What is claimed is

1. A genetically modified microorganism capable of converting a C1 carbon to 2,3-BDO, wherein the microorganism is from the species *Methylococcus capsulatus* and comprises ~~at least one~~ heterologous genes ~~gene~~ encoding: ~~i) an acetoin reductase; ii) an alpha-acetolactate decarboxylase; and/or iii) an acetolactate synthase~~

(a) an acetolactate synthase comprising an amino acid sequence at least 95% identical to any one of SEQ ID NO: 1, 3, or 19;

(b) an alpha-acetolactate decarboxylase comprising an amino acid sequence at least 95% identical to SEQ ID NO: 5 or 7; and

(c) an acetoin reductase comprising an amino acid sequence at least 95% identical to any one of SEQ ID NO: 9, 11, or 13;

wherein:

the heterologous acetolactate synthase is non-constitutively expressed; and

when the acetolactate synthase comprises an amino acid sequence at least 95% identical to SEQ ID NO: 3, the acetoin reductase comprises an amino acid sequence at least 95% identical to SEQ ID NO: 9 or 11.

2. The microorganism of claim 1, wherein the heterologous genes are ~~gene(s) is/are~~ integrated by an integration vector into the genome of said microorganism.

3. The microorganism of claim 1, wherein the heterologous genes are ~~gene(s) is/are~~ expressed on an episomal vector.

4. The microorganism of claim 1, wherein: ~~comprising:~~

(a) the ~~a~~ heterologous gene encoding acetolactate synthase ~~that~~ is 5' in relation to any other heterologous gene;

(b) the ~~a~~ heterologous gene encoding acetoin reductase ~~that~~ is 3' in relation to any other heterologous gene; and ~~and/or~~

(c) the ~~a~~ heterologous gene encoding alpha-acetolactate decarboxylase ~~that~~ is neither 5' or 3' in relation to any other heterologous gene.

5. The microorganism of claim 1, wherein the heterologous genes are ~~gene(s) is/are~~ under the control of a switch.

6. The microorganism of claim 1, wherein: (a) ~~(i)~~ the acetolactate synthase comprises the ~~an~~ amino acid sequence of ~~at least 90% identical to~~ any one of SEQ ID NOs: 1, 3, or 19, or differs therefrom by conservative substitutions; (b) ~~(ii)~~ the alpha-acetolactate decarboxylase comprises the ~~an~~ amino acid sequence of ~~at least 90% identical to~~ SEQ ID NO: 5 or 7, or differs therefrom by conservative substitutions; and (c) ~~and/or (iii)~~ the acetoin reductase comprises the ~~an~~ amino acid sequence of ~~at least 90% identical to~~ any one of SEQ ID NO: 9, 11, or 13, or differs therefrom by conservative substitutions.

7. The microorganism of claim 1, wherein: (a) the acetolactate synthase comprises the amino acid sequence of any one of SEQ ID NOs: 1, 3, or 19; (b) the alpha-acetolactate decarboxylase comprises the amino acid sequence of SEQ ID NO: 5 or 7; and (c) the acetoin reductase comprises the amino acid sequence of any one of SEQ ID NO: 9, 11, or 13. ~~comprising: (i) a heterologous acetoin reductase; (ii) a heterologous alpha-acetolactate decarboxylase; and/or (iii) a heterologous acetolactate synthase.~~

8. The microorganism of claim 1, ~~7,~~ wherein the heterologous gene encoding acetolactate synthase is under the control of a pBAD promoter or a pMxaF promoter. ~~non-constitutively expressed.~~

9. The microorganism of claim 1, ~~7,~~ wherein: (a) ~~(i)~~ the acetolactate synthase comprises an amino acid sequence that is at least 95% ~~90%~~ identical to SEQ ID NO: 1 or 19; (b) ~~(ii)~~ the alpha-acetolactate decarboxylase comprises an amino acid sequence that is at least 95% ~~90%~~ identical to SEQ ID NO: 7; and (c) ~~and/or (iii)~~ the acetoin reductase comprises an amino acid sequence that is at least 95% ~~90%~~ identical to SEQ ID NO: 9.

10. The microorganism of claim 7, wherein the acetoin reductase is NADPH-dependent.

11. A method of making the microorganism of claim 1, the method comprising transforming the microorganism with a heterologous genes ~~nucleic acid comprising a gene~~ encoding an acetoin reductase, an alpha-acetolactate decarboxylase, and ~~and/or~~ an acetolactate synthase.

12. A method of making 2,3-BDO, the method comprising:

(a) ~~a)~~ contacting the microorganism of claim 1 with a C1 carbon; and

(b) ~~b)~~ growing the microorganism to produce 2,3-BDO.

13. The method of claim 12, wherein the C1 carbon is methane.

14. The method of claim 12, wherein the microorganism is grown at a temperature between 32 °C and 49 °C.

15. The method of claim 12, further comprising contacting the microorganism with media containing at least 1 μM lanthanum before growing the microorganism to produce 2,3-BDO.

16. The method of claim 15, further comprising diluting the lanthanum in media before growing the microorganism to produce 2,3-BDO.

17. The method of claim 12, wherein the microorganism ~~comprises a heterologous gene encoding alpha-acetolactate decarboxylase and~~ is grown to produce acetoin.

18. The method of claim 12, further comprising contacting the 2,3-BDO with a catalyst to produce butadiene or methyl ethyl ketone.