7. A method according to claim 6, wherein PrfA-dependent promoter is selected from the group consisting of the *inlA* promoter, the *inlB* promoter, the *inlC* promoter, the *hpt* promoter, the *hly* promoter, the *plcA* promoter, the *mpl* promoter, and the *actA* promoter.

8. A method according to claim 6, wherein the PrfA-dependent promoter is an *actA* promoter.

9. A method according to claim 1, wherein the recombinase is selected from the group consisting of ϕC31 integrase, R4 integrase, TP901 integrase, ϕBT1 integrase, BxB1 integrase, PSA integrase, Cre recombinase, Flp recombinase, XerC recombinase, λ integrase, HK022 integrase, P22 integrase, HP1 integrase, L5 integrase, γδ recombinase, Tn3 recombinase, gin recombinase, RV integrase, SPBc integrase, TG1 integrase, ϕC1 integrase, MR11 integrase, ϕ370 integrase, ϕK38 integrase, Wβ integrase, and BL3 integrase.

10. A method according to claim 1, wherein the first attachment site is an *attB* site and the second attachment site is an *attP* site.

11. A method according to claim 1, wherein the one or more genes essential for multiplication of the bacterium comprise at least one gene involved in DNA replication.

12. A method according to claim 11, wherein the at least one gene involved in DNA replication is selected from the group consisting of *ori, dnaA, dnaN, gyrA, gyrB, polC, dnaE, ftsK, ftsZ, ligA, dnaG, parC, parE, holB, dnaX, SMC,* and *ftsY.*

13. A method according to claim 1, wherein the one or more genes essential for multiplication of the bacterium are part of an operon, and the first attachment site is upstream of all or a portion of the operon, and the second attachment site is downstream of all or a portion of the operon.

14. A method according to claim 13, wherein the first attachment site is upstream of the operon, and the second attachment site is downstream of the operon.

15. A method according to claim 1, wherein the recombinase is a Cre recombinase, the regulatory sequences comprise an *actA* promoter, the first and second attachment sites comprise loxP sites, and the gene(s) essential for multiplication of the bacterium flanked by the first and second attachment sites are involved in DNA replication.

30. A bacterium according to claim 22, wherein the recombinase is selected from the group consisting of ϕC31 integrase, R4 integrase, TP901 integrase, ϕBT1 integrase, BxB1 integrase, PSA integrase, Cre recombinase, Flp recombinase, XerC recombinase, λ integrase, HK022 integrase, P22 integrase, HP1 integrase, L5 integrase, γδ recombinase, Tn3 recombinase, gin recombinase, RV integrase, SPBc integrase, TG1 integrase, ϕC1 integrase, MR11 integrase, ϕ370 integrase, ϕK38 integrase, Wβ integrase, and BL3 integrase.

31. A bacterium according to claim 22, wherein the first attachment site is an *attB* site and the second attachment site is an *attP* site.

32. A bacterium according to claim 22, wherein the one or more genes essential for multiplication of the bacterium comprise at least one gene involved in DNA replication.

33. A bacterium according to claim 30, wherein the at least one gene involved in DNA replication is selected from the group consisting of *ori, dnaA, dnaN, gyrA, gyrB, polC, dnaE, ftsK, ftsZ, ligA, dnaG, parC, parE, holB, dnaX, SMC,* and *ftsY.*

34. A bacterium according to claim 22, wherein the one or more genes essential for multiplication of the bacterium are part of an operon, and the first attachment site is upstream of all or a portion of the operon, and the second attachment site is downstream of all or a portion of the operon.

35. A bacterium according to claim 34, wherein the first attachment site is upstream of the operon, and the second attachment site is downstream of the operon.

36. A bacterium according to claim 22, wherein the recombinase is a Cre recombinase, the regulatory sequences comprise an *actA* promoter, the first and second attachment sites comprise loxP sites, and the gene(s) essential for multiplication of the bacterium flanked by the first and second attachment sites are involved in DNA replication.

37. A bacterium according to claim 22, wherein the first and second attachment sites flank a nucleic acid sequence about 20kb in length or less.

38. A bacterium according to claim 37, wherein the nucleic acid sequence is 10kb in length or less.

39. A bacterium according to claim 38, wherein the nucleic acid sequence is about 6kb in length.