

## Supplementary methods

### *Analysis of human milk oligosaccharides*

The composition of each individual HM sample with regard to its HMOS was qualitatively and quantitatively determined using highly sensitive multiplexed capillary-gel-electrophoresis with laser-induced-florescence detection (xCGE-LIF) [1] as described in the Supplementary methods.

In brief and in accordance with the glyXera GmbH kit protocol (KIT-glyX-Quant-DPV, glyXera GmbH, Magdeburg, Germany), the pure HM samples were diluted 1:100 and then spiked with an internal standard (IS) (oligosaccharide quantification standard solution, OS-A5-N-1mL-01, glyXera GmbH, Magdeburg, Germany). For this step, 2 µL of an IS solution and 3 µL of ultrapure water [2] were added to 20 µL of each diluted HM sample. Subsequently, the IS spiked samples were treated with denaturation solution (C-DeNatSol-100uL-01, glyXera GmbH, Magdeburg, Germany). Next, the free oligosaccharides within the denaturized HM/IS samples, comprising the free HMOS and IS, were labeled with APTS dye (KIT-glyX-OSP-A-96-01, glyXera GmbH, Magdeburg, Germany). Afterwards, the excess of APTS (not reacted) and salt were removed using hydrophilic interaction chromatography solid phase extraction (HILIC-SPE, in accordance with the glyXera GmbH kit protocol KIT-glyX-OS.H-APTS-96-01, glyXera GmbH, Magdeburg, Germany). In the next step, the purified APTS-labeled oligosaccharides (HILIC-SPE eluates) were analyzed via xCGE-LIF in accordance with the glyXera GmbH measurement kit protocol (KIT-glyX-OS.M-96-01, glyXera GmbH, Magdeburg, Germany). Finally, data processing, analysis, and qualitative evaluation of the HMOS *Fingerprints* (normalized electropherograms) were performed via glyXtool™ software (version 5.3.1, glyXera GmbH, Magdeburg, Germany), and data analysis and quantitative evaluation of the HMOS *Fingerprints* was performed via glyXtoolGUI™ software (Beta v0.4 [r166+], glyXera GmbH, Magdeburg, Germany).

The limit of quantification (LOQ) was determined using the signal-to-noise ratio (S/N) of each HMOS *Fingerprint* that was calculated according to Ullsten et al. [3]. The LOQ was defined at an S/N of 10. The respective noise within each sample was determined after the migration time alignment of the unsmoothed data in the late migration time range (approximation range = degree of polymerization (DP) 18<DP<20). Consequently, the LOQ is specific with regard to each sample and measurement. All HMOS-peaks  $\geq$ LOQ were taken into account and their IS-normalized peak areas were calculated.

For the low-abundant GLs (i.e.  $\beta$ 6'-,  $\beta$ 4'-,  $\beta$ 3'-, and  $\alpha$ 3'-GL), which were of particular interest in this study, the relative and absolute levels were determined down to the limit of detection (LOD), defined at an S/N of 3. Absolute concentrations ( $c$ ) were determined according to the following formula:  $c = \text{IS-normalized peak height of the analyte} \times \text{concentration of IS} \times \text{dilution factor} \times \text{response factor}$  (KIT-glyX-Quant-DPV, glyXera GmbH, Magdeburg, Germany).

**Supplemental Table S1.** Overview of the number of human milk (HM) samples collected at different time-points over the first 4 months (middle column) and for the subset of 24 Dutch women over the first 12 months (right column) of lactation.

Lactation month	First 4 months	First 12 months (Dutch subset)
	Number of HM samples	Number of HM samples
1 month postpartum	240	21
2 months postpartum	92	24
3 months postpartum	54	23
4 months postpartum	249	23
5 months postpartum	-	23
6 months postpartum	-	21
7 months postpartum	-	12
8 months postpartum	-	9
9 months postpartum	-	7
10 months postpartum	-	4
11 months postpartum	-	2
12 months postpartum	-	2
<b>Total</b>	635 (371 donors)	171 (24 donors)

**Supplemental Table S2.** Total peak area of the selected human milk oligosaccharides (HMOS) (nTPA) and relative peak area (rPA, %) of the HMOS (median (Q1-Q3)) according to maternal human milk (HM) group [4–6] in HM samples (n=171) collected longitudinally over the first year postpartum from 24 Dutch mothers (Dutch subset).

	<b>HM Group I (n = 126 Samples, 18 Donors) median (Q1-Q3)</b>	<b>HM Group II (n = 21 Samples, 3 Donors) median (Q1-Q3)</b>	<b>HM Group III (n = 15 Samples, 2 Donors) median (Q1-Q3)</b>	<b>HM Group IV (n = 9 Samples, 1 Donor) median (Q1-Q3)</b>
nTPA <sup>1</sup>	11.4 (9.33-13.4) <sup>a</sup>	9.30 (7.53-10.8) <sup>b</sup>	9.95 (8.51-10.7) <sup>a,b</sup>	6.22 (5.27-9.83) <sup>b</sup>
<b>rPA (%)</b>				
2'-FL	22.2 (15.0-29.5) <sup>a</sup>	0.00 (0.00-0.00) <sup>2 b</sup>	42.0 (35.5-53.0) <sup>c</sup>	0.00 (0.00-0.00) <sup>2 b</sup>
3-FL	11.7 (5.53-21.4) <sup>a</sup>	35.9 (26.4-45.3) <sup>b</sup>	0.00 (0.00-3.38) <sup>c</sup>	6.78 (3.04-7.31) <sup>d</sup>
DFL	1.86 (1.29-2.50) <sup>a</sup>	0.00 (0.00-0.00) <sup>2 b</sup>	1.01 (0.62-1.48) <sup>a</sup>	0.00 (0.00-0.00) <sup>2 b</sup>
LNT	10.6 (7.87-13.1) <sup>a</sup>	15.3 (11.3-20.6) <sup>b</sup>	9.77 (6.50-13.8) <sup>a</sup>	51.8 (47.8-59.3) <sup>c</sup>
LNnT	0.98 (0.67-1.48) <sup>a</sup>	0.66 (0.00-0.91) <sup>b</sup>	1.21 (0.83-1.78) <sup>a</sup>	1.35 (0.94-1.89) <sup>a,b</sup>
LNFP I+V	7.56 (3.29-12.5) <sup>a</sup>	1.51 (1.36-1.63) <sup>2 b</sup>	18.8 (15.6-21.5) <sup>c</sup>	1.29 (1.16-1.55) <sup>2 b</sup>
LNFP II	5.79 (3.31-9.01) <sup>a</sup>	19.7 (17.1-21.2) <sup>b</sup>	0.00 (0.00-0.00) <sup>2 c</sup>	0.00 (0.00-0.00) <sup>2 c</sup>
LNFP III	7.52 (5.66-9.12) <sup>a</sup>	9.28 (8.06-10.6) <sup>b</sup>	8.94 (6.99-12.3) <sup>a,b</sup>	15.6 (10.1-18.4) <sup>b</sup>
LNDFH I	16.3 (13.5-19.1) <sup>a</sup>	0.00 (0.00-0.00) <sup>2 b</sup>	0.00 (0.00-0.00) <sup>2 b</sup>	0.00 (0.00-0.00) <sup>2 b</sup>
LNDFH II	0.00 (0.00-0.00) <sup>2 a</sup>	3.50 (2.87-4.16) <sup>b</sup>	0.00 (0.00-0.00) <sup>2 a</sup>	0.00 (0.00-0.00) <sup>2 a</sup>
3'-SL	1.08 (0.78-1.43) <sup>a</sup>	1.37 (1.04-1.91) <sup>b</sup>	1.18 (1.04-2.15) <sup>a,b</sup>	1.76 (1.05-2.21) <sup>c</sup>
6'-SL	0.83 (0.47-1.64) <sup>a</sup>	0.70 (0.50-1.64) <sup>a</sup>	0.91 (0.37-1.62) <sup>a</sup>	1.74 (0.66-2.71) <sup>a</sup>
DSLNT	1.97 (1.40-2.47) <sup>a</sup>	3.20 (2.86-3.71) <sup>b</sup>	2.95 (1.94-4.10) <sup>a,b</sup>	5.53 (5.00-8.83) <sup>c</sup>
LSTa	0.00 (0.00-0.20) <sup>a</sup>	0.00 (0.00-0.21) <sup>a</sup>	0.00 (0.00-0.21) <sup>a</sup>	0.78 (0.75-0.93) <sup>b</sup>
LSTb	0.92 (0.68-1.08) <sup>a</sup>	1.43 (1.29-1.89) <sup>b</sup>	0.64 (0.51-0.98) <sup>a</sup>	2.36 (2.18-2.72) <sup>c</sup>
LSTc	0.34 (0.00-0.84) <sup>a</sup>	0.28 (0.00-0.77) <sup>a</sup>	0.26 (0.00-0.57) <sup>a</sup>	0.99 (0.27-1.60) <sup>a</sup>
3'-F-LNH	2.38 (1.42-3.85) <sup>a</sup>	3.65 (0.76-6.23) <sup>ab</sup>	2.51 (1.44-3.94) <sup>a</sup>	7.46 (4.94-8.41) <sup>b</sup>
2'-F-LNH	0.00 (0.00-0.00) <sup>2 a</sup>	0.00 (0.00-0.00) <sup>2 a</sup>	0.00 (0.00-0.00) <sup>2 a</sup>	0.00 (0.00-0.00) <sup>2 a</sup>
$\beta$ 3'-GL <sup>3</sup>	0.074 (0.049-0.12) <sup>a</sup>	0.10 (0.080-0.13) <sup>a</sup>	0.11 (0.00-0.13) <sup>a</sup>	0.42 (0.38-0.51) <sup>b</sup>
$\beta$ 6'-GL <sup>3</sup>	0.36 (0.25-0.53) <sup>a</sup>	0.52 (0.44-0.61) <sup>b</sup>	0.42 (0.38-1.01) <sup>ab</sup>	1.07 (0.87-1.36) <sup>c</sup>
$\alpha$ 3'-GL <sup>3</sup>	0.00 (0.00-0.00) <sup>2 a</sup>	0.00 (0.00-0.00) <sup>2 a</sup>	0.00 (0.00-0.00) <sup>2 a</sup>	0.00 (0.00-0.00) <sup>2 a</sup>

<sup>1</sup> Displayed as the internal standard (IS)-normalized total peak area of selected HMOS (nTPA); <sup>2</sup> '0.00' does not necessarily mean that the respective HMOS is not present at any level, but it means that any amount of HMOS present is below the limit of quantification (LOQ); <sup>3</sup> For  $\beta$ 6'-GL,  $\beta$ 3'-GL and  $\alpha$ 3'-GL, the limit of

detection was defined at a signal-to-noise ratio (S/N) of 3. For all other HMOS, the limit of quantification was defined at a S/N of 10; <sup>a,b,c</sup> and <sup>d</sup> Different superscript letters indicate statistical significance ( $p<0.05$ ). Significance values have been adjusted by the Bonferroni correction for multiple tests.

Abbreviations used: 2'-FL: 2'-fucosyllactose; 3-FL: 3-fucosyllactose; DFL: difucosyllactose; LNT: lacto-N-tetraose; LNnT: lacto-N-neotetraose; LNFP I: lacto-N-fucopentaose I; LNFP II: lacto-N-fucopentaose II; LNFP III: lacto-N-fucopentaose III; LNFP V: lacto-N-fucopentaose V; LNDFH I: lacto-N-difucohexaose I; LNDFH II: lacto-N-difucohexaose II; 3'-SL: 3-sialyllactose; 6'-SL: 6-sialyllactose; DSLNT: disialyllacto-N-tetraose; LSTa: sialyl-lacto-N-tetraose a; LSTb: sialyl-lacto-N-tetraose b; LSTc: sialyl-lacto-N-tetraose c; 2'-F-LNH: 2'-fucosyllacto-N-hexaose; 3'-F-LNH: 3'-fucosyllacto-N-hexaose;  $\beta$ 3'-GL:  $\beta$ 3'-galactosyllactose;  $\beta$ 6'-GL:  $\beta$ 6'-galactosyllactose;  $\alpha$ 3'-GL:  $\alpha$ 3'-galactosyllactose.

**Supplemental Table S3.** Percentage of human milk (HM) samples (n=635) in which the specific human milk oligosaccharide (HMOS) was detected (Presence, % of total) and relative peak area (rPA, %) of the selected HMOS (median (Q1-Q3)) according to maternal HM group [4-6]. HM samples were collected in the first 4 months postpartum from 371 donors. Three samples could not be assigned to a HM group and are for this reason not depicted in this table.

	HM Group I (n = 420 Samples, 241 Donors)		HM Group II (n = 137 Samples, 83 Donors)		HM Group III (n = 53 Samples, 32 Donors)		HM Group IV (n = 22 Samples, 14 Donors)	
	Presence % of total <sup>1</sup>	rPA (%) median (Q1-Q3)	Presence % of total <sup>1</sup>	rPA (%) median (Q1-Q3)	Presence % of total <sup>1</sup>	rPA (%) median (Q1-Q3)	Presence % of total <sup>1</sup>	rPA (%) median (Q1-Q3)
2'-FL	100	23.2 (18.4-29.0) <sup>a</sup>	0	-	100	40.9 (34.2-48.9) <sup>b</sup>	0	-
3-FL	95	7.76 (4.17-14.5) <sup>a</sup>	100	28.4 (17.2-35.8) <sup>b</sup>	15	2.86 (2.47-4.18) <sup>c</sup>	100	6.25 (4.03-11.3) <sup>a</sup>
DFL	100	1.61 (1.13-2.20) <sup>a</sup>	4.4	0.44 (0.25-0.65) <sup>b</sup>	89	0.68 (0.54-1.15) <sup>c</sup>	4.5	1.29 (1.29-1.29) <sup>b</sup>
LNT	100	11.9 (9.20-14.6) <sup>a</sup>	99	19.3 (14.6-26.5) <sup>b</sup>	100	11.8 (9.10-13.8) <sup>a</sup>	100	51.8 (46.4-56.7) <sup>c</sup>
LNnT	99	1.45 (1.03-2.06) <sup>a</sup>	85	0.78 (0.54-1.26) <sup>b</sup>	98	1.10 (0.83-1.54) <sup>c</sup>	95	1.04 (0.45-1.50) <sup>a,b,c</sup>
LNFP II	100	5.14 (3.58-7.34) <sup>a</sup>	100	20.6 (17.6-25.4) <sup>b</sup>	3.8	0.18 (0.13- .) <sup>2 c</sup>	0	-
LNFP III	100	6.81 (4.62-8.83) <sup>a</sup>	100	9.25 (7.30-11.3) <sup>b</sup>	100	6.44 (3.85-8.49) <sup>a</sup>	100	14.3 (9.58-18.0) <sup>c</sup>
LNFP I+V	100	9.69 (6.00-14.0) <sup>a</sup>	100	1.65 (1.39-1.97) <sup>b</sup>	100	24.9 (19.3-31.5) <sup>c</sup>	100	1.60 (1.32-2.36) <sup>b</sup>
LNDFH I	100	17.4 (14.9-20.2) <sup>a</sup>	1.5	1.44 (0.043- .) <sup>2 b</sup>	3.8	0.59 (0.46- .) <sup>2 b</sup>	0	-
LNDFH II	2.1	1.25 (0.99-1.59) <sup>a</sup>	100	3.77 (2.84-4.88) <sup>b</sup>	0	-	0	-
3'-SL	100	0.89 (0.70-1.07) <sup>a</sup>	100	1.00 (0.82-1.25) <sup>b</sup>	98	0.95 (0.77-1.22) <sup>a,b</sup>	100	1.45 (1.09-1.63) <sup>c</sup>
6'-SL	100	1.22 (0.76-2.23) <sup>a</sup>	100	1.58 (0.92-2.67) <sup>a,b</sup>	98	1.35 (0.89-2.52) <sup>a</sup>	100	2.42 (1.80-3.45) <sup>b</sup>
DSLNT	100	1.71 (1.33-2.27) <sup>a</sup>	99	2.37 (1.72-3.14) <sup>b</sup>	98	1.94 (1.33-2.48) <sup>a,b</sup>	100	4.09 (3.22-5.05) <sup>c</sup>
LSTa	60	0.24 (0.18-0.30) <sup>a</sup>	58	0.29 (0.23-0.44) <sup>a</sup>	45	0.33 (0.27-0.45) <sup>a</sup>	95	0.48 (0.34-0.78) <sup>b</sup>
LSTb	99	0.80 (0.61-1.04) <sup>a</sup>	99	1.21 (1.04-1.50) <sup>b</sup>	92	0.76 (0.62-0.93) <sup>a</sup>	100	2.21 (1.89-2.75) <sup>c</sup>
LSTc	96	0.79 (0.46-1.42) <sup>a</sup>	93	0.84 (0.42-1.33) <sup>a</sup>	92	0.71 (0.47-1.71) <sup>a</sup>	95	1.02 (0.76-1.82) <sup>a</sup>
3'-F-LNH	98	3.46 (2.40-4.61) <sup>a</sup>	99	4.63 (2.77-7.18) <sup>b</sup>	98	2.71 (2.05-4.76) <sup>a</sup>	100	10.5 (8.48-11.3) <sup>c</sup>
2'-F-LNH	12	1.72 (1.17-2.45) <sup>a</sup>	0	-	36	1.69 (1.04-3.19) <sup>a</sup>	0	-

<sup>1</sup> Percentage of HM samples in which the specific HMOS was detected ( $\geq$ limit of quantification (LOQ)); <sup>2</sup> In only two samples, the respective HMOS was present and hence Q3 could not be calculated; <sup>a,b,c</sup>and <sup>d</sup> Different superscript letters indicate statistical significance (p<0.05). Significance values have been adjusted by the Bonferroni correction for multiple tests.

Abbreviations used: 2'-FL: 2'-fucosyllactose; 3-FL: 3-fucosyllactose; DFL: difucosyllactose; LNT: lacto-N-tetraose; LNnT: lacto-N-neotetraose; LNFP I: lacto-N-fucopentaose I; LNFP II: lacto-N-fucopentaose II; LNFP III: lacto-N-fucopentaose III; LNFP V: lacto-N-fucopentaose V; LNDFH I: lacto-N-

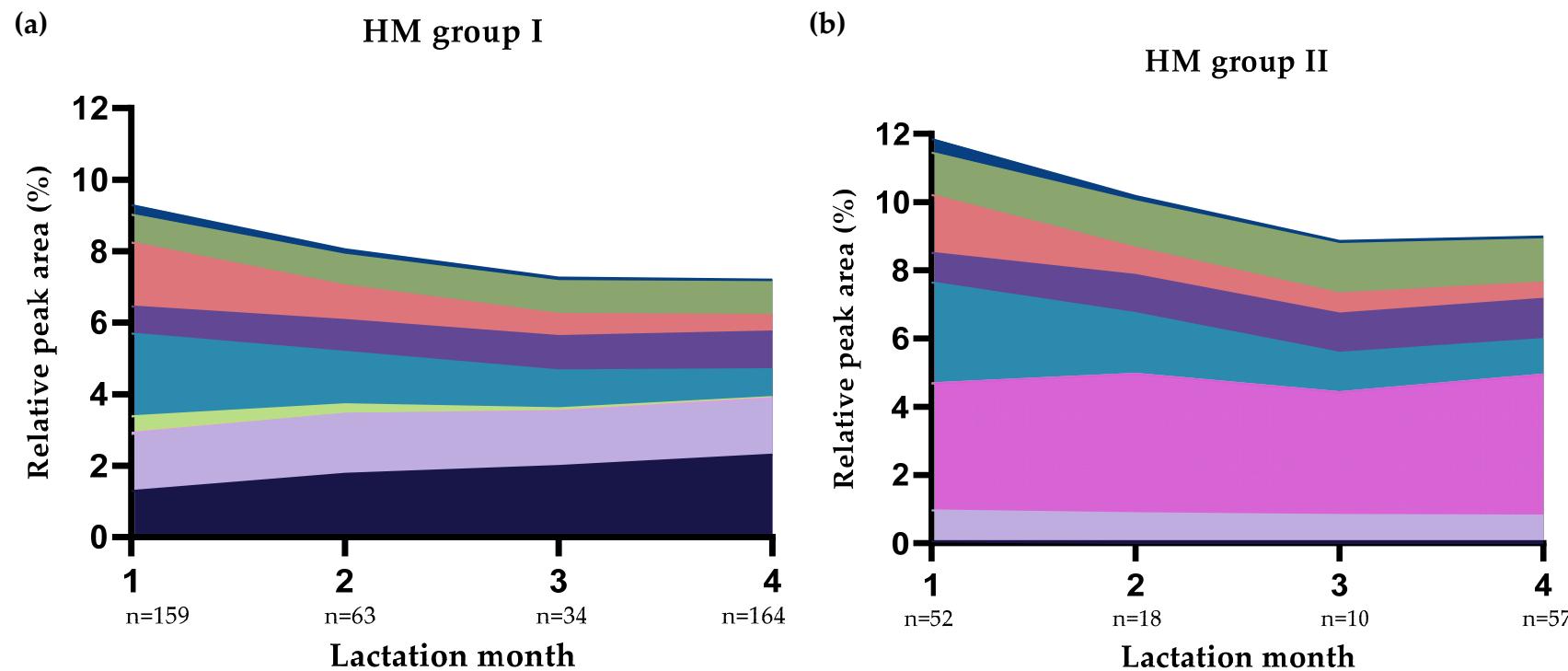
difucohexaose I; LNDFH II: lacto-N-difucohexaose II; 3'-SL: 3-sialyllactose; 6'-SL: 6-sialyllactose; DSLNT: disialyllacto-N-tetraose; LSTA: sialyl-lacto-N-tetraose a; LSTb: sialyl-lacto-N-tetraose b; LSTc: sialyl-lacto-N-tetraose c; 2'-F-LNH: 2'- fucosyllacto-N-hexaose; 3'-F-LNH: 3'-fucosyllacto-N-hexaose

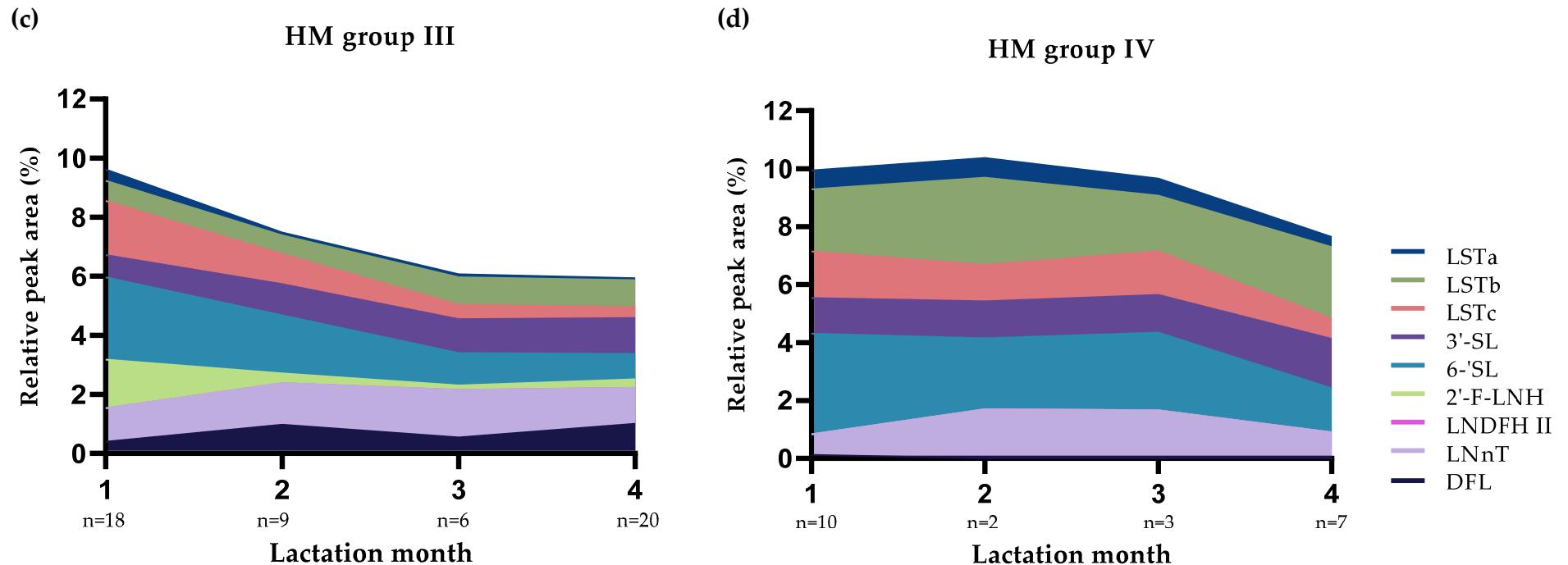
**Supplemental Table S4.** Percentage of human milk (HM) samples (n=171) in which the specific human milk oligosaccharide (HMOS) was detected (Presence, % of total) and relative peak area (rPA, %) of the selected HMOS (median (Q1-Q3)) according to maternal HM group [4–6]. HM samples were collected longitudinally over the first year postpartum from 24 Dutch mothers.

	HM Group I (n = 126 Samples, 18 Donors)		HM Group II (n = 21 Samples, 3 Donors)		HM Group III (n = 15 Samples, 2 Donors)		HM Group IV (n = 9 Samples, 1 Donor)	
	Presence % of total <sup>1</sup>	rPA (%) Median (Q1-Q3)	Presence % of total <sup>1</sup>	rPA (%) Median (Q1-Q3)	Presence % of total <sup>1</sup>	rPA (%) Median (Q1-Q3)	Presence % of total <sup>1</sup>	rPA (%) Median (Q1-Q3)
2'-FL	100	22.3 (15.0-29.9) <sup>a</sup>	0	-	100	42.0 (35.5-53.0) <sup>b</sup>	0	-
3-FL	96	12.2 (6.29-21.7) <sup>a</sup>	100	35.9 (26.4-45.3) <sup>b</sup>	33	3.61 (3.04-4.40) <sup>c</sup>	100	6.78 (3.04-7.31) <sup>d</sup>
DFL	100	1.86 (1.29-2.50) <sup>a</sup>	0	-	100	1.01 (0.62-1.48) <sup>a</sup>	0	-
LNT	100	10.6 (7.87-13.1) <sup>a</sup>	100	15.3 (11.3-20.6) <sup>b</sup>	100	9.77 (6.50-13.8) <sup>a</sup>	100	51.8 (47.8-59.3) <sup>c</sup>
LNnT	94	1.03 (0.73-1.51) <sup>a</sup>	71	0.73 (0.55-1.13) <sup>b</sup>	93	1.22 (0.96-1.80) <sup>a</sup>	100	1.35 (0.94-1.89) <sup>a,b</sup>
LNFP I+V	100	7.56 (3.29-12.5) <sup>a</sup>	100	1.51 (1.36-1.63)	100	18.8 (15.6-24.5) <sup>b</sup>	100	1.29 (1.16-1.55)
LNFP II	100	5.79 (3.31-9.01) <sup>a</sup>	100	19.7 (17.1-21.2) <sup>b</sup>	0	-	0	-
LNFP III	100	7.52 (5.66-9.12) <sup>a</sup>	100	9.28 (8.06-10.6) <sup>b</sup>	100	8.94 (6.99-12.3) <sup>a,b</sup>	100	15.6 (10.1-18.4) <sup>b</sup>
LNDFH I	100	16.3 (13.5-19.1) <sup>a</sup>	0	-	0	-	0	-
LNDFH II	6.3	1.20 (1.04-1.85) <sup>a</sup>	90	3.91 (3.09-4.19) <sup>b</sup>	0	-	0	-
3'-SL	100	1.08 (0.78-1.43) <sup>a</sup>	100	1.37 (1.04-1.91) <sup>a</sup>	100	1.18 (1.04-2.15) <sup>a</sup>	100	1.76 (1.05-2.21) <sup>a</sup>
6'-SL	95	0.88 (0.52-1.66) <sup>a</sup>	95	0.74 (0.51-1.71) <sup>a</sup>	100	0.91 (0.37-1.62) <sup>a</sup>	100	1.74 (0.66-2.71) <sup>a</sup>
DSLNT	100	1.97 (1.40-2.47) <sup>a</sup>	95	3.30 (2.91-3.75) <sup>b</sup>	100	2.95 (1.94-4.10) <sup>a,b</sup>	100	5.53 (5.00-8.83) <sup>c</sup>
LSTa	46	0.20 (0.17-0.28) <sup>a</sup>	33	0.26 (0.20-0.31) <sup>a</sup>	27	0.23 (0.21-0.42) <sup>a</sup>	100	0.78 (0.75-0.93) <sup>b</sup>
LSTb	99	0.93 (0.69-1.08) <sup>a</sup>	100	1.43 (1.29-1.89) <sup>b</sup>	100	0.64 (0.51-0.98) <sup>a</sup>	100	2.36 (2.18-2.72) <sup>c</sup>
LSTc	73	0.57 (0.27-1.08) <sup>a</sup>	57	0.70 (0.32-1.20) <sup>a</sup>	60	0.53 (0.29-0.77) <sup>a</sup>	89	1.17 (0.51-1.64) <sup>a</sup>
3'-F-LNH	93	2.49 (1.59-3.90) <sup>a</sup>	86	4.06 (1.23-6.82) <sup>a,b</sup>	87	2.76 (1.75-4.37) <sup>a</sup>	100	7.46 (4.94-8.41) <sup>b</sup>
2'-F-LNH	16	1.00 (0.61-2.14) <sup>a</sup>	0	-	20	0.90 (0.32-.) <sup>3 a</sup>	0	-
$\beta$ 3'-GL <sup>2</sup>	83	0.087 (0.062-0.15) <sup>a</sup>	95	0.11 (0.081-0.14) <sup>a</sup>	73	0.12 (0.11-0.13) <sup>a</sup>	100	0.42 (0.38-0.51) <sup>b</sup>
$\beta$ 6'-GL <sup>2</sup>	100	0.36 (0.25-0.53) <sup>a</sup>	100	0.52 (0.44-0.61) <sup>b</sup>	100	0.42 (0.38-1.01) <sup>a,b</sup>	100	1.07 (0.87-1.36) <sup>c</sup>
$\alpha$ 3'-GL <sup>2</sup>	1.6	0.18 (0.13-.) <sup>3 a</sup>	0	-	0	-	0	-

<sup>1</sup> Percentage of HM samples in which the specific HMOS was detected ( $\geq$ limit of quantification (LOQ)); <sup>2</sup> For  $\beta$ 6'-GL,  $\beta$ 3'-GL and  $\alpha$ 3'-GL, the limit of detection was defined at a signal-to-noise ratio (S/N) of 3. For all other HMOS, the limit of quantification was defined at an S/N of 10; <sup>3</sup> In only two samples, the respective HMOS was present and hence Q3 could not be calculated; <sup>a, b, c</sup> and <sup>d</sup> Different superscript letters indicate statistical significance (p<0.05). Significance values have been adjusted by the Bonferroni correction for multiple tests.

Abbreviations used: 2'-FL: 2'-fucosyllactose; 3-FL: 3-fucosyllactose; DFL: difucosyllactose; LNT: lacto-N-tetraose; LNnT: lacto-N-neotetraose; LNFP I: lacto-N-fucopentaose I; LNFP II: lacto-N-fucopentaose II; LNFP III: lacto-N-fucopentaose III; LNFP V: lacto-N-fucopentaose V; LNDFH I: lacto-N-difucohexaose I; LNDFH II: lacto-N-difucohexaose II; 3'-SL: 3-sialyllactose; 6'-SL: 6-sialyllactose; DSLNT: disialyllacto-N-tetraose; LSTa: sialyl-lacto-N-tetraose a; LSTb: sialyl-lacto-N-tetraose b; LSTc: sialyl-lacto-N-tetraose c; 2'-F-LNH: 2'-fucosyllacto-N-hexaose; 3'-F-LNH: 3'- fucosyllacto-N-hexaose;  $\beta$ 3'-GL:  $\beta$ 3'-galactosyllactose;  $\beta$ 6'-GL:  $\beta$ 6'-galactosyllactose;  $\alpha$ 3'-GL:  $\alpha$ 3'-galactosyllactose.





**Supplemental Figure S1.** Median relative peak areas (rPA) of low-abundant human milk oligosaccharides (HMOS) in the human milk (HM) samples (n=635) collected in the first 4 months of lactation according to HM group [4–6] and lactation stage. (a) HM group I; (b): HM group II; (c): HM group III and (d): HM group IV. Three samples could not be assigned to a HM group and are for this reason not depicted in these figures.

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