precursor of a cofactor used by an enzyme that functions in a flavonoid pathway, such as, for examples, bicarbonate, biotin, thiamine, pantothenate, alpha-ketoglutarate, ascorbate, or 5-aminolevulinic acid.

Further provided are methods for producing flavonoids and anthocyanins that include culturing a cell engineered for the production of flavonoids or anthocyanins as provided herein under conditions in which the cell produces flavonoids or anthocyanins. In some examples, the methods include culturing the engineered cells in a culture medium that includes at least one feed molecule or supplement such as but not limited to: tyrosine, phenylalanine, malonate, p-coumarate, bicarbonate, acetate, pantothenate, biotin, thiamine, alpha-ketoglutarate, ascorbate, and 5-aminolevulinic acid. The methods can further include recovering at least one of the flavonoids from culture medium, whole culture, or the cells.

In one aspect, the present disclosure provides an engineered host cell that comprises one or more genetic modifications resulting in production of flavonoid or anthocyanin from a carbon source that can also be an energy source, through multiple chemical intermediates, by the engineered host cell, wherein the engineered host cell comprises at least one genetic modification to an endogenous gene to increase the production and/or availability of malonyl-CoA in comparison to a wild-type host cell, wherein the engineered host cell expresses acetyl-CoA carboxylase (ACC) having an amino acid sequence at least 85% identical to the polypeptide set forth in SEQ ID NO: 15. In a first example, provided herein are cells engineered to produce one or more flavonoids or anthocyanins, wherein the cells include, in addition to nucleic acid sequences encoding either tyrosine ammonia lyase activity and/or phenylalanine ammonia lyase activity and cinnamate-4-hydroxylase activity, 4-coumarate-CoA ligase activity, chalcone synthase activity, chalcone isomerase activity, flavanone-3-hydroxylase activity, flavonoid 3'-hydroxylase activity or flavonoid 3'5'-hydroxylase activity, cytochrome P450 reductase activity,

leucoanthocyanidin reductase activity, and dihydroflavonol-4- reductase activity, one or more genetic modifications for improving production of the flavonoids or anthocyanins. As set forth herein, a cell that is engineered to produce one or more of the flavonoids is engineered to include an exogenous nucleic acid sequence encoding tyrosine ammonia lyase activity that can form 4-coumaric acid using tyrosine as substrate (e.g., tyrosine ammonia lyase TAL, EC: 4.3.1.25) or, alternatively or in addition, an exogenous nucleic acid sequence encoding phenylalanine ammonia lyase activity that can convert phenylalanine to trans-cinnamic acid and an exogenous nucleic acid sequence encoding cinnamate-4-hydroxylase activity that forms 4-coumaric acid from trans-cinnamic acid, an exogenous nucleic acid sequence encoding CoA ligase activity that forms p-coumaroyl-CoA from coumaric acid (e.g., 4-coumarate--CoA ligase, 4CL, EC:6.2.1.12), an exogenous nucleic acid sequence encoding polyketide synthase activity that forms naringenin chalcone using malonyl-CoA and p-coumaroyl-CoA as substrates (e.g., chalcone synthase, CHS, EC:2.3.1.74), an exogenous nucleic acid sequence encoding chalcone isomerase activity that forms naringenin

chalcone isomerase; (ii) chalcone synthase; (iii) a fusion protein comprises a chalcone synthase and a chalcone isomerase; and (iv) any combination thereof. In certain examples, the engineered cell is *E. coli*. In certain examples, one or more genetic modifications decreases fatty acid biosynthesis. In certain examples, the engineered host cell comprises an exogenous nucleic acid sequence selected from: (i) nucleic acid sequence encoding tyrosine ammonia lyase, wherein the encoded tyrosine ammonia lyase forms 4-coumaric acid using tyrosine as a substrate; (ii) nucleic acid sequence encoding phenylalanine ammonia lyase, wherein the encoded phenylalanine ammonia lyase converts phenylalanine to trans-cinnamic acid; (iii) nucleic acid sequence encoding cinnamate-4-hydroxylase, wherein the cinnamate-4-hydroxylase produces 4-coumaric acid from trans-cinnamic acid; (iv) nucleic acid sequence encoding flavanone-3-hydroxylase, wherein flavanone-3-hydroxylase forms dihydrokaempferol from naringenin; and (v) any combinations thereof. In certain examples, the engineered host cell comprises an exogenous nucleic acid sequence selected from the group consisting of: (i) nucleic acid sequences encoding tyrosine ammonia lyase, wherein the encoded tyrosine ammonia lyase forms 4-coumaric acid using tyrosine as a substrate; (ii) nucleic acid sequence encoding phenylalanine ammonia lyase, wherein the encoded phenylalanine ammonia lyase converts phenylalanine to trans-cinnamic acid; (iii) nucleic acid sequence encoding cinnamate-4-hydroxylase, wherein the cinnamate-4-hydroxylase produces 4-coumaric acid from trans-cinnamic acid; (iv) nucleic acid sequence encoding 4-courmarate-CoA ligase activity, wherein 4-courmarate-CoA ligase forms p-coumaroyl-CoA from coumaric acid (v) nucleic acid sequence encoding chalcone synthase activity, wherein chalcone synthase forms naringenin chalcone from malonyl-CoA and p-coumaroyl-CoA; (vi) nucleic acid sequence encoding chalcone isomerase activity, wherein chalcone isomerase forms naringenin from naringenin chalcone; (vii) nucleic acid sequence encoding flavanone-3-hydroxylase, wherein flavanone-3-hydroxylase forms dihydrokaempferol from naringenin; and (viii) any combinations thereof. In certain examples, the flavonoid is catechin.

In yet another example, the disclosure provides a method of increasing the production of flavonoids or anthocyanins, the method comprising: providing an engineered host cell that comprises one or more genetic modifications resulting in production of flavonoid or anthocyanin from a carbon source that can also be an energy source, through multiple chemical intermediates, by the engineered host cell. In certain examples, the production of flavonoid or anthocyanin

encoded phenylalanine ammonia lyase converts phenylalanine to trans-cinnamic acid; (iii) nucleic acid sequence encoding cinnamate-4-hydroxylase, wherein the cinnamate-4-hydroxylase produces 4-coumaric acid from trans-cinnamic acid; (iv) nucleic acid sequence encoding flavanone-3-hydroxylase, wherein flavanone-3-hydroxylase forms dihydrokaempferol from naringenin; and (v) any combinations thereof. In certain examples, the engineered host cell comprises an exogenous nucleic acid sequence selected from the group consisting of: (i) nucleic acid sequence encoding tyrosine ammonia lyase, wherein the encoded tyrosine ammonia lyase forms 4-coumaric acid using tyrosine as a substrate; (ii) nucleic acid sequence encoding phenylalanine ammonia lyase, wherein the encoded phenylalanine ammonia lyase converts phenylalanine to trans-cinnamic acid; (iii) nucleic acid sequence encoding cinnamate-4-hydroxylase, wherein the cinnamate-4-hydroxylase produces 4-coumaric acid from trans-cinnamic acid; (iv) nucleic acid sequence encoding 4-courmarate-CoA ligase activity, wherein 4-courmarate-CoA ligase forms p-coumaroyl-CoA from coumaric acid (v) nucleic acid sequence encoding chalcone synthase activity, wherein chalcone synthase forms naringenin chalcone from malonyl-CoA and p-coumaroyl-CoA; (vi) nucleic acid sequence encoding chalcone isomerase activity, wherein chalcone isomerase forms naringenin from naringenin chalcone; (vii) nucleic acid sequence encoding flavanone-3-hydroxylase, wherein flavanone-3-hydroxylase forms dihydrokaempferol from naringenin; and (viii) any combinations thereof. In certain examples, the flavonoid is catechin.

In yet another example, the disclosure provides a plurality of engineered host cells, wherein each of the plurality of the engineered host cells comprises one or more genetic modifications resulting in production of flavonoid or

from naringenin; and (v) any combinations thereof. In certain examples, the engineered host cell comprises an exogenous nucleic acid sequence selected from the group consisting of: (i) nucleic acid sequence encoding tyrosine ammonia lyase, wherein the encoded tyrosine ammonia lyase forms 4-coumaric acid using tyrosine as a substrate; (ii) nucleic acid sequence encoding phenylalanine ammonia lyase, wherein the encoded phenylalanine ammonia lyase converts phenylalanine to trans-cinnamic acid; (iii) nucleic acid sequence encoding cinnamate-4-hydroxylase, wherein the cinnamate-4-hydroxylase produces 4-coumaric acid from trans-cinnamic acid; (iv) nucleic acid sequence encoding 4-courmarate-CoA ligase activity, wherein 4-courmarate-CoA ligase forms p-coumaroyl-CoA from coumaric acid (v) nucleic acid sequence encoding chalcone synthase activity, wherein chalcone synthase forms naringenin chalcone from malonyl-CoA and p-coumaroyl-CoA; (vi) nucleic acid sequence encoding chalcone isomerase activity, wherein chalcone isomerase forms naringenin from naringenin chalcone; (vii) nucleic acid sequence encoding flavanone-3-hydroxylase, wherein flavanone-3-hydroxylase forms dihydrokaempferol from naringenin; and (viii) any combinations thereof. In certain examples, the flavonoid is catechin.

In yet another example, the disclosure provides a method of increasing the production of flavonoids or anthocyanins, the method comprising: providing a plurality of engineered host cells, wherein each of the plurality of the engineered host cell comprises one or more genetic modifications resulting production of flavonoid or anthocyanin from a carbon source that can also be an energy source, through multiple chemical

ammonia lyase, wherein the encoded tyrosine ammonia lyase forms 4-coumaric acid using tyrosine as a substrate; (ii) nucleic acid sequence encoding phenylalanine ammonia lyase, wherein the encoded phenylalanine ammonia lyase converts phenylalanine to trans-cinnamic acid; (iii) nucleic acid sequence encoding cinnamate-4-hydroxylase, wherein the cinnamate-4-hydroxylase produces 4-coumaric acid from trans-cinnamic acid; (iv) nucleic acid sequence encoding 4-courmarate-CoA ligase activity, wherein 4-courmarate-CoA ligase forms p-coumaroyl-CoA from coumaric acid (v) nucleic acid sequence encoding chalcone synthase activity, wherein chalcone synthase forms naringenin chalcone from malonyl-CoA and p-coumaroyl-CoA; (vi) nucleic acid sequence encoding chalcone isomerase activity, wherein chalcone isomerase forms naringenin from naringenin chalcone; (vii) nucleic acid sequence encoding flavanone-3-hydroxylase, wherein flavanone-3-hydroxylase forms dihydrokaempferol from naringenin; and (viii) any combinations thereof. In certain examples, the flavonoid is catechin.

In yet another example, the engineered host cell comprises one or more genetic modifications to increase the production and/or availability of malonyl-CoA. In certain examples, the production and/or availability of malonyl-CoA is increased by transformation of acetyl-CoA to malonyl-CoA. In certain examples, the engineered host cell comprises one or more genetic modifications selected from: (i) expression of acetyl-CoA carboxylase (ACC); and (ii) overexpression of acetyl-CoA carboxylase. In another example, the engineered host cell is an *E. coli*. In certain examples, the *E. coli* cell further comprises genes from fungi. In certain examples, the acetyl-CoA carboxylase is from: *Mucor circinelloides*, *Rhodotorula toruloides*, *Lipomyces starkeyi*, and *Ustilago maydis*, and orthologs of acetyl-CoA carboxylase having at least 50% amino acid identity to the acetyl-CoA carboxylase of these aforementioned species. In certain examples, one or more genetic modification is deletion or attenuation of one or more fatty biosynthetic genes resulting in decrease in fatty acid biosynthesis. In certain examples, one or more genetic modification is overexpression of acetyl-CoA synthase (ACS). In certain examples, the acetyl-CoA synthase is selected from: acetyl-CoA

pyruvate dehydrogenase (PDH), wherein the PDH may include E354K mutation; (ii) exogenous nucleic acid sequence encoding a malonyl-CoA synthetase; (iii) upregulation of endogenous pantothenate kinase (PanK), wherein PanK is not feedback inhibited by coenzyme A; (iv) exogenous nucleic acid sequence encoding a malonate transporter; and (v) any combinations thereof. In certain examples, the malonyl-CoA synthetase is selected from of malonyl-CoA synthetases of *Streptomyces coelicolor*, *Rhodopseudomonas palustris*, or a malonyl-CoA synthetase having at least 50% identity to any of these or other naturally occurring malonyl-CoA synthetases. In certain examples, one or more genetic modifications to decrease fatty acid biosynthesis is selected from: (i) mutation or downregulation of a gene encoding malonyl-CoA-ACP transacylase (*E. coli* fabD); (ii) modifications to the gene beta-ketoacyl-ACP synthase II (*E. coli* fabF); (iii) downregulation of beta-ketoacyl-ACP synthase I enzyme (*E. coli* fabB); (iv) downregulation of acyl carrier protein (*E. coli* acpP); and (v) any combinations thereof. In certain examples, the engineered host cell comprises peptides selected from: (i) acetyl-CoA carboxylase (ACC) having an amino acid sequence at least 80% identical to the polypeptide set forth in SEQ ID NO: 15 or SEQ ID NO: 16; (ii) malonate CoA-transferase having an amino acid sequence at least 80% identical to the polypeptide set forth in SEQ ID NO: 19; (iii) acetyl-CoA synthase (ACS) having an amino acid sequence at least 80% identical to the polypeptide set forth in SEQ ID NO: 16; (iv) malonyl-CoA synthase having an amino acid sequence at least 80% identical SEQ ID NO: 77, SEQ ID NO: 78, or SEQ ID NO: 79; (v) malonate transporter having an amino acid sequence at least 80% identical to SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO: 84, SEQ ID NO: 85, SEQ ID NO: 86, or SEQ ID NO: 87; (vi) pantothenate kinase having an amino acid sequence at least 80% identical to SEQ ID NO: 88, SEQ ID NO: 89, or SEQ ID NO: 90; and (vii) any combinations thereof.

In another example, the disclosure provides a method of increasing the production of flavonoids comprising an engineered host cell, wherein the one or more engineered host cells comprise one or more genetic modifications to increase the

identical to SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO: 84, SEQ ID NO: 85, SEQ ID NO: 86, or SEQ ID NO: 87; (vi) pantothenate kinase having an amino acid sequence at least 80% identical to SEQ ID NO: 88, SEQ ID NO: 89, or SEQ ID NO: 90; and (vii) any combinations thereof.

In another example, the disclosure provides an engineered host cell, wherein the engineered host cell comprises one or more genetic modifications to increase endogenous biosynthesis of tyrosine. In certain examples, one or more genetic modifications comprises upregulation of 3-deoxy-D-arabino-heptulosonate synthase. In certain examples, one or more genetic modifications are selected from: (i) upregulation of 13horismite mutase; (ii) upregulation of prephenate dehydrogenase; (iii) overexpression of shikimate kinase; (iv) overexpression of shikimate dehydrogenase; and (v) any combinations thereof. In certain examples, one or more genetic modifications comprises downregulation of L-phenylalanine biosynthetic pathway. In certain examples, one or more genetic modifications comprises expression of exogenous phosphoenolpyruvate synthase (ppsA). In certain examples, one or more genetic modifications comprises expression of exogenous transketolase (tktA). In certain examples, wherein the one or more genetic modifications comprises disruption of tyrR gene. In certain examples, one or more genetic modifications are selected from a group consisting of: (i) expression or overexpression of (D146N) variant of 13horismi-2-dehydro-3-deoxyheptonate aldolase; (ii) expression or

overexpression of variant of 3-dehydroquinate synthase (aroB); (iii) overexpression of transketolase tktA; (iv) deletion of shikimate kinase (aroK); (v) deletion of tyrR; (vi) expression or overexpression of A354V variant of 13horismite mutase (tyrA); (vi) and any combination thereof.

In another example, the disclosure provides a method of increasing endogenous biosynthesis of tyrosine comprising an engineered cell, wherein the engineered host cell comprises one or more genetic modifications to increase endogenous biosynthesis of tyrosine. In certain examples, one or more genetic modifications comprises upregulation of 3-deoxy-D-arabino-heptulosonate synthase. In certain examples, one or more genetic modifications are selected from: (i) upregulation of chorismate mutase; (ii) upregulation of prephenate dehydrogenase; (iii) overexpression of shikimate kinase; (iv) overexpression of shikimate dehydrogenase; and (v) any combinations thereof. In certain examples, one or more genetic modifications comprises

downregulation of L-phenylalanine biosynthetic pathway. In certain examples, one or more genetic modifications comprises expression of exogenous phosphoenolpyruvate synthase (ppsA). In certain examples, one or more genetic modifications comprises expression of exogenous transketolase (tktA). In certain examples, wherein the one or more genetic modifications comprises disruption of tyrR gene. In certain examples, one or more genetic modifications are selected from a group consisting of: (i) expression or overexpression of (D146N) variant of phospho-2-dehydro-3-deoxyheptonate aldolase; (ii) expression or overexpression of variant of 3-dehydroquinate synthase (aroB); (iii) overexpression of transketolase tktA; (iv) deletion of shikimate kinase (aroK); (v) deletion of tyrR; (vi) expression or overexpression of A354V variant of chorismate mutase (tyrA); (vi) and any combination thereof.

In another example, the disclosure provides an engineered host cell, wherein the engineered host cell comprises one or more genetic modifications to increase transformation of leucocyanidin or catechin to cyanidin-3-glucoside (Cy3G). In certain examples, one or more genetic modifications comprises overexpression of anthocyanin synthase. In certain examples, the anthocyanin synthase is selected from: (i) anthocyanin synthase of *Carica papaya* (SEQ. ID NO:13); (ii) the anthocyanin synthase has an amino acid sequence at least 80% identical to SEQ. ID NO: 66, SEQ. ID NO: 67, SEQ. ID NO: 68, or SEQ. ID NO: 69; (iii) the anthocyanin synthase has an amino acid sequence at least 80% identical to SEQ. ID NO: 13; and (iv) any combinations thereof. In certain examples, one or more engineered host cells comprises flavonoid-3-glucosyl transferase (3GT). In certain examples, flavonoid-3-glucosyl transferase is selected from: (i) flavonoid-3-glucosyl

In another example, the disclosure provides a method for increasing the production of flavonoids comprising an engineered host cell, wherein the engineered host cell comprises one or more genetic modifications to increase transformation of leucocyanidin or catechin to cyanidin-3-glucoside (Cy3G). In certain examples, one or more genetic modifications comprises overexpression of anthocyanin synthase. In certain examples, the anthocyanin synthase is selected from: (i) anthocyanin synthase of *Carica papaya* (SEQ. ID NO:13); (ii) the anthocyanin synthase has an amino acid sequence at least 80% identical to SEQ. ID NO: 66, SEQ. ID NO: 67, SEQ. ID NO: 68, or SEQ. ID NO: 69; (iii) the anthocyanin synthase has an amino acid sequence at least 80% identical to SEQ. ID NO: 13; and (iv) any combinations thereof. In certain examples, one or more engineered host cells comprises flavonoid-3-glucosyl transferase (3GT). In certain examples, flavonoid-3-glucosyl transferase is selected from: (i) flavonoid-3-glucosyl transferase in *Vitis labrusca* (SEQ. ID NO:14); (ii) the flavonoid-3-glucosyl transferase has an amino acid sequence at least 80% identical to SEQ. ID NO: 70, SEQ. ID NO: 71, SEQ. ID NO: 72, or SEQ. ID NO: 73; and (iii) any combinations thereof. In certain examples, one or more genetic modifications comprises overexpression of anthocyanin synthase and flavonoid-3-glucosyl transferase (3GT). In certain examples, the one or more genetic modifications comprises overexpression of anthocyanin synthase and flavonoid-3-glucosyl transferase (3GT). In certain examples, the one or more genetic modifications are selected from a group consisting of: (i) anthocyanin synthase, (ii) flavonoid-3-glucosyl transferase (3GT), and (iii) a combination thereof.

In another aspect, the present disclosure provides a method of increasing the production of flavonoids or anthocyanins, the method comprising providing an engineered host cell as disclosed herein. In yet another aspect, the present disclosure provides a plurality of engineered host cells, wherein each of the plurality of the engineered host cells is an engineered host cell as disclosed herein. In yet another aspect, the present disclosure provides a method of increasing the production of flavonoids or anthocyanins, the method comprising providing a plurality of engineered host cells, wherein each of the plurality of the engineered host cells is an engineered host cell as disclosed herein.

In another example, the disclosure provides a method of increasing the transformation of leucocyanidin or catechin to cyanidin-3-glucoside (Cy3G), delphinidin or gallocatechin to delphindin-3-glucoside (De3G), or afzelechin or pelargonidin to pelargonidin-3-glucoside (Pe3G) comprising anthocyanin synthase, wherein the anthocyanin synthase is selected from: (i) anthocyanin synthase of *Carica papaya* (SEQ. ID NO:13); (ii) the anthocyanin synthase has an amino acid sequence at least 80% identical to SEQ. ID NO: 66, SEQ. ID NO: 67, SEQ. ID NO: 68, or SEQ. ID NO: 69; (iii) the anthocyanin synthase has an amino acid sequence at least 80% identical to SEQ. ID NO: 13; and (iv) any combinations thereof. In certain examples, one or more genetic modifications comprises overexpression of anthocyanin synthase and flavonoid-3-glucosyl transferase (3GT). In certain examples, the one or more genetic modifications are

CLAIMS

1. An engineered host cell that comprises one or more genetic modifications resulting in production of flavonoid or anthocyanin from a carbon source that can also be an energy source, through multiple chemical intermediates, by the engineered host cell, wherein the engineered host cell comprises at least one genetic modification to an endogenous gene to increase the production and/or availability of malonyl-CoA in comparison to a wild-type host cell, wherein the engineered host cell expresses acetyl-CoA carboxylase (ACC) having an amino acid sequence at least 85% identical to the polypeptide set forth in SEQ ID NO: 15.

2. The engineered host cell of claim 1, wherein the production of flavonoid or anthocyanin from a carbon source that can also be an energy source occurs through enzymatic transformation.

3. The engineered host cell of claim 1, wherein the carbon source is selected from a group consisting of: (i) glycerol, (ii) a sugar, (iii) an organic acid, (iv) an amino acid, (v) a biomass comprising glycerol; and (vi) any combination thereof.

4. The engineered host cell of claim 1, wherein the engineered host cell is cultured in a medium comprising molecules selected from a group consisting of: (i) glycerol, (ii) a sugar, (iii) an organic acid, (iv) an amino acid, (v) a biomass comprising glycerol, and (vi) any combination thereof.

5. The engineered host cell of claim 1, wherein the one or more genetic modifications lead to increase in metabolic flux to flavonoid precursors or cofactors.

6. The engineered host cell of claim 1, wherein the one or more genetic modifications cause reduction of formation of byproducts.

7. The engineered host cell of claim 1, wherein the engineered host cell is cultured in a medium comprising molecules selected from a group consisting of tyrosine, phenylalanine, malonate, p-coumarate, bicarbonate, acetate, pantothenate, biotin, thiamine, alpha-ketoglutarate, ascorbate, and 5-aminolevulinic acid.

8. The engineered host cell of claim 1, wherein the engineered host cell comprises an exogenous nucleic acid sequence selected from the group consisting of: (i) nucleic acid sequence encoding tyrosine ammonia lyase, wherein the encoded tyrosine ammonia lyase forms 4-coumaric acid using tyrosine as a substrate; (ii) nucleic acid sequence encoding phenylalanine ammonia lyase, wherein the encoded phenylalanine ammonia lyase converts phenylalanine to trans-cinnamic acid; (iii) nucleic acid sequence encoding cinnamate-4-hydroxylase, wherein the cinnamate-4-hydroxylase produces 4-coumaric acid from trans-cinnamic acid; (iv) nucleic acid sequence encoding 4-coumarate-CoA ligase activity, wherein 4-coumarate-CoA ligase forms p-coumaroyl-CoA from coumaric acid (v) nucleic acid sequence encoding chalcone synthase activity, wherein chalcone synthase forms naringenin chalcone from malonyl-CoA and p-coumaroyl-CoA; (vi) nucleic acid sequence encoding chalcone isomerase activity, wherein chalcone isomerase forms naringenin from naringenin chalcone; (vii) nucleic acid sequence encoding flavanone-3-hydroxylase, wherein flavanone-3-hydroxylase forms dihydrokaempferol from naringenin; and (viii) any combinations thereof.

9. The engineered host cell of claim 1, wherein the flavonoid is catechin.

10. The engineered host cell of claim 1, wherein the production and/or availability of malonyl-CoA is increased by transformation of acetyl-CoA to malonyl-CoA.

11. The engineered host cell of claim 1, wherein the engineered host cell comprises one or more genetic modifications to increase expression of acetyl-CoA carboxylase (ACC) in comparison to a wild-type host cell.

12. The engineered host cell of claim 1, wherein the engineered host cell is *E. coli*.

13. The engineered host cell of claim 12, wherein the *E. coli* further comprises genes from fungi.

14. The engineered host cell of claim 11, wherein the acetyl-CoA carboxylase is from a species selected from the group consisting of *Mucor circinelloides*, *Rhodotorula toruloides*, *Lipomyces starkeyi*, and *Ustilago maydis*, and orthologs of acetyl-CoA carboxylase having at least 50% amino acid identity to the acetyl-CoA carboxylase of these aforementioned species.

15. The engineered host cell of claim 1, wherein the one or more genetic modifications is deletion or attenuation of one or more fatty acid biosynthetic genes resulting in decrease in fatty acid biosynthesis in comparison to a wild-type host cell.

16. The engineered host cell of claim 1, wherein the engineered host cell further comprises peptides selected from a group consisting of: (i) malonate CoA-transferase having an amino acid sequence at least 80% identical to the polypeptide set forth in SEQ ID NO: 19; (ii) acetyl-CoA synthase (ACS) having an amino acid sequence at least 80% identical to the polypeptide set forth in SEQ ID NO: 16; (iii) malonyl-CoA synthase having an amino acid sequence at least 80% identical SEQ ID NO: 77, SEQ ID NO: 78, or SEQ ID NO: 79; (iv) malonate transporter having an amino acid sequence at least 80% identical to SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO: 84, SEQ ID NO: 85, SEQ ID NO: 86, or SEQ ID NO: 87; (v) pantothenate kinase having an amino acid sequence at least 80% identical to SEQ ID NO: 88, SEQ ID NO: 89, or SEQ ID NO: 90; and (vi) any combinations thereof.

17. The engineered host cell of claim 1, wherein the engineered host cell expresses acetyl-CoA carboxylase (ACC) having an amino acid sequence at least 90% identical to the polypeptide set forth in SEQ ID NO: 15.

18. The engineered host cell of claim 1, wherein the engineered host cell expresses acetyl-CoA carboxylase (ACC) having an amino acid sequence at least 95% identical to the polypeptide set forth in SEQ ID NO: 15.

19. The engineered host cell of claim 1, wherein the engineered host cell further comprises one or more genetic modifications for production of cyanidin-3-glucoside (Cy3G) from catechin, wherein the one more genetic modifications for production of cyanidin-3-glucoside (Cy3G) from

catechin compriseoverexpression of anthocyanin synthase, wherein the anthocyanin synthase is selected from a group consisting of: (i) the anthocyanin synthase of *Carica papaya* (SEQ ID NO:13); (ii) the anthocyanin synthase has an amino acid sequence at least 80% identical to SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, or SEQ ID NO: 69; (iii) the anthocyanin synthase has an amino acid sequence at least 80% identical to SEQ ID NO: 13; and (iv) any combinations thereof.

20. The engineered host cell of claim 1, wherein the one or more genetic modifications for production of cyanidin-3-glucoside (Cy3G) from catechin further comprise overexpression of flavonoid-3-glucosyl transferase (3GT), wherein the flavonoid-3-glucosyl transferase is selected from a group consisting of: (i) the flavonoid-3-glucosyl transferase of *Vitis labrusca* (SEQ ID NO:14); (ii) the flavonoid-3-glucosyl transferase has an amino acid sequence at least 80% identical to SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, or SEQ ID NO: 73; (iii) the flavonoid-3-glucosyl transferase has an amino acid sequence at least 80% identical to SEQ ID NO: 14; and (iv) any combinations thereof.

21. The engineered host cell of claim 1, wherein the engineered host cell further comprises one or more genetic modifications to increase the production of dihydroquercetin (DHQ), dihydromyricein (DHM), eriodictoyl (EDL), and/or pentahydroxyflayaone (PHF), wherein the engineered host cell comprises cytochrome P450 reductase (CPR) and at least one of flavanone-3-hydroxylase (F3H), flavanone-3’-hydroxylase (F3’H), or flavonoid 3’,5’-hydroxylase (F3’5’H), wherein:

the flavonoid 3’-hydroxylase (F3’H) is truncated to remove the N-terminal leader sequence;

the flavonoid 3’,5’-hydroxylase (F3’5’H) is truncated to remove the N-terminal leader sequence;

cytochrome P450 reductase (CPR) is truncated to remove the N-terminal leader sequence;

flavonoid 3’-hydroxylase (F3’H) is fused with cytochrome P450 reductase (CPR); and/or

flavonoid 3’,5’-hydroxylase (F3’5’H) is fused with cytochrome P450 reductase (CPR).

22. The engineered host cell of claim 21, wherein the precursor for increase in production of dihydroquercetin (DHQ), dihydromyricein (DHM), eriodictoyl (EDL), and/or pentahydroxyflayanone (PHF) is naringenin and/or dihydrokaempferol (DHK).

23. The engineered host cell of claim 21, wherein the flavanone-3'-hydroxylase (F3'H) has an amino acid sequence at least 80% identical to the polypeptide set forth in SEQ ID NO. 8; the cytochrome P450 reductase (CPR) has an amino acid sequence at least 80% identical to the polypeptide set forth in SEQ ID NO. 9; flavanone-3-hydroxylase (F3H) has an amino acid sequence at least 80% identical to the polypeptides selected from a group consisting of: (i) SEQ ID NO. 7, (ii) SEQ ID NO. 45, (iii) SEQ ID NO. 46, (iv) SEQ ID NO. 47, and (v) SEQ ID NO. 48; and/or the flavonoid 3',5'-hydroxylase (F3'5'H) has an amino acid sequence at least 80% identical to the polypeptides selected from a group consisting of: (i) SEQ ID NO. 10, (ii) SEQ ID NO. 56, and (iii) SEQ ID NO. 57.

24. The engineered host cell of any one of claims 21-23, wherein the engineered host cell further comprises cytochrome $b_{5,}$ wherein the cytochrome b_5 has an amino acid sequence at least 80% identical to the polypeptide set forth in SEQ ID NO. 98.

25. A method of increasing the production of flavonoids or anthocyanins, the method comprising providing an engineered host cell according to any one of claims 1-24.

26. A plurality of engineered host cells, wherein each of the plurality of the engineered host cells is an engineered host cell according to any one of claims 1-24.

27. A method of increasing the production of flavonoids or anthocyanins, the method comprising providing a plurality of engineered host cells, wherein each of the plurality of the engineered host cells is an engineered host cell according to any one of claims 1-24.