WHAT IS CLAIMED IS:

1. A recombinant *Thraustochytrium* microorganism comprising: (i) two or more copies of a nucleic acid sequence encoding xylose isomerase, wherein the nucleic acid encoding xylose isomerase is an exogenous nucleic acid; (ii) at least one nucleic acid sequence encoding a xylulose kinase; and (iii) at least one nucleic acid sequence encoding a xylose transporter,

wherein the isomerase, kinase and transporter are integrated into the genome of the *Thraustochytrium* microorganism.

2. The recombinant *Thraustochytrium* microorganism of claim 1, wherein the nucleic acid sequence encoding the xylulose kinase is an exogenous nucleic acid sequence.

3. The recombinant *Thraustochytrium* microorganism of claim 1 or claim 2, wherein the nucleic acid sequence encoding the xylose transporter is an exogenous nucleic acid sequence.

4. The recombinant *Thraustochytrium* microorganism of any one of claims 1-3, wherein the nucleic acid sequence encoding the xylose isomerase is a heterologous nucleic acid.

5. The recombinant *Thraustochytrium* microorganism of any one of claims 1-4, wherein the microorganism comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 copies of the exogenous nucleic acid sequence encoding xylose isomerase.

6. The recombinant *Thraustochytrium* microorganism of claim 4 or claim 5, wherein the heterologous nucleic acid sequence encoding the xylose isomerase comprises SEQ ID NO:2.

7. The recombinant *Thraustochytrium* microorganism of any one of claims 1-6, wherein the microorganism comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 copies of the nucleic acid sequence encoding the xylulose kinase.

8. The recombinant *Thraustochytrium* microorganism of any one of claims 1-7, wherein the nucleic acid sequence encoding xylulose kinase is a heterologous nucleic acid.

9. The recombinant *Thraustochytrium* microorganism of claim 8, wherein the heterologous nucleic acid sequence encoding the xylulose kinase comprises SEQ ID NO:5.

10. The recombinant *Thraustochytrium* microorganism of any one of claims 1-9, wherein the microorganism comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17,

18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 copies of the nucleic acid sequence encoding the xylose transporter.

11. The recombinant *Thraustochytrium* microorganism of any one of claims 1-10, wherein the nucleic acid encoding the xylose transporter is a heterologous nucleic acid.

12. The recombinant *Thraustochytrium* microorganism of claim 11, wherein the heterologous nucleic acid encoding the xylose transporter is GXS1 from *Candida intermedia*.

13. The recombinant *Thraustochytrium* microorganism of claim 11, wherein the heterologous nucleic acid sequence encoding the xylose transporter comprises SEQ ID NO:23.

14. The recombinant *Thraustochytrium* microorganism of any one of claims 1-13, wherein the recombinant microorganism has increased xylose transport activity as compared to a non-recombinant control microorganism, increased xylose isomerase activity as compared to a non-recombinant control microorganism, increased xylulose kinase activity as compared to a non-recombinant control microorganism, or any combination thereof.

15. The recombinant *Thraustochytrium* microorganism of any one of claims 1-14, wherein the recombinant microorganism grows with xylose as the sole carbon source.

16. The recombinant *Thraustochytrium* microorganism of any one of claims 1-15, wherein the exogenous nucleic acid sequence encoding the xylose isomerase is operably linked to a promoter sequence.

17. The recombinant *Thraustochytrium* microorganism of any one of claims 8-16, wherein the nucleic acid sequence encoding the xylulose kinase is operably linked to a promoter sequence.

18. The recombinant *Thraustochytrium* microorganism of any one of claims 11-17, wherein the nucleic acid sequence encoding the xylose transporter is operably linked to a promoter sequence.

19. The recombinant *Thraustochytrium* microorganism of any one of claims 16-18, wherein the promoter is a tubulin promoter sequence.

20. The recombinant *Thraustochytrium* microorganism of claim 19, wherein the promoter sequence comprises SEQ ID NO:25 or SEQ ID NO:26.

21. The recombinant *Thraustochytrium* microorganism of any one of claims 1-20, wherein the exogenous nucleic acid sequence encoding the xylose isomerase comprises a terminator sequence.

22. The recombinant *Thraustochytrium* microorganism of any one of claims 8-21, wherein the nucleic acid sequence encoding the xylulose kinase comprises a terminator sequence.

23. The recombinant *Thraustochytrium* microorganism of any one of claims 11-22, wherein the nucleic acid sequence encoding the xylose transporter comprises a terminator sequence.

24. The recombinant *Thraustochytrium* microorganism of any one of claims 21-23, wherein the terminator sequence is a tubulin terminator sequence.

25. The recombinant *Thraustochytrium* microorganism of claim 24, wherein the terminator sequence comprises SEQ ID NO:27, SEQ ID NO:28, or SEQ ID NO:30.

26. The recombinant *Thraustochytrium* microorganism of any one of claims 1-25, wherein the microorganism further comprises a selectable marker.

27. The recombinant *Thraustochytrium* microorganism of claim 26, wherein the selectable marker is an antibiotic resistance gene.

28. The recombinant *Thraustochytrium* microorganism of claim 27, wherein the antibiotic resistance gene is zeocin, hygromycin B, kanamycin or neomycin.

29. The recombinant *Thraustochytrium* microorganism of claim 28, wherein the microorganism has ATCC Accession No. PTA-6245.

30. A method of making a recombinant xylose-metabolizing *Thraustochytrium* microorganism comprising:

transforming the *Thraustochytrium* microorganism with one or more nucleic acid constructs comprising a nucleic acid sequence encoding a xylose isomerase, a nucleic acid sequence encoding a xylulose kinase and a nucleic acid sequence encoding a xylose transporter; and

isolating *Thraustochytrium* microorganisms comprising at least two or more copies of the nucleic acid sequences encoding the xylose isomerase, at least one copy of the nucleic acid sequence encoding the xylulose kinase and at least one copy of the xylose transporter, wherein the isomerase, kinase and transporter are integrated into the genome of the *Thraustochytrium* microorganism.

31. The method of claim 30, wherein one or more nucleic acid constructs further comprise a selectable marker sequence.

32. The method of claim 30 or claim 31, wherein the one or more nucleic acid constructs comprise a first nucleic acid construct comprising a nucleic acid sequence encoding a xylose isomerase, a second nucleic acid construct comprising a nucleic acid sequence encoding a xylulose kinase and a third nucleic acid construct comprising a nucleic acid sequence encoding a xylose transporter.

33. The method of claim 32, wherein the first, second and third nucleic acid constructs comprise the same selectable marker sequence.

34. The method of claim 32 or claim 33, wherein the first nucleic acid construct comprises a promoter, the selectable marker sequence, a nucleic acid sequence encoding a 2A peptide, the nucleic acid sequence encoding the xylose isomerase, and a terminator.

35. The method of any one of claims 32-34, wherein the second nucleic acid construct comprises a promoter, the selectable marker sequence, a nucleic acid sequence encoding a 2A peptide, the nucleic acid sequence encoding the xylulose kinase, and a terminator.

36. The method of any one of claims 32-35, wherein the third nucleic acid construct comprises a promoter, the nucleic acid sequence encoding the xylose transporter, a nucleic acid sequence encoding a 2A peptide, the selectable marker sequence, and a terminator.

37. The method of any one of claims 31-36, wherein the selectable marker sequence is an antibiotic resistance gene.

38. The method of claim 37, wherein the antibiotic resistance gene is zeocin, hygromycin B, kanamycin or neomycin.

39. The method of any one of claims 34-38, wherein the promoter is a tubulin promoter.

40. The method of claim 39, wherein the promoter comprises SEQ ID NO:25 or SEQ ID NO:26.

41. The method of any one of claims 34-40, wherein the terminator is a tubulin terminator.

42. The method of claim 41, wherein the terminator comprises SEQ ID NO:27, SEQ ID NO:28, or SEQ ID NO:30.

43. The method of any one of claims 30-42, wherein the isolated recombinant *Thraustochytrium* microorganism comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15,

16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 copies of the nucleic acid sequence encoding xylose isomerase.

44. The method of any one of claims 30-43, wherein the xylose isomerase is a heterologous xylose isomerase.

45. The method of any one of claims 30-43, wherein the nucleic acid sequence encoding the xylose isomerase comprises SEQ ID NO:2.

46. The method of any one of claims 30-45, wherein the isolated recombinant microorganism comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 copies of the nucleic acid sequence encoding the xylulose kinase.

47. The method of any one of claims 30-46, wherein the xylulose kinase is a heterologous xylulose kinase.

48. The method of any one of claims 30-46, wherein the nucleic acid sequence encoding the xylulose kinase comprises SEQ ID NO:5.

49. The method of any one of claims 30-48, wherein the isolated recombinant microorganism comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 copies of the nucleic acid sequence encoding the xylose transporter.

50. The method of any one of claims 30-49, wherein the xylose transporter is a heterologous xylose transporter.

51. The method of any one of claims 30-49, wherein the xylose transporter is GXS1 from *Candida intermedia*.

52. The method of any one of claims 30-49, wherein the nucleic acid sequence encoding the xylose transporter comprises SEQ ID NO:23.

53. The method of any one of claims 30-52, wherein the isolated recombinant microorganism has increased xylose transport activity as compared to a control non-recombinant microorganism, increased xylose isomerase activity as compared to a control non-recombinant microorganism, increased xylulose kinase activity as compared to a control non-recombinant microorganism, or a combination thereof.

54. The method of any one of claims 30-53, wherein the isolated recombinant microorganism grows with xylose as the sole carbon source.

55. The method of claim 54, wherein the microorganism has ATCC Accession No. PTA-6245.

56. A method of producing oil, comprising culturing the recombinant *Thraustochytrium* microorganism of any one of claims 1-29 in a culture medium under suitable conditions to produce the oil, wherein the microorganism grows on xylose as the sole carbon source.

57. The method of claim 56, wherein the oil comprises triglycerides.

58. The method of claim 56, wherein the oil comprises alpha linolenic acid, arachidonic acid, docosahexanenoic acid, docosapentaenoic acid, eicosapentaenoic acid, gamma-linolenic acid, linoleic acid, linolenic acid, or a combination thereof.

59. The method of any one of claims 56-58, further comprising isolating the oil.