14 | 66010319 | C | FUT8 | intron\_variant | FG2n total/G2n | -0.212 | 4.47E-12 | Negative | 0.868 | 0.030 | Negative | 0.106 |
| rs4581615 | 14 | 66055943 | C | FUT8 | intron\_variant | Fn total | -0.212 | 4.55E-12 | Negative | 0.863 | 0.025 | Negative | 0.101 |
| rs7161123 | 14 | 66052901 | G | FUT8 | intron\_variant | Fn total | -0.212 | 4.55E-12 | Negative | 0.866 | 0.028 | Negative | 0.103 |
| rs12889002 | 14 | 66063582 | C | FUT8 | intron\_variant | Fn total | -0.212 | 4.55E-12 | Negative | 0.862 | 0.024 | Negative | 0.101 |
| rs3783709 | 14 | 66058664 | T | FUT8 | intron\_variant | Fn total | -0.212 | 4.55E-12 | Negative | 0.864 | 0.025 | Negative | 0.101 |
| rs743085 | 14 | 66068133 | G | FUT8 | intron\_variant | Fn total | 0.212 | 4.55E-12 | Positive | 1.158 | 0.024 | Positive | 0.101 |
| rs2184603 | 14 | 65930670 | C | FUT8, RPL21P8 | intron\_variant, downstream\_gene\_variant | Fn total | 0.213 | 4.68E-12 | Positive | 1.149 | 0.033 | Positive | 0.109 |
| rs4899179 | 14 | 65926748 | G | FUT8 | intron\_variant, downstream\_gene\_variant | Fn total | 0.213 | 4.83E-12 | Positive | 1.191 | 0.008 | Positive | 0.101 |
| rs2149841 | 14 | 66010319 | C | FUT8 | intron\_variant | Fn total | -0.212 | 5.16E-12 | Negative | 0.868 | 0.030 | Negative | 0.106 |
| rs12589698 | 14 | 65920435 | G | FUT8 | intron\_variant, non\_coding\_transcript\_variant | FG2n total/G2n | -0.212 | 5.36E-12 | Negative | 0.843 | 0.009 | Negative | 0.101 |
| rs12887134 | 14 | 66045543 | C | FUT8 | intron\_variant | FG2n total/G2n | 0.211 | 5.49E-12 | Positive | 1.155 | 0.027 | Positive | 0.101 |
| rs7155541 | 14 | 66046242 | C | FUT8 | intron\_variant | FG2n total/G2n | 0.211 | 5.51E-12 | Positive | 1.156 | 0.026 | Positive | 0.101 |
| rs11624104 | 14 | 66196137 | G | FUT8 | intron\_variant | FG2n total/G2n | 0.210 | 6.44E-12 | Positive | 1.153 | 0.029 | Positive | 0.103 |

1. Fn total: the percentage of all fucosylated structures (+/- bisecting GlcNAc) in total neutral IgG glycans;

   FG0n total/G0n: the percentage of fucosylation of agalactosylated structures in total neutral IgG glycans;

   FG2n total/G2n : the percentage of fucosylation of digalactosylated structures in total neutral IgG glycans [↑](#endnote-ref-1)