We claim:

1. A method for configuring a bacterium to delete one or more genes in the bacterial genome which are essential for multiplication of the bacterium, the deletion occurring preferentially when the bacterium is introduced into a mammalian host, comprising:

(i) introducing into the bacterium a nucleic acid encoding a recombinase heterologous to the bacterium operably connected to regulatory sequences which preferentially induce expression of the recombinase in the mammalian host, and

(ii) introducing in the bacterial genome a first attachment site for the recombinase upstream from the gene(s) essential for multiplication of the bacterium, and a second attachment site for the recombinase downstream from the gene(s) essential for multiplication of the bacterium, such that the recombinase, when expressed in the mammalian host, catalyzes a site specific recombination event which deletes the gene(s) essential for multiplication of the bacterium flanked by the first and second attachment sites, wherein the bacterium is deficient for multiplication following the site specific recombination event.

2. A method according to claim 1, wherein the bacterium is an intracellular pathogen, and the regulatory sequences preferentially induce expression of the recombinase when the bacterium is in a mammalian host cell~~, and is most preferably a facultative intracellular bacterium~~.

3. A method according to claim 1, wherein the bacterium is of a genus selected from the group consisting of *Listeria, Neisseria, Mycobacterium, Francisella, Bacillus, Salmonella, Shigella, Yersinia, Brucella, Legionella, Rickettsia,* and *Chlamydia.*

4. A method according to claim 1, wherein the bacterium is *Listeria monocytogenes.*

5. A method according to claim 4, wherein the bacterium is *Listeria monocytogenes.*, wherein the Listeria monocytogenes is Δ*ActA*/Δ*InlB.*

6. A method according to claim 4, wherein the regulatory sequences comprise a *Listeria monocytogenes* promoter which is PrfA-dependent.

22. A bacterium comprising:

(i) a nucleic acid encoding a recombinase heterologous to the bacterium operably connected to regulatory sequences which preferentially induce expression of the recombinase in a mammalian host, and

(ii) a first attachment site for the recombinase upstream from one or more genes in the bacterial genome which are essential for multiplication of the bacterium, and a second attachment site for the recombinase downstream from the gene(s) genes in the bacterial genome which are essential for multiplication of the bacterium.

23. A bacterium according to claim 22, wherein the bacterium is an intracellular pathogen, ~~and is most preferably a facultative intracellular bacterium,~~ and the regulatory sequences preferentially induce expression of the recombinase when the bacterium is in a mammalian host cell.

24. A bacterium according to claim 22, wherein the bacterium is of a genus selected from the group consisting of *Listeria, Neisseria, Mycobacterium, Francisella, Bacillus, Salmonella, Shigella, Yersinia, Brucella, Legionella, Rickettsia,* and *Chlamydia*.

25. A bacterium according to claim 22, wherein the bacterium is *Listeria monocytogenes*.

26. A method according to claim 25, wherein the bacterium is *Listeria monocytogenes*., wherein the Listeria monocytogenes is Δ*ActA*/Δ*InlB*.

27. A bacterium according to claim 22, wherein the regulatory sequences comprise a *Listeria monocytogenes* promoter which is PrfA-dependent.

28. A bacterium according to claim 27, 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.

29. A bacterium according to claim 27, wherein the PrfA-dependent promoter is an *actA* promoter.

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 virulence 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.

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

~~39~~40. A bacterium according to claim 22, wherein the bacterium comprises within the bacterial genome an exogenous nucleic acid sequence encoding a heterologous polypeptide, wherein the exogenous nucleic acid sequence is operably connected to regulatory sequences which preferentially induce expression of the heterologous polypeptide when the bacterium is in a mammalian host.

41. A method according to claim 1, wherein the bacterium is a facultative intracellular bacterium.

42. A bacterium according to claim 22, wherein the bacterium is a facultative intracellular bacterium.