What is claimed is:

1. A method for producing a fucosylated oligosaccharide in a bacterium comprising providing bacterium comprising an exogenous lactose-utilizing α(1,2) fucosyltransferase enzyme, wherein the amino acid sequence of said enzyme comprises
    (i) the amino acid sequence of SEQ ID NO: 11;
    (ii) the amino acid sequence of SEQ ID NO: 12;
    (iii) the amino acid sequence of SEQ ID NO: 13;
    (iv) the amino acid sequence of SEQ ID NO: 14;
    (v) the amino acid sequence of SEQ ID NO: 17; or
    (vi) the amino acid sequence of SEQ ID NO: 19.

2. The method of claim 1, further comprising retrieving the fucosylated oligosaccharide from said bacterium or from a culture supernatant of said bacterium.

3. The method of claim 1 or 2, wherein said fucosylated oligosaccharide comprises 2'-fucosyllactose (2'-FL), lactodifucotetraose (LDFT), Lacto-N-fucopentaose I (LNF I), or lacto-N-difucohexaose I (LDFH I).

4. The method of any one of the preceding claims, wherein the bacterium further comprises an exogenous lactose-utilizing α(1,3) fucosyltransferase enzyme and/or an exogenous lactose-utilizing α(1,4) fucosyltransferase enzyme.

5. The method of claim 4, wherein the exogenous lactose-utilizing α(1,3) fucosyltransferase enzyme comprises (i) a *Helicobacter pylori* 26695 *futA* gene; or (ii) a Helicobacter pylori UA948 FucTa gene or a Helicobacter pylori strain DMS6709 FucT III gene.

6. The method of claim 5, wherein
    (i) said method further comprises culturing said bacterium in the presence of tryptophan and in the absence of thymidine;

(ii) said bacterium comprises a deleted or inactivated endogenous lacZ gene and/or a deleted or inactivated endogenous lacI gene of said bacterium;

(iii) said bacterium comprises a deleted or inactivated endogenous lacZ gene and/or a deleted or inactivated endogenous lacI gene of said bacterium, wherein said bacterium further comprises an exogenous lacZ gene or variant thereof, wherein said exogenous lacZ gene or variant thereof comprises an β-galactosidase activity level less than wild-type bacterium;

(iv) said bacterium comprises less than 6,000 units of β-galactosidase activity;

(v) said bacterium comprises less than 1,000 units of β-galactosidase activity;

(vi) said bacterium comprises a lacIq gene promoter immediately upstream of a lacY gene;

(vii) said bacterium comprises an inactivation of the wcaJ gene;

(viii) said bacterium comprises a null mutation, inactivating mutation, or deletion of an endogenous lon gene;

(ix) said bacterium comprises an inactivating mutation of an endogenous lon gene, wherein said inactivating mutation of an endogenous lon gene comprises the insertion of a functional E. coli $lacZ^+$ gene;

(x) said bacterium further comprises a functional lactose permease gene;

(xi) said bacterium further comprises a functional lactose permease gene, wherein said bacterium comprises E. coli lacY;

(xii) said bacterium further comprises an exogenous E. coli rcsA or E. coli rcsB gene;

(xiii) said bacterium further comprises a mutation in the thyA gene;

(xiv) said bacterium accumulates intracellular lactose in the presence of exogenous lactose;

(xv) said bacterium accumulates intracellular GDP-fucose; or

(xvi) said bacterium comprises the genotype ΔampC::$P_{trp}{}^{B}$cI, Δ(lacI-lacZ)::FRT,P_{lacIq}lacY$^+$, ΔwcaJ::FRT, thyA::Tn10, Δlon:(npt3, lacZ$^{+)}$.

7. The method of any one of the preceding claims, wherein said bacterium is a member of the *Bacillus, Pantoea, Lactobacillus, Lactococcus, Streptococcus, Proprionibacterium, Enterococcus, Bifidobacterium, Sporolactobacillus, Micromomospora, Micrococcus, Rhodococcus,* or *Pseudomonas* genus, preferably wherein said production strain is selected from the group consisting of *Bacillus*

licheniformis, Bacillus subtilis, Bacillus coagulans, Bacillus thermophilus, Bacillus laterosporus, Bacillus megaterium, Bacillus mycoides, Bacillus pumilus, Bacillus lentus, Bacillus cereus, and Bacillus circulans, Erwinia herbicola (*Pantoea agglomerans*), *Citrobacter freundii, Pantoea citrea, Pectobacterium carotovorum, Xanthomonas campestris Lactobacillus acidophilus, Lactobacillus salivarius, Lactobacillus plantarum, Lactobacillus helveticus, Lactobacillus delbrueckii, Lactobacillus rhamnosus, Lactobacillus bulgaricus, Lactobacillus crispatus, Lactobacillus gasseri, Lactobacillus casei, Lactobacillus reuteri, Lactobacillus jensenii, Lactococcus lactis, Streptococcus thermophiles, Proprionibacterium freudenreichii, Enterococcus faecium, Enterococcus thermophiles*), *Bifidobacterium longum, Bifidobacterium infantis, Bifidobacterium bifidum, Pseudomonas fluorescens* and *Pseudomonas aeruginosa*.

8. The method of any of the preceding claims, wherein said bacterium comprises a nucleic acid construct comprising an isolated nucleic acid encoding said α(1,2) fucosyltransferase enzyme.

9. An isolated bacterium comprising an isolated nucleic acid encoding a lactose-accepting α (1,2) fucosyltransferase enzyme, wherein the amino acid sequence of said enzyme encoded by said nucleic acid comprises
   (i) the amino acid sequence of SEQ ID NO: 11;
   (ii) the amino acid sequence of SEQ ID NO: 12;
   (iii) the amino acid sequence of SEQ ID NO: 13;
   (iv) the amino acid sequence of SEQ ID NO: 14;
   (v) the amino acid sequence of SEQ ID NO: 17; or
   (vi) the amino acid sequence of SEQ ID NO: 19; and
   wherein the isolated bacterium further comprising a α(1,3) fucosyltransferase enzyme and/or a α(1,4) fucosyltransferase enzyme.

10. The method of any one of claims 1 to 8, or the isolated bacterium of claim 9, wherein said bacterium is *Escherichia coli*.

11. The method of any one of claims 1 to 8 or 10, or the isolated bacterium of any one of claims 9 to 10, wherein said bacterium further comprises reduced level of

β-galactosidase activity, a defective colanic acid synthesis pathway, an inactivated adenosine-5'-triphosphate (ATP)-dependent intracellular protease, an inactivated endogenous *lacA* gene, or any combination thereof.

12. The method of any one of claims 1 to 8 or 10 to 11, or the isolated bacterium of any one of claims 9 to 11, wherein the enzyme comprises the amino acid sequence of SEQ ID NO: 13.