Claims

1. Method for the production of fucosyllactose by a genetically modified cell, comprising the steps of:
   - providing a cell capable of producing fucosyllactose, said cell comprising at least one nucleic acid sequence coding for a fucosyltransferase that transfers a fucose residue from a guanosine-diphosphate fucose (GDP-fucose) donor to a lactose acceptor thereby synthesizing fucosyllactose,
   - said cell further comprising i) a modified expression of an endogenous membrane protein enabling and/or enhancing fucosyllactose transport and/or ii) an expression of a heterologous membrane protein enabling and/or enhancing fucosyllactose transport, and wherein said membrane protein in i) and/or ii) is selected from the group of porters and wherein said membrane protein is not belonging to the SET family;
   - cultivating the cell in a medium under conditions permissive for the production of the desired fucosyllactose
   - preferably separating the fucosyllactose from the cultivation.
2. Method according to claim 1, wherein said membrane protein is a porter selected from:
   - the group of eggnog families 05BZS, 05C0R, 05C2C, 05CT4, 05CXP, 05CZQ, 05D94, 05DXI, 05E5M, 05E5W, 05E8G, 05EAM, 05EDR, 05EGZ, 05F9N, 05JHE, 05PSV, 05W2Y, 05W3H, 05XJ5, 070Q9, 07CWC, 07QF7, 07QNK, 07RBJ, 07RJ1, 07T5E, 07VQ3, 0814C, 088QT, 08H15, 08N8A, 08SC4, 08Z4Q, as defined by eggnogdb 1.0.2 as released on 3rd Nov 2017,
   - the PFAM list of PF00083, PF00474, PF00873, PF00893, PF01895, PF01943, PF02690, PF03083, PF04193, PF05977, PF07690, PF07690, PF13347, PF13440 and PF14667, as defined by Pfam 32.0 as released on Sept 2018,
   - the interpro list IPR000390, IPR001036, IPR001411, IPR001734, IPR001927, IPR002797, IPR003663, IPR003841, IPR004316, IPR004633, IPR004638, IPR004734, IPR004812, IPR005275, IPR005828, IPR005829, IPR006603, IPR010290, IPR011701, IPR020846, IPR023008, IPR023721, IPR023722, IPR026022, IPR027417, IPR027463, IPR029303, IPR032896, IPR036259, IPR038078, IPR038377, IPR039672, as defined by InterPro 75.0 as released on 4th July 2019.
3. Method according to any one of claim 1 or 2, wherein said membrane protein is a porter selected from MdfA from *Escherichia coli K12 MG1655* with SEQ ID NO 02, IceT from *Escherichia coli K12 MG1655* with SEQ ID NO 06, Blon_2331 from *B. longum subsp. Infantis* (strain ATCC 15697) with SEQ ID NO 40, Blon_2332 from *B. longum subsp. Infantis* (strain ATCC 15697) with SEQ ID NO 42, wzx-like protein of *Chitinophaga sp. CF118* with SEQ ID NO 58, *Prevotella ruminicola (AR32)* with SEQ ID NO 66, *Lactococcus raffinolactis (ATCC 43920)* with SEQ ID NO 64, or *Dyadobacter soli DSM 25329* with SEQ ID NO 62, or functional homolog or functional fragment of any one of the above porter membrane protein with SEQ

ID NO 02, 06, 40, 42, 58, 66, 64 or 62, respectively, enabling and/or enhancing fucosyllactose transport or a sequence having at least 80% sequence identity to any one of said MdfA, IceT, Blon_2331, Blon_2332 membrane proteins or wzx-like membrane protein with SEQ ID NOs 02, 06, 40, 42, 58, 66, 64 or 62, respectively, enabling and/or enhancing fucosyllactose transport.

4. Method according to any one of claim 1 or 2, wherein said membrane protein is a porter selected from MdfA from *Escherichia coli* K12 MG1655 with SEQ ID NO 02, IceT from *Escherichia coli* K12 MG1655 with SEQ ID NO 06, YnfM from *Escherichia coli* K12 MG1655 with SEQ ID NO 04, Yhhs from *Escherichia coli* K12 MG1655 with SEQ ID NO 08, EmrD from *Escherichia coli* K12 MG1655 with SEQ ID NO 10, YdhC from *Escherichia coli* K12 MG1655 with SEQ ID NO 12, YbdA from *Escherichia coli* K12 MG1655 with SEQ ID NO 14, YdeE from *Escherichia coli* K12 MG1655 with SEQ ID NO 16, MhpT from *Escherichia coli* K12 MG1655 with SEQ ID NO 18, YebQ from *Escherichia coli* K12 MG1655 with SEQ ID NO 20, YjhB from *Escherichia coli* K12 MG1655 with SEQ ID NO 22, Bcr from *Escherichia coli* K12 MG1655 with SEQ ID NO 24, FucP from *Escherichia coli* K12 MG1655 with SEQ ID NO 26, WzxE from *Escherichia coli* K12 MG1655 with SEQ ID NO 32, EmrE from *Escherichia coli* K12 MG1655 with SEQ ID NO 38, Blon_2331 from *Bifidobacterium longum subsp. Infantis* (strain ATCC 15697) with SEQ ID NO 40, Blon_2332 from *Bifidobacterium longum subsp. Infantis* (strain ATCC 15697) with SEQ ID NO 42, Blon_0247 from *Bifidobacterium longum subsp. Infantis* (strain ATCC 15697) with SEQ ID NO 46, Blon_0245 from *Bifidobacterium longum subsp. Infantis* (strain ATCC 15697) with SEQ ID NO 48, Blon_0345 from *Bifidobacterium longum subsp. Infantis* (strain ATCC 15697) with SEQ ID NO 50, CDT2 from *Neurospora crassa* OR74A with SEQ ID NO 52, CDT2 from *Aspergillus oryzae* RIB40 with SEQ ID NO 54, Wzx from *Chitinophaga* sp. CF118 with SEQ ID NO 58, Wzx from *Eubacterium* sp. CAG:581 with SEQ ID NO 60, Wzx from *Dyadobacter soli* (DSM 25329) with SEQ ID NO 62, Wzx from *Lactococcus raffinolactis* (ATCC 43920) with SEQ ID NO 64, Wzx from *Prevotella ruminicola* (AR32) with SEQ ID NO 66, NAPO from *Brachyspira hampsonii* P280/1 with SEQ ID NO 86, NAm from *Actinobaculum suis* (DSM 20639) with SEQ ID NO 98, NAm from R*uminococcus gnavus* with SEQ ID NO 100, NAm from *Curtobacterium* sp. 314Chir4.1 with SEQ ID NO 102, Nap from *Niabella drilacis* (DSM25811) with SEQ ID NO 104, Nap from *Saccharicrinis fermentans* (DSM 9555) with SEQ ID NO 106, mdtD from *Citrobacter freundii* MGH152 with SEQ ID NO 108, mdtD from *Citrobacter werkmanii* NBRC 105721 with SEQ ID NO 110, mdtD from *Citrobacter amalonaticus* with SEQ ID NO 112, mdtD from *Klebsiella oxytoca* with SEQ ID NO 114, mdtD from *Escherichia albertii* B156 with SEQ ID NO 116, yegB from *Salmonella enterica subsp. Salamae* with SEQ ID NO 118, mdtD from *Klebsiella pneumoniae* 30684/NJST258_2 with SEQ ID NO 120, Tcr_1_D38215 from *Klebsiella pneumoniae* with SEQ ID NO 122, mdtD from *Pseudocitrobacter faecalis* with SEQ ID NO 124, Cmr from *Yokenella regensburgei* (ATCC43003) with SEQ ID NO 126, MdfA from

Cronobacter muytjensii with SEQ ID NO 128, MdfA from *Klebsiella oxytoca* with SEQ ID NO130, MFS from *Citrobacter koseri* with SEQ ID NO 132, MdfA from *Escherichia marmotae* with SEQ ID NO 134, Cmr from *Shigella flexneri* with SEQ ID NO 136, MdfA from *Salmonella enterica subsp. Salamae* with SEQ ID NO 138, Cmr from *Citrobacter youngae* (ATCC 29220) with SEQ ID NO 140, MdfA from *Citrobacter freundii* with SEQ ID NO 142, MdfA from *Enterobacter kobei* with SEQ ID NO 144, MdfA from *Enterobacter* sp. with SEQ ID NO 146, MdfA from *Lelliottia sp*. WB101 with SEQ ID NO 148, MdfA from *Enterobacter ludwigii* EcWSU1 with SEQ ID NO 150, Sweet-like protein from *Actinoplanes utahensis* with SEQ ID NO 152, Sweet-like protein from *Chitinophagaceae bacterium* PMG_246 with SEQ ID NO 154, Sweet-like protein from *Rhizobium* sp. PDC82 with SEQ ID NO 156, Sweet-like protein from *Kineococcus rhizosphaerae* (DSM 19711) with SEQ ID NO 158, Sweet-like protein from *Morganella morganii* IS15 with SEQ ID NO 160, Sweet-like protein from *Geodermatophilus obscurus* (strain ATCC 25078) with SEQ ID NO 162, Sweet-like protein from *Bradyrhizobium* sp. BTAi1 with SEQ ID NO 164, Sweet-like protein from *Bradyrhizobium japonicum* USDA 110 with SEQ ID NO 166, Sweet-like protein from *Xanthomonas campestris pv. vesicatoria* str. 85-10 with SEQ ID NO 168, Sweet-like protein from *Herbaspirillum aquaticum* with SEQ ID NO 170, Sweet-like protein from *Flavobacteria bacterium* MS024-2A with SEQ ID NO 172, rnd-like from *Sinorhizobium medicae* WSM419 with SEQ ID NO 182, arabinose efflux from *Azospirillum brasiliense* LMG 04375 with SEQ ID NO 184 or functional homolog or functional fragment of any of the above porter membrane protein with SEQ ID NO 02, 06, 04, 08, 10, 12, 14, 16, 18, 20, 22, 24, 26, 32, 38, 40, 42, 46, 48, 50, 52, 54, 58, 60, 62, 64, 66, 86, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 182 or 184, respectively, enabling and/or enhancing fucosyllactose transport or a protein having an amino acid sequence having at least 80% sequence identity to any of said MdfA, IceT, YnfM, Yhhs, EmrD, YdhC, YbdA, YdeE, MhpT, YebQ, YjhB, Bcr, FucP, WzxE, EmrE, Wzx, Blon_2331, Blon_2232, Blon_0247, Blon_0245, Blon_0345, NAPO, NAm, Nap, mdtD, YegB, Tcr_1_D38215, cmr, MFS, CDT2, rnd, Sweet-like or arabinose efflux membrane proteins with SEQ ID NO 02, 06, 04, 08, 10, 12, 14, 16, 18, 20, 22, 24, 26, 32, 38, 40, 42, 46, 48, 50, 52, 54, 58, 60, 62, 64, 66, 86, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 182 or 184, respectively, enabling and/or enhancing fucosyllactose transport.

5. Method for the production of fucosyllactose by a genetically modified cell, comprising the steps of:
    - providing a cell capable of producing fucosyllactose, said cell comprising at least one nucleic acid sequence coding for a fucosyltransferase that transfers a fucose residue from a GDP-fucose donor to a lactose acceptor thereby synthesizing fucosyllactose

- said cell further comprising i) a modified expression of an endogenous membrane protein enabling and/or enhancing fucosyllactose transport and/or ii) an expression of a heterologous membrane protein enabling and/or enhancing fucosyllactose transport, and wherein said membrane protein in i) and/or ii) is selected from the group of membrane proteins consisting of the porter membrane proteins MdfA from *Escherichia coli* K12 MG1655 with SEQ ID NO 02, IceT from *Escherichia coli* K12 MG1655 with SEQ ID NO 06, YnfM from *Escherichia coli* K12 MG1655 with SEQ ID NO 04, Yhhs from *Escherichia coli* K12 MG1655 with SEQ ID NO 08, EmrD from *Escherichia coli* K12 MG1655 with SEQ ID NO 10, YdhC from *Escherichia coli* K12 MG1655 with SEQ ID NO 12, YbdA from *Escherichia coli* K12 MG1655 with SEQ ID NO 14, YdeE from *Escherichia coli* K12 MG1655 with SEQ ID NO 16, MhpT from *Escherichia coli* K12 MG1655 with SEQ ID NO 18, YebQ from *Escherichia coli* K12 MG1655 with SEQ ID NO 20, YjhB from *Escherichia coli* K12 MG1655 with SEQ ID NO 22, Bcr from *Escherichia coli* K12 MG1655 with SEQ ID NO 24, FucP from *Escherichia coli* K12 MG1655 with SEQ ID NO 26, WzxE from *Escherichia coli* K12 MG1655 with SEQ ID NO 32, EmrE from *Escherichia coli* K12 MG1655 with SEQ ID NO 38, Blon_2331 from *Bifidobacterium longum subsp. Infantis* (strain ATCC 15697) with SEQ ID NO 40, Blon_2332 from *Bifidobacterium longum subsp. Infantis* (strain ATCC 15697) with SEQ ID NO 42, Blon_0247 from *Bifidobacterium longum subsp. Infantis* (strain ATCC 15697) with SEQ ID NO 46, Blon_0245 from *Bifidobacterium longum subsp. Infantis* (strain ATCC 15697) with SEQ ID NO 48, Blon_0345 from *Bifidobacterium longum subsp. Infantis* (strain ATCC 15697) with SEQ ID NO 50, CDT2 from *Neurospora crassa* OR74A with SEQ ID NO 52, CDT2 from *Aspergillus oryzae* RIB40 with SEQ ID NO 54, Wzx from *Chitinophaga* sp. CF118 with SEQ ID NO 58, Wzx from *Eubacterium* sp. CAG:581 with SEQ ID NO 60, Wzx from *Dyadobacter soli* (DSM 25329) with SEQ ID NO 62, Wzx from *Lactococcus raffinolactis* (ATCC 43920) with SEQ ID NO 64, Wzx from *Prevotella ruminicola* (AR32) with SEQ ID NO 66, NAPO from *Brachyspira hampsonii* P280/1 with SEQ ID NO 86, NAm from *Actinobaculum suis* (DSM 20639) with SEQ ID NO 98, NAm from R*uminococcus gnavus* with SEQ ID NO 100, NAm from *Curtobacterium* sp. 314Chir4.1 with SEQ ID NO 102, Nap from *Niabella drilacis* (DSM25811) with SEQ ID NO 104, Nap from *Saccharicrinis fermentans* (DSM 9555) with SEQ ID NO 106, mdtD from *Citrobacter freundii* MGH152 with SEQ ID NO 108, mdtD from *Citrobacter werkmanii* NBRC 105721 with SEQ ID NO 110, mdtD from *Citrobacter amalonaticus* with SEQ ID NO 112, mdtD from *Klebsiella oxytoca* with SEQ ID NO 114, mdtD from *Escherichia albertii* B156 with SEQ ID NO 116, yegB from *Salmonella enterica subsp. Salamae* with SEQ ID NO 118, mdtD from *Klebsiella pneumoniae* 30684/NJST258_2 with SEQ ID NO 120, Tcr_1_D38215 from *Klebsiella pneumoniae* with SEQ ID NO 122, mdtD from *Pseudocitrobacter faecalis* with SEQ ID NO 124, Cmr from *Yokenella regensburgei* (ATCC43003) with SEQ ID NO 126,

MdfA from *Cronobacter muytjensii* with SEQ ID NO 128, MdfA from *Klebsiella oxytoca* with SEQ ID NO130, MFS from *Citrobacter koseri* with SEQ ID NO 132, MdfA from *Escherichia marmotae* with SEQ ID NO 134, Cmr from *Shigella flexneri* with SEQ ID NO 136, MdfA from *Salmonella enterica subsp. Salamae* with SEQ ID NO 138, Cmr from *Citrobacter youngae* (ATCC 29220) with SEQ ID NO 140, MdfA from *Citrobacter freundii* with SEQ ID NO 142, MdfA from *Enterobacter kobei* with SEQ ID NO 144, MdfA from *Enterobacter* sp. with SEQ ID NO 146, MdfA from *Lelliottia sp*. WB101 with SEQ ID NO 148, MdfA from *Enterobacter ludwigii* EcWSU1 with SEQ ID NO 150, Sweet-like protein from *Actinoplanes utahensis* with SEQ ID NO 152, Sweet-like protein from *Chitinophagaceae bacterium* PMG_246 with SEQ ID NO 154, Sweet-like protein from *Rhizobium* sp. PDC82 with SEQ ID NO 156, Sweet-like protein from *Kineococcus rhizosphaerae* (DSM 19711) with SEQ ID NO 158, Sweet-like protein from *Morganella morganii* IS15 with SEQ ID NO 160, Sweet-like protein from *Geodermatophilus obscurus* (strain ATCC 25078) with SEQ ID NO 162, Sweet-like protein from *Bradyrhizobium* sp. BTAi1 with SEQ ID NO 164, Sweet-like protein from *Bradyrhizobium japonicum* USDA 110 with SEQ ID NO 166, Sweet-like protein from *Xanthomonas campestris pv. vesicatoria* str. 85-10 with SEQ ID NO 168, Sweet-like protein from *Herbaspirillum aquaticum* with SEQ ID NO 170, Sweet-like protein from *Flavobacteria bacterium* MS024-2A with SEQ ID NO 172, rnd-like from *Sinorhizobium medicae* WSM419 with SEQ ID NO 182, arabinose efflux from *Azospirillum brasiliense* LMG 04375 with SEQ ID NO 184 or functional homolog or functional fragment of any of the above porter membrane protein with SEQ ID NO 02, 06, 04, 08, 10, 12, 14, 16, 18, 20, 22, 24, 26, 32, 38, 40, 42, 46, 48, 50, 52, 54, 58, 60, 62, 64, 66, 86, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 182 or 184, respectively, enabling and/or enhancing fucosyllactose transport or a protein having an amino acid sequence having at least 80% sequence identity to any of said MdfA, IceT, YnfM, Yhhs, EmrD, YdhC, YbdA, YdeE, MhpT, YebQ, YjhB, Bcr, FucP, WzxE, EmrE, Wzx, Blon_2331, Blon_2232, Blon_0247, Blon_0245, Blon_0345, NAPO, NAm, Nap, mdtD, YegB, Tcr_1_D38215, cmr, MFS, CDT2, rnd, Sweet-like or arabinose efflux membrane proteins with SEQ ID NO 02, 06, 04, 08, 10, 12, 14, 16, 18, 20, 22, 24, 26, 32, 38, 40, 42, 46, 48, 50, 52, 54, 58, 60, 62, 64, 66, 86, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 182 or 184, respectively, enabling and/or enhancing fucosyllactose transport.

6. Method for the production of fucosyllactose according to any one of the previous claims, wherein said membrane protein is a transporter protein involved in transport of compounds across the outer membrane of the cell wall.

7. Method for the production of fucosyllactose according to any one of the previous claims, the method further comprising at least one of the following steps:
   i) adding to the culture medium a lactose feed comprising at least 50, more preferably at least 75, more preferably at least 100, more preferably at least 120, more preferably at least 150 gram of lactose per litre of initial reactor volume wherein the reactor volume ranges from 250 mL to 10.000 m^3, preferably in a continuous manner, and preferably so that the final volume of the culture medium is not more than three-fold, preferably not more than two-fold, more preferably less than 2-fold of the volume of the culture medium before the addition of said lactose feed;
   ii) adding a lactose feed in a continuous manner to the culture medium over the course of 1 day, 2 days, 3 days, 4 days, 5 days by means of a feeding solution;
   iii) adding a lactose feed in a continuous manner to the culture medium over the course of 1 day, 2 days, 3 days, 4 days, 5 days by means of a feeding solution and wherein the concentration of said lactose feeding solution is 50 g/L, preferably 75 g/L, more preferably 100 g/L, more preferably 125 g/L, more preferably 150 g/L, more preferably 175 g/L, more preferably 200 g/L, more preferably 225 g/L, more preferably 250 g/L, more preferably 275 g/L, more preferably 300 g/L, more preferably 325 g/L, more preferably 350 g/L, more preferably 375 g/L, more preferably, 400 g/L, more preferably 450 g/L, more preferably 500 g/L, even more preferably, 550 g/L, most preferably 600 g/L; and wherein preferably the pH of said solution is set between 3 and 7 and wherein preferably the temperature of said feed solution is kept between 20°C and 80°C;

   said method resulting in a fucosyllactose concentration of at least 50 g/L, preferably at least 75 g/L, more preferably at least 90 g/L, more preferably at least 100 g/L, more preferably at least 125 g/L, more preferably at least 150 g/L, more preferably at least 175 g/L, more preferably at least 200 g/L in the final volume of said culture medium.
8. The method of claim 7, wherein the lactose feed is accomplished by adding lactose from the beginning of the cultivating in a concentration of at least 5 mM, preferably in a concentration of 30, 40, 50, 60, 70, 80, 90, 100, 150 mM, more preferably in a concentration > 300 mM.
9. The method of any one of claim 7 or 8, wherein a first phase of exponential cell growth is provided by adding a carbon-based substrate, preferably glucose or sucrose, to the culture medium before the lactose is added to the culture medium in a second phase.
10. Method according to any one of the claims 1 to 9, wherein the method is producing a mixture of fucosyllactoses.
11. Method according to any one of claims 1 to 10, wherein said fucosyllactose is 2'-fucosyllactose, 3-fucosyllactose and/or difucosyllactose.
12. Method according to any one of claims 1 to 11, wherein said genetically modified cell is selected from the group consisting of microorganism, plant, or animal cells, preferably said microorganism is a bacterium, fungus or a yeast, preferably said plant is a rice, cotton,

rapeseed, soy, maize or corn plant, preferably said animal is an insect, fish, bird or non-human mammal, more preferably said cell is an *Escherichia coli* cell, more preferably said yeast belongs to the phylum of the Ascomycota or the phylum of the Basidiomycota or the phylum of the Deuteromycota or the phylum of the Zygomycetes.

13. Host cell genetically modified for the production of a fucosyllactose, wherein the host cell comprises at least one nucleic acid sequence coding for a fucosyltransferase that transfers a fucose residue from a GDP-fucose donor to a lactose acceptor thereby synthesizing fucosyllactose, said cell further comprising i) a modified expression of an endogenous membrane protein enabling and/or enhancing fucosyllactose transport and/or ii) an expression of a heterologous membrane protein enabling and/or enhancing fucosyllactose transport, and wherein said membrane protein in i) and/or ii) is selected from the group of porters and wherein said membrane protein is not belonging to the SET family.
14. Host cell according to claim 13, wherein said membrane protein is chosen from the group of membrane proteins as defined in any one of the claims 2 to 6.
15. Host cell according to claim 13, wherein said membrane protein is a porter selected from MdfA from *Escherichia coli* K12 MG1655 with SEQ ID NO 02, IceT from *Escherichia coli* K12 MG1655 with SEQ ID NO 06, YnfM from *Escherichia coli* K12 MG1655 with SEQ ID NO 04, Yhhs from *Escherichia coli* K12 MG1655 with SEQ ID NO 08, EmrD from *Escherichia coli* K12 MG1655 with SEQ ID NO 10, YdhC from *Escherichia coli* K12 MG1655 with SEQ ID NO 12, YbdA from *Escherichia coli* K12 MG1655 with SEQ ID NO 14, YdeE from *Escherichia coli* K12 MG1655 with SEQ ID NO 16, MhpT from *Escherichia coli* K12 MG1655 with SEQ ID NO 18, YebQ from *Escherichia coli* K12 MG1655 with SEQ ID NO 20, YjhB from *Escherichia coli* K12 MG1655 with SEQ ID NO 22, Bcr from *Escherichia coli* K12 MG1655 with SEQ ID NO 24, FucP from *Escherichia coli* K12 MG1655 with SEQ ID NO 26, WzxE from *Escherichia coli* K12 MG1655 with SEQ ID NO 32, EmrE from *Escherichia coli* K12 MG1655 with SEQ ID NO 38, Blon_2331 from *Bifidobacterium longum subsp. Infantis* (strain ATCC 15697) with SEQ ID NO 40, Blon_2332 from *Bifidobacterium longum subsp. Infantis* (strain ATCC 15697) with SEQ ID NO 42, Blon_0247 from *Bifidobacterium longum subsp. Infantis* (strain ATCC 15697) with SEQ ID NO 46, Blon_0245 from *Bifidobacterium longum subsp. Infantis* (strain ATCC 15697) with SEQ ID NO 48, Blon_0345 from *Bifidobacterium longum subsp. Infantis* (strain ATCC 15697) with SEQ ID NO 50, CDT2 from *Neurospora crassa* OR74A with SEQ ID NO 52, CDT2 from *Aspergillus oryzae* RIB40 with SEQ ID NO 54, Wzx from *Chitinophaga* sp. CF118 with SEQ ID NO 58, Wzx from *Eubacterium* sp. CAG:581 with SEQ ID NO 60, Wzx from *Dyadobacter soli* (DSM 25329) with SEQ ID NO 62, Wzx from *Lactococcus raffinolactis* (ATCC 43920) with SEQ ID NO 64, Wzx from *Prevotella ruminicola* (AR32) with SEQ ID NO 66, NAPO from *Brachyspira hampsonii* P280/1 with SEQ ID NO 86, NAm from *Actinobaculum suis* (DSM 20639) with SEQ ID NO 98, NAm from R*uminococcus gnavus* with SEQ ID NO 100, NAm from *Curtobacterium* sp. 314Chir4.1 with SEQ ID NO 102, Nap from *Niabella*

drilacis (DSM25811) with SEQ ID NO 104, Nap from *Saccharicrinis fermentans* (DSM 9555) with SEQ ID NO 106, mdtD from *Citrobacter freundii* MGH152 with SEQ ID NO 108, mdtD from *Citrobacter werkmanii* NBRC 105721 with SEQ ID NO 110, mdtD from *Citrobacter amalonaticus* with SEQ ID NO 112, mdtD from *Klebsiella oxytoca* with SEQ ID NO 114, mdtD from *Escherichia albertii* B156 with SEQ ID NO 116, yegB from *Salmonella enterica subsp. Salamae* with SEQ ID NO 118, mdtD from *Klebsiella pneumoniae* 30684/NJST258_2 with SEQ ID NO 120, Tcr_1_D38215 from *Klebsiella pneumoniae* with SEQ ID NO 122, mdtD from *Pseudocitrobacter faecalis* with SEQ ID NO 124, Cmr from *Yokenella regensburgei* (ATCC43003) with SEQ ID NO 126, MdfA from *Cronobacter muytjensii* with SEQ ID NO 128, MdfA from *Klebsiella oxytoca* with SEQ ID NO130, MFS from *Citrobacter koseri* with SEQ ID NO 132, MdfA from *Escherichia marmotae* with SEQ ID NO 134, Cmr from *Shigella flexneri* with SEQ ID NO 136, MdfA from *Salmonella enterica subsp. Salamae* with SEQ ID NO 138, Cmr from *Citrobacter youngae* (ATCC 29220) with SEQ ID NO 140, MdfA from *Citrobacter freundii* with SEQ ID NO 142, MdfA from *Enterobacter kobei* with SEQ ID NO 144, MdfA from *Enterobacter* sp. with SEQ ID NO 146, MdfA from *Lelliottia sp*. WB101 with SEQ ID NO 148, MdfA from *Enterobacter ludwigii* EcWSU1 with SEQ ID NO 150, Sweet-like protein from *Actinoplanes utahensis* with SEQ ID NO 152, Sweet-like protein from *Chitinophagaceae bacterium* PMG_246 with SEQ ID NO 154, Sweet-like protein from *Rhizobium* sp. PDC82 with SEQ ID NO 156, Sweet-like protein from *Kineococcus rhizosphaerae* (DSM 19711) with SEQ ID NO 158, Sweet-like protein from *Morganella morganii* IS15 with SEQ ID NO 160, Sweet-like protein from *Geodermatophilus obscurus* (strain ATCC 25078) with SEQ ID NO 162, Sweet-like protein from *Bradyrhizobium* sp. BTAi1 with SEQ ID NO 164, Sweet-like protein from *Bradyrhizobium japonicum* USDA 110 with SEQ ID NO 166, Sweet-like protein from *Xanthomonas campestris pv. vesicatoria* str. 85-10 with SEQ ID NO 168, Sweet-like protein from *Herbaspirillum aquaticum* with SEQ ID NO 170, Sweet-like protein from *Flavobacteria bacterium* MS024-2A with SEQ ID NO 172, rnd-like from *Sinorhizobium medicae* WSM419 with SEQ ID NO 182, arabinose efflux from *Azospirillum brasiliense* LMG 04375 with SEQ ID NO 184 or functional homolog or functional fragment of any of the above porter membrane protein with SEQ ID NO 02, 06, 04, 08, 10, 12, 14, 16, 18, 20, 22, 24, 26, 32, 38, 40, 42, 46, 48, 50, 52, 54, 58, 60, 62, 64, 66, 86, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 182 or 184, respectively, enabling and/or enhancing fucosyllactose transport or a protein having an amino acid sequence having at least 80% sequence identity to any of said MdfA, IceT, YnfM, Yhhs, EmrD, YdhC, YbdA, YdeE, MhpT, YebQ, YjhB, Bcr, FucP, WzxE, EmrE, Wzx, Blon_2331, Blon_2232, Blon_0247, Blon_0245, Blon_0345, NAPO, NAm, Nap, mdtD, YegB, Tcr_1_D38215, cmr, MFS, CDT2, rnd, Sweet-like or arabinose efflux membrane proteins with SEQ ID NO 02, 06, 04, 08, 10, 12, 14, 16, 18, 20, 22, 24, 26, 32, 38, 40, 42, 46, 48, 50, 52,

54, 58, 60, 62, 64, 66, 86, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 182 or 184, respectively, enabling and/or enhancing fucosyllactose transport.

16. Host cell according to any one of the claims 13 to 15, wherein said membrane protein is a transporter protein involved in transport of compounds across the outer membrane of the cell wall.

17. Host cell according to any one of the claims 13 to 16, wherein said cell is selected from the group consisting of microorganism, plant, or animal cells, preferably said microorganism is a bacterium, fungus or a yeast, preferably said plant is a rice, cotton, rapeseed, soy, maize or corn plant, preferably said animal is an insect, fish, bird or non-human mammal, more preferably said cell is an Escherichia coli cell, more preferably said yeast belongs to the phylum of the Ascomycota or the phylum of the Basidiomycota or the phylum of the Deuteromycota or the phylum of the Zygomycetes.

18. Host cell according to any one of the claims 13 to 17, wherein the cell comprises a catabolic pathway for selected mono-, di- or oligosaccharides which is at least partially inactivated, the mono-, di-, or oligosaccharides being involved in and/or required for the synthesis of fucosyllactose.

19. Host cell according to any one of the claims 13 to 18, wherein said fucosyllactose is 2'-fucosyllactose, 3-fucosyllactose or difucosyllactose.

20. Use of a host cell according to any one of the claims 13 to 19, for the production of fucosyllactose, preferably said fucosyllactose is 2'-fucosyllactose, 3-fucosyllactose or difucosyllactose.