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 is i) selected from the group of membrane proteins comprising any one of the PFAM domains found by searching the genomic neighbourhood of GT10 and GT11 fucosyltransferase families with interpro number IPR001503 and IPR002516 as defined on InterPro 75.0 released on 4th July 2019 respectively, wherein said genomic neighbourhood window size is 14 genes before and 14 genes after the respective fucosyltransferase and wherein said membrane protein is not belonging to the SET family, or ii) selected from the group of membrane proteins comprising SEQ ID NOs 204, 206, 208, 210, 212, 214, 216, 218, or functional homolog or functional fragment of any one of the membrane proteins comprising SEQ ID NOs 204, 206, 208, 210, 212, 214, 216, 218 or a sequence having at least 80% sequence identity to any one of said membrane proteins with SEQ ID NOs 204, 206, 208, 210, 212, 214, 216, 218
   - 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 selected from the group of
   a) porters;
   b) P-P-bond-hydrolysis-driven transporters;
   c) β-Barrel Porins;
   d) Auxiliary transport proteins;
   e) Putative transport proteins; and
   f) Phosphotransfer-driven group translocators.

3.1. 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~~ 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
  - ~~a)~~ porters and wherein said membrane protein is not belonging to the SET family;
  ~~b) P-P-bond-hydrolysis-driven transporters;~~
  ~~c) β-Barrel Porins;~~
  ~~d) Auxiliary transport proteins;~~
  ~~e) Putative transport proteins; and~~
  ~~f) Phosphotransfer-driven group translocators~~
- cultivating the cell in a medium under conditions permissive for the production of the desired fucosyllactose
- preferably separating the fucosyllactose from the cultivation.

~~4. Method according to any one of claims 2 or 3, wherein said porter is selected from the group of TCDB classes 2.A.1.1, 2.A.1.12, 2.A.1.15, 2.A.1.2, 2.A.1.3, 2.A.1.36, 2.A.1.38, 2.A.1.46, 2.A.1.68, 2.A.1.7, 2.A.1.81, 2.A.123, 2.A.2, 2.A.21, 2.A.58, 2.A.6.3, 2.A.66 and 2.A.7.1, as defined by TCDB.org as released on 17th June 2019.~~

~~5. Method according to any one of claims 2 or 3, wherein said P-P-bond-hydrolysis-driven transporter is selected from the group of TCDB classes 3.A.1.1, 3.A.1.2, 3.A.1.10, 3.A.1.11 and 3.A.1.5, as defined by TCDB.org as released on 17th June 2019.~~

~~6. Method according to any one of claims 2 or 3, wherein said β-Barrel Porin is selected from TCDB classes 1.B.3.1 and 1.B.18, as defined by TCDB.org as released on 17th June 2019.~~

~~7. Method according to any one of specific claims 2 or 3, wherein said Auxiliary transport protein is selected from TCDB class 8.A.3, as defined by TCDB.org as released on 17th June 2019.~~

~~8. Method according to any one of claims 2 or 3, wherein said Putative transport protein is selected from the group of TCDB classes 9.B.14 and 9.B.158, as defined by TCDB.org as released on 17th June 2019.~~

~~9. Method according to any one of claims 2 or 3, wherein said phosphotransfer-driven group translocators is selected from the group of TCDB classes 4.A.1.1 and 4.A.4.1, as defined by TCDB.org as released on 17th June 2019.~~

2. Method according to ~~any one of~~ claim~~s 2 or 3~~ 1, wherein said membrane protein is a porter ~~is~~ selected from:

~~10.~~ 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.~~,~~

11. Method according to any one of claims 2 or 3, wherein said P-P-bond-hydrolysis-driven transporter is selected from the group of eggnog families 05BZ1, 05CJ1, 05EY8, 05HAC, 05DMK, 05DFW, 05MFV, 07FKK, 07R5U, 07V1T, 08IJ9, 08JQ7, 172T7, as defined by eggnogdb 1.0.2 as released on 3rd Nov 2017.

12. Method according to any one of claims 2 or 3, wherein said β-Barrel Porin is selected from the group of eggnog family 05DAY, 08KDD, as defined by eggnogdb 1.0.2 as released on 3rd Nov 2017.

13. Method according to any one of claims 2 or 3, wherein said Auxiliary transport protein is selected from the group of eggnog family 07SYR, as defined by eggnogdb 1.0.2 as released on 3rd Nov 2017.

14. Method according to any one of claims 2 or 3, wherein said Putative transport protein is selected from the group of eggnog families 05CRE, 05GWF, 06N3A, as defined by eggnogdb 1.0.2 as released on 3rd Nov 2017.

15. Method according to any one of claims 2 or 3, wherein said phosphotransfer-driven group translocators is selected from the group of eggnog families 05CI1 and 05VI0, as defined by eggnogdb 1.0.2 as released on 3rd Nov 2017.

16. Method according to any one of claims 2 or 3, wherein said porter is chosen from 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.

17. Method according to any one of claims 2 or 3, wherein said P-P-bond-hydrolysis-driven transporter is chosen from PFAM list PF00005, PF00532, PF00664, PF01061, PF08352, PF14524, PF13407, PF13416 and PF17912, as defined by Pfam 32.0 as released on Sept 2018.

18. Method according to any one of claims 2 or 3, wherein said β-Barrel Porin is chosen from PFAM list PF02264, PF02563, PF10531 and PF18412, as defined by Pfam 32.0 as released on Sept 2018.

19. Method according to any one of claims 2 or 3, wherein said Auxiliary transport protein is chosen from PFAM list PF13807 and PF02706, as defined by Pfam 32.0 as released on Sept 2018.

20. Method according to any one of claims 2 or 3, wherein said Putative transport protein is chosen from PFAM list PF01578, PF03932, PF05140 and PF11045, as defined by Pfam 32.0 as released on Sept 2018.

21. Method according to any one of claims 2 or 3, wherein said phosphotransfer-driven group translocators is chosen from PFAM list PF00367, PF00358, PF02378, PF03829, as defined by Pfam 32.0 as released on Sept 2018.

22. Method according to any one of claims 2 or 3, wherein said porter is chosen from 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.

~~23. Method according to any one of claims 2 or 3, wherein said P-P-bond-hydrolysis-driven transporter is chosen from interpro list IPR000412, IPR001734, IPR001761, IPR003439, IPR003593, IPR005829, IPR005978, IPR005981, IPR006059, IPR006060, IPR006061, IPR008995, IPR011527, IPR011701, IPR013456, IPR013525, IPR013563, IPR015851, IPR015855, IPR017871, IPR019554, IPR020846, IPR025997, IPR026266, IPR027417, IPR028082, IPR029439, IPR033893, IPR036259, IPR036640, IPR038377, IPR039421 and IPR040582, as defined by InterPro 75.0 as released on 4th July 2019.~~

~~24. Method according to any one of claims 2 or 3, wherein said β-Barrel Porin is chosen from interpro list IPR003192, IPR003715, IPR019554, IPR023738, IPR036998 and IPR040716, as defined by InterPro 75.0 as released on 4th July 2019.~~

~~25. Method according to any one of claims 2 or 3, wherein said Auxiliary transport protein is chosen from interpro list IPR003856, IPR020846, IPR027417, IPR032807 and IPR036259, as defined by InterPro 75.0 as released on 4th July 2019.~~

~~26. Method according to any one of claims 2 or 3, wherein said Putative transport protein is chosen from interpro list IPR002541, IPR003439, IPR003593, IPR004316, IPR005627, IPR006603, IPR007816, IPR017871, IPR020368, IPR020846, IPR023648, IPR027417, IPR036259 and IPR036822, as defined by InterPro 75.0 as released on 4th July 2019.~~

~~27. Method according to any one of claims 2 or 3, wherein said phosphotransfer-driven group translocators is chosen from interpro list IPR001127, IPR001996, IPR003352, IPR004716, IPR010974, IPR011055, IPR013013, IPR018113, IPR018454, IPR036665 and IPR036878, as defined by InterPro 75.0 as released on 4th July 2019.~~

~~28.~~3. Method according to any one of claim~~s~~ 1 or 2 ~~or 3~~, wherein said ~~porter~~ 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.

29. Method according to any one of claims 2 or 3, wherein said P-P-bond-hydrolysis driven transporter membrane protein is selected from lmrA from *Lactococcus lactis* strain SRCM103457 with SEQ ID NO 28, LpsE membrane protein from *Sporomusa sphaeroides DSM 2875* with SEQ ID NOs 70 or 74, *Flavobacterium spartansii* with SEQ ID NOs 68 or 72, TolC from *Candidatus Planktophila sulfonica* with SEQ ID NO 76, MsbA from *Pedobacter ginsengisoli* with SEQ ID NO 82 or *Verrucomicrobia bacterium CG1_02_43_26* with SEQ ID NO 84, malE from *Escherichia coli* K-12 MG1655 with SEQ ID NO 206, malK from *Escherichia coli* K-12 MG1655 with SEQ ID NO 208, araF from *Escherichia coli* K-12 MG1655 with SEQ ID NO 214, xylF from *Escherichia coli* K-12 MG1655 with SEQ ID NO 216, or ytfQ from *Escherichia coli* K-12 MG1655 with SEQ ID NO 218 or functional homolog or functional fragment of any of the above P-P-bond-hydrolysis driven transporter membrane protein or a sequence having at least 80% sequence identity to any of said lmrA, LpsE, TolC, MsbA, malE, malK, araF, xylF or ytfQ membrane protein with SEQ ID NOs 28, 70, 74, 68, 72, 76, 82, 84, 206, 208, 214, 216, or 218, respectively.
30. Method according to any one of claims 2 or 3, wherein said β-barrel porin is selected from Wza from *Escherichia coli K12 MG1655* with SEQ ID NO 34 or lamB from *Escherichia coli* K12 MG1655 with SEQ ID NO 204 or functional homolog or functional fragment thereof or a sequence having at least 80% sequence identity to said Wza or lamB membrane proteins with SEQ ID NOs 34 or 204, respectively.
31. Method according to any one of claims 2 or 3, wherein said auxiliary transport protein is selected from Wzc from *Thermotoga maritima* (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) with SEQ ID NO 88, or functional homolog or functional fragment thereof or a sequence having at least 80% sequence identity to said Wzc membrane protein with SEQ ID NO 88.
32. Method according to any one of claims 2 or 3, wherein said putative transport protein is selected from CutC from *Clostridium* sp. CAG: 1013 with SEQ ID NO 90, *Odoribacter splanchnicus* DSM 20712 with SEQ ID NO 92, *Mitsuaria* sp. PDC51 with SEQ ID NO 94 or *Prevotella intermedia* ATCC 25611 (DSM 20706) with SEQ ID NO 96, or functional homolog or functional fragment of any of said CutC membrane proteins or a sequence having at least 80% sequence identity to any of said CutC membrane protein with SEQ ID NOs 90, 92, 94 or 96, respectively.
33. Method according to any one of claims 2 or 3, wherein said phosphotransfer-driven group translocator is selected from nagE from *Escherichia coli* K12 MG1655 with SEQ ID NO 210, srlB from *Escherichia coli* K12 MG1655 with SEQ ID NO 212 or functional homolog or functional fragment of any of said nagE or srlB membrane protein or a sequence having at

~~least 80% sequence identity to any of said nagE or srlB membrane protein with SEQ ID NOs 210 or 212, respectively.~~

~~34.~~4. Method according to any one of claim~~s~~ 1 or 2 ~~or 3~~, wherein said ~~porter~~ 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~~s~~ 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.

~~35. Method according to any one of claims 2 or 3, wherein said P-P-bond-hydrolysis-driven transporter is selected from LmrA from *Lactococcus lactis* strain SRCM103457 with SEQ ID NO 28, OppF from *Escherichia coli* strain K12 MG1655 with SEQ ID NO 30, Wzk from *Helicobacter pylori* (strain ATCC 700392 / 26695) with SEQ ID NO 36, Blon_2475 from *Bifidobacterium longum* subsp. Infantis (strain ATCC 15697) with SEQ ID NO 44, LpsE from *Flavobacterium spartansii* with SEQ ID NOs 68 or 72, LpsE from *Sporomusa sphaeroides* DSM 2875 with SEQ ID NOs 70 or 74, TolC from *Candidatus Planktophila sulfonica* with SEQ ID NO 76, TolC from *Butyrivibrio hungatei* XBD2006 with SEQ ID NO 78, MsbA from~~

~~*Roseburia intestinalis* CAG:13 with SEQ ID NO 80, MsbA from *Pedobacter ginsengisoli* with SEQ ID NO 82, MsbA from *Verrucomicrobia bacterium* CG1_02_43_26 with SEQ ID NO 84, Wzm from *Rhizobium* sp. Root149 with SEQ ID NO 174, Wzm from *Azospirillum brasiliense* LMG 04375 with SEQ ID NO 176, Wzm from *Escherichia coli* 113303 with SEQ ID NO 196, Wzt from *Rhizobium* sp. Root149 with SEQ ID NO 178, Wzt from *Azospirillum brasiliense* LMG 04375 with SEQ ID NO 180, Wzt from *Escherichia coli* 113303 with SEQ ID NO 194, Nodj from *Bradyrhizobium japonicum* USDA 110 with SEQ ID NOs 188 or 190, malE from *Escherichia coli* K-12 MG1655 with SEQ ID NO 206, malK from *Escherichia coli* K-12 MG1655 with SEQ ID NO 208, araF from *Escherichia coli* K-12 MG1655 with SEQ ID NO 214, xylF from *Escherichia coli* K-12 MG1655 with SEQ ID NO 216, or ytfQ from *Escherichia coli* K-12 MG1655 with SEQ ID NO 218 or functional homolog or functional fragment of any one of the above P-P-bond-hydrolysis-driven transporter membrane protein or a protein having an amino acid sequence having at least 80% sequence identity to any of said LmrA, OppF, Wzk, Blon_2475, LpsE, TolC, MsbA, Wzm, Wzt, Nodj, malE, malK, araF, xylF or ytfQ membrane proteins with SEQ ID NOs 28, 30, 36, 44, 68, 72, 70, 74, 76, 78, 80, 82, 84, 174, 176, 196, 178, 180, 194, 188, 190, 206, 208, 214, 216 or 218, respectively.~~

~~36. Method according to any one of claims 2 or 3, wherein said putative transport protein is selected from Cytochrome C biogenesis protein from *Helicobacter pylori* with SEQ ID NO 56, CutC from *Clostridium* sp. CAG: 1013 with SEQ ID NO 90, CutC from *Odoribacter splanchnicus* DSM 20712 with SEQ ID NO 92, CutC from *Mitsuaria* sp. PDC51 with SEQ ID NO 94, CutC from *Prevotella intermedia* ATCC 25611 (DSM 20706) with SEQ ID NO 96, ybjM from *Escherichia coli K12 MG1655* with SEQ ID NO 190, ybjM from *Enterobacteriaceae bacterium* ENNIH1 with SEQ ID NO 192 or functional homolog or functional fragment of any one of the above putative transport protein or protein having an amino acid sequence having at least 80% sequence identity to any one of said CytC, CutC or ybjM membrane protein with SEQ ID NOs 56, 90, 92, 94, 96, 190 or 192, respectively.~~

~~37.~~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~~s~~ 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.; and the P-P-bond-hydrolysis-driven transporters LmrA from *Lactococcus lactis* strain SRCM103457 with SEQ ID NO 28, OppF from *Escherichia coli* strain K12 MG1655 with SEQ ID NO 30, Wzk from *Helicobacter pylori* (strain ATCC 700392 / 26695) with SEQ ID NO 36, Blon_2475 from *Bifidobacterium longum* subsp. Infantis (strain ATCC 15697) with SEQ ID NO 44, LpsE from *Flavobacterium spartansii* with SEQ ID NOs 68 or 72, LpsE from *Sporomusa sphaeroides* DSM 2875 with SEQ ID NOs 70 or 74, TolC from *Candidatus Planktophila sulfonica* with SEQ ID NO 76, TolC from *Butyrivibrio hungatei* XBD2006 with SEQ ID NO 78, MsbA from *Roseburia intestinalis* CAG:13 with SEQ ID NO 80, MsbA from *Pedobacter ginsengisoli* with SEQ ID NO 82, MsbA from *Verrucomicrobia bacterium* CG1_02_43_26 with SEQ ID NO 84, Wzm from *Rhizobium* sp. Root149 with SEQ ID NO 174, Wzm from

Azospirillum brasiliense LMG 04375 with SEQ ID NO 176, Wzm from *Escherichia coli* 113303 with SEQ ID NO 196, Wzt from *Rhizobium* sp. Root149 with SEQ ID NO 178, Wzt from *Azospirillum brasiliense* LMG 04375 with SEQ ID NO 180, Wzt from *Escherichia coli* 113303 with SEQ ID NO 194, Nodj from *Bradyrhizobium japonicum* USDA 110 with SEQ ID NOs 188 or 190, malE from *Escherichia coli* K-12 MG1655 with SEQ ID NO 206, malK from *Escherichia coli* K-12 MG1655 with SEQ ID NO 208, araF from *Escherichia coli* K-12 MG1655 with SEQ ID NO 214, xylF from *Escherichia coli* K-12 MG1655 with SEQ ID NO 216, or ytfQ from *Escherichia coli* K-12 MG1655 with SEQ ID NO 218 or functional homolog or functional fragment of any one of the above P-P-bond-hydrolysis-driven transporter membrane protein or a protein having an amino acid sequence having at least 80% sequence identity to any of said LmrA, OppF, Wzk, Blon_2475, LpsE, TolC, MsbA, Wzm, Wzt, Nodj, malE, malK, araF, xylF or ytfQ membrane proteins with SEQ ID NOs 28, 30, 36, 44, 68, 72, 70, 74, 76, 78, 80, 82, 84, 174, 176, 196, 178, 180, 194, 188, 190, 206, 208, 214, 216, or 218, respectively.; and a β-barrel porin membrane protein Wza from *Escherichia coli K12 MG1655* with SEQ ID NO 34 or lamB from *Escherichia coli* K12 MG1655 with SEQ ID NO 204 or functional homolog or functional fragment of any one of said Wza or lamB protein or a sequence having at least 80% sequence identity to any one of said Wza or lamB membrane protein with SEQ ID NO 34 or 204, respectively; and auxiliary transport protein Wzc from *Thermotoga maritima* (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) with SEQ ID NO 88, or functional homolog or functional fragment thereof or a sequence having at least 80% sequence identity to said Wzc membrane protein with SEQ ID NO 88; putative transport proteins Cytochrome C biogenesis protein from *Helicobacter pylori* with SEQ ID NO 56, CutC from *Clostridium* sp. CAG: 1013 with SEQ ID NO 90, CutC from *Odoribacter splanchnicus* DSM 20712 with SEQ ID NO 92, CutC from *Mitsuaria* sp. PDC51 with SEQ ID NO 94, CutC from *Prevotella intermedia* ATCC 25611 (DSM 20706) with SEQ ID NO 96, ybjM from *Escherichia coli K12 MG1655* with SEQ ID NO 190, ybjM from *Enterobacteriaceae bacterium* ENNIH1 with SEQ ID NO 192 or functional homolog or functional fragment of any one of the above putative transport protein or protein having an amino acid sequence having at least 80% sequence identity to any one of said CytC, CutC or ybjM membrane protein with SEQ ID NOs 56, 90, 92, 94, 96, 190 or 192, respectively; and phosphotransfer-driven group translocators nagE from *Escherichia coli* K12 MG1655 with SEQ ID NO 210, srlB from *Escherichia coli* K12 MG1655 with SEQ ID NO 212 or functional homolog or functional fragment of any of said nagE or srlB membrane protein or a sequence having at least 80% sequence identity to any one of said nagE or srlB membrane protein with SEQ ID NOs 210 or 212, respectively.

~~38.~~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.

~~39.~~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.

~~40.~~8. The method of claim 7~~39~~, 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.

~~41. The method of any one of the claims 39 or 40, wherein said lactose feed is accomplished by adding lactose to the cultivation medium in a concentration, such, that throughout the production phase of the cultivation a lactose concentration of at least 5 mM, preferably 10 mM or 30 mM is obtained.~~

~~42. The method of any of the claims 39, 40 or 41, wherein the host cells are cultivated for at least about 60, 80, 100, or about 120 hours or in a continuous manner.~~

~~43. The method of any one of claims 39 to 42, wherein a carbon and energy source, preferably sucrose, glucose, fructose, glycerol, maltose, maltodextrines, trehalose, polyols, starch, succinate, malate, pyruvate, lactate, ethanol, citrate, lactose, is also added, preferably continuously to the culture medium, preferably with the lactose.~~

~~44.~~9. The method of any one of claim~~s~~ 7 or 8~~39 to 43~~, 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.

~~45.~~10. Method according to any one of the claims 1 to 9~~44~~, wherein the method is producing a mixture of fucosyllactoses.

~~46.~~11. Method according to any one of claims 1 to 10~~45~~, wherein said fucosyllactose is 2'-fucosyllactose, 3-fucosyllactose and/or difucosyllactose.

~~47.~~12. Method according to any one of claims 1 to 11~~46~~, 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.

~~48. Method according to claim 47, wherein the cell is an *Escherichia coli* cell.~~

~~49. 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 is i) selected from the group of membrane proteins comprising any one of the PFAM domains found by searching the genomic neighbourhood of GT10 and GT11 fucosyltransferase families with interpro number IPR001503 and IPR002516 as defined on InterPro 75.0 released on 4th July 2019 respectively, wherein said genomic neighbourhood window size is 14 genes before and 14 genes after the respective fucosyltransferase and wherein said membrane protein is not belonging to the SET family, or ii) selected from the group of membrane proteins comprising SEQ ID NOs 204, 206, 208, 210, 212, 214, 216, 218, or functional homolog or functional fragment of any one of the membrane proteins comprising SEQ ID NOs 204, 206, 208, 210, 212, 214, 216, 218 or a sequence having at least 80% sequence identity to any one of said membrane proteins with SEQ ID NOs 204, 206, 208, 210, 212, 214, 216, 218.~~

~~50. Host cell according to claim 49, wherein said membrane protein is selected from the group of a) porters;~~

b) P-P-bond-hydrolysis-driven transporters;

c) β-Barrel Porins;

d) Auxiliary transport proteins;

e) Putative transport proteins; and

f) Phosphotransfer-driven group translocators.

51. 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

a) porters and wherein said membrane protein is not belonging to the SET family;

b) P-P-bond-hydrolysis-driven transporters;

c) β-Barrel Porins;

d) Auxiliary transport proteins;

e) Putative transport proteins; and

13. f) Phosphotransfer-driven group translocators.

52. 14. Host cell according to any one of the claims 50 or 51 13, wherein said membrane protein is chosen from the group of membrane proteins as defined in any one of the claims 2 to 64 to 38.

53. 15. Host cell genetically modified for the production of a fucosyllactose according to any one of the claim 13s 50 or 51, wherein said membrane protein is a porter membrane protein is 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 NOs 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.

54. Host cell according to any one of the claims 50 or 51, wherein said P-P-bond-hydrolysis-driven transporter is selected from LmrA from *Lactococcus lactis* strain SRCM103457 with SEQ ID NO 28, OppF from *Escherichia coli* strain K12 MG1655 with SEQ ID NO 30, Wzk from *Helicobacter pylori* (strain ATCC 700392 / 26695) with SEQ ID NO 36, Blon_2475 from *Bifidobacterium longum* subsp. Infantis (strain ATCC 15697) with SEQ ID NO 44, LpsE from *Flavobacterium spartansii* with SEQ ID NOs 68 or 72, LpsE from *Sporomusa sphaeroides* DSM 2875 with SEQ ID NOs 70 or 74, TolC from *Candidatus Planktophila sulfonica* with SEQ ID NO 76, TolC from *Butyrivibrio hungatei* XBD2006 with SEQ ID NO 78, MsbA from *Roseburia intestinalis* CAG:13 with SEQ ID NO 80, MsbA from *Pedobacter ginsengisoli* with SEQ ID NO 82, MsbA from *Verrucomicrobia bacterium* CG1_02_43_26 with SEQ ID NO 84, Wzm from *Rhizobium* sp. Root149 with SEQ ID NO 174, Wzm from *Azospirillum brasiliense* LMG 04375 with SEQ ID NO 176, Wzm from *Escherichia coli* 113303 with SEQ ID NO 196, Wzt from *Rhizobium* sp. Root149 with SEQ ID NO 178, Wzt from *Azospirillum brasiliense* LMG 04375 with SEQ ID NO 180, Wzt from *Escherichia coli* 113303 with SEQ ID NO 194, Nodj from *Bradyrhizobium japonicum* USDA 110 with SEQ ID NOs 188 or 190, malE from *Escherichia coli* K-12 MG1655 with SEQ ID NO 206, malK from *Escherichia coli* K-12 MG1655 with SEQ ID NO 208, araF from *Escherichia coli* K-12 MG1655 with SEQ ID NO 214, xylF from *Escherichia coli* K-12 MG1655 with SEQ ID NO 216, or ytfQ from *Escherichia coli* K-12 MG1655 with SEQ ID NO 218 or functional homolog or functional fragment of any one of the above P-P-bond-hydrolysis-driven transporter membrane protein or a protein having an amino acid sequence having at least 80% sequence identity to any of said LmrA, OppF, Wzk, Blon_2475, LpsE, TolC, MsbA, Wzm, Wzt, Nodj, malE, malK, araF, xylF or ytfQ membrane proteins with SEQ ID NOs 28, 30, 36, 44, 68, 72, 70, 74, 76, 78, 80, 82, 84, 174, 176, 196, 178, 180, 194, 188, 190, 206, 208, 214, 216, or 218 respectively.

55. Host cell according to any one of the claims 50 or 51, wherein said putative transport protein is selected from Cytochrome C biogenesis protein from *Helicobacter pylori* with SEQ ID NO 56, CutC from *Clostridium* sp. CAG: 1013 with SEQ ID NO 90, CutC from *Odoribacter splanchnicus* DSM 20712 with SEQ ID NO 92, CutC from *Mitsuaria* sp. PDC51 with SEQ ID NO 94, CutC from *Prevotella intermedia* ATCC 25611 (DSM 20706) with SEQ ID NO 96, ybjM from *Escherichia coli K12 MG1655* with SEQ ID NO 190, ybjM from *Enterobacteriaceae bacterium* ENNIH1 with SEQ ID NO 192 or functional homolog or functional fragment of any one of the above putative transport protein or protein having an amino acid sequence having at least 80% sequence identity to any one of said CytC, CutC or ybjM membrane protein with SEQ ID NOs 56, 90, 92, 94, 96, 190 or 192, respectively.

56. Host cell according to any one of the claims 50 or 51, wherein said β-barrel porin is selected from Wza from *Escherichia coli K12 MG1655* with SEQ ID NO 34 or lamB from *Escherichia coli* K12 MG1655 with SEQ ID NO 204 or functional homolog or functional fragment to any one of said Wza or lamB protein or a sequence having at least 80% sequence identity to any one of said Wza or lamB membrane protein with SEQ ID NO 34 or 204, respectively.

57. Host cell according to any one of the claims 50 or 51, wherein said auxiliary transport protein is selected from Wzc from *Thermotoga maritima* (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) with SEQ ID NO 88, or functional homolog or functional fragment thereof or a sequence having at least 80% sequence identity to said Wzc membrane protein with SEQ ID NO 88.

58. Host cell according to any one of the claims 50 or 51, wherein said phosphotransfer-driven group translocators is selected from nagE from *Escherichia coli* K12 MG1655 with SEQ ID NO 210 or srlB from *Escherichia coli* K12 MG1655 with SEQ ID NO 212 or functional homolog or functional fragment of any of said nagE or srlB membrane protein or a sequence having at least 80% sequence identity to any one of said nagE or srlB membrane protein with SEQ ID NOs 210 or 212, respectively.

59.16. Host cCell according to any one of the previous claims 13 to 1549 to 58, wherein said membrane protein is a transporter protein involved in transport of compounds across the outer membrane of the cell wall.

60. Cell according to any one of the claims 49 to 59, wherein the cell is stably cultured in a medium.

61.17. Host cCell according to any one of the claims 13 to 1649 to 60, 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.

~~62. Host cell according to claim 61, wherein the cell is an Escherichia coli cell.~~

~~63.~~18. Host c~~C~~ell according to any one of the claims ~~49 to 62~~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.

~~64.~~19. Host c~~C~~ell according to any one of the claims ~~49 to 63~~13 to 18, wherein said fucosyllactose is 2'-fucosyllactose, 3-fucosyllactose or difucosyllactose.

~~65. Method for the production of fucosyllactose, comprising the steps of:~~

~~a) providing a cell according to any one of the claims 49 to 64,~~

~~b) culturing the cell in a medium under conditions permissive for the production of said fucosyllactose,~~

~~c) separating said fucosyllactose from the cultivation.~~

~~66. Use of a membrane protein selected from the group of membrane proteins as defined in any one of the claims 1 to 38, for fucosyllactose transport, in the fermentative production of fucosyllactose.~~

~~67~~20. Use of a host cell according to any one of the claims ~~49 to 64~~13 to 19, for the production of fucosyllactose, preferably ~~.~~

~~68. Use of a cell according to claim 67 wherein~~ said fucosyllactose is 2'-fucosyllactose, 3-fucosyllactose or difucosyllactose.