



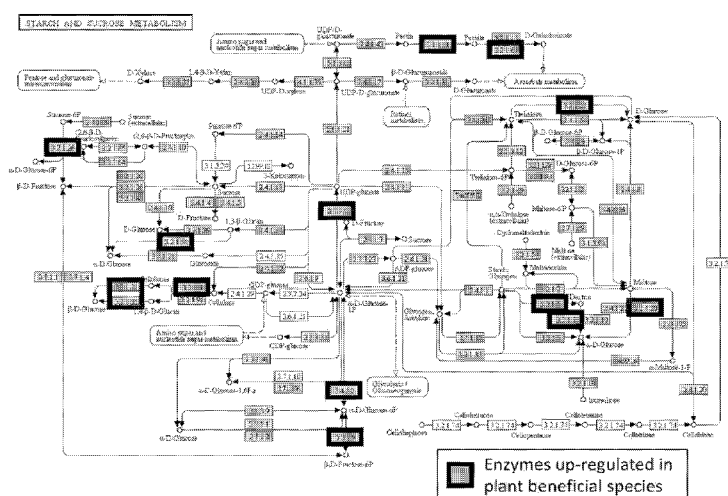
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- (71) Applicants: SYMBIOTA, LLC [US/US]; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US). SYMBIOTA, INC. [US/US]; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US).
- (72) Inventors; and
- (71) Applicants : SAMAYOA, Phillip; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US). VON MALTZAHN, Geoffrey; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US).

- (72) Inventors: AMBROSE, Karen, V.; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US). BILLINGS, Nathan, A.; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US). DJONOVIC, Slavica; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US). FLAVELL, Richard, Bailey; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US). GULICK, Trudi, A.; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US). JOHNSTON, David, Morris; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US). LEFF, Jonathan, W.; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US). LIVA, Stephanie, M.; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US). LYFORD, Jeffrey; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US). MARQUEZ, Luis, Miguel; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US). MILLET, Yves, Alain; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US). SADOWSKI, Craig; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US). SAMAYOA, Phillip; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US). TOLEDO, Gerardo, V.; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US). WEISMAN, David, R.; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US). ZHANG, Xuecheng; 101 Main Street, 14th Floor, Cambridge, MA 02142 (US).
- (74) Agent: HUBL, Susan T.; Fenwick & West LLP, Silicon Valley Center, 801 California Street, Mountain View, CA 94041 (US).
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(54) Title: SEED ENDOPHYTES ACROSS CULTIVARS AND SPECIES, ASSOCIATED COMPOSITIONS, AND METHODS OF USE THEREOF

FIG. 2



(57) Abstract: Materials and methods for improving plant traits and for providing plant fitness benefits are provided. In some embodiments, the materials, and methods employing the same, can comprise endophytes.



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**SEED ENDOPHYTES ACROSS CULTIVARS AND SPECIES, ASSOCIATED
COMPOSITIONS, AND METHODS OF USE THEREOF**

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of International Application No. PCT/US2015/038187, filed June 26, 2015, U.S. Provisional Application No. 62/156,021, filed May 1, 2015, U.S. Provisional Application No. 62/156,028, filed May 1, 2015, U.S. Provisional Application No. 62/098,296, filed December 30, 2014, U.S. Provisional Application No. 62/098,298, filed December 30, 2014, U.S. Provisional Application No. 62/098,299, filed December 30, 2014, U.S. Provisional Application No. 62/098,302, filed December 30, 2014, and U.S. Provisional Application No. 62/098,304, filed December 30, 2014, each of which is incorporated by reference in its entirety.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on December 30, 2015, is named 10035_Final_ST25.txt, and is 20 bytes in size.

FIELD OF THE INVENTION

[0003] Among other things, inventions disclosed herein relate to compositions and methods for improving the cultivation of plants, particularly agricultural plants. In an aspect, inventions described herein relate to beneficial bacteria and fungi that are capable of living in a plant, which may be used to impart improved agronomic traits to the plants. In another aspect, inventions described herein relate to methods of improving plant characteristics by introducing synthetic combinations of such beneficial bacteria and/or fungi to those plants. Further, inventions described herein also provide methods of treating seeds and other plant elements with synthetic combinations of beneficial bacteria and/or fungi that are capable of living within a plant, to impart improved agronomic characteristics to plants, particularly agricultural plants.

BACKGROUND

[0004] Agriculture faces numerous challenges that are making it increasingly difficult to provide food, materials, and fuels to the world's population. Population growth and changes in diet associated with rising incomes are increasing global food demand, while many key

resources for agriculture are becoming increasingly scarce. By 2050, the FAO projects that total food production must increase by 70% to meet the needs of the growing population, a challenge that is exacerbated by numerous factors, including diminishing freshwater resources, increasing competition for arable land, rising energy prices, increasing input costs, and the likely need for crops to adapt to the pressures of a more extreme global climate. The need to grow nearly twice as much food in more uncertain climates is driving a critical need for new innovations.

[0005] Today, crop performance is optimized via of technologies directed towards the interplay between crop genotype (e.g., plant breeding, genetically-modified (GM) crops) and its surrounding environment (e.g., fertilizer, synthetic herbicides, pesticides). While these paradigms have assisted in doubling global food production in the past fifty years, yield growth rates have stalled in many major crops and shifts in the climate have been linked to production declines in important crops such as wheat. In addition to their long development and regulatory timelines, public fears of GM-crops and synthetic chemicals has challenged their use in many key crops and countries, resulting in a complete lack of acceptance for GM traits in wheat and the exclusion of GM crops and many synthetic chemistries from European markets. Thus, there is a significant need for innovative, effective, and publically-acceptable approaches to improving the intrinsic yield and resilience of crops to severe stresses.

SUMMARY OF THE INVENTION

[0006] The disclosures of PCT/US2014/044427, filed June 26, 2014, U.S. Application Serial No. 14/316,469, filed June 26, 2014, and PCT/US2014/054160, filed September 4, 2014, are incorporated by reference in their entirety, including the sequence listings containing SEQ ID NOs: 1-1448.

[0007] The present invention is based on the discovery that a plant element (e.g., a whole plant, seedling, meristematic tissue, ground tissue, vascular tissue, dermal tissue, seed, leaf, root, shoot, stem, flower, fruit, stolon, bulb, tuber, corm, kelkis, shoot, bud) can be effectively augmented by associating its surface with a single endophyte strain or a plurality of endophytes in an amount that is not normally found on the plant element. Endophytes described herein can be isolated from inside the same plant or a different plant, or from inside a part or tissue of the same plant or different plant. The plant element thus associated with a single endophyte strain or a plurality of endophytes can be used to confer improved

agronomic trait or traits to the seed or the plant that is grown or derived from the plant element.

[0008] In an embodiment, the invention features a method for improving an agricultural trait in an agricultural plant. In an embodiment, the method includes providing an agricultural plant, seed or tissue thereof; contacting the plant, seed or tissue thereof with a formulation comprising an endophyte that is common to at least two donor plant types that is present in the formulation in an amount effective to colonize the plant; and growing the plants under conditions that allow the endophyte to improve a trait in the plant. In some embodiments, the two donor plants are of the same family. In some embodiments, the two donor plants are of the same genus. In some embodiments, the two donor plants are of the same species. In some embodiments, the agricultural plant tissue is a seed. In a further embodiment, the population is disposed on the surface of the seed.

[0009] In an embodiment, the method for improving an agricultural trait in an agricultural plant includes providing a modern agricultural plant, seed or tissue thereof; contacting the plant, seed, or tissue thereof with a formulation comprising an endophyte derived from an ancestral plant in an amount effective to colonize the plant; and allowing the plant to grow under conditions that allow the endophyte to colonize the plant.

[0010] The invention also features a method for preparing a seed comprising an endophyte population. The method comprising applying to an exterior surface of a seed a formulation comprising an endophyte population consisting essentially of an endophyte comprising a 16S rRNA or ITS rRNA nucleic acid sequence at least 95% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455.

[0011] In some embodiments, provided herein is a method for treating seedlings. The method includes contacting foliage or the rhizosphere of a plurality of agricultural plant seedlings with a seed a formulation comprising an endophyte population consisting essentially of an endophyte comprising a 16S rRNA or ITS rRNA nucleic acid sequence at least 95% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455; and growing the contacted seedlings.

[0012] The invention also features a method for modulating a plant trait. The method includes applying to vegetation or an area adjacent the vegetation, a seed a formulation comprising an endophyte population consisting essentially of an endophyte comprising a 16S rRNA or ITS rRNA nucleic acid sequence at least 95% identical to a nucleic acid sequence

selected from the group consisting of SEQ ID NOs: 1-455, wherein the formulation is capable of providing a benefit to the vegetation, or to a crop produced from the vegetation.

[0013] A method for modulating a plant trait also is featured. The method comprising applying a formulation to soil, the seed a formulation comprising an endophyte population consisting essentially of an endophyte comprising a 16S rRNA or ITS rRNA nucleic acid sequence at least 95% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455, wherein the formulation is capable of providing a benefit to seeds planted within the soil, or to a crop produced from plants grown in the soil.

[0014] In some embodiments, the endophyte comprises a 16S rRNA or ITS rRNA nucleic acid sequence at least 95% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455. In some embodiments, the endophyte is capable of a function or activity selected from the group consisting of auxin production, nitrogen fixation, production of an antimicrobial compound, mineral phosphate solubilization, siderophore production, cellulase production, chitinase production, xylanase production, and acetoin production. In some embodiments, the endophyte exhibits at least two of: auxin production, nitrogen fixation, production of an antimicrobial compound, mineral phosphate solubilization, siderophore production, cellulase production, chitinase production, xylanase production, and acetoin production.

[0015] In some embodiments, the endophyte is capable of metabolizing at least one substrate selected from the group consisting of: α -D-glucose, arabinose, arbutin, β -methyl-D-galactoside, β -methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, γ -amino-N-butyric acid, γ -cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, α -erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid- γ -lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose.

[0016] In some embodiments, the endophyte is capable of metabolizing at least two substrates selected from the group consisting of: α -D-glucose, arabinose, arbutin, β -methyl-

D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose.

[0017] In some embodiments, the endophyte is present at a concentration of at least 10^2 CFU or spores per seed on the surface of seeds after contacting. In some embodiments, the applying or contacting comprises spraying, immersing, coating, encapsulating, or dusting the seeds or seedlings with the formulation.

[0018] In some embodiments, the benefit or agricultural trait is selected from the group consisting of: increased root biomass, increased root length, increased height, increased shoot length, increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency, increased overall biomass, increased grain yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance, increased salt tolerance, increased resistance to nematode stress, increased resistance to a fungal pathogen, increased resistance to a bacterial pathogen, increased resistance to a viral pathogen, a detectable modulation in the level of a metabolite, a detectable modulation in the transcriptome, and a detectable modulation in the proteome, relative to reference seeds or agricultural plants derived from reference seeds. In some embodiments, the benefit or agricultural trait comprises at least two benefits or agricultural traits selected from the group consisting of: increased root biomass, increased root length, increased height, increased shoot length, increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency, increased overall biomass, increased grain yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance, increased salt tolerance, increased resistance to nematode stress, increased resistance to a fungal pathogen, increased resistance to a bacterial pathogen, increased resistance to a viral pathogen, a detectable modulation in the level of a metabolite, a detectable modulation in the transcriptome, and a detectable modulation in the proteome, relative to reference seeds or

agricultural plants derived from reference seeds. In some embodiments, the benefit is increased tolerance to low nitrogen stress or increased nitrogen use efficiency, and the endophyte is non-diazotrophic.

[0019] In some embodiments, the formulation comprises at least one member selected from the group consisting of an agriculturally compatible carrier, a tackifier, a microbial stabilizer, a fungicide, an antibacterial agent, an herbicide, a nematocide, an insecticide, a plant growth regulator, a rodenticide, and a nutrient.

[0020] In some embodiments, the endophyte comprises a nucleic acid sequence that is at least 97% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455, wherein the endophyte is present in the formulation in an amount effective to colonize the mature agricultural plant. In some embodiments, the endophyte comprises a nucleic acid sequence that is at least 99% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455, wherein the endophyte is present in the formulation in an amount effective to colonize the mature agricultural plant. In some embodiments, the endophyte comprises a nucleic acid sequence that is at least 99.5% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455, wherein the endophyte is present in the formulation in an amount effective to colonize the mature agricultural plant.

[0021] In some embodiments, the plant, seed or tissue thereof is contacted with at least 10 CFU or spores, at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores, at least 30,000 CFU or spores, at least 100,000 CFU or spores, at least 300,000 CFU or spores, at least 1,000,000 CFU or spores, or more, of the endophyte.

[0022] In some embodiments, the formulation comprises at least two endophytes comprising a nucleic acid sequence that is at least 97% identical, at least 98% identical, at least 99% identical, at least 99.5% identical, or 100% identical, to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455, wherein the at least two endophytes are present in the formulation in an amount effective to colonize the mature agricultural plant. In some embodiments, the formulation comprises at least two endophytes provided in Table 1, Table 2, Table 7 and Table 8.

[0023] In some embodiments, the plant is a monocot. The monocot can be corn, wheat, barley or rice. In some embodiments, the plant is a dicot. The dicot can be a soybean, peanut,

canola, cotton, Brassica Napus, cabbage, lettuce, melon, strawberry, turnip, watermelon, tomato or pepper.

[0024] In some embodiments, the endophyte is present in the formulation in an amount effective to be detectable within a target tissue of the agricultural plant selected from a fruit, seed, leaf, root or portion thereof.

[0025] In some embodiments, the endophyte is detected in an amount of at least 10 CFU or spores, at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores, at least 30,000 CFU or spores, at least 100,000 CFU or spores, at least 300,000 CFU or spores, at least 1,000,000 CFU or spores, or more, in the target tissue.

[0026] In some embodiments, the endophyte is present in the formulation in an amount effective to increase the biomass and/or yield of the fruit or seed produced by the plant by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, or more, when compared with the fruit or seed of a reference agricultural plant.

[0027] In some embodiments, the endophyte is present in the formulation in an amount effective to detectably increase the biomass of the plant or tissue thereof. In some embodiments, the biomass of the plant, or tissue thereof is detectably increased by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, or more, when compared with a reference agricultural plant.

[0028] In some embodiments, the endophyte is present in the formulation in an amount effective to detectably increase the rate of germination of the seed. In some embodiments, the rate of germination of the seed is increased by at least 0.5%, at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100% or more, when compared with a reference agricultural plant.

[0029] In some embodiments, the endophyte is present in the formulation in an amount effective to detectably induce production of auxin in the plant. In some embodiments, the production of auxin in the plant is increased by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least

70%, at least 80%, at least 90%, at least 100% or more, when compared with a reference agricultural plant.

[0030] The invention also features an agricultural plant, or portion of tissue thereof, comprising a formulation comprising an endophyte that is common to at least two donor plant types that is disposed on an exterior surface of the plant or portion of tissue thereof, or within the plant or portion of tissue thereof, in an amount effective to colonize the plant, and in an amount effective to provide a benefit to the modern agricultural plant.

[0031] In some embodiments of the agricultural plant, or portion of tissue thereof, the endophyte comprises a nucleic acid sequence that is at least 97% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455. In some embodiments of the agricultural plant, or portion of tissue thereof, the endophyte comprises a nucleic acid sequence that is at least 99% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455. In some embodiments of the agricultural plant, or portion of tissue thereof, the endophyte comprises a nucleic acid sequence that is at least 99.5% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455.

[0032] In some embodiments of the agricultural plant, or portion of tissue thereof, the endophyte is capable of a function or activity selected from the group consisting of auxin production, nitrogen fixation, production of an antimicrobial compound, mineral phosphate solubilization, siderophore production, cellulase production, chitinase production, xylanase production, and acetoin production.

[0033] In some embodiments of the agricultural plant, or portion of tissue thereof, the endophyte exhibits at least two of: auxin production, nitrogen fixation, production of an antimicrobial compound, mineral phosphate solubilization, siderophore production, cellulase production, chitinase production, xylanase production, and acetoin production.

[0034] In some embodiments of the agricultural plant, or portion of tissue thereof, the endophyte is capable of metabolizing at least one substrate selected from the group consisting of: a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycy-L-

aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose.

[0035] In some embodiments of the agricultural plant, or portion of tissue thereof, the endophyte is capable of metabolizing at least two substrates selected from the group consisting of: a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose.

[0036] In some embodiments of the agricultural plant, or portion of tissue thereof, the formulation is disposed on an exterior surface of the plant or portion of tissue thereof, or within the plant or portion of tissue thereof, by spraying, immersing, coating, encapsulating, or dusting the plant or portion of tissue thereof with the formulation.

[0037] In some embodiments, the agricultural plant, or portion of tissue thereof further comprises a formulation that comprises at least one member selected from the group consisting of an agriculturally compatible carrier, a tackifier, a microbial stabilizer, a fungicide, an antibacterial agent, an herbicide, a nematicide, an insecticide, a plant growth regulator, a rodenticide, and a nutrient.

[0038] In some embodiments of the agricultural plant, or portion of tissue thereof, the benefit is selected from the group consisting of: increased root biomass, increased root length, increased height, increased shoot length, increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency,

increased overall biomass, increased yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance, increased salt tolerance, increased resistance to nematode stress, increased resistance to a fungal pathogen, increased resistance to a bacterial pathogen, increased resistance to a viral pathogen, increased resistance to herbivory, a detectable modulation in the level of a metabolite, a detectable modulation in the proteome, and a detectable modulation in the transcriptome, relative to a reference agricultural plant.

[0039] In some embodiments of the agricultural plant, or portion of tissue thereof, the benefit comprises at least two benefits selected from the group consisting of increased: root biomass, increased root length, increased height, increased shoot length, increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency, increased overall biomass, increased yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance, increased salt tolerance, increased resistance to nematode stress, increased resistance to a fungal pathogen, increased resistance to a bacterial pathogen, increased resistance to a viral pathogen, increased resistance to herbivory, a detectable modulation in the level of a metabolite, a detectable modulation in the proteome, and a detectable modulation in the transcriptome, relative to a reference agricultural plant. In some embodiments of the agricultural plant, or portion of tissue thereof, the benefit is increased tolerance to low nitrogen stress or increased nitrogen use efficiency, and the endophyte is non-diazotrophic.

[0040] In some embodiments of the agricultural plant, or portion of tissue thereof, the plant or portion of tissue thereof is contacted with at least 10 CFU or spores, at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores, at least 30,000 CFU or spores, at least 100,000 CFU or spores, at least 300,000 CFU or spores, at least 1,000,000 CFU or spores, or more, of the endophyte. In some embodiments of the agricultural plant, or portion of tissue thereof, the plant tissue is a seed. In a further embodiment, the endophyte is disposed on the surface of the seed.

[0041] In some embodiments, the agricultural plant, or portion of tissue thereof comprises at least two endophytes comprising a nucleic acid sequence that is at least 97% identical, at least 98% identical, at least 99% identical, at least 99.5% identical, or 100% identical, to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455 in an amount effective to colonize the mature agricultural plant. In some embodiments of

the agricultural plant, or portion of tissue thereof, the two endophytes are selected from the groups disclosed in Table 1, Table 2, Table 7 and Table 8.

[0042] In some embodiments, the agricultural plant is a monocot. In some embodiments, the portion of tissue thereof is derived from a monocot. The monocot can be corn, wheat, barley or rice.

[0043] In some embodiments, the agricultural plant is a dicot. In some embodiments, the portion of tissue thereof is derived from a dicot. The dicot can be a soybean, canola, cotton, Brassica Napus, tomato or pepper.

[0044] In some embodiments of the agricultural plant, or portion of tissue thereof, the endophyte is disposed in an amount effective to be detectable within a target tissue of the mature target tissue of the mature agricultural plant selected from a fruit, seed, leaf, root or portion thereof.

[0045] In some embodiments of the agricultural plant, or portion of tissue thereof, the population is disposed in an amount effective to increase the rate of germination of the seed. The rate of germination of the seed can be increased by at least 0.5%, at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100% or more, when compared with a reference agricultural plant.

[0046] In some embodiments of the agricultural plant, or portion of tissue thereof, the population is disposed in an amount effective to be detectable within a target tissue of the mature plant. The target tissue can be the root, shoot, leaf, flower, fruit or seed.

[0047] In some embodiments of the agricultural plant, or portion of tissue thereof, the population is detected in an amount of at least 10 CFU or spores, at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores, at least 30,000 CFU or spores, at least 100,000 CFU or spores, at least 300,000 CFU or spores, at least 1,000,000 CFU or spores, or more, in the plant or target tissue thereof.

[0048] In some embodiments of the agricultural plant, or portion of tissue thereof, the population of is disposed in an amount effective to be detectable in the rhizosphere surrounding the plant. The population can be detected in an amount of at least 10 CFU or spores, at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores, at least 30,000 CFU or spores, at

least 100,000 CFU or spores, at least 300,000 CFU or spores, at least 1,000,000 CFU or spores, or more, in the rhizosphere surrounding the plant.

[0049] In some embodiments of the agricultural plant, or portion of tissue thereof, the population is disposed in an amount effective to detectably increase the biomass of the plant. The biomass of the plant can be detectably increased by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, or more, when compared with a reference agricultural plant.

[0050] In some embodiments of the agricultural plant, or portion of tissue thereof, the population is disposed in an amount effective to increase the biomass of a fruit or seed of the plant. The biomass of the fruit or seed of the plant can be detectably increased by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, or more, when compared with the fruit or seed of a reference agricultural plant.

[0051] In some embodiments of the agricultural plant, or portion of tissue thereof, the population is disposed in an amount effective to increase the height of the plant. The height of the plant can be increased by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, or more, when compared with the height of a reference agricultural plant.

[0052] In some embodiments of the agricultural plant, or portion of tissue thereof, the population is disposed in an amount effective to increase production of auxin in the plant. The auxin production of the plant can be increased by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, or more, when compared with the auxin production of a reference agricultural plant.

[0053] In some embodiments of the agricultural plant, or portion of tissue thereof, the population is disposed in an amount effective to increase production of acetoin in the plant. The acetoin production of the plant can be increased by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, or more, when compared with the acetoin production of a reference agricultural plant.

[0054] In some embodiments of the agricultural plant, or portion of tissue thereof, the population is disposed in an amount effective to increase production of siderophore in the plant. The siderophore production of the plant can be increased by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, or more, when compared with the siderophore production of a reference agricultural plant.

[0055] In some embodiments of the agricultural plant, or portion of tissue thereof, the population is disposed in an amount effective to increase resistance to one or more stress conditions selected from the group consisting of a drought stress, heat stress, cold stress, salt stress, and low mineral stress.

[0056] In some embodiments of the agricultural plant, or portion of tissue thereof, the population is disposed in an amount effective to increase resistance to one or more biotic stress conditions selected from the group consisting of a nematode stress, insect herbivory stress, fungal pathogen stress, bacterial pathogen stress, and viral pathogen stress.

[0057] The invention also features bag comprising at least 1,000 seeds, wherein each seed comprises a formulation comprising an endophyte that is common to at least two donor plant types that is disposed on an exterior surface of the plant or portion of tissue thereof, or within the plant or portion of tissue thereof, in an amount effective to colonize the plant, and in an amount effective to provide a benefit to the modern agricultural plant, wherein each seed is contacted with at least 10 CFU or spores, at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores, at least 30,000 CFU or spores, at least 100,000 CFU or spores, at least 300,000 CFU or spores, at least 1,000,000 CFU or spores, or more, of the endophyte, and wherein the bag further comprises a label describing the seeds and/or the population.

[0058] In an embodiment, the invention features an agricultural formulation comprising an endophyte comprising a nucleic acid sequence that is at least 97% identical, at least 98% identical, at least 99% identical, at least 99.5% identical, or 100% identical, to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455 that is present in an amount effective to colonize a mature agricultural plant, wherein the formulation further comprises at least one member selected from the group consisting of an agriculturally compatible carrier, a tackifier, a microbial stabilizer, a fungicide, an antibacterial agent, an herbicide, a nematicide, an insecticide, a plant growth regulator, a rodenticide, and a nutrient.

[0059] In some embodiments of the agricultural formulation, the agricultural plant is a monocot. The monocot can be maize, barley, rice, or wheat. In some embodiments of the agricultural formulation, the agricultural plant is a dicot. The dicot can be soybean, canola, cotton, Brassica Napus, tomato, squash, cucumber, pepper, peanut, sunflower, or sugar beet.

[0060] In some embodiments of the agricultural formulation, the population consists essentially of an endophyte comprising a nucleic acid sequence that is at least 99% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455. In some embodiments of the agricultural formulation, the population consists essentially of an endophyte comprising a nucleic acid sequence that is at least 99.5% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455.

[0061] The preparation of claim 87, comprising at least two different endophytes each comprise a nucleic acid sequence that is at least 97% identical, at least 98% identical, at least 99% identical, at least 99.5% identical, or 100% identical, to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455.

[0062] In some embodiments of the agricultural formulation, each of the two different endophytes comprises the nucleic acid sequence disclosed in Table 1, Table 2, Table 7, and Table 8.

[0063] In some embodiments of the agricultural formulation, at least 1%, at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 75%, at least 80%, at least 90%, or at least 95% or more, of the population is in spore form.

[0064] In some embodiments of the agricultural formulation, the endophytes were adapted to culture on growth medium.

[0065] In some embodiments of the agricultural formulation, the preparation is substantially stable at temperatures between about 0°C and about 50°C for at least three days. In some embodiments of the agricultural formulation, the preparation is substantially stable at temperatures between about 4°C and about 37°C for at least thirty days.

[0066] In some embodiments, the agricultural formulation is formulated to provide a population of plants that demonstrates a substantially homogenous growth rate when introduced into agricultural production.

[0067] The invention also features a method for making the plant comprising a formulation comprising an endophyte that is common to at least two donor plant types that is

disposed on an exterior surface of the plant or portion of tissue thereof, or within the plant or portion of tissue thereof, in an amount effective to colonize the plant, and in an amount effective to provide a benefit to the modern agricultural plant. The method includes providing a modern agricultural plant, and applying to the plant a formulation comprising an endophyte comprising an endophytic microbe comprising a nucleic acid sequence that is at least 97% identical, at least 98% identical, at least 99% identical, at least 99.5% identical, or 100% identical, to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455 that is present in an amount effective to colonize the plant.

[0068] The invention also features a commodity plant product comprising a plant, or a portion or part thereof, comprising a formulation comprising an endophyte that is common to at least two donor plant types that is disposed on an exterior surface of the plant or portion of tissue thereof, or within the plant or portion of tissue thereof, in an amount effective to colonize the plant, and in an amount effective to provide a benefit to the modern agricultural plant. The commodity plant product can be a grain, a flour, a starch, a syrup, a meal, an oil, a film, a packaging, a nutraceutical product, a pulp, an animal feed, a fish fodder, a bulk material for industrial chemicals, a cereal product, a processed human-food product, a sugar or an alcohol and protein.

[0069] The invention also features a method of producing a commodity plant product. The method includes obtaining a plant or plant tissue from a plant, progeny or derivative thereof, the plant comprising a formulation comprising an endophyte that is common to at least two donor plant types that is disposed on an exterior surface of the plant or portion of tissue thereof, or within the plant or portion of tissue thereof, in an amount effective to colonize the plant, and in an amount effective to provide a benefit to the modern agricultural plant; and producing the commodity plant product therefrom.

[0070] The invention also features a synthetic combination comprising a purified microbial population in association with a plurality of seeds or seedlings of an agricultural plant, wherein the purified microbial population comprises a first endophyte, wherein the first endophyte comprises a 16S rRNA or ITS rRNA nucleic acid sequence at least 97% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455, and wherein the endophyte is present in the synthetic combination in an amount effective to provide a benefit to the seeds or seedlings or the plants derived from the seeds or seedlings.

[0071] In some embodiments of the synthetic combination comprising a purified microbial population, the first endophyte is capable of at least one of: production of an auxin, nitrogen fixation, production of an antimicrobial, production of a siderophore, mineral phosphate solubilization, production of a cellulase, production of a chitinase, production of a xylanase, and production of acetoin, or a combination of two or more thereof.

[0072] In some embodiments of the synthetic combination comprising a purified microbial population, the microbial population further comprises a second endophyte. In a further embodiment, the microbial population comprises a second microbial endophyte having an 16S rRNA or ITS rRNA nucleic acid sequence that is less than 95% identical to that of the first microbial endophyte.

[0073] In some embodiments of the synthetic combination comprising a purified microbial population, the microbial population further comprises a second endophyte, and wherein the first and second endophytes are independently capable of at least one of production of an auxin, nitrogen fixation, production of an antimicrobial, production of a siderophore, mineral phosphate solubilization, production of a cellulase, production of a chitinase, production of a xylanase, or production of acetoin, or a combination of two or more thereof.

[0074] In some embodiments of the synthetic combination comprising a purified microbial population, the first and second endophytes are independently capable of at least one of production of an auxin, nitrogen fixation, production of an antimicrobial, production of a siderophore, mineral phosphate solubilization, production of a cellulase, production of a chitinase, production of a xylanase, or production of acetoin, or a combination of two or more thereof.

[0075] In some embodiments of the synthetic combination comprising a purified microbial population, the microbial population further comprises a second endophyte, wherein the first and second endophytes are independently capable of metabolizing at least one substrate selected from the group consisting of: α -D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid,

glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose, or a combination of two or more thereof.

[0076] The invention also features a synthetic combination comprising at least two endophytes associated with a seed, wherein at least the first endophyte is heterologous to the seed and wherein the first endophyte comprises a 16S rRNA or ITS rRNA nucleic acid sequence at least 97% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455, wherein the endophytes are present in the formulation in an amount effective to provide a benefit to the seeds or seedlings or the plants derived from the seeds or seedlings.

[0077] In some embodiments of the synthetic combination comprising at least two endophytes, the second endophyte is a bacterial endophyte. In some embodiments of the synthetic combination comprising at least two endophytes, the second endophyte is a fungal endophyte.

[0078] In some embodiments of the synthetic combination comprising at least two endophytes, the first endophyte is a fungal endophyte. In some embodiments of the synthetic combination comprising at least two endophytes, the first endophyte is a fungal endophyte and the second endophyte is a fungal endophyte. In some embodiments of the synthetic combination comprising at least two endophytes, the first endophyte is a fungal endophyte and the second endophyte is a bacterial endophyte.

[0079] In some embodiments of the synthetic combination comprising at least two endophytes, the first and second endophytes are independently capable of metabolizing at least one substrate selected from the group consisting of: a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-

arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose, or a combination of two or more thereof.

[0080] In some embodiments of any of the synthetic combinations, the first endophyte is capable of metabolizing at least one substrate selected from the group of: a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose. In some embodiments of the synthetic combination comprising at least two endophytes associated with a seed, both of the endophytes are heterologous to the seed.

[0081] In some embodiments of any of the synthetic combinations, the synthetic combination is disposed within a packaging material selected from a bag, box, bin, envelope, carton, or container. In an embodiment of any of the synthetic combinations, the synthetic combination comprises 1000 seed weight amount of seeds, wherein the packaging material optionally comprises a desiccant, and wherein the synthetic combination optionally comprises an anti-fungal agent.

[0082] In some embodiments of any of the synthetic combinations, the first endophyte is localized on the surface of the seeds or seedlings. In some embodiments of any of the synthetic combinations, the first endophyte is obtained from a plant species other than the seeds or seedlings of the synthetic combination. In some embodiments of any of the synthetic combinations, the first endophyte is obtained from a plant cultivar different from the cultivar of the seeds or seedlings of the synthetic combination. In some embodiments of any of the synthetic combinations, the first endophyte is obtained from a plant cultivar that is the same as the cultivar of the seeds or seedlings of the synthetic combination.

[0083] In some embodiments of any of the synthetic combinations, the first endophyte is a bacterial endophyte.

[0084] In some embodiments of any of the synthetic combinations, the first endophyte is capable of at least two of auxin production, nitrogen fixation, production of an antimicrobial compound, mineral phosphate solubilization, siderophore production, cellulase production, chitinase production, xylanase production, and acetoin production.

[0085] In some embodiments of any of the synthetic combinations, the first endophyte is capable of metabolizing at least two substrates selected from the group consisting of: a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose.

[0086] In some embodiments of any of the synthetic combinations, the benefit is selected from the group consisting of: increased root biomass, increased root length, increased height, increased shoot length, increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency, increased overall biomass, increased grain yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance, increased salt tolerance, increased resistance to nematode stress, increased resistance to a fungal pathogen, increased resistance to a bacterial pathogen, increased resistance to a viral pathogen, a detectable modulation in the level of a metabolite, a detectable modulation in the transcriptome, and a detectable modulation in the proteome, relative to reference seeds or agricultural plants derived from reference seeds. In some embodiments, the benefit comprises at least two benefits selected from the group consisting of: increased root biomass, increased root length, increased height, increased shoot length, increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency, increased overall biomass, increased grain yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance,

increased salt tolerance, increased resistance to nematode stress, increased resistance to a fungal pathogen, increased resistance to a bacterial pathogen, increased resistance to a viral pathogen, a detectable modulation in the level of a metabolite, a detectable modulation in the transcriptome, and a detectable modulation in the proteome, relative to reference seeds or agricultural plants derived from reference seeds.

[0087] In some embodiments of any of the synthetic combinations, the combination comprises seeds and the first endophyte is associated with the seeds as a coating on the surface of the seeds. In some embodiments of any of the synthetic combinations, the combination comprises seedlings and the first endophyte is contacted with the seedlings as a spray applied to one or more leaves and/or one or more roots of the seedlings. In some embodiments of any of the synthetic combinations, the synthetic combination further comprises one or more additional endophyte species.

[0088] In some embodiments of any of the synthetic combinations, the effective amount is at least 1×10^2 CFU or spores/per seed. In some embodiments of any of the synthetic combinations, the effective amount is at least 1×10^3 CFU or spores/per seed. In some embodiments of any of the synthetic combinations, the combination comprises seeds and the effective amount is from about 1×10^2 CFU or spores/per seed to about 1×10^8 CFU or spores/per seed.

[0089] In some embodiments of any of the synthetic combinations, the seed is a seed from an agricultural plant. In some embodiments of any of the synthetic combinations, the seed is a transgenic seed.

[0090] In some embodiments of any of the synthetic combinations, the first endophytes are present in an amount of at least 10 CFU or spores, at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores, at least 30,000 CFU or spores, at least 100,000 CFU or spores, at least 300,000 CFU or spores, or at least 1,000,000 CFU spores per seed.

[0091] In some embodiments, any of the synthetic combinations further comprise one or more of the following: a stabilizer, or a preservative, or a carrier, or a surfactant, an anticomplex agent, or any combination thereof. In some embodiments, any of the synthetic combinations further comprise one or more of the following: fungicide, nematicide, bactericide, insecticide, and herbicide.

[0092] The invention also features a plurality of any of the synthetic combinations placed in a medium that promotes plant growth, the medium selected from the group consisting of: soil, hydroponic apparatus, and artificial growth medium. The invention also features a plurality of any of the synthetic combinations, wherein the synthetic combinations are shelf-stable.

[0093] The invention also features a plant grown from any of the synthetic combinations disclosed herein, the plant exhibiting an improved phenotype of agronomic interest, selected from the group consisting of: increased root biomass, increased root length, increased height, increased shoot length, increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency, increased overall biomass, increased grain yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance, increased salt tolerance, increased resistance to nematode stress, increased resistance to a fungal pathogen, increased resistance to a bacterial pathogen, increased resistance to a viral pathogen, a detectable modulation in the level of a metabolite, a detectable modulation in the transcriptome, and a detectable modulation in the proteome.

[0094] In some embodiments, the invention features a method for preparing an agricultural seed composition comprising contacting the surface of a plurality of seeds with a formulation comprising a purified microbial population that comprises at least two endophytes that are heterologous to the seed, wherein the first endophyte is capable of metabolizing at least one of a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose, wherein the endophytes are present in the formulation in an amount capable of modulating a trait of agronomic importance, as compared to isoline plants grown from seeds not contacted with the formulation.

[0095] In some embodiments, the invention features a method for preparing an agricultural seed composition, comprising contacting the surface of a plurality of seeds with a formulation comprising a purified microbial population that comprises at least two endophytes that are heterologous to the seed, wherein the first endophyte is capable of at least one function or activity selected from the group consisting of auxin production, nitrogen fixation, production of an antimicrobial compound, mineral phosphate solubilization, siderophore production, cellulase production, chitinase production, xylanase production, and acetoin production, wherein the endophytes are present in the formulation in an amount capable of modulating a trait of agronomic importance, as compared to isoline plants grown from seeds not contacted with the formulation.

[0096] In some embodiments, the invention features a method of improving a phenotype during water limited conditions of a plurality of host plants grown from a plurality of seeds, comprising treating the seeds with a formulation comprising at least two endophytes that are heterologous to the seeds, wherein the first endophyte is capable of metabolizing at least one of a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose, the phenotype improvement selected from the group consisting of: increased root biomass, increased root length, increased height, increased shoot length, increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency, increased overall biomass, increased grain yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance, increased salt tolerance, increased resistance to nematode stress, increased resistance to a fungal pathogen, increased resistance to a bacterial pathogen, increased resistance to a viral pathogen, a detectable modulation in the level of a metabolite, a detectable modulation in the transcriptome, and a detectable modulation in the proteome.

[0097] In some embodiments of the methods, the first endophyte is a bacterial endophyte. In some embodiments of the methods, the first endophyte is a bacterial endophyte and the second endophyte is a bacterial endophyte. In some embodiments of the methods, the first endophyte is a bacterial endophyte and the second endophyte is a fungal endophyte. In some embodiments of the methods, the first endophyte is a fungal endophyte. In some embodiments of the methods, the first endophyte is a fungal endophyte and the second endophyte is a fungal endophyte. In some embodiments of the methods, the first endophyte is a fungal endophyte and the second endophyte is a bacterial endophyte.

[0098] In some embodiments of the methods, the first endophyte is capable of metabolizing at least two of a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose.

[0099] In some embodiments of the methods, the second endophyte is capable of metabolizing at least two of a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose.

[0100] In some embodiments of the methods, the formulation comprises the purified microbial population at a concentration of at least about 1×10^2 CFU/ml or spores/ml in a liquid formulation or about 1×10^2 CFU/gm or spores/ml in a non-liquid formulation.

[0101] In some embodiments of the methods for preparing an agricultural seed composition, the trait of agronomic importance is selected from the group consisting of: increased root biomass, increased root length, increased height, increased shoot length, increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency, increased overall biomass, increased grain yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance, increased salt tolerance, increased resistance to nematode stress, increased resistance to a fungal pathogen, increased resistance to a bacterial pathogen, increased resistance to a viral pathogen, a detectable modulation in the level of a metabolite, a detectable modulation in the transcriptome, and a detectable modulation in the proteome.

[0102] In some embodiments of the methods, at least one of the endophytes is capable of localizing in a plant element of a plant grown from the seed, the plant element selected from the group consisting of: whole plant, seedling, meristematic tissue, ground tissue, vascular tissue, dermal tissue, seed, leaf, root, shoot, stem, flower, fruit, stolon, bulb, tuber, corm, keikis, and bud.

[0103] In some embodiments of the methods, at least one of the endophytes is capable of colonizing a plant element of a plant grown from the seed, the plant element selected from the group consisting of: whole plant, seedling, meristematic tissue, ground tissue, vascular tissue, dermal tissue, seed, leaf, root, shoot, stem, flower, fruit, stolon, bulb, tuber, corm, keikis, and bud.

[0104] In some embodiments of the methods, the formulation further comprises one or more of the following: a stabilizer, or a preservative, or a carrier, or a surfactant, or an anticomplex agent, or any combination thereof. In some embodiments of the methods, the formulation further comprises one or more of the following: fungicide, nematicide, bactericide, insecticide, and herbicide.

[0105] In some embodiments of the methods, the seed is a transgenic seed.

[0106] The invention also features a plant derived from one of the methods for preparing an agricultural seed composition, wherein the plant comprises in at least one of its plant elements the endophytes. In some embodiments, the invention also features progeny of the

plant derived from one of the methods for preparing an agricultural seed composition wherein the progeny comprises in at least one of its plant elements the endophytes.

[0107] In some embodiments of any of the methods, the endophyte expresses one or more genes encoding a protein whose amino acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 479, 483, 519, 532, 549, 557, 561, 562, 577, 578, 611, 626, 640, 656, 660, 666, 674, 676, 677, 678, 679, 680, 682, 683, 684, 685, 686, 688, 689, 690, 691, 692, 693, 696, 697, 698, 701, 704, 706, 710, 711, 716, 717, 718, 719, 720, 721, 722, 723, 724, 727, 728, 729, 730, 731, 732, 733, 734, 735, 737, 738, 741, 743, 744, 745, 746, 747, 748, 749, 751, 753, 756, 757, 759, 761, 762, 763, 764, 765, 766, 767, 768, 769, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 782, 783, 784, 785, 786, 788, 790, 793, 795, 796, 797, 798, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 815, 816, 817, 818, 819, 820, 822, 823, 824, 825, 826, 829, 830, 833, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 846, 848, 850, 851, 853, 854, 855, 856, 857, 858, 859, 860, 864, 865, 866, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 884, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 897, 898, 899, 901, 902, 903, 904, 905, 906, 907, 908, 910, 911, 912, 913, 914, 915, 916, 917, 918, 920, 921, 922, 923, 924, 926, 927, 928, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 968, 969, 971, 974, 976, 978, 979, 980, 984, 985, 987, 988, 989, 992, 993, 994, 995, 996, 998, 1000, 1001, 1002, 1003, 1006, 1008, 1010, 1011, 1012, 1014, 1015, 1016, 1017, 1018, 1019, 1021, 1022, 1023, 1024, 1025, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1036, 1037, 1038, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1055, 1056, 1058, 1059, 1060, 1062, 1064, 1065, 1066, 1068, 1070, 1071, 1072, 1076, 1077, 1079, 1080, 1081, 1083, 1085, 1086, 1087, 1088, 1090, 1091, 1092, 1094, 1095, 1096, 1097, 1098, 1099, 1101, 1102, 1103, 1104, 1106, 1107, 1108, 1110, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1121, 1122, 1123, 1124, 1126, 1127, 1129, 1130, 1131, 1132, 1133, 1134, 1136, 1137, 1138, 1139, 1140, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1151, 1153, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1174, 1176, 1178, 1179, 1180, 1181, 1182, 1183, 1184, 1185, 1186, 1188, 1189, 1190, 1191, 1192, 1193, 1194, 1196, 1197, 1198, 1199, 1200, 1201, 1203, 1205, 1206, 1207, 1208, 1209, 1210, 1211, 1213, 1214, 1216, 1217, 1218, 1219, 1221, 1222, 1223, 1225, 1226, 1228, 1229, 1230, 1231, 1232, 1233, 1235, 1237, 1238, 1239, 1241, 1242, 1243, 1244, 1245,

1246, 1247, 1248, 1249, 1250, 1251, 1252, 1253, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266, 1267, 1268, 1269, 1270, 1271, 1272, 1273, 1274, 1275, 1276, 1277, 1279, 1280, 1281, 1282, 1283, 1284, 1285, 1286, 1287, 1288, 1290, 1292, 1293, 1296, 1297, 1298, 1300, 1301, 1303, 1304, 1306, 1307, 1308, 1309, 1311, 1312, 1313, 1314, 1317, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1330, 1331, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1345, 1346, 1347, 1348, 1350, 1351, 1352, 1353, 1355, 1356, 1357, 1358, 1359, 1360, 1361, 1362, 1363, 1364, 1365, 1366, 1368, 1369, 1370, 1371, 1372, 1374, 1375, 1376, 1379, 1380, 1382, 1383, 1384, 1385, 1386, 1388, 1389, 1390, 1391, 1392, 1393, 1396, 1397, 1398, 1399, 1400, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1424, 1425, 1426, 1427, 1428, 1430, 1431, 1432, 1433, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 1448, 1449, 1450, 1452, 1453, 1456, 1459, 1466, 1467, 1469, 1471, 1478, 1479, 1482, 1483, 1484, 1485, 1487, 1488, 1489, 1490, 1495, 1497, 1498, 1499, 1500, 1501, 1504, 1505, 1506, 1508, 1511, 1513, 1514, 1516, 1520, 1526, 1529, 1534, 1535, 1537, 1538, 1540, 1545, 1547, 1548, 1549, 1550, 1551, 1552, 1553, 1554, 1556, 1559, 1561, 1562, 1565, 1566, 1568, 1569, 1570, 1571, 1573, 1574, 1575, 1576, 1577, 1578, 1579, 1580, 1581, 1582, 1583, 1585, 1588, 1589, 1591, 1592, 1593, 1594, 1595, 1596, 1597, 1598, 1601, 1603, 1604, 1605, 1607, 1608, 1609, 1611, 1612, 1613, 1614, 1615, 1616, 1617, 1618, 1619, 1620, 1622, 1624, 1625, 1626, 1627, 1628, 1629, 1630, 1632, 1633, 1636, 1637, 1638, 1639, 1640, 1641, 1642, 1643, 1644, 1646, 1647, 1648, 1650, 1651, 1652, 1654, 1657, 1659, 1660, 1661, 1664, 1665, 1666, 1667, 1668, 1671, 1673, 1675, 1676, 1678, 1679, 1681, 1684, 1685, 1686, 1689, 1690, 1692, 1693, 1694, 1695, 1696, 1697, 1698, 1701, 1705, 1706, 1707, 1709, 1711, 1712, 1713, 1714, 1716, 1717, 1718, 1720, 1721, 1723, 1724, 1725, 1726, 1728, 1729, 1731, 1732, 1734, 1735, 1736, 1737, 1738, 1739, 1740, 1741, 1743, 1744, 1745, 1746, 1747, 1750, 1751, 1753, 1754, 1755, 1760, 1761, 1762, 1763, 1764, 1765, 1767, 1770, 1771, 1772, 1775, 1776, 1777, 1778, 1779, 1780, 1781, 1782, 1786, 1787, 1788, 1789, 1791, 1792, 1793, 1794, 1795, 1797, 1798, 1799, 1800, 1801, 1803, 1804, 1805, 1806, 1809, 1810, 1811, 1814, 1815, 1818, 1819, 1820, 1821, 1822, 1823, 1824, 1825, 1826, 1828, 1830, 1831, 1833, 1835, 1836, 1837, 1838, 1839, 1840, 1841, 1842, 1843, 1846, 1851, 1852, 1854, 1857, 1858, 1860, 1861, 1862, 1863, 1864, 1866, 1868, 1869, 1870, 1872, 1873, 1874, 1875, 1876, 1878, 1879, 1880, 1881, 1883, 1884, 1885, 1887, 1888, 1892, 1893, 1894, 1896, 1898, 1899, 1900, 1901, 1902, 1903, 1904, 1905, 1906, 1907, 1910, 1911, 1913, 1915, 1916, 1917, 1918, 1920, 1921, 1924, 1925, 1926, 1927, 1928, 1930, 1932, 1933, 1934, 1935, 1938, 1939, 1940, 1942, 1943, 1945, 1946, 1948, 1949, 1950, 1951, 1953, 1954, 1955, 1959, 1960, 1961, 1962, 1963,

1965, 1966, 1967, 1970, 1971, 1973, 1975, 1976, 1977, 1979, 1981, 1982, 1983, 1984, 1985, 1986, 1988, 1990, 1994, 1995, 1996, 1998, 1999, 2000, 2001, 2002, 2003, 2006, 2007, 2008, 2009, 2010, 2011, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2052, 2054, 2055, 2059, 2060, 2062, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2074, 2076, 2077, 2080, 2081, 2082, 2083, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2095, 2096, 2097, 2098, 2100, 2101, 2102, 2103, 2104, 2105, 2108, 2109, 2110, 2112, 2113, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2125, 2127, 2128, 2129, 2131, 2132, 2134, 2135, 2136, 2138, 2140, 2141, 2142, 2143, 2145, 2146, 2147, 2148, 2149, 2150, 2153, 2154, 2155, 2156, 2158, 2159, 2160, 2162, 2163, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2174, 2176, 2177, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2188, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2200, 2202, 2204, 2205, 2206, 2207, 2208, 2210, 2211, 2212, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2238, 2239, 2241, 2242, 2243, 2244, 2245, 2246, 2248, 2249, 2251, 2253, 2254, 2255, 2257, 2258, 2259, 2261, 2262, 2265, 2267, 2268, 2269, and 2270.

[0108] In some embodiments of the methods, protein expression is modulated in response to the first endophyte contacting a plant element. In some embodiments, protein expression is upregulated in response to the first endophyte contacting a plant element. In some embodiments, the amino acid sequence of the upregulated protein is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 549, 640, 656, 676, 684, 690, 937, 1456, 1467, 1479, 1484, 1488, 1490, 1498, 1499, 1500, 1504, 1505, 1508, 1513, 1529, 1534, 1538, 1540, 1547, 1551, 1554, 1561, 1566, 1568, 1570, 1571, 1574, 1578, 1581, 1583, 1591, 1592, 1593, 1597, 1598, 1604, 1605, 1609, 1615, 1616, 1619, 1622, 1624, 1626, 1629, 1630, 1632, 1636, 1638, 1642, 1643, 1647, 1650, 1651, 1652, 1659, 1661, 1664, 1666, 1671, 1675, 1676, 1678, 1684, 1685, 1689, 1692, 1694, 1695, 1696, 1701, 1706, 1709, 1711, 1712, 1718, 1723, 1725, 1728, 1729, 1732, 1737, 1738, 1740, 1741, 1744, 1746, 1747, 1751, 1755, 1761, 1763, 1771, 1772, 1775, 1778, 1779, 1782, 1787, 1788, 1791, 1792, 1797, 1798, 1799, 1800, 1805, 1819, 1824, 1828, 1835, 1840, 1842, 1843, 1846, 1854, 1860, 1862, 1868, 1875, 1892, 1893, 1900, 1901, 1910, 1918, 1924, 1925, 1926, 1928, 1932, 1933, 1934, 1938, 1943, 1946, 1949, 1950, 1953, 1963, 1967, 1971, 1973, 1975, 1985, 1990, 1994, 1998, 2000, 2003, 2006, 2010, 2013, 2016, 2018, 2021, 2025, 2027, 2028, 2030, 2034, 2035, 2036, 2048, 2050, 2052, 2054,

2059, 2062, 2065, 2066, 2067, 2068, 2074, 2080, 2091, 2092, 2093, 2095, 2097, 2098, 2100, 2101, 2104, 2108, 2110, 2112, 2117, 2119, 2125, 2131, 2134, 2135, 2145, 2149, 2150, 2156, 2159, 2162, 2168, 2181, 2185, 2193, 2195, 2196, 2206, 2211, 2216, 2217, 2219, 2220, 2221, 2223, 2231, 2236, 2239, 2242, 2243, 2248, 2255, 2257, 2258, 2259, or 2262.

[0109] In some embodiments of the methods, protein expression is repressed in response to the first endophyte contacting a plant element. In some embodiments, the repressed protein amino acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 479, 483, 519, 532, 557, 626, 674, 678, 680, 683, 685, 688, 690, 696, 697, 701, 704, 706, 710, 711, 717, 720, 722, 723, 724, 728, 729, 730, 732, 733, 734, 737, 741, 744, 745, 748, 749, 751, 753, 756, 757, 761, 764, 766, 768, 769, 772, 773, 774, 778, 779, 782, 783, 784, 788, 790, 793, 795, 796, 797, 800, 802, 803, 806, 807, 808, 810, 812, 817, 818, 819, 820, 822, 825, 826, 833, 836, 837, 839, 841, 846, 848, 851, 853, 854, 855, 856, 857, 860, 864, 865, 866, 870, 872, 874, 876, 878, 879, 880, 881, 882, 884, 886, 887, 890, 891, 893, 894, 895, 898, 901, 903, 905, 907, 908, 910, 911, 912, 913, 915, 917, 918, 921, 924, 926, 927, 928, 933, 934, 935, 936, 937, 938, 940, 942, 944, 945, 946, 947, 950, 952, 954, 955, 957, 960, 961, 962, 963, 964, 968, 971, 976, 978, 979, 985, 987, 989, 992, 1000, 1001, 1002, 1003, 1006, 1008, 1012, 1014, 1018, 1019, 1021, 1022, 1024, 1025, 1028, 1031, 1032, 1034, 1037, 1038, 1040, 1042, 1043, 1046, 1047, 1050, 1051, 1056, 1059, 1064, 1065, 1068, 1070, 1072, 1077, 1079, 1083, 1086, 1087, 1091, 1094, 1095, 1098, 1102, 1103, 1104, 1110, 1111, 1112, 1113, 1114, 1116, 1117, 1118, 1121, 1126, 1130, 1132, 1133, 1134, 1136, 1139, 1143, 1146, 1147, 1151, 1155, 1156, 1158, 1159, 1160, 1162, 1163, 1165, 1168, 1170, 1172, 1174, 1176, 1180, 1182, 1183, 1186, 1188, 1192, 1193, 1194, 1196, 1197, 1198, 1209, 1214, 1217, 1218, 1219, 1221, 1222, 1223, 1225, 1226, 1230, 1237, 1242, 1244, 1249, 1251, 1253, 1256, 1260, 1261, 1262, 1264, 1270, 1272, 1274, 1276, 1279, 1280, 1283, 1284, 1285, 1286, 1288, 1290, 1292, 1298, 1300, 1303, 1307, 1309, 1311, 1312, 1313, 1320, 1321, 1324, 1325, 1328, 1330, 1331, 1333, 1336, 1337, 1339, 1340, 1344, 1346, 1352, 1353, 1355, 1357, 1358, 1359, 1360, 1361, 1363, 1364, 1365, 1370, 1375, 1376, 1379, 1380, 1383, 1384, 1386, 1390, 1391, 1392, 1393, 1396, 1399, 1400, 1402, 1405, 1408, 1411, 1412, 1418, 1420, 1422, 1427, 1428, 1431, 1433, 1438, 1439, 1440, 1442, 1444, 1445, 1449, or 1450.

[0110] In some embodiments of the methods, the protein is expressed with at least a two-fold difference, at least a three-fold difference, at least a four-fold difference, at least a five-fold difference, at least a six-fold difference, at least a seven-fold difference, at least an eight-

fold difference, at least a nine-fold difference, at least a ten-fold difference or more in expression level as compared to the protein expression level of a reference microorganism. In some embodiments, the difference in expression level of the protein is positive. In some embodiments, the difference in expression level of the protein is negative.

[0111] In some embodiments of the methods, the protein is involved in at least one KEGG pathway selected from the group consisting of: endocytosis, purine metabolism, inositol phosphate metabolism, and peroxisome. In some embodiments of the methods, the protein is involved in at least one KEGG pathway selected from the group consisting of: ko00403 (indole diterpene alkaloid biosynthesis), ko00522 (biosynthesis of 12-, 14- and 16-membered macrolides), ko00550 (peptidoglycan biosynthesis), ko00601 (glycosphingolipid biosynthesis – lacto and neolacto series), ko0901 (indole alkaloid biosynthesis), ko01052 (type I polyketide structures), ko010503 (biosynthesis of siderophore group nonribosomal peptides), ko01501 (beta-Lactam resistance), and ko04071 (sphingolipid signaling pathway).

[0112] In some embodiments of any of the methods, the plant, crop, seedling, or plant grown from the seed expresses one or more genes whose nucleic acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 4127, 4128, 4129, 4130, 4131, 4132, 4133, 4134, 4135, 4136, 4137, 4138, 4139, 4140, 4141, 4142, 4143, 4144, 4145, 4146, 4147, 4148, 4149, 4150, 4151, 4152, 4153, 4154, 4155, 4156, 4157, 4158, 4159, 4160, 4161, 4162, 4163, 4164, 4165, 4166, 4167, 4168, 4169, 4170, 4171, 4172, 4173, 4174, 4175, 4176, 4177, 4178, 4179, 4180, 4181, 4182, 4183, 4184, 4185, 4186, 4187, 4188, 4189, 4190, 4191, 4192, 4193, 4194, 4195, 4196, 4197, 4198, 4199, 4200, 4201, 4202, 4203, 4204, 4205, 4206, 4207, 4208, 4209, 4210, 4211, 4212, 4213, 4214, 4215, 4216, 4217, 4218, 4219, 4220, 4221, 4222, 4223, 4224, 4225, 4226, 4227, 4228, 4229, 4230, 4231, 4232, 4233, 4234, 4235, 4236, 4237, 4238, 4239, 4240, 4241, 4242, 4243, 4244, 4245, 4246, 4247, 4248, 4249, 4250, 4251, 4252, 4253, 4254, 4255, 4256, 4257, 4258, 4259, 4260, 4261, 4262, 4263, 4264, 4265, 4266, 4267, 4268, or 4269.

[0113] In some embodiments, the one or more plant genes are modulated in response to the first endophyte contacting the plant or plant element as compared to a reference microorganism contacting the plant or plant element. In some embodiments, the one or more plant genes are upregulated in response to the first endophyte contacting a plant element as compared to a reference microorganism contacting the plant or plant element. In some embodiments, the upregulated genes nucleic acid sequence is at least 95%, at least 96%, at

least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 4131, 4140, 4142, 4153, 4162, 4167, 4181, 4183, 4184, 4195, 4199, 4201, 4206, 4213, 4222, 4223, 4250, 4253, or 4269.

[0114] In some embodiments, the transcription of one or more genes are repressed in response to the first endophyte contacting a plant element as compared to a reference microorganism contacting the plant or plant element. In some embodiments, the repressed genes nucleic acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 4150.

[0115] In some embodiments, the one or more genes are expressed with at least a 0.5-fold difference, at least a 0.6-fold difference, at least a 0.7-fold difference, at least a 0.8-fold difference, at least a 0.9-fold difference, at least a 1.0-fold difference, at least a 1.1-fold difference, at least a 1.2-fold difference, at least a 1.3-fold difference or more in expression level as compared to the gene expression level of a reference microorganism. In some embodiments, the difference in expression level is positive. In some embodiments, the difference in expression level is negative.

[0116] In some embodiments, the one or more genes has at least one gene function selected from the group consisting of: cell wall modification, defense response, oxidation-reduction process, biological process, regulation of transcription, metabolic process, glucosinolate biosynthetic process, response to karrikin, protein phosphorylation, protein folding, response to chitin, proteolysis, response to auxin stimulus, DNA-dependent regulation of transcription, N-terminal protein myristoylation, response to oxidative stress, cellular component, leaf senescence, resistance gene-dependent defense response signaling pathway, zinc ion binding, response to cold, malate metabolic process, transport, catalytic activity, response to ozone, VQ motif, regulation of systemic acquired resistance, potassium ion transport, anaerobic respiration, multicellular organismal development, response to heat, methyltransferase activity, response to wounding, oxidation-reduction process, monooxygenase activity, oxidation-reduction process, carbohydrate metabolic process, exocytosis, nuclear-transcribed mRNA poly(A) tail shortening, sodium ion transport, glycerol metabolic process, on willebrand factor A3, response to water deprivation, response to salt stress, and chlorophyll biosynthetic process. In some embodiments, the gene has a gene ontology (GO) identifier selected from the group consisting of: GO:0003824, GO, catalytic activity; GO:0006355, GO, regulation of transcription, DNA-dependent; GO:0009870, GO,

defense response signaling pathway, resistance gene-dependent; GO:0008150, GO, biological_process; GO:0010200, GO, response to chitin; GO:0006508, GO, proteolysis; GO:0010193, GO, response to ozone; GO:0006979, GO, response to oxidative stress; and GO:0005975, GO, carbohydrate metabolic process.

[0117] In some embodiments, the gene function is selected from the following group: single-stranded DNA specific endodeoxyribonuclease activity, sequence-specific DNA binding transcription factor activity, NAD⁺ ADP-ribosyltransferase activity, metalloendopeptidase activity, DNA catabolic process, cellular iron ion homeostasis, response to osmotic stress, metallopeptidase activity, zinc ion binding, response to wounding, camalexin biosynthetic process, endoribonuclease activity, producing 5'-phosphomonoesters, cellular response to heat, T/G mismatch-specific endonuclease activity, polyamine oxidase activity, flavin adenine dinucleotide binding, cellular heat acclimation, cellular response to ethylene stimulus, cellular response to nitric oxide, and reactive oxygen species metabolic process.

[0118] In some embodiments, the endophyte comprises an ITS rRNA nucleic acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the nucleic acid sequence of SEQ ID NO: 344.

[0119] In some embodiments of any of the methods, the endophyte expresses one or more genes encoding a protein whose amino acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 477-501, 505, 514, 518, 521, 528, 530, 531, 550, 566, 567, 572, 579, 580, 581, 587, 593, 600, 602, 614, 623, 630, 635, 643, 645, 652, 657, 661, 662, 667, 670, 672, 673, 4510-4535, 4540, 4541, 4542, 4547, 4555, 4558, 4560, 4569, 4570, 4571, 4572, 4577, 4582, 4592, 4594, 4602, 4608, 4609, 4622, 4626, 4641, 4643, 4653, 4654, 4742-4766, 4734, 4739, 4740, 477, 478, 480, 482, 484, 485, 487, 489, 494, 496, 497, 501, 530, 567, 587, 602, 614, 633, 645, 649, 651, 652, 658, 665, 666, 667, 673, 874, 934, 1013, 1249, 1342, 2252, 2272, 2273, 2281, 2282, 2284, 2285, 2286, 2287, 2289, 2290, 2291, 2292, 2293, 2296, 4510, 4514, 4515, 4518, 4520, 4521, 4525, 4526, 4527, 4529, 4532, 4538, 4539, 4540, 4555, 4559, 4560, 4562, 4569, 4570, 4571, 4572, 4577, 4581, 4582, 4594, 4595, 4597, 4608, 4615, 4618, 4623, 4624, 4626, 4630, 4632, 4635, 4641, 4642, 4646, 4650, 4658, 4659, 4661, 4662, 4663, 4666, 4667, 4668, 4670, 4799, 4801, 4802, 4803, 4804, 4805, 4826, 4827, 4828, 4829, 4830, 4831, 4832, 4833, 4834, 4835, 4836, 4837, 4838, 4839, 4840, 4841, 4863, 4864, 4865, 4866, 4867, 4868, 4869, 4870, 4871, 4872, 4873, 4874, 4875, 4876, 4877, 4878,

4879, 4880, 4881, 4882, 4883, 4884, 4885, 4886, 4887, 4888, 4889, 4890, 4891, 4892, 4893, 4894, 4917, 4918, 4919, 4920, 4921, 4922, 4923, 4924, 4925, 4939, 4940, 4941, 4943, 4947, 4948, 4950, 4951, 4955, 4956, 4957, 2315, 2320, 2322, 2326, 2349, 2350, 2352, 2377, 2382, 2390, 2407, 2422, 2436, 2443, 2457, 2463, 2464, 2470, 2477, 2483, 2721, 2968, 3093, 3185, 4096, 4097, 4098, 4099, 4100, 4101, 4102, 4103, 4104, 4105, 4106, 4107, 4108, 4109, 4110, 4111, 4112, 4113, 4114, 4115, 4116, 4117, 4118, 4119, 4120, 4121, 4122, 4123, 4124, 4125, 4126, 4346, 4353, 4362, 4369, 4386, 4391, 4394, 4408, 4410, 4413, 4415, 4422, 4423, 4432, 4433, 4442, 4469, 4487, 4489, 4491, 4493, 4494, 4495, 4496, 4497, 4498, 4499, 4500, 4501, 4502, 4503, 4504, 4505, 4506, 4507, 4508, 4509, 4343, 4484, 4485, 4486, 4488, 4490, and 4492. In some embodiments of any of the methods, the endophyte expresses one or more genes involved in starch and sucrose metabolism, cell wall degradation, or protection from oxidative stress.

[0120] In some embodiments, the protein is expressed with at least a two-fold difference, at least a three-fold difference, at least a four-fold difference, at least a five-fold difference, at least a six-fold difference, at least a seven-fold difference, at least an eight-fold difference, at least a nine-fold difference, at least a ten-fold difference or more in expression level as compared to the protein expression level of a reference microorganism. In some embodiments, the difference in expression level is positive. In some embodiments, the difference in expression level is negative.

[0121] In some embodiments, the endophyte comprises an ITS rRNA nucleic acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 344 and 447. In some embodiments, the endophyte comprises a 16S rRNA nucleic acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 439 or 441.

[0122] In some embodiments of any of the methods, the endophyte expresses one or more genes encoding a protein whose amino acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 479, 483, 519, 532, 549, 557, 561, 562, 577, 578, 611, 626, 640, 656, 660, 666, 674, 676, 677, 678, 679, 680, 682, 683, 684, 685, 686, 688, 689, 690, 691, 692, 693, 696, 697, 698, 701, 704, 706, 710, 711, 716, 717, 718, 719, 720, 721, 722, 723, 724, 727, 728, 729, 730, 731, 732, 733, 734, 735, 737, 738, 741, 743, 744, 745, 746, 747, 748, 749, 751, 753, 756, 757, 759, 761, 762, 763, 764, 765, 766, 767, 768, 769,

771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 782, 783, 784, 785, 786, 788, 790, 793, 795, 796, 797, 798, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 815, 816, 817, 818, 819, 820, 822, 823, 824, 825, 826, 829, 830, 833, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 846, 848, 850, 851, 853, 854, 855, 856, 857, 858, 859, 860, 864, 865, 866, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 884, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 897, 898, 899, 901, 902, 903, 904, 905, 906, 907, 908, 910, 911, 912, 913, 914, 915, 916, 917, 918, 920, 921, 922, 923, 924, 926, 927, 928, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 968, 969, 971, 974, 976, 978, 979, 980, 984, 985, 987, 988, 989, 992, 993, 994, 995, 996, 998, 1000, 1001, 1002, 1003, 1006, 1008, 1010, 1011, 1012, 1014, 1015, 1016, 1017, 1018, 1019, 1021, 1022, 1023, 1024, 1025, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1036, 1037, 1038, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1055, 1056, 1058, 1059, 1060, 1062, 1064, 1065, 1066, 1068, 1070, 1071, 1072, 1076, 1077, 1079, 1080, 1081, 1083, 1085, 1086, 1087, 1088, 1090, 1091, 1092, 1094, 1095, 1096, 1097, 1098, 1099, 1101, 1102, 1103, 1104, 1106, 1107, 1108, 1110, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1121, 1122, 1123, 1124, 1126, 1127, 1129, 1130, 1131, 1132, 1133, 1134, 1136, 1137, 1138, 1139, 1140, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1151, 1153, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1174, 1176, 1178, 1179, 1180, 1181, 1182, 1183, 1184, 1185, 1186, 1188, 1189, 1190, 1191, 1192, 1193, 1194, 1196, 1197, 1198, 1199, 1200, 1201, 1203, 1205, 1206, 1207, 1208, 1209, 1210, 1211, 1213, 1214, 1216, 1217, 1218, 1219, 1221, 1222, 1223, 1225, 1226, 1228, 1229, 1230, 1231, 1232, 1233, 1235, 1237, 1238, 1239, 1241, 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1252, 1253, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266, 1267, 1268, 1269, 1270, 1271, 1272, 1273, 1274, 1275, 1276, 1277, 1279, 1280, 1281, 1282, 1283, 1284, 1285, 1286, 1287, 1288, 1290, 1292, 1293, 1296, 1297, 1298, 1300, 1301, 1303, 1304, 1306, 1307, 1308, 1309, 1311, 1312, 1313, 1314, 1317, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1330, 1331, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1345, 1346, 1347, 1348, 1350, 1351, 1352, 1353, 1355, 1356, 1357, 1358, 1359, 1360, 1361, 1362, 1363, 1364, 1365, 1366, 1368, 1369, 1370, 1371, 1372, 1374, 1375, 1376, 1379, 1380, 1382, 1383, 1384, 1385, 1386, 1388, 1389, 1390, 1391, 1392, 1393, 1396, 1397, 1398, 1399, 1400, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1424, 1425, 1426, 1427, 1428, 1430, 1431, 1432, 1433, 1437, 1438, 1439, 1440, 1441,

1442, 1443, 1444, 1445, 1446, 1447, 1448, 1449, 1450, 1452, 1453, 1456, 1459, 1466, 1467, 1469, 1471, 1478, 1479, 1482, 1483, 1484, 1485, 1487, 1488, 1489, 1490, 1495, 1497, 1498, 1499, 1500, 1501, 1504, 1505, 1506, 1508, 1511, 1513, 1514, 1516, 1520, 1526, 1529, 1534, 1535, 1537, 1538, 1540, 1545, 1547, 1548, 1549, 1550, 1551, 1552, 1553, 1554, 1556, 1559, 1561, 1562, 1565, 1566, 1568, 1569, 1570, 1571, 1573, 1574, 1575, 1576, 1577, 1578, 1579, 1580, 1581, 1582, 1583, 1585, 1588, 1589, 1591, 1592, 1593, 1594, 1595, 1596, 1597, 1598, 1601, 1603, 1604, 1605, 1607, 1608, 1609, 1611, 1612, 1613, 1614, 1615, 1616, 1617, 1618, 1619, 1620, 1622, 1624, 1625, 1626, 1627, 1628, 1629, 1630, 1632, 1633, 1636, 1637, 1638, 1639, 1640, 1641, 1642, 1643, 1644, 1646, 1647, 1648, 1650, 1651, 1652, 1654, 1657, 1659, 1660, 1661, 1664, 1665, 1666, 1667, 1668, 1671, 1673, 1675, 1676, 1678, 1679, 1681, 1684, 1685, 1686, 1689, 1690, 1692, 1693, 1694, 1695, 1696, 1697, 1698, 1701, 1705, 1706, 1707, 1709, 1711, 1712, 1713, 1714, 1716, 1717, 1718, 1720, 1721, 1723, 1724, 1725, 1726, 1728, 1729, 1731, 1732, 1734, 1735, 1736, 1737, 1738, 1739, 1740, 1741, 1743, 1744, 1745, 1746, 1747, 1750, 1751, 1753, 1754, 1755, 1760, 1761, 1762, 1763, 1764, 1765, 1767, 1770, 1771, 1772, 1775, 1776, 1777, 1778, 1779, 1780, 1781, 1782, 1786, 1787, 1788, 1789, 1791, 1792, 1793, 1794, 1795, 1797, 1798, 1799, 1800, 1801, 1803, 1804, 1805, 1806, 1809, 1810, 1811, 1814, 1815, 1818, 1819, 1820, 1821, 1822, 1823, 1824, 1825, 1826, 1828, 1830, 1831, 1833, 1835, 1836, 1837, 1838, 1839, 1840, 1841, 1842, 1843, 1846, 1851, 1852, 1854, 1857, 1858, 1860, 1861, 1862, 1863, 1864, 1866, 1868, 1869, 1870, 1872, 1873, 1874, 1875, 1876, 1878, 1879, 1880, 1881, 1883, 1884, 1885, 1887, 1888, 1892, 1893, 1894, 1896, 1898, 1899, 1900, 1901, 1902, 1903, 1904, 1905, 1906, 1907, 1910, 1911, 1913, 1915, 1916, 1917, 1918, 1920, 1921, 1924, 1925, 1926, 1927, 1928, 1930, 1932, 1933, 1934, 1935, 1938, 1939, 1940, 1942, 1943, 1945, 1946, 1948, 1949, 1950, 1951, 1953, 1954, 1955, 1959, 1960, 1961, 1962, 1963, 1965, 1966, 1967, 1970, 1971, 1973, 1975, 1976, 1977, 1979, 1981, 1982, 1983, 1984, 1985, 1986, 1988, 1990, 1994, 1995, 1996, 1998, 1999, 2000, 2001, 2002, 2003, 2006, 2007, 2008, 2009, 2010, 2011, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2052, 2054, 2055, 2059, 2060, 2062, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2074, 2076, 2077, 2080, 2081, 2082, 2083, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2095, 2096, 2097, 2098, 2100, 2101, 2102, 2103, 2104, 2105, 2108, 2109, 2110, 2112, 2113, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2125, 2127, 2128, 2129, 2131, 2132, 2134, 2135, 2136, 2138, 2140, 2141, 2142, 2143, 2145, 2146, 2147, 2148, 2149, 2150, 2153, 2154, 2155, 2156, 2158, 2159, 2160, 2162, 2163, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2174, 2176, 2177, 2179, 2180, 2181, 2182, 2183,

2184, 2185, 2186, 2188, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2200, 2202, 2204, 2205, 2206, 2207, 2208, 2210, 2211, 2212, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2238, 2239, 2241, 2242, 2243, 2244, 2245, 2246, 2248, 2249, 2251, 2253, 2254, 2255, 2257, 2258, 2259, 2261, 2262, 2265, 2267, 2268, 2269, and 2270.

[0123] In some embodiments of any of the methods, expression of the protein is modulated in response to the first endophyte contacting a plant element.

[0124] In some embodiments, expression of the protein is upregulated in response to the first endophyte contacting a plant element. In some embodiments, the amino acid sequence of the upregulated protein is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 549, 640, 656, 676, 684, 690, 937, 1456, 1467, 1479, 1484, 1488, 1490, 1498, 1499, 1500, 1504, 1505, 1508, 1513, 1529, 1534, 1538, 1540, 1547, 1551, 1554, 1561, 1566, 1568, 1570, 1571, 1574, 1578, 1581, 1583, 1591, 1592, 1593, 1597, 1598, 1604, 1605, 1609, 1615, 1616, 1619, 1622, 1624, 1626, 1629, 1630, 1632, 1636, 1638, 1642, 1643, 1647, 1650, 1651, 1652, 1659, 1661, 1664, 1666, 1671, 1675, 1676, 1678, 1684, 1685, 1689, 1692, 1694, 1695, 1696, 1701, 1706, 1709, 1711, 1712, 1718, 1723, 1725, 1728, 1729, 1732, 1737, 1738, 1740, 1741, 1744, 1746, 1747, 1751, 1755, 1761, 1763, 1771, 1772, 1775, 1778, 1779, 1782, 1787, 1788, 1791, 1792, 1797, 1798, 1799, 1800, 1805, 1819, 1824, 1828, 1835, 1840, 1842, 1843, 1846, 1854, 1860, 1862, 1868, 1875, 1892, 1893, 1900, 1901, 1910, 1918, 1924, 1925, 1926, 1928, 1932, 1933, 1934, 1938, 1943, 1946, 1949, 1950, 1953, 1963, 1967, 1971, 1973, 1975, 1985, 1990, 1994, 1998, 2000, 2003, 2006, 2010, 2013, 2016, 2018, 2021, 2025, 2027, 2028, 2030, 2034, 2035, 2036, 2048, 2050, 2052, 2054, 2059, 2062, 2065, 2066, 2067, 2068, 2074, 2080, 2091, 2092, 2093, 2095, 2097, 2098, 2100, 2101, 2104, 2108, 2110, 2112, 2117, 2119, 2125, 2131, 2134, 2135, 2145, 2149, 2150, 2156, 2159, 2162, 2168, 2181, 2185, 2193, 2195, 2196, 2206, 2211, 2216, 2217, 2219, 2220, 2221, 2223, 2231, 2236, 2239, 2242, 2243, 2248, 2255, 2257, 2258, 2259, or 2262.

[0125] In some embodiments, expression of the protein is repressed in response to the first endophyte contacting a plant element. In some embodiments, the repressed protein amino acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 479, 483, 519, 532, 557, 626, 674, 678, 680, 683, 685, 688, 690, 696, 697, 701, 704, 706, 710, 711, 717, 720, 722, 723, 724, 728, 729, 730, 732, 733, 734, 737, 741, 744, 745,

748, 749, 751, 753, 756, 757, 761, 764, 766, 768, 769, 772, 773, 774, 778, 779, 782, 783, 784, 788, 790, 793, 795, 796, 797, 800, 802, 803, 806, 807, 808, 810, 812, 817, 818, 819, 820, 822, 825, 826, 833, 836, 837, 839, 841, 846, 848, 851, 853, 854, 855, 856, 857, 860, 864, 865, 866, 870, 872, 874, 876, 878, 879, 880, 881, 882, 884, 886, 887, 890, 891, 893, 894, 895, 898, 901, 903, 905, 907, 908, 910, 911, 912, 913, 915, 917, 918, 921, 924, 926, 927, 928, 933, 934, 935, 936, 937, 938, 940, 942, 944, 945, 946, 947, 950, 952, 954, 955, 957, 960, 961, 962, 963, 964, 968, 971, 976, 978, 979, 985, 987, 989, 992, 1000, 1001, 1002, 1003, 1006, 1008, 1012, 1014, 1018, 1019, 1021, 1022, 1024, 1025, 1028, 1031, 1032, 1034, 1037, 1038, 1040, 1042, 1043, 1046, 1047, 1050, 1051, 1056, 1059, 1064, 1065, 1068, 1070, 1072, 1077, 1079, 1083, 1086, 1087, 1091, 1094, 1095, 1098, 1102, 1103, 1104, 1110, 1111, 1112, 1113, 1114, 1116, 1117, 1118, 1121, 1126, 1130, 1132, 1133, 1134, 1136, 1139, 1143, 1146, 1147, 1151, 1155, 1156, 1158, 1159, 1160, 1162, 1163, 1165, 1168, 1170, 1172, 1174, 1176, 1180, 1182, 1183, 1186, 1188, 1192, 1193, 1194, 1196, 1197, 1198, 1209, 1214, 1217, 1218, 1219, 1221, 1222, 1223, 1225, 1226, 1230, 1237, 1242, 1244, 1249, 1251, 1253, 1256, 1260, 1261, 1262, 1264, 1270, 1272, 1274, 1276, 1279, 1280, 1283, 1284, 1285, 1286, 1288, 1290, 1292, 1298, 1300, 1303, 1307, 1309, 1311, 1312, 1313, 1320, 1321, 1324, 1325, 1328, 1330, 1331, 1333, 1336, 1337, 1339, 1340, 1344, 1346, 1352, 1353, 1355, 1357, 1358, 1359, 1360, 1361, 1363, 1364, 1365, 1370, 1375, 1376, 1379, 1380, 1383, 1384, 1386, 1390, 1391, 1392, 1393, 1396, 1399, 1400, 1402, 1405, 1408, 1411, 1412, 1418, 1420, 1422, 1427, 1428, 1431, 1433, 1438, 1439, 1440, 1442, 1444, 1445, 1449, or 1450.

[0126] In some embodiments, the protein is expressed with at least a two-fold difference, at least a three-fold difference, at least a four-fold difference, at least a five-fold difference, at least a six-fold difference, at least a seven-fold difference, at least an eight-fold difference, at least a nine-fold difference, at least a ten-fold difference or more in expression level as compared to the protein expression level of a reference microorganism. In some embodiments of any of the methods, the difference in expression level is positive. In some embodiments, the difference in expression level is negative.

[0127] In some embodiments, the protein is involved in at least one KEGG pathway selected from the group consisting of: endocytosis, purine metabolism, inositol phosphate metabolism, and peroxisome. In some embodiments, the protein is involved in at least one KEGG pathway selected from the group consisting of: ko00403 (indole diterpene alkaloid biosynthesis), ko00522 (biosynthesis of 12-, 14- and 16-membered macrolides), ko00550 (peptidoglycan biosynthesis), ko00601 (glycosphingolipid biosynthesis – lacto and neolacto

series), ko0901 (indole alkaloid biosynthesis), ko01052 (type I polyketide structures), ko010503 (biosynthesis of siderophore group nonribosomal peptides), ko01501 (beta-Lactam resistance), and ko04071 (sphingolipid signaling pathway).

[0128] In some embodiments of any of the plants, formulations, synthetic combinations, or other compositions of the invention, the plant, crop, seedling, or plant grown from the seed expresses one or more genes whose nucleic acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 4127, 4128, 4129, 4130, 4131, 4132, 4133, 4134, 4135, 4136, 4137, 4138, 4139, 4140, 4141, 4142, 4143, 4144, 4145, 4146, 4147, 4148, 4149, 4150, 4151, 4152, 4153, 4154, 4155, 4156, 4157, 4158, 4159, 4160, 4161, 4162, 4163, 4164, 4165, 4166, 4167, 4168, 4169, 4170, 4171, 4172, 4173, 4174, 4175, 4176, 4177, 4178, 4179, 4180, 4181, 4182, 4183, 4184, 4185, 4186, 4187, 4188, 4189, 4190, 4191, 4192, 4193, 4194, 4195, 4196, 4197, 4198, 4199, 4200, 4201, 4202, 4203, 4204, 4205, 4206, 4207, 4208, 4209, 4210, 4211, 4212, 4213, 4214, 4215, 4216, 4217, 4218, 4219, 4220, 4221, 4222, 4223, 4224, 4225, 4226, 4227, 4228, 4229, 4230, 4231, 4232, 4233, 4234, 4235, 4236, 4237, 4238, 4239, 4240, 4241, 4242, 4243, 4244, 4245, 4246, 4247, 4248, 4249, 4250, 4251, 4252, 4253, 4254, 4255, 4256, 4257, 4258, 4259, 4260, 4261, 4262, 4263, 4264, 4265, 4266, 4267, 4268, or 4269.

[0129] In some embodiments, the one or more plant genes are modulated in response to the first endophyte contacting the plant or plant element as compared to a reference microorganism contacting the plant or plant element.

[0130] In some embodiments, the one or more plant genes are upregulated in response to the first endophyte contacting a plant element as compared to a reference microorganism contacting the plant or plant element. In some embodiments, the upregulated gene's nucleic acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 4131, 4140, 4142, 4153, 4162, 4167, 4181, 4183, 4184, 4195, 4199, 4201, 4206, 4213, 4222, 4223, 4250, 4253, or 4269.

[0131] In some embodiments, the transcription of one or more genes are repressed in response to the first endophyte contacting a plant element as compared to a reference microorganism contacting the plant or plant element. In some embodiments, the repressed genes nucleic acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least

99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 4150.

[0132] In some embodiments, the one or more genes are expressed with at least a 0.5-fold difference, at least a 0.6-fold difference, at least a 0.7-fold difference, at least a 0.8-fold difference, at least a 0.9-fold difference, at least a 1.0-fold difference, at least a 1.1-fold difference, at least a 1.2-fold difference, at least a 1.3-fold difference or more in expression level as compared to the gene expression level of a reference microorganism. In some embodiments, the difference in expression level is positive. In some embodiments, the difference in expression level is negative.

[0133] In some embodiments, the one or more genes has at least one gene function selected from the group consisting of: cell wall modification, defense response, oxidation-reduction process, biological process, regulation of transcription, metabolic process, glucosinolate biosynthetic process, response to karrikin, protein phosphorylation, protein folding, response to chitin, proteolysis, response to auxin stimulus, DNA-dependent regulation of transcription, N-terminal protein myristoylation, response to oxidative stress, cellular component, leaf senescence, resistance gene-dependent defense response signaling pathway, zinc ion binding, response to cold, malate metabolic process, transport, catalytic activity, response to ozone, VQ motif, regulation of systemic acquired resistance, potassium ion transport, anaerobic respiration, multicellular organismal development, response to heat, methyltransferase activity, response to wounding, oxidation-reduction process, monooxygenase activity, oxidation-reduction process, carbohydrate metabolic process, exocytosis, nuclear-transcribed mRNA poly(A) tail shortening, sodium ion transport, glycerol metabolic process, on willebrand factor A3, response to water deprivation, response to salt stress, and chlorophyll biosynthetic process. In some embodiments, the gene has a gene ontology (GO) identifier selected from the group consisting of: GO:0003824, GO, catalytic activity; GO:0006355, GO, regulation of transcription, DNA-dependent; GO:0009870, GO, defense response signaling pathway, resistance gene-dependent; GO:0008150, GO, biological_process; GO:0010200, GO, response to chitin; GO:0006508, GO, proteolysis; GO:0010193, GO, response to ozone; GO:0006979, GO, response to oxidative stress; and GO:0005975, GO, carbohydrate metabolic process.

[0134] In some embodiments, the gene function is selected from the following group: single-stranded DNA specific endodeoxyribonuclease activity, sequence-specific DNA binding transcription factor activity, NAD⁺ ADP-ribosyltransferase activity,

metalloendopeptidase activity, DNA catabolic process, cellular iron ion homeostasis, response to osmotic stress, metallopeptidase activity, zinc ion binding, response to wounding, camalexin biosynthetic process, endoribonuclease activity, producing 5'-phosphomonoesters, cellular response to heat, T/G mismatch-specific endonuclease activity, polyamine oxidase activity, flavin adenine dinucleotide binding, cellular heat acclimation, cellular response to ethylene stimulus, cellular response to nitric oxide, and reactive oxygen species metabolic process.

[0135] In some embodiments, the endophyte comprises an ITS rRNA nucleic acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the nucleic acid sequence of SEQ ID NO: 344.

[0136] In some embodiments of any of the plants, formulations, synthetic combinations, or other compositions of the invention, the endophyte expresses one or more genes encoding a protein whose amino acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 477-501, 505, 514, 518, 521, 528, 530, 531, 550, 566, 567, 572, 579, 580, 581, 587, 593, 600, 602, 614, 623, 630, 635, 643, 645, 652, 657, 661, 662, 667, 670, 672, 673, 4510-4535, 4540, 4541, 4542, 4547, 4555, 4558, 4560, 4569, 4570, 4571, 4572, 4577, 4582, 4592, 4594, 4602, 4608, 4609, 4622, 4626, 4641, 4643, 4653, 4654, 4742-4766, 4734, 4739, 4740, 477, 478, 480, 482, 484, 485, 487, 489, 494, 496, 497, 501, 530, 567, 587, 602, 614, 633, 645, 649, 651, 652, 658, 665, 666, 667, 673, 874, 934, 1013, 1249, 1342, 2252, 2272, 2273, 2281, 2282, 2284, 2285, 2286, 2287, 2289, 2290, 2291, 2292, 2293, 2296, 4510, 4514, 4515, 4518, 4520, 4521, 4525, 4526, 4527, 4529, 4532, 4538, 4539, 4540, 4555, 4559, 4560, 4562, 4569, 4570, 4571, 4572, 4577, 4581, 4582, 4594, 4595, 4597, 4608, 4615, 4618, 4623, 4624, 4626, 4630, 4632, 4635, 4641, 4642, 4646, 4650, 4658, 4659, 4661, 4662, 4663, 4666, 4667, 4668, 4670, 4799, 4801, 4802, 4803, 4804, 4805, 4826, 4827, 4828, 4829, 4830, 4831, 4832, 4833, 4834, 4835, 4836, 4837, 4838, 4839, 4840, 4841, 4863, 4864, 4865, 4866, 4867, 4868, 4869, 4870, 4871, 4872, 4873, 4874, 4875, 4876, 4877, 4878, 4879, 4880, 4881, 4882, 4883, 4884, 4885, 4886, 4887, 4888, 4889, 4890, 4891, 4892, 4893, 4894, 4917, 4918, 4919, 4920, 4921, 4922, 4923, 4924, 4925, 4939, 4940, 4941, 4943, 4947, 4948, 4950, 4951, 4955, 4956, 4957, 2315, 2320, 2322, 2326, 2349, 2350, 2352, 2377, 2382, 2390, 2407, 2422, 2436, 2443, 2457, 2463, 2464, 2470, 2477, 2483, 2721, 2968, 3093, 3185, 4096, 4097, 4098, 4099, 4100, 4101, 4102, 4103, 4104, 4105, 4106, 4107, 4108, 4109, 4110, 4111, 4112, 4113, 4114, 4115, 4116, 4117, 4118, 4119, 4120, 4121, 4122, 4123, 4124, 4125, 4126, 4346, 4353,

4362, 4369, 4386, 4391, 4394, 4408, 4410, 4413, 4415, 4422, 4423, 4432, 4433, 4442, 4469, 4487, 4489, 4491, 4493, 4494, 4495, 4496, 4497, 4498, 4499, 4500, 4501, 4502, 4503, 4504, 4505, 4506, 4507, 4508, 4509, 4343, 4484, 4485, 4486, 4488, 4490, and 4492.

[0137] In some embodiments of any of the plants, formulations, synthetic combinations, or other compositions of the invention, the endophyte expresses one or more genes involved in starch and sucrose metabolism, cell wall degradation, or protection from oxidative stress. In some embodiments, the protein is expressed with at least a two-fold difference, at least a three-fold difference, at least a four-fold difference, at least a five-fold difference, at least a six-fold difference, at least a seven-fold difference, at least an eight-fold difference, at least a nine-fold difference, at least a ten-fold difference or more in expression level as compared to the protein expression level of a reference microorganism. In some embodiments, the difference in expression level is positive.

[0138] In some embodiments, the difference in expression level is negative. In some embodiments, the endophyte comprises an ITS rRNA nucleic acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 344 and 447. In some embodiments, the wherein the endophyte comprises a 16S rRNA nucleic acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 439 or 441.

[0139] Therefore, in a first aspect, inventions described herein provide a synthetic combination of a plant element of a first plant and a preparation of an endophyte that is coated onto the surface of the plant element of the first plant such that the endophyte is present at a higher level on the surface of the plant element than is present on the surface of an uncoated reference plant element, wherein the endophyte is isolated from the inside of the plant element of a second plant. In some embodiments, a synthetic combination comprises a plant element of a first plant and a preparation of one or more endophytes. In some embodiments, the one or more endophytes are selected from the group consisting of fungi, bacteria, and combinations thereof. In some embodiments, the one or more endophytes of the synthetic combination are fungi. In some embodiments, at least 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 or more endophytes of the synthetic combination are fungi. In some embodiments, one or more endophytes of the synthetic combination are bacteria. In some embodiments, at least 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 or more endophytes of the synthetic combination are bacteria. In some embodiments, one or more endophytes of the synthetic combination comprise both fungi and

bacteria. In some embodiments, one or more endophytes of the synthetic combination comprise at least one fungus and at least one bacterium. In some embodiments, one or more endophytes of the synthetic combination comprise at least 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 or more bacteria, at least 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 or more fungi, and combinations thereof.

[0140] In some embodiments, the endophyte comprises a taxon that is present in at least two species that are selected from cereal, fruit and vegetable, wild grassland and oilseed plants. In some embodiments, the endophyte comprises a nucleic acid that is at least 97% identical, for example, at least 98% identical, at least 99% identical, at least 99.5% identical, or 100% identical to the nucleic acid sequence selected from the groups provided in Table 1, Table 2, Table 7, and Table 8.

[0141] In some embodiments, the isolated endophyte is cultured, for example, prior to being coated onto the surface of the plant element. The endophyte can be cultured in a synthetic or semi-synthetic medium.

[0142] The isolated endophyte can be associated with the surface of the seed of the first plant. In some embodiments, the endophyte is not associated with the surface of the plant element of the first plant.

[0143] The present invention contemplates a synthetic combination in which the first plant and the second plant are the same species. In a particular embodiment, the first plant and the second plant are the same cultivar. The synthetic combination may also make use of an endophyte that is isolated from a plant that is a different species from the first plant.

[0144] In some embodiments, the plant element of the first plant is from a monocotyledonous plant. For example, the plant element of the first plant is from a cereal plant. The plant element of the first plant can be selected from the group consisting of maize, wheat, barley, onion, rice, or sorghum. In an alternative embodiment, the seed of the first plant is from a dicotyledonous plant. The plant element of the first plant can be selected from the group consisting of cotton, *Brassica napus*, tomato, pepper, cabbage, lettuce, melon, strawberry, turnip, watermelon, peanut or soybean. In a particular embodiment, the plant is not a cotton plant. In still another embodiment, the plant is not a soybean. In another embodiment, the plant is not maize. In yet another embodiment, the plant is not wheat.

[0145] In some embodiments, the plant element of the first plant can be from a genetically modified plant. In another embodiment, the plant element of the first plant can be a hybrid plant element.

[0146] The synthetic combination can comprise a plant element of the first plant that is surface-sterilized prior to combining with the endophytes.

[0147] As stated above, the endophyte used in the synthetic combination is derived from within the plant element of a second plant. In some embodiments, the second plant is a monocotyledonous plant or tissue thereof. In a particular embodiment, the second plant is a cereal plant or tissue thereof. In some embodiments, the second plant is selected from the group consisting of a maize plant, a barley plant, a wheat plant, an onion plant, a rice plant, or a sorghum plant. In some embodiments, the plant element is a seed that is a naked grain (i.e., without hulls or fruit cases). In an alternative embodiment, the second plant is a dicotyledonous plant. For example, the second plant can be selected from the group consisting of a cotton plant, a *Brassica Napus* plant, a tomato plant, a pepper plant, a cabbage plant, a lettuce plant, a melon plant, a strawberry plant, a turnip plant, a watermelon plant, a peanut plant or a soybean plant.

[0148] In some embodiments, the endophyte is coated on the surface of the plant element of the first plant in an amount effective to confer in the plant element or resulting plant thereof an improved agronomic trait. For example, in one embodiment, the agronomic trait is selected from the group consisting of: improved leaf biomass, improved vigor, improved fruit mass, improved grain yield, improved root mass, increased flower number, increased plant height, earlier flowering, and enhanced germination rate. Alternatively, or in addition, the agronomic trait is selected from the group consisting of: improved resistance to drought, improved water use efficiency, improved nitrogen use efficiency, improved nitrogen uptake, improved resistance to salt stress, improved resistance to heat, improved resistance to cold, improved metal tolerance, and improved nutritional content, improved uptake of micronutrients including metal ions, improved uptake of phosphorus and improved uptake of potassium. In some embodiments, the agronomic trait is selected from the group consisting of: improved nematode resistance, improved fungal pathogen resistance, improved pathogen resistance, improved herbivore resistance, improved viral pathogen resistance.

[0149] In some embodiments, the seed of the first plant is coated with at least 1 CFU or spores of the endophyte per seed, for example, at least 2 CFU or spores, at least 5 CFU or spores, at least 10 CFU or spores, at least 30 CFU or spores, at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores, at least 30,000 CFU or spores or more per seed.

[0150] The synthetic combination can additionally comprise a seed coating composition. The seed coating composition can comprise an agent selected from the group consisting of: a fungicide, an antibacterial agent, an herbicide, a nematicide, an insecticide, a plant growth regulator, a rodenticide, a nutrient, and combinations thereof. The seed coating composition can further comprise an agent selected from the group consisting of an agriculturally acceptable carrier, a tackifier, a microbial stabilizer, and combinations thereof. In some embodiments, the seed coating composition can contain a second microbial preparation, including but not limited to a rhizobial bacterial preparation.

[0151] The present invention contemplates the use of endophytes that are unmodified, as well as those that are modified. In some embodiments, the endophyte is a recombinant endophyte. In one particular embodiment, the endophyte is modified prior to coating onto the surface of the seed such that it has enhanced compatibility with an antimicrobial agent when compared with the unmodified. For example, the endophyte can be modified such that it has enhanced compatibility with an antibacterial agent. In an alternative embodiment, the endophyte has enhanced compatibility with an antifungal agent. The endophyte can be modified such that it exhibits at least 3 fold greater, for example, at least 5 fold greater, at least 10 fold greater, at least 20 fold greater, at least 30 fold greater or more resistance to an antimicrobial agent when compared with the unmodified endophyte. The endophyte can be substantially purified from any other microbial entity. In one embodiment, the antimicrobial agent is an antibacterial agent. In another embodiment, the antimicrobial agent is an antifungal agent.

[0152] In one particular embodiment, the antimicrobial agent is glyphosate. For example, the modified endophyte exhibits at least 3 fold greater, for example, at least 5 fold greater, at least 10 fold greater, at least 20 fold greater, at least 30 fold greater or more resistance to the antimicrobial agent when compared with the unmodified endophyte. In the alternative, the modified endophyte has a doubling time in growth medium containing at least 1 mM glyphosate, for example, at least 2 mM glyphosate, at least 5mM glyphosate, at least 10mM glyphosate, at least 15mM glyphosate or more, that is no more than 250%, for example, no more than 200%, no more than 175%, no more than 150%, or no more than 125%, of the doubling time of the endophyte in the same growth medium containing no glyphosate. In still another embodiment, the modified endophyte has a doubling time in a plant tissue containing at least 10 ppm glyphosate, for example, at least 15 ppm glyphosate, at least 20 ppm glyphosate, at least 30 ppm glyphosate, at least 40 ppm glyphosate or more, that is no more

than 250%, for example, no more than 200%, no more than 175%, no more than 150%, or no more than 125%, of the doubling time of the unmodified endophyte in a reference plant tissue containing no glyphosate.

[0153] The present invention also contemplates the use of multiple endophytes. For example, in some embodiments, the synthetic combination described above can comprise a plurality of purified endophytes, for example, 2, 3, 4 or more different types of endophytes.

[0154] In another aspect, the present invention provides for a method for improving a trait in an agricultural plant, the method comprising: Providing an agricultural plant, contacting the plant with a formulation comprising a endophytic microbial entity comprising a nucleic acid sequence that is at least 97% identical, at least 98% identical, at least 99% identical, at least 99.5% identical, or 100% identical, to the nucleic acid sequence selected from the groups provided in **Table 1**, **Table 2**, **Table 7**, and **Table 8** that is present in the formulation in an amount effective to colonize the plant and allowing the plant to grow under conditions that allow the endophytic microbial entity to colonize the plant.

[0155] Also described herein are preparations comprising a population of isolated modified endophytes described above. Preparations described herein further comprise an agriculturally acceptable carrier, and the preparation comprises an amount of endophytes sufficient to improve an agronomic trait of the population of seeds. For example, in one embodiment, the agronomic trait is selected from the group consisting of: improved leaf biomass, improved vigor, improved fruit mass, improved grain yield, improved root mass, increased flower number, increased plant height, earlier flowering, enhanced germination rate and combinations thereof. Alternatively, or in addition, the agronomic trait is selected from the group consisting of: improved resistance to drought, improved water use efficiency, improved nitrogen use efficiency, improved nitrogen uptake, improved resistance to salt stress, improved resistance to heat, improved resistance to cold, improved metal tolerance, improved nutritional content, improved uptake of micronutrients including metal ions, improved uptake of phosphorus, improved uptake of potassium and combinations thereof. In some embodiments, the agronomic trait is selected from the group consisting of: improved nematode resistance, improved fungal pathogen resistance, improved pathogen resistance, improved herbivore resistance, improved viral pathogen resistance, and combinations thereof. In some embodiments, the preparation is substantially stable at temperatures between about 2 °C and about 45 °C for at least about thirty days.

[0156] Preparations can be conveniently formulated to provide the ideal number of endophytes onto a seed to produce synthetic combinations described above. In some embodiments, a preparation is formulated to provide at least 100 endophytes, for example, at least 300 endophyte, 1,000 endophytes, 3,000 endophytes, 10,000 endophytes or more per seed. In some embodiments, a preparation is formulated to provide a population of plants that demonstrates a substantially homogenous growth rate when introduced into agricultural production. Inventions described herein also contemplate a preparation comprising two or more different purified endophytes.

[0157] Also described herein are commodity plant products comprising a plant or part of a plant (including a seed) and further comprising the modified endophyte described above that is present in a detectable level, for example, as detected by the presence of its nucleic acid by PCR.

[0158] In another aspect of the present invention, a seed comprising synthetic combinations described herein is provided. In still another aspect, disclosed is a substantially uniform population of seeds comprising a plurality of such seeds. In one embodiment, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 90%, at least 95% or more of the seeds in the population, contains a viable endophyte or endophytes disposed on the surface of the seeds. In a particular embodiment, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 90%, at least 95% or more of the seeds in the population contains at least 10 CFU or spores, for example, at least 30 CFU or spores, at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores or more, of the endophyte or endophytes coated onto the surface of the seed.

[0159] In still another aspect, the present invention discloses a substantially uniform population of plants produced by growing the population of seeds described above. In one embodiment, at least 75%, at least 80%, at least 90%, at least 95% or more of the plants comprise in one or more tissues an effective amount of the endophyte or endophytes. In another embodiment, at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, at least 80%, at least 90%, at least 95% or more of the plants comprise a microbe population that is substantially similar.

[0160] In another aspect, described herein is an agricultural field, including a greenhouse comprising the population of plants described above. In one embodiment, the agricultural field comprises at least 100 plants. In another embodiment, the population occupies at least about 100 square feet of space, wherein at least about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or more than 90% of the population comprises an effective amount of the microbe. In another embodiment, the population occupies at least about 100 square feet of space, wherein at least about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or more than 90% of the population comprises the microbe in reproductive tissue. In still another embodiment, the population occupies at least about 100 square feet of space, wherein at least about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or more than 90% of the population comprises at least 10 CFUs or spores, 100 CFUs or spores, 1,000 CFUs or spores, 10,000 CFUs or spores or more of the microbe. In yet another embodiment, the population occupies at least about 100 square feet of space, wherein at least about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or more than 90% of the population comprises an exogenous microbe (i.e., the endophyte) of monoclonal origin.

[0161] In another aspect, disclosed is a method of producing a commodity plant product, comprising obtaining a plant or plant tissue from the synthetic combination described above, and producing the commodity plant product therefrom. The commodity plant product can be produced from the seed, or the plant (or a part of the plant) grown from the seed. The commodity plant product can also be produced from the progeny of such plant or plant part. The commodity plant product can be selected from the group consisting of grain, flour, starch, seed oil, syrup, meal, flour, oil, film, packaging, nutraceutical product, an animal feed, a fish fodder, a cereal product, a processed human-food product, a sugar or an alcohol and protein.

BRIEF DESCRIPTION OF THE DRAWINGS

[0001] The drawings are for illustration purposes only not for limitation.

[0002] FIG. 1 depicts an exemplary schematic of a KEGG pathway for Glycolysis / Gluconeogenesis. The secreted proteome of a beneficial and neutral *Agrobacterium* were contrasted, and KEGG IDs that were enriched are depicted. 5AY represents beneficial SYM01004 (SEQ ID NO: 441). 5BY represents neutral SYM00091 (SEQ ID NO: 427). Light grey ovals represent proteins corresponding to 5AY. Dark grey ovals represent proteins corresponding to 5BY. Medium grey ovals represent proteins corresponding with both 5AY and 5BY. $P\text{-value} = 1.36\text{e-}8$

[0003] FIG. 2 depicts an exemplary schematic of a KEGG pathway for starch and sucrose metabolism. The secreted proteome of a beneficial and neutral bacteria and fungi were contrasted, and KEGG IDs that were enriched are depicted.

DETAILED DESCRIPTION

Definitions

[0004] In order for the present invention to be more readily understood, certain terms are first defined below. Additional definitions for the following terms and other terms are set forth throughout the specification.

[0005] As used herein, an “agricultural seed” is a seed used to grow a plant typically used in agriculture (an “agricultural plant”). The seed may be of a monocot or dicot plant, and may be planted for the production of an agricultural product, for example grain, food, feed, fiber, fuel, etc. As used herein, an agricultural seed is a seed that is prepared for planting, for example, in farms for growing.

[0006] An “endophyte” or “endophytic entity” or “endophytic microbe” is a symbiotic organism (e.g., a microorganism, e.g., a bacterium, e.g., a fungi) capable of living within a plant or is otherwise associated therewith, and does not cause disease or harm the plant otherwise, and confers one or more beneficial properties to the host plant. In some embodiments, an endophyte is a microorganism. In some embodiments, an endophyte is a microorganism that is associated with one or more host plant tissues and is in a symbiotic, e.g., beneficial relationship with said host plant tissues. In some embodiments, an endophyte is a microorganism, e.g., a bacterial or fungal organism, that confers an increase in yield, an increase in biomass, an increase in stress resistance, an increase in fitness, or combinations

thereof, in its host plant. Endophytes may occupy the intracellular or extracellular spaces of plant tissue, including the leaves, stems, flowers, fruits, seeds, roots and combinations thereof. As used herein, the term “endophytic component” refers to a composition and/or structure that is part of the endophyte.

5 [0007] As used herein, the term “microbe” or “microorganism” refers to any species or taxon of microorganism, including, but not limited to, archaea, bacteria, microalgae, fungi (including mold and yeast species), mycoplasmas, microspores, nanobacteria, oomycetes, and protozoa. In some embodiments, a microbe or microorganism is an endophyte. In some
0 embodiments, a microbe is an endophyte. In some embodiments, a microbe or microorganism encompasses individual cells (e.g., unicellular microorganisms) or more than one cell (e.g., multi-cellular microorganism). A “population of microorganisms” may thus refer to a multiple cells of a single microorganism, in which the cells share common genetic derivation. As used herein, the term “neutral” microbe or “neutral” microorganism refers to a microorganism that is both non-beneficial *and* non-pathogenic to a host plant.

5 [0008] As used herein, the term “bacteria” or “bacterium” refers in general to any prokaryotic organism, and may reference an organism from either Kingdom Eubacteria (Bacteria), Kingdom Archaeobacteria (Archae), or both.

[0009] As used herein, the term “fungus” or “fungi” refers in general to any organism from Kingdom Fungi.

0 [0010] A “spore” or a population of “spores” refers to bacteria or fungi that are generally viable, more resistant to environmental influences such as heat and bactericidal or fungicidal agents than other forms of the same bacteria or fungi, and typically capable of germination and out-growth. Bacteria and fungi that are “capable of forming spores” are those bacteria and fungi comprising the genes and other necessary abilities to produce spores under suitable
5 environmental conditions.

[0011] “Internal Transcribed Spacer” (ITS) refers to the spacer DNA (non-coding DNA) situated between the small-subunit ribosomal RNA (rRNA) and large-subunit rRNA genes in the chromosome or the corresponding transcribed region in the polycistronic rRNA precursor transcript.

0 [0012] A “plurality of endophytes” means two or more types of endophyte entities, e.g., of simple bacteria or simple fungi, complex fungi, or combinations thereof. In some embodiments, the two or more types of endophyte entities are two or more strains of

endophytes. In other embodiments, the two or more types of endophyte entities are two or more species of endophytes. In yet other embodiments, the two or more types of endophyte entities are two or more genera of endophytes. In yet other embodiments, the two or more types of endophyte entities are two or more families of endophytes. In yet other
5 embodiments, the two or more types of endophyte entities are two or more orders of endophytes.

[0013] A “population” of endophytes refers to a plurality of cells of a single endophyte, in which the cells share common genetic derivation.

[0014] A “complex network” means a plurality of endophytes co-localized in an
0 environment, such as on or within an agricultural plant. Preferably, a complex network includes two or more types of endophyte entities that synergistically interact, such synergistic endophytic populations capable of providing a benefit to the agricultural seed, seedling, or plant derived thereby.

[0015] The terms “pathogen” and “pathogenic” in reference to a bacterium or fungus
5 includes any such organism that is capable of causing or affecting a disease, disorder or condition of a host comprising the organism.

[0016] A “spore” or a population of “spores” refers to bacteria or fungi that are generally viable, more resistant to environmental influences such as heat and bactericidal or fungicidal agents than other forms of the same bacteria or fungi, and typically capable of germination
20 and out-growth. Bacteria and fungi that are “capable of forming spores” are those bacteria and fungi comprising the genes and other necessary abilities to produce spores under suitable environmental conditions.

[0017] As used herein, a “colony-forming unit” (“CFU”) is used as a measure of viable microorganisms in a sample. A CFU is an individual viable cell capable of forming on a solid
25 medium a visible colony whose individual cells are derived by cell division from one parental cell.

[0018] The term “isolated” is intended to specifically reference an organism, cell, tissue, polynucleotide, or polypeptide that is removed from its original source and purified from additional components with which it was originally associated. For example, an endophyte
30 may be considered isolated from a seed if it is removed from that seed source and purified so that it is isolated from any additional components with which it was originally associated.

Similarly, an endophyte may be removed and purified from a plant or plant element so that it is isolated and no longer associated with its source plant or plant element.

[0019] As used herein, an isolated strain of a microbe is a strain that has been removed from its natural milieu. “Pure cultures” or “isolated cultures” are cultures in which the organisms present are only of one strain of a particular genus and species. This is in contrast to “mixed cultures,” which are cultures in which more than one genus and/or species of microorganism are present. As such, the term “isolated” does not necessarily reflect the extent to which the microbe has been purified. A “substantially pure culture” of the strain of microbe refers to a culture which contains substantially no other microbes than the desired strain or strains of microbe. In other words, a substantially pure culture of a strain of microbe is substantially free of other contaminants, which can include microbial contaminants. Further, as used herein, a “biologically pure” strain is intended to mean the strain separated from materials with which it is normally associated in nature. A strain associated with other strains, or with compounds or materials that it is not normally wound with in nature, is still defined as “biologically pure.” A monoculture of a particular strain is, of course, “biologically pure.” As used herein, the term “enriched culture” of an isolated microbial strain refers to a microbial culture that contains more than 50%, 60%, 70%, 80%, 90%, or 95% of the isolated strain.

[0020] A “plant element” is intended to generically reference either a whole plant or a plant component, including but not limited to plant tissues, parts, and cell types. A plant element is preferably one of the following: whole plant, seedling, meristematic tissue, ground tissue, vascular tissue, dermal tissue, seed, leaf, root, shoot, stem, flower, fruit, stolon, bulb, tuber, corm, keikis, shoot, bud. As used herein, a “plant element” is synonymous to a “portion” of a plant, and refers to any part of the plant, and can include distinct tissues and/or organs, and may be used interchangeably with the term “tissue” throughout.

[0021] Similarly, a “plant reproductive element” is intended to generically reference any part of a plant that is able to initiate other plants via either sexual or asexual reproduction of that plant, for example but not limited to: seed, seedling, root, shoot, stolon, bulb, tuber, corm, keikis, or bud.

[0022] A “population” of plants, as used herein, refers to a plurality of plants that are of the same taxonomic category, typically of the same species, and will also typically share a common genetic derivation.

[0023] As used herein, an “agricultural seed” is a seed used to grow a plant typically used in agriculture (an “agricultural plant”). The seed may be of a monocot or dicot plant, and may be planted for the production of an agricultural product, for example feed, food, fiber, fuel, etc. As used herein, an agricultural seed is a seed that is prepared for planting, for example, in farms for growing.

[0024] “Agricultural plants”, or “plants of agronomic importance”, include plants that are cultivated by humans for food, feed, fiber, and fuel purposes. Agricultural plants include monocotyledonous species such as: maize (*Zea mays*), common wheat (*Triticum aestivum*), spelt (*Triticum spelta*), einkorn wheat (*Triticum monococcum*), emmer wheat (*Triticum dicoccum*), durum wheat (*Triticum durum*), Asian rice (*Oryza sativa*), African rice (*Oryza glaberrima*), wild rice (*Zizania aquatica*, *Zizania latifolia*, *Zizania palustris*, *Zizania texana*), barley (*Hordeum vulgare*), Sorghum (*Sorghum bicolor*), Finger millet (*Eleusine coracana*), Proso millet (*Panicum miliaceum*), Pearl millet (*Pennisetum glaucum*), Foxtail millet (*Setaria italica*), Oat (*Avena sativa*), Triticale (*Triticosecale*), rye (*Secale cereal*), Russian wild rye (*Psathyrostachys juncea*), bamboo (*Bambuseae*), or sugarcane (e.g., *Saccharum arundinaceum*, *Saccharum barberi*, *Saccharum bengalense*, *Saccharum edule*, *Saccharum munja*, *Saccharum officinarum*, *Saccharum procerum*, *Saccharum ravennae*, *Saccharum robustum*, *Saccharum sinense*, or *Saccharum spontaneum*); as well as dicotyledonous species such as: soybean (*Glycine max*), canola and rapeseed cultivars (*Brassica napus*), cotton (genus *Gossypium*), alfalfa (*Medicago sativa*), cassava (genus *Manihot*), potato (*Solanum tuberosum*), tomato (*Solanum lycopersicum*), pea (*Pisum sativum*), chick pea (*Cicer arietinum*), lentil (*Lens culinaris*), flax (*Linum usitatissimum*), peanut (*Arachis hypogaea*) and many varieties of vegetables.

[0025] A “host plant” includes any plant, particularly a plant of agronomic importance, which an endophyte can colonize. As used herein, an endophyte is said to “colonize” a plant or plant element when it can be stably detected within the plant or plant element over a period time, such as one or more days, weeks, months or years, in other words, a colonizing entity is not transiently associated with the plant or plant element. Such host plants are preferably plants of agronomic importance.

[0026] A “non-host target” means an organism or chemical compound that is altered in some way after contacting a host plant or host fungus that comprises an endophyte, as a result of a property conferred to the host plant or host fungus by the endophyte.

[0027] As used herein, a “hybrid plant” refers generally refers to a plant that is the product of a cross between two genetically different parental plants. A hybrid plant is generated by either a natural or artificial process of hybridization whereby the entire genome of one species, variety cultivar, breeding line or individual plant is combined intra- or interspecifically into the genome of species, variety or cultivar or line, breeding line or individual plant by crossing.

[0028] An “inbred plant”, as used herein, refers to a plant or plant line that has been repeatedly crossed or inbred to achieve a high degree of genetic uniformity, and low heterozygosity, as is known in the art.

[0029] The term “isoline” is a comparative term, and references organisms that are genetically identical, but may differ in treatment. In one example, two genetically identical maize plant embryos may be separated into two different groups, one receiving a treatment (such as transformation with a heterologous polynucleotide, to create a genetically modified plant) and one control that does not receive such treatment. Any phenotypic differences between the two groups may thus be attributed solely to the treatment and not to any inherency of the plant’s genetic makeup. In another example, two genetically identical seeds may be treated with a formulation that introduces an endophyte composition. Any phenotypic differences between the plants derived from those seeds may be attributed to the treatment, thus forming an isoline comparison.

[0030] Similarly, by the terms “reference plant”, “reference agricultural plant” or “reference seed”, it is meant an agricultural plant or seed of the same species, strain, or cultivar to which a treatment, formulation, composition or endophyte preparation as described herein is not administered/contacted. A reference agricultural plant or seed, therefore, is identical to the treated plant with the exception of the presence of the endophyte and can serve as a control for detecting the effects of the endophyte that is conferred to the plant.

[0031] A “reference environment” refers to the environment, treatment or condition of the plant in which a measurement is made. For example, production of a compound in a plant associated with an endophyte can be measured in a reference environment of drought stress, and compared with the levels of the compound in a reference agricultural plant under the same conditions of drought stress. Alternatively, the levels of a compound in plant associated

with an endophyte and reference agricultural plant can be measured under identical conditions of no stress.

[0032] A “population” of plants refers to more than one plant, that are of the same taxonomic category, typically be of the same species, and will also typically share a
5 common genetic derivation.

[0033] In some embodiments, the invention contemplates the use of microbes that are “exogenous” to a seed or plant. As used herein, a microbe is considered exogenous to the seed or plant if the plant element that is unmodified (e.g., a plant element that is not treated with the plurality of endophytes described herein) does not contain the microbe.

0 [0034] In some embodiments, a microbe can be “endogenous” to a seed or plant. As used herein, a microbe is considered “endogenous” to a plant or seed, if the endophyte or endophyte component is derived from, or is otherwise found in, a plant element of the plant specimen from which it is sourced. In embodiments in which an endogenous endophyte is applied, the endogenous microbe is applied in an amount that differs from the levels typically
5 found in the plant.

[0035] In some embodiments, the present invention contemplates the synthetic compositions comprising the combination of a plant element, seedling, or whole plants and an endophyte population, in which the endophyte population is “heterologously disposed”.

[0036] In some aspects, “heterologously disposed” means that the plant element, seedling,
0 or plant does not contain detectable levels of the microbe in that same plant element, seedling, or plant. For example if said plant element or seedling or plant does not naturally have the endophyte associated with it and the endophyte is applied, the endophyte would be considered to be heterologously disposed. In some aspects, “heterologously disposed” means that the endophyte is being applied to a different plant element than that with which the
5 endophyte is naturally associated. For example, if said plant element or seedling or plant has the endophyte normally found in the root tissue but not in the leaf tissue, and the endophyte is applied to the leaf, the endophyte would be considered to be heterologously disposed. In some aspects, “heterologously disposed” means that the endophyte being applied to a different tissue or cell layer of the plant element than that in which the microbe is naturally
0 found. For example, if endophyte is naturally found in the mesophyll layer of leaf tissue but is being applied to the epithelial layer, the endophyte would be considered to be heterologously disposed. In some aspects, “heterologously disposed” means that the

endophyte being applied is at a greater concentration, number, or amount of the plant element, seedling, or plant, than that which is naturally found in said plant element, seedling, or plant. For example, an endophyte concentration that is being applied is at least 1.5 times, between 1.5 and 2 times, 2 times, between 2 and 3 times, 3 times, between 3 and 5 times, 5 times, between 5 and 7 times, 7 times, between 7 and 10 times, 10 times greater, or even greater than 10 times higher number, amount, or concentration than that which is naturally present, the endophyte would be considered to be heterologously disposed. In some aspects, “heterologously disposed” means that the endophyte is applied to a developmental stage of the plant element, seedling, or plant in which said endophyte is not naturally associated, but may be associated at other stages. For example, if an endophyte is normally found at the flowering stage of a plant and no other stage, an endophyte applied at the seedling stage may be considered to be heterologously disposed. For the avoidance of doubt, “heterologously disposed” contemplates use of microbes that are “exogenous” to a seed or plant.

[0037] In some cases, the present invention contemplates the use of microbes that are “compatible” with agricultural chemicals, including but not limited to, a fungicide, an anti-complex compound, a bactericide, a virucide, an herbicide, a nematocide, a parasiticide, a pesticide, or any other agent widely used in agriculture which has the effect of killing or otherwise interfering with optimal growth of another organism. As used herein, a microbe is “compatible” with an agricultural chemical, when the microbe is modified, such as by genetic modification, e.g., contains a transgene that confers resistance to an herbicide, or otherwise adapted to grow in, or otherwise survive, the concentration of the agricultural chemical used in agriculture. For example, a microbe disposed on the surface of plant element is compatible with the fungicide metalaxyl if it is able to survive the concentrations that are applied on the plant element surface.

[0038] “Biomass” means the total mass or weight (fresh or dry), at a given time, of a plant tissue, plant tissues, an entire plant, or population of plants, usually given as weight per unit area. The term may also refer to all the plants or species in the community (community biomass).

[0039] Some of the compositions and methods described herein involve single endophyte strains or plurality of endophytes in an amount effective to colonize a plant. As used herein, a microbe is said to “colonize” a plant or seed when it can exist in an endophytic relationship with the plant in the plant environment, for example inside the plant or a part or tissue thereof, including the seed.

[0040] The compositions and methods herein may provide for an improved “agronomic trait” or “trait of agronomic importance” to a host plant, which may include, but not be limited to, the following: altered oil content, altered protein content, altered seed carbohydrate composition, altered seed oil composition, and altered seed protein composition, chemical tolerance, cold tolerance, delayed senescence, disease resistance, drought tolerance, ear weight, growth improvement, health enhancement, heat tolerance, herbicide tolerance, herbivore resistance, improved nitrogen fixation, improved nitrogen utilization, improved root architecture, improved water use efficiency, increased biomass, increased root length, increased seed weight, increased shoot length, increased yield, increased yield under water-limited conditions, kernel mass, kernel moisture content, metal tolerance, number of ears, number of kernels per ear, number of pods, nutrition enhancement, pathogen resistance, pest resistance, photosynthetic capability improvement, salinity tolerance, stay-green, vigor improvement, increased dry weight of mature seeds, increased fresh weight of mature seeds, increased number of mature seeds per plant, increased chlorophyll content, increased number of pods per plant, increased length of pods per plant, reduced number of wilted leaves per plant, reduced number of severely wilted leaves per plant, and increased number of non-wilted leaves per plant, a detectable modulation in the level of a metabolite, a detectable modulation in the level of a transcript, and a detectable modulation in the proteome, compared to an isoline plant grown from a seed without said seed treatment formulation.

[0041] Additionally, “altered metabolic function” or “altered enzymatic function” may include, but not be limited to, the following: altered production of an auxin, altered nitrogen fixation, altered production of an antimicrobial compound, altered production of a siderophore, altered mineral phosphate solubilization, altered production of a cellulase, altered production of a chitinase, altered production of a xylanase, altered production of acetoin and altered ability to metabolize a carbon source.

[0042] An “increased yield” can refer to any increase in biomass or seed or fruit weight, seed size, seed number per plant, seed number per unit area, bushels per acre, tons per acre, kilo per hectare, or carbohydrate yield. Typically, the particular characteristic is designated when referring to increased yield, e.g., increased grain yield or increased seed size.

[0043] “Agronomic trait potential” is intended to mean a capability of a plant element for exhibiting a phenotype, preferably an improved agronomic trait, at some point during its life cycle, or conveying said phenotype to another plant element with which it is associated in the

same plant. For example, a plant element may comprise an endophyte that will provide benefit to leaf tissue of a plant from which the plant element is grown; in such case, the plant element comprising such endophyte has the agronomic trait potential for a particular phenotype (for example, increased biomass in the plant) even if the seed itself does not display said phenotype.

[0044] By the term “capable of metabolizing” a particular carbon substrate, it is meant that the endophyte is able to utilize that carbon substrate as an energy source.

[0045] The term “synthetic combination” means a plurality of elements associated by human endeavor, in which said association is not found in nature. In some embodiments, “synthetic combination” is used to refer to a treatment formulation associated with a plant element. In some aspects of the present invention, “synthetic combination” refers to a purified population of endophytes in a treatment formulation comprising additional compositions with which said endophytes are not found associated in nature. The combination may be achieved, for example, by coating the surface of the seed of a plant, such as an agricultural plant, or host plant elements with an endophyte. In some embodiments of the present invention, “synthetic combination” refers to one or more plant elements in association with an isolated, purified population of endophytes in a treatment formulation comprising additional compositions with which said endophytes are not found associated in nature.

[0046] A “treatment formulation” refers to a mixture of chemicals that facilitate the stability, storage, and/or application of the endophyte composition(s). In some embodiments, an agriculturally compatible carrier can be used to formulate an agricultural formulation or other composition that includes a purified endophyte preparation. As used herein an “agriculturally compatible carrier” refers to any material, other than water, that can be added to a plant element without causing or having an adverse effect on the plant element (e.g., reducing seed germination) or the plant that grows from the plant element, or the like.

[0047] In some cases, the present invention contemplates the use of compositions that are “compatible” with agricultural chemicals, for example, a fungicide, an anti-complex compound, or any other agent widely used in agriculture which has the effect of killing or otherwise interfering with optimal growth of another organism.

[0048] Some compositions described herein contemplate the use of an agriculturally compatible carrier. As used herein an “agriculturally compatible carrier” is intended to refer

to any material, other than water, which can be added to a seed or a seedling without causing/having an adverse effect on the seed, the plant that grows from the seed, seed germination, or the like.

[0049] As used herein, a nucleic acid has “homology” or is “homologous” to a second
5 nucleic acid if the nucleic acid sequence has a similar sequence to the second nucleic acid sequence. The terms “identity”, “percent sequence identity” or “identical” in the context of nucleic acid sequences refer to the residues in the two sequences that are the same when aligned for maximum correspondence. There are a number of different algorithms known in the art that can be used to measure nucleotide sequence identity. For instance, polynucleotide
0 sequences can be compared using FASTA, Gap or Bestfit, which are programs in Wisconsin Package Version 10.0, Genetics Computer Group (GCG), Madison, Wis. FASTA provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences. In some embodiments, sequences can be compared using Geneious (Biomatters, Ltd., Auckland, New Zealand). In other embodiments, polynucleotide
5 sequences can be compared using the multiple sequence alignment algorithm MUSCLE. In some embodiments the nucleic acid sequence to be aligned is a complete gene. In some embodiments, the nucleic acid sequence to be aligned is a gene fragment. In some embodiments, if the nucleic acid sequence to be aligned is a gene fragment, the percent identity to a second nucleic acid sequence is considered X% identical if the two
10 sequences are X% identical the length of the shortest sequence.

[0050] The term “substantial homology” or “substantial similarity,” when referring to a nucleic acid or fragment thereof, indicates that, when optimally aligned with appropriate nucleotide insertions or deletions with another nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least about 76%, 80%, 85%, or at least about 90%,
15 or at least about 95%, 96%, 97%, 98% or 99% of the nucleotide bases, as measured by any well-known algorithm of sequence identity, such as FASTA, BLAST, MUSCLE or Gap, as discussed above.

[0051] As used herein, the terms “operational taxonomic unit,” “OTU,” “taxon,” “hierarchical cluster,” and “cluster” are used interchangeably. An operational taxon unit
20 (OTU) refers to a group of one or more organisms that comprises a node in a clustering tree. The level of a cluster is determined by its hierarchical order. In some embodiments, an OTU is a group tentatively assumed to be a valid taxon for purposes of phylogenetic analysis. In other embodiments, an OTU is any of the extant taxonomic units under study. In yet another

embodiment, an OTU is given a name and a rank. For example, an OTU can represent a domain, a sub-domain, a kingdom, a sub-kingdom, a phylum, a sub-phylum, a class, a sub-class, an order, a sub-order, a family, a subfamily, a genus, a subgenus, or a species. In some embodiments, OTUs can represent one or more organisms from the kingdoms eubacteria, protista, or fungi at any level of a hierarchical order. In some embodiments, an OTU represents a prokaryotic or fungal order.

[0052] As used herein, the terms “water-limited condition”, “water stress condition” and “drought condition”, or “water-limited”, “water stress”, and “drought”, may be used interchangeably. For example, a method or composition for improving a plant’s ability to grow under drought conditions means the same as the ability to grow under water-limited conditions. In such cases, the plant can be further said to display improved tolerance to drought stress.

[0053] The terms “decreased”, “fewer”, “slower” and “increased” “faster” “enhanced” “greater” as used herein refers to a decrease or increase in a characteristic of the endophyte treated seed or resulting plant compared to an untreated seed or resulting plant. For example, a decrease in a characteristic may be at least 1%, at least 2%, at least 3%, at least 4%, at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least about 60%, at least 75%, at least about 80%, at least about 90%, at least 100%, at least 200%, at least about 300%, at least about 400% or more lower than the untreated control. For example, a decrease may be between 1% and 5%, or between 5% and 10%, or between 10% and 15%, or between 15% and 20%, or between 20% and 25%, or between 25% and 30%, or between 30% and 35%, or between 35% and 40%, or between 45% and 50% lower than the untreated control or the formulation control. An increase may be at least 1%, at least 2%, at least 3%, at least 4%, at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least about 60%, at least 75%, at least about 80%, at least about 90%, at least 100%, at least 200%, at least about 300%, at least about 400% or more higher than the untreated control. For example, an increase may be between 1% and 5%, or between 5% and 10%, or between 10% and 15%, or between 15% and 20%, or between 20% and 25%, or between 25% and 30%, or between 30% and 35%, or between 35% and 40%, or between 45% and 50% higher than the untreated control or the formulation control.

Endophytes

[0054] Agricultural plants appear to associate with symbiotic microorganisms termed endophytes, particularly bacteria and fungi, that may have been important during evolution and may contribute to plant survival and performance. However, modern agricultural processes may have perturbed this relationship, resulting in increased crop losses, diminished stress resilience, biodiversity losses, and increasing dependence on external chemicals, fertilizers, and other unsustainable agricultural practices. There is a need for novel methods for generating plants with novel microbiome properties that can sustainably increase yield, stress resilience, and decrease fertilizer and chemical use.

[0055] The inventors have undertaken a systematic comparison of the microbial communities that reside within a wide diversity of plants. As such, the endophytic microbes useful for the invention generally relate to endophytic microbes that are present in agricultural plants.

[0056] In part, the present invention describes preparations of novel endophytes, and the creation of synthetic combinations of agricultural seeds and/or seedlings with heterologous endophytes and formulations containing the synthetic combinations, as well as the recognition that such synthetic combinations display a diversity of beneficial properties present in the agricultural plants and the associated endophyte populations newly created by the present inventors. Such beneficial properties include metabolism, transcript expression, proteome alterations, morphology, and the resilience to a variety of environmental stresses, and the combination of a plurality of such properties.

Provided are novel compositions, methods, and products related our invention's ability to overcome the limitations of the prior art in order to provide reliable increases in crop yield, biomass, germination, vigor, stress resilience, and other properties to agricultural crops.

[0057] We find that beneficial microbes can be robustly derived from plant elements, optionally cultured, administered heterologously to agricultural plant elements such as seeds, and colonize the resulting plant tissues with high efficiency to confer multiple beneficial properties.

We find that microbes can confer beneficial properties across a range of concentrations.

[0058] We find that endophytes can be heterologously disposed onto seedlings of a distinct cultivar, species, or crop type and confer benefits to those new recipients. For example, endophytes from corn cultivars are heterologously provided to wheat cultivars to confer a benefit. This is surprising given the observations of distinct microbiome preferences in

distinct plant and mammalian hosts and, in particular, the likelihood that microbes derived from seeds have been co-evolved to be specialized to a particular host.

[0059] We further find that combinations of heterologously disposed endophytes confer additive advantages to plants, including multiple functional properties and resulting in seed, seedling, and plant hosts that display single or multiple improved agronomic properties.

[0060] Endophytes are microbes that grow inside a plant. Recent appreciation that endophytes can confer remarkable traits upon the host plant is the basis for the present invention. The inventors have developed a method to introduce isolated endophytes to another plant by coating the microbes onto the surface of a seed of a plant. By combining an endophyte sourced from one plant, it is possible to transfer the beneficial agronomic trait onto an agricultural plant, and therefore holds great promise for increasing agricultural productivity.

[0061] Combining a selected plant species, OTU, strain or cultivar with one or more types of endophytes thus provides mechanisms by which, alone or in parallel with plant breeding and transgenic technologies, is provided improved yield from crops and generation of products thereof. Therefore, in a first aspect, the present invention provides a synthetic combination comprising the combination of a plant element, seedling, or whole plants and a single endophyte strain or a plurality of endophytes, in which the single endophyte strain or a plurality of endophytes are "heterologously disposed."

Synthetic compositions of plant elements and endophytes

[0062] The present invention contemplates a synthetic combination of a plant element of a plant that is coated with an endophyte on its surface. The plant element can be any agricultural plant element, for example an agricultural seed. In one embodiment, the plant element of the first plant is from a monocotyledonous plant. For example, the plant element of the first plant is from a cereal plant. The plant element of the first plant can be selected from the group consisting of a maize plant, a wheat plant, a barley plant, an onion plant, a sorghum plant, or a rice plant. In an alternative embodiment, the plant element of the first plant is from a dicotyledonous plant. The plant element of the first plant can be selected from the group consisting of a cotton plant, a *Brassica napus* plant, a tomato plant, a pepper plant, a cabbage plant, a lettuce plant, a melon plant, a strawberry plant, a turnip plant, a watermelon plant, a peanut plant, or a soybean plant. In a particular embodiment, the plant is not a cotton plant. In still another embodiment, the seed of the first plant can be from a

genetically modified plant. In another embodiment, the seed of the first plant can be a hybrid seed.

5 [0063] The synthetic combination can comprise a plant element of the first plant that is surface-sterilized prior to combining with the endophytes. Such pre-treatment prior to coating the plant element with endophytes removes the presence of other microbes that may interfere with the optimal colonization, growth and/or function of the endophyte. Surface sterilization of plant elements can be accomplished without killing the plant elements as described herein elsewhere (see, for example, the section *Isolation of endophytes*).

Sources of Endophytes

0 [0064] As described herein, endophytes can be derived from heterologous, homologous, or engineered sources, optionally cultured, administered heterologously as a single endophyte strain or a plurality of endophytes to plant elements, and, as a result of the administration, confer multiple beneficial properties. In some embodiments, endophytes are derived from plant elements or soil. In some embodiments, the plant element from which the endophyte is
15 derived is a monocotyledonous plant. In a particular embodiment, the plant is a cereal plant or tissue thereof. In yet another embodiment, plant is selected from the group consisting of a maize plant, a barley plant, a wheat plant, a sugarcane plant, a sorghum plant, or a rice plant. In some embodiments, the plant element is a naked grain (i.e., without hulls or fruit cases). In an alternative embodiment, the plant element from which the endophyte is derived is a
20 dicotyledonous plant. For example, a plant can be selected from the group consisting of a cotton plant, a *Brassica napus* plant, a tomato plant, a pepper plant, a cabbage plant, a lettuce plant, a melon plant, a strawberry plant, a turnip plant, a watermelon plant, a peanut plant, or a soybean plant.

[0065] In some embodiments, the endophytes can be obtained from a plant element of the
25 same or different crop, and can be from the same or different cultivar or variety as the plant element to which the composition is heterologously associated. For example, endophytes from a particular corn variety can be isolated and coated onto the surface of a corn seed of the same variety. In other embodiments, the endophytes can be isolated from a related species (e.g., an endophyte isolated from *Triticum monococcum* (einkorn wheat) can be coated onto
30 the surface of a *T. aestivum* (common wheat) plant element; or, an endophyte from *Hordeum vulgare* (barley) can be isolated and coated onto the plant element of another member of the Triticeae family, for example, plant elements of the rye plant, *Secale cereale*). In still another

embodiment, the endophytes can be isolated from a plant part of a plant that is distantly related to the plant element onto which the endophyte is to be coated. For example, tomato-derived endophytes are isolated and coated onto a rice plant element. In still another embodiment, endophytes used in a composition or used to make a synthetic composition can be obtained from a plant element of a plant that is distantly related to the plant element onto which the endophyte is to be coated. For example, a tomato-derived endophyte can be isolated and coated onto a rice plant element.

[0066] In some embodiments, the present invention contemplates the use of endophytes that can confer a beneficial agronomic trait upon the seed or resulting plant onto which it is coated. In another embodiment, the seed endophytes useful for the present invention can also be isolated from seeds of plants adapted to a particular environment, including, but not limited to, an environment with water deficiency, salinity, acute and/or chronic heat stress, acute and/or chronic cold stress, nutrient deprived soils including, but not limited to, micronutrient deprived soils, macronutrient (e.g., potassium, phosphate, nitrogen) deprived soils, pathogen stress, including fungal, nematode, insect, viral, bacterial pathogen stress. In one example, the endophyte is isolated from the seed of a plant that grows in a water deficient environment.

[0067] The synthetic combination of the present invention contemplates the presence of an endophyte on the surface of the seed of the first plant. In one embodiment, the seed of the first plant is coated with at least 10 CFU or spores of the endophyte per seed, for example, at least 20 CFU or spores, at least 50 CFU or spores, at least 100 CFU or spores, at least 200 CFU or spores, at least 300 CFU or spores, at least 500 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores, at least 30,000 CFU or spores or more per plant element. In another embodiment, the plant element is coated with at least 10, for example, at least 20, at least 50, at least 100, at least 200, at least 300, at least 500, at least 1,000, at least 3,000, at least 10,000, at least 30,000, at least 100,000, at least 300,000, at least 1,000,000 or more of the endophyte as detected by the number of copies of a particular endophyte gene detected, for example, by quantitative PCR.

[0068] The endophyte useful for the present invention can be a fungus. In another embodiment, the endophyte can be a bacterium. In one embodiment, the endophyte is not an *Agrobacterium*. In another embodiment, the endophyte is not capable of nitrogen fixation (for example, from the genus *Rhizobium*). In still another embodiment, the endophyte is not from the genus *Acetobacter*. In yet another embodiment, the endophyte is not from the genus

Bacillus. In a particular embodiment, the endophyte is not *Bacillus mojavensis*. In yet another embodiment, the endophyte is not from the genus *Neotyphodium*.

[0069] Historical taxonomic classification of fungi has been according to morphological presentation. Beginning in the mid-1800's, it was recognized that some fungi have a pleomorphic life cycle, and that different nomenclature designations were being used for different forms of the same fungus. In 1981, the Sydney Congress of the International Mycological Association laid out rules for the naming of fungi according to their status as anamorph, teleomorph, or holomorph. With the development of genomic sequencing, it became evident that taxonomic classification based on molecular phylogenetics did not align with morphological-based nomenclature. As a result, in 2011 the International Botanical Congress adopted a resolution approving the International Code of Nomenclature for Algae, Fungi, and Plants (Melbourne Code) (2012), with the stated outcome of designating "One Fungus = One Name". However, systematics experts have not aligned on common nomenclature for all fungi, nor are all existing databases and information resources inclusive of updated taxonomies. As such, many fungi referenced herein may be described by their anamorph form but it is understood that based on identical genomic sequencing, any pleomorphic state of that fungus may be considered to be the same organism. For example, the genus *Alternaria* is the anamorph form of the teleomorph genus *Lewia*, ergo both would be understood to be the same organism with the same DNA sequence.

Exogenous Endophytes

[0070] In one embodiment, the endophyte is an endophytic microbe that was isolated from a different plant than the inoculated plant. For example, in one embodiment, the endophyte can be an endophyte isolated from a different plant of the same species as the inoculated plant. In some cases, the endophyte can be isolated from a species related to the inoculated plant.

[0071] The breeding of plants for agriculture, as well as cultural practices used to combat microbial pathogens, may have resulted in the loss in modern cultivars of the endophytes present in their wild ancestors or other wild plants, or such practices may have inadvertently promoted other novel or rare plant-endophyte interactions, or otherwise altered the microbial population. The former is the case in maize and its phylogenetically confirmed, direct wild ancestor, Parviglumis teosinte (*Zea mays* ssp. *Parviglumis*). Although both species have seeds that appear to contain a common core of endophytic bacterial species, the relative abundance

of certain groups is higher in seeds of teosinte than modern corn. It is possible that this higher diversity and titer of endophytes in the ancestor is correlated with an equally wide range of physiological responses derived from the symbiosis that allow the plant to better adapt to the environment and tolerate stress. In order to survey plant groups for potentially useful endophytes, seeds of their wild ancestors, wild relatives, primitive landraces, modern landraces, modern breeding lines, and elite modern agronomic varieties can be screened for microbial endophytes by culture and culture independent methods as described herein. In addition, microbial endophytes can be isolated from other wild plants, such as grassland plants.

[0072] In some cases, plants are inoculated with endophytes that are exogenous to the seed of the inoculated plant. In one embodiment, the endophyte is derived from a plant of another species. For example, an endophyte that is normally found in dicots is applied to a monocot plant (e.g., inoculating corn with a soy bean-derived endophyte), or vice versa. In other cases, the endophyte to be inoculated onto a plant can be derived from a related species of the plant that is being inoculated. In one embodiment, the endophyte can be derived from a related taxon, for example, from a related species. The plant of another species can be an agricultural plant. For example, an endophyte derived from *Hordeum irregulare* can be used to inoculate a *Hordeum vulgare* L., plant. Alternatively, it can be derived from a 'wild' plant (i.e., a non-agricultural plant). For example, endophytes normally associated with the wild cotton *Gossypium klotzschianum* can be used to inoculate commercial varieties of *Gossypium hirsutum* plants. Endophytes normally associated with a wild turnip plant or a wild watermelon plant can be used to inoculate commercial varieties of turnip or watermelon plants, respectively. As an alternative example of deriving an endophyte from a 'wild' plant, endophytic bacteria isolated from the South East Asian jungle orchid, *Cymbidium eburneum*, can be isolated and testing for their capacity to benefit seedling development and survival of agricultural crops such as wheat, maize, soy and others. In another example, endophytes may be isolated from wild grassland plants. In other cases, the endophyte can be isolated from an ancestral species of the inoculated plant. For example, an endophyte derived from *Zea diploperennis* can be used to inoculate a commercial variety of modern corn, or *Zea mays*.

Selection of plant species from desired habitats for isolation of microbial endophytes

[0073] Different environments can contain significantly different populations of endophytes. For example, geographically isolated soils from different parts of the Americas have been shown to differ in 96% of the bacterial species they contain. Soils containing

different microbial populations can strongly influence the endophytic bacterial population observed inside *Arabidopsis* illustrating that the environment can at least partially alter a plant's associated microbial population. This suggests that plants growing and especially thriving in choice environments are colonized by different and perhaps beneficial endophytes, whose isolation and inoculation onto crop plants may aid these plants to better survive in the same choice environment or to better resist certain stresses encountered in a normal agricultural environment. For instance, at least some of the bacteria isolated from plants growing in arid environments are expected to confer drought tolerance to host plants they are transplanted onto. Additionally, novel endophytes may be found in related crop varieties grown in the choice environment. Once a choice environment is selected, seeds of choice plants to be sampled will be identified by their healthy and/or robust growth, and will then be sampled at least 5 at a time by excavating the entire plants plus small root ball including roots and associated soil and any seeds or fruit present on the plant. These will be placed in a cool (4°C environment) for storage and prompt transport back to the lab for extraction of endophytes and DNA using methods described herein. Identification of choice environments or ecosystems for bioprospecting of plant associated endophytes from either wild plants or crop plants growing in the choice environments or ecosystems follows protocols described herein.

[0074] In one embodiment, the endophyte-associated plant is harvested from a soil type different than the normal soil type that the crop plant is grown on, for example from a gelisol (soils with permafrost within 2 m of the surface), for example from a histosol (organic soil), for example from a spodosol (acid forest soils with a subsurface accumulation of metal-humus complexes), for example from an andisol (soils formed in volcanic ash), for example from a oxisol (intensely weathered soils of tropical and subtropical environments), for example from a vertisol (clayey soils with high shrink/swell capacity), for example from an aridisol (CaCO₃-containing soils of arid environments with subsurface horizon development), for example from a ultisol (strongly leached soils with a subsurface zone of clay accumulation and <35% base saturation), for example from a mollisol (grassland soils with high base status), for example from an alfisol (moderately leached soils with a subsurface zone of clay accumulation and >35% base saturation), for example from an inceptisol (soils with weakly developed subsurface horizons), for example from an entisol (soils with little or no morphological development).

[0075] In another embodiment, the endophyte-associated plant is harvested from an ecosystem where the agricultural plant is not normally found, for example a tundra ecosystem as opposed to a temperate agricultural farm, for example from tropical and subtropical moist broadleaf forests (tropical and subtropical, humid), for example from tropical and subtropical dry broadleaf forests (tropical and subtropical, semihumid), for example from tropical and subtropical coniferous forests (tropical and subtropical, semihumid), for example from temperate broadleaf and mixed forests (temperate, humid), for example from temperate coniferous forests (temperate, humid to semihumid), from for example from boreal forests/taiga (subarctic, humid), for example from tropical and subtropical grasslands, savannas, and shrublands (tropical and subtropical, semiarid), for example from temperate grasslands, savannas, and shrublands (temperate, semiarid), for example from flooded grasslands and savannas (temperate to tropical, fresh or brackish water inundated), for example from montane grasslands and shrublands (alpine or montane climate), for example from Mediterranean forests, woodlands, and scrub or sclerophyll forests (temperate warm, semihumid to semiarid with winter rainfall), for example from mangrove forests, and for example from deserts and xeric shrublands (temperate to tropical, arid).

[0076] In another embodiment, the endophyte-associated plant is harvested from a soil with an average pH range that is different from the optimal soil pH range of the crop plant, for example the plant may be harvested from an ultra acidic soil (< 3.5), from an extreme acid soil ($3.5-4.4$), from a very strong acid soil ($4.5-5.0$), from a strong acid soil ($5.1-5.5$), from a moderate acid soil ($5.6-6.0$), from an slight acid soil ($6.1-6.5$), from an neutral soil ($6.6-7.3$), from an slightly alkaline soil ($7.4-7.8$), from an moderately alkaline soil ($7.9-8.4$), from a strongly alkaline soil ($8.5-9.0$), or from an very strongly alkaline soil (> 9.0).

[0077] In one embodiment, the endophyte-associated plant is harvested from an environment with average air temperatures lower than the normal growing temperature of the crop plant, for example $2-5^{\circ}\text{C}$ colder than average, for example, at least $5-10^{\circ}\text{C}$ colder, at least $10-15^{\circ}\text{C}$ colder, at least at least $15-20^{\circ}\text{C}$ colder, at least $20-25^{\circ}\text{C}$ colder, at least $25-30^{\circ}\text{C}$ colder, at least $30-35^{\circ}\text{C}$ colder, at least $35-40^{\circ}\text{C}$ colder, at least $40-45^{\circ}\text{C}$ colder, at least $45-50^{\circ}\text{C}$ colder, at least $50-55^{\circ}\text{C}$ colder or more, when compared with crop plants grown under normal conditions during an average growing season.

[0078] In one embodiment, the endophyte-associated plant is harvested from an environment with average air temperatures higher than the normal growing temperature of the crop plant, for example $2-5^{\circ}\text{C}$ hotter than average, for example, at least $5-10^{\circ}\text{C}$ hotter, at

least 10-15°C hotter, at least at least 15-20°C hotter, at least 20-25°C hotter, at least 25-30°C hotter, at least 30-35°C hotter, at least 35-40°C hotter, at least 40-45°C hotter, at least 45-50°C hotter, at least 50-55°C hotter or more, when compared with crop plants grown under normal conditions during an average growing season.

5 [0079] In another embodiment, the endophyte-associated plant is harvested from an environment with average rainfall lower than the optimal average rainfall received by the crop plant, for example 2-5% less rainfall than average, for example, at least 5-10% less rainfall, at least 10-15% less rainfall, at least 15-20% less rainfall, at least 20-25% less rainfall, at least 25-30% less rainfall, at least 30-35% less rainfall, at least 35-40% less
0 rainfall, at least 40-45% less rainfall, at least 45-50% less rainfall, at least 50-55% less rainfall, at least 55-60% less rainfall, at least 60-65% less rainfall, at least 65-70% less rainfall, at least 70-75% less rainfall, at least 80-85% less rainfall, at least 85-90% less rainfall, at least 90-95% less rainfall, or less, when compared with crop plants grown under normal conditions during an average growing season.

5 [0080] In one embodiment, the endophyte-associated plant is harvested from an environment with average rainfall higher than the optimal average rainfall of the crop plant, for example 2-5% more rainfall than average, for example, at least 5-10% more rainfall, at least 10-15% more rainfall, at least 15-20% more rainfall, at least 20-25% more rainfall, at least 25-30% more rainfall, at least 30-35% more rainfall, at least 35-40% more rainfall, at
0 least 40-45% more rainfall, at least 45-50% more rainfall, at least 50-55% more rainfall, at least 55-60% more rainfall, at least 60-65% more rainfall, at least 65-70% more rainfall, at least 70-75% more rainfall, at least 80-85% more rainfall, at least 85-90% more rainfall, at least 90-95% more rainfall, at least 95-100% more rainfall, or even greater than 100% more rainfall, or even greater than 200% more rainfall, or even greater than 300% more rainfall, or
5 even greater than 400% more rainfall, or even greater than 500% more rainfall, when compared with crop plants grown under normal conditions during an average growing season.

[0081] In another embodiment, the endophyte-associated plant is harvested from a soil type with different soil moisture classification than the normal soil type that the crop plant is
0 grown on, for example from an aquic soil (soil is saturated with water and virtually free of gaseous oxygen for sufficient periods of time, such that there is evidence of poor aeration), for example from an udic soil (soil moisture is sufficiently high year-round in most years to meet plant requirement), for example from an ustic soil (soil moisture is intermediate

between udic and aridic regimes; generally, plant-available moisture during the growing season, but severe periods of drought may occur), for example from an aridic soil (soil is dry for at least half of the growing season and moist for less than 90 consecutive days), for example from a xeric soil (soil moisture regime is found in Mediterranean-type climates, with cool, moist winters and warm, dry summers).

[0082] In one embodiment, the endophyte-associated plant is harvested from an environment with average rainfall lower than the optimal average rainfall of the crop plant, for example 2-95% less rainfall than average, for example, at least 5-90% less rainfall, at least 10-85% less rainfall, at least 15-80% less rainfall, at least 20-75% less rainfall, at least 25-70% less rainfall, at least 30-65% less rainfall, at least 35-60% less rainfall, at least 40-55% less rainfall, at least 45-50% less rainfall, when compared with crop plants grown under normal conditions during an average growing season.

[0083] In one embodiment, the endophyte-associated plant is harvested from an environment with average rainfall higher than the optimal average rainfall of the crop plant, for example 2-5% more rainfall than average, for example, at least 5-10% more rainfall, at least 10-15% more rainfall, at least 15-20% more rainfall, at least 20-25% more rainfall, at least 25-30% more rainfall, at least 30-35% more rainfall, at least 35-40% more rainfall, at least 40-45% more rainfall, at least 45-50% more rainfall, at least 50-55% more rainfall, at least 55-60% more rainfall, at least 60-65% more rainfall, at least 65-70% more rainfall, at least 70-75% more rainfall, at least 80-85% more rainfall, at least 85-90% more rainfall, at least 90-95% more rainfall, at least 95-100% more rainfall, or even greater than 100% more rainfall, or even greater than 200% more rainfall, or even greater than 300% more rainfall, or even greater than 400% more rainfall, or even greater than 500% more rainfall, when compared with crop plants grown under normal conditions during an average growing season.

[0084] In another embodiment, the endophyte-associated plant is harvested from an agricultural environment with a crop yield lower than the average crop yield expected from the crop plant grown under average cultivation practices on normal agricultural land, for example 2-5% lower yield than average, for example, at least 5-10% lower yield, at least 10-15% lower yield, at least 15-20% lower yield, at least 20-25% lower yield, at least 25-30% lower yield, at least 30-35% lower yield, at least 35-40% lower yield, at least 40-45% lower yield, at least 45-50% lower yield, at least 50-55% lower yield, at least 55-60% lower yield, at least 60-65% lower yield, at least 65-70% lower yield, at least 70-75% lower yield, at least

80-85% lower yield, at least 85-90% lower yield, at least 90-95% lower yield, or less, when compared with crop plants grown under normal conditions during an average growing season.

5 [0085] In a related embodiment, the endophyte-associated plant is harvested from an agricultural environment with a crop yield lower than the average crop yield expected from the crop plant grown under average cultivation practices on normal agricultural land, for example 2-95% lower yield than average, for example, at least 5-90% lower yield, at least 10-85% lower yield, at least 15-80% lower yield, at least 20-75% lower yield, at least 25-70% lower yield, at least 30-65% lower yield, at least 35-60% lower yield, at least 40-55% lower
0 yield, at least 45-50% lower yield, when compared with crop plants grown under normal conditions during an average growing season.

[0086] In one embodiment, the endophyte-associated plant is harvested from an environment with average crop yield higher than the optimal average crop yield of the crop plant, for example 2-5% more yield than average, for example, at least 5-10% more yield, at
5 least 10-15% more yield, at least 15-20% more yield, at least 20-25% more yield, at least 25-30% more yield, at least 30-35% more yield, at least 35-40% more yield, at least 40-45% more yield, at least 45-50% more yield, at least 50-55% more yield, at least 55-60% more yield, at least 60-65% more yield, at least 65-70% more yield, at least 70-75% more yield, at
0 least 80-85% more yield, at least 85-90% more yield, at least 90-95% more yield, at least 95-100% more yield, or even greater than 100% more yield, or even greater than 200% more yield, or even greater than 300% more yield, or even greater than 400% more yield, or even greater than 500% more yield, when compared with crop plants grown under normal conditions during an average growing season.

[0087] In a related embodiment, the endophyte-associated plant is harvested from an
5 environment with average crop yield higher than the optimal average crop yield of the crop plant, 2-500% more yield than average, 2-400% more yield than average, 2-300% more yield than average, 2-200% more yield than average, 2-95% more yield than average, for example, at least 5-90% more yield, at least 10-85% more yield, at least 15-80% more yield, at least
20-75% more yield, at least 25-70% more yield, at least 30-65% more yield, at least 35-60%
0 more yield, at least 40-55% more yield, at least 45-50% more yield, when compared with crop plants grown under normal conditions during an average growing season.

[0088] In another embodiment, the endophyte-associated plant is harvested from a environment where soil contains lower total nitrogen than the optimum levels recommended in order to achieve average crop yields for a plant grown under average cultivation practices on normal agricultural land, for example 2-5% less nitrogen than average, for example, at
5 least 5-10% less nitrogen, at least 10-15% less nitrogen, at least 15-20% less nitrogen, at least 20-25% less nitrogen, at least 25-30% less nitrogen, at least 30-35% less nitrogen, at least 35-40% less nitrogen, at least 40-45% less nitrogen, at least 45-50% less nitrogen, at least 50-55% less nitrogen, at least 55-60% less nitrogen, at least 60-65% less nitrogen, at least 65-70% less nitrogen, at least 70-75% less nitrogen, at least 80-85% less nitrogen, at least 85-
10 90% less nitrogen, at least 90-95% less nitrogen, or less, when compared with crop plants grown under normal conditions during an average growing season.

[0089] In another embodiment, the endophyte-associated plant is harvested from a environment where soil contains higher total nitrogen than the optimum levels recommended in order to achieve average crop yields for a plant grown under average cultivation practices
15 on normal agricultural land, for example 2-5% more nitrogen than average, for example, at least 5-10% more nitrogen, at least 10-15% more nitrogen, at least 15-20% more nitrogen, at least 20-25% more nitrogen, at least 25-30% more nitrogen, at least 30-35% more nitrogen, at least 35-40% more nitrogen, at least 40-45% more nitrogen, at least 45-50% more nitrogen, at least 50-55% more nitrogen, at least 55-60% more nitrogen, at least 60-65% more nitrogen, at
20 least 65-70% more nitrogen, at least 70-75% more nitrogen, at least 80-85% more nitrogen, at least 85-90% more nitrogen, at least 90-95% more nitrogen, at least 95-100% more nitrogen, or even greater than 100% more nitrogen, or even greater than 200% more nitrogen, or even greater than 300% more nitrogen, or even greater than 400% more nitrogen, or even greater than 500% more nitrogen, when compared with crop plants grown under normal conditions.
25 during an average growing season.

[0090] In another embodiment, the endophyte-associated plant is harvested from a environment where soil contains lower total phosphorus than the optimum levels recommended in order to achieve average crop yields for a plant grown under average cultivation practices on normal agricultural land, for example 2-5% less phosphorus than
30 average, for example, at least 5-10% less phosphorus, at least 10-15% less phosphorus, at least 15-20% less phosphorus, at least 20-25% less phosphorus, at least 25-30% less phosphorus, at least 30-35% less phosphorus, at least 35-40% less phosphorus, at least 40-45% less phosphorus, at least 45-50% less phosphorus, at least 50-55% less phosphorus, at

least 55-60% less phosphorus, at least 60-65% less phosphorus, at least 65-70% less phosphorus, at least 70-75% less phosphorus, at least 80-85% less phosphorus, at least 85-90% less phosphorus, at least 90-95% less phosphorus, or less, when compared with crop plants grown under normal conditions during an average growing season.

5 [0091] In another embodiment, the endophyte-associated plant is harvested from a environment where soil contains higher total phosphorus than the optimum levels recommended in order to achieve average crop yields for a plant grown under average cultivation practices on normal agricultural land, for example 2-5% more phosphorus than average, for example, at least 5-10% more phosphorus, at least 10-15% more phosphorus, at
0 least 15-20% more phosphorus, at least 20-25% more phosphorus, at least 25-30% more phosphorus, at least 30-35% more phosphorus, at least 35-40% more phosphorus, at least 40-45% more phosphorus, at least 45-50% more phosphorus, at least 50-55% more phosphorus, at least 55-60% more phosphorus, at least 60-65% more phosphorus, at least 65-70% more phosphorus, at least 70-75% more phosphorus, at least 80-85% more phosphorus, at least 85-
5 90% more phosphorus, at least 90-95% more phosphorus, at least 95-100% more phosphorus, or even greater than 100% more phosphorus, or even greater than 200% more phosphorus, or even greater than 300% more phosphorus, or even greater than 400% more phosphorus, or even greater than 500% more phosphorus, when compared with crop plants grown under normal conditions during an average growing season.

10 [0092] In another embodiment, the endophyte-associated plant is harvested from a environment where soil contains lower total potassium than the optimum levels recommended in order to achieve average crop yields for a plant grown under average cultivation practices on normal agricultural land, for example 2-5% less potassium than average, for example, at least 5-10% less potassium, at least 10-15% less potassium, at least
15 15-20% less potassium, at least 20-25% less potassium, at least 25-30% less potassium, at least 30-35% less potassium, at least 35-40% less potassium, at least 40-45% less potassium, at least 45-50% less potassium, at least 50-55% less potassium, at least 55-60% less potassium, at least 60-65% less potassium, at least 65-70% less potassium, at least 70-75% less potassium, at least 80-85% less potassium, at least 85-90% less potassium, at least 90-
20 95% less potassium, or less, when compared with crop plants grown under normal conditions during an average growing season.

[0093] In another embodiment, the endophyte-associated plant is harvested from a environment where soil contains higher total potassium than the optimum levels

recommended in order to achieve average crop yields for a plant grown under average cultivation practices on normal agricultural land, for example 2-5% more potassium than average, for example, at least 5-10% more potassium, at least 10-15% more potassium, at least 15-20% more potassium, at least 20-25% more potassium, at least 25-30% more potassium, at least 30-35% more potassium, at least 35-40% more potassium, at least 40-45% more potassium, at least 45-50% more potassium, at least 50-55% more potassium, at least 55-60% more potassium, at least 60-65% more potassium, at least 65-70% more potassium, at least 70-75% more potassium, at least 80-85% more potassium, at least 85-90% more potassium, at least 90-95% more potassium, at least 95-100% more potassium, or even greater than 100% more potassium, or even greater than 200% more potassium, or even greater than 300% more potassium, or even greater than 400% more potassium, or even greater than 500% more potassium, when compared with crop plants grown under normal conditions during an average growing season.

[0094] In another embodiment, the endophyte-associated plant is harvested from a environment where soil contains lower total sulfur than the optimum levels recommended in order to achieve average crop yields for a plant grown under average cultivation practices on normal agricultural land, for example 2-5% less sulfur than average, for example, at least 5-10% less sulfur, at least 10-15% less sulfur, at least 15-20% less sulfur, at least 20-25% less sulfur, at least 25-30% less sulfur, at least 30-35% less sulfur, at least 35-40% less sulfur, at least 40-45% less sulfur, at least 45-50% less sulfur, at least 50-55% less sulfur, at least 55-60% less sulfur, at least 60-65% less sulfur, at least 65-70% less sulfur, at least 70-75% less sulfur, at least 80-85% less sulfur, at least 85-90% less sulfur, at least 90-95% less sulfur, or less, when compared with crop plants grown under normal conditions during an average growing season.

[0095] In another embodiment, the endophyte-associated plant is harvested from a environment where soil contains higher total sulfur than the optimum levels recommended in order to achieve average crop yields for a plant grown under average cultivation practices on normal agricultural land, for example 2-5% more sulfur than average, for example, at least 5-10% more sulfur, at least 10-15% more sulfur, at least 15-20% more sulfur, at least 20-25% more sulfur, at least 25-30% more sulfur, at least 30-35% more sulfur, at least 35-40% more sulfur, at least 40-45% more sulfur, at least 45-50% more sulfur, at least 50-55% more sulfur, at least 55-60% more sulfur, at least 60-65% more sulfur, at least 65-70% more sulfur, at least 70-75% more sulfur, at least 80-85% more sulfur, at least 85-90% more sulfur, at least

90-95% more sulfur, at least 95-100% more sulfur, or even greater than 100% more sulfur, or even greater than 200% more sulfur, or even greater than 300% more sulfur, or even greater than 400% more sulfur, or even greater than 500% more sulfur, when compared with crop plants grown under normal conditions during an average growing season.

5 [0096] In another embodiment, the endophyte-associated plant is harvested from a environment where soil contains lower total calcium than the optimum levels recommended in order to achieve average crop yields for a plant grown under average cultivation practices on normal agricultural land, for example 2-5% less calcium than average, for example, at least 5-10% less calcium, at least 10-15% less calcium, at least 15-20% less calcium, at least
0 20-25% less calcium, at least 25-30% less calcium, at least 30-35% less calcium, at least 35-40% less calcium, at least 40-45% less calcium, at least 45-50% less calcium, at least 50-55% less calcium, at least 55-60% less calcium, at least 60-65% less calcium, at least 65-70% less calcium, at least 70-75% less calcium, at least 80-85% less calcium, at least 85-90% less calcium, at least 90-95% less calcium, or less, when compared with crop plants grown under
5 normal conditions during an average growing season.

[0097] In another embodiment, the endophyte-associated plant is harvested from a environment where soil contains lower total magnesium than the optimum levels recommended in order to achieve average crop yields for a plant grown under average cultivation practices on normal agricultural land, for example 2-5% less magnesium than
0 average, for example, at least 5-10% less magnesium, at least 10-15% less magnesium, at least 15-20% less magnesium, at least 20-25% less magnesium, at least 25-30% less magnesium, at least 30-35% less magnesium, at least 35-40% less magnesium, at least 40-45% less magnesium, at least 45-50% less magnesium, at least 50-55% less magnesium, at least 55-60% less magnesium, at least 60-65% less magnesium, at least 65-70% less
5 magnesium, at least 70-75% less magnesium, at least 80-85% less magnesium, at least 85-90% less magnesium, at least 90-95% less magnesium, or less, when compared with crop plants grown under normal conditions during an average growing season.

[0098] In another embodiment, the endophyte-associated plant is harvested from a environment where soil contains higher total sodium chloride (salt) than the optimum levels
0 recommended in order to achieve average crop yields for a plant grown under average cultivation practices on normal agricultural land, for example 2-5% more salt than average, for example, at least 5-10% more salt, at least 10-15% more salt, at least 15-20% more salt, at least 20-25% more salt, at least 25-30% more salt, at least 30-35% more salt, at least 35-40%

more salt, at least 40-45% more salt, at least 45-50% more salt, at least 50-55% more salt, at least 55-60% more salt, at least 60-65% more salt, at least 65-70% more salt, at least 70-75% more salt, at least 80-85% more salt, at least 85-90% more salt, at least 90-95% more salt, at least 95-100% more salt, or even greater than 100% more salt, or even greater than 200% more salt, or even greater than 300% more salt, or even greater than 400% more salt, or even greater than 500% more salt, when compared with crop plants grown under normal conditions during an average growing season.

Relocalization of Endophytes

[0099] In some embodiments, a single endophyte strain or a plurality of endophytes that are used to treat a plant element are capable of localizing to a different tissue of the plant, regardless of the original source of the endophyte. For example, the endophyte can be capable of localizing to any one of the tissues in the plant, including: the root, adventitious root, seminal root, root hair, shoot, leaf, flower, bud, tassel, meristem, pollen, pistil, ovaries, stamen, fruit, stolon, rhizome, nodule, tuber, trichome, guard cells, hydathode, petal, sepal, glume, rachis, vascular cambium, phloem, and xylem. In one embodiment, the endophyte is capable of localizing to the root and/or the root hair of the plant. In another embodiment, the endophyte is capable of localizing to the photosynthetic tissues, for example, leaves and shoots of the plant. In other cases, the endophyte is localized to the vascular tissues of the plant, for example, in the xylem and phloem. In still another embodiment, the endophyte is capable of localizing to the reproductive tissues (flower, pollen, pistil, ovaries, stamen, fruit) of the plant. In another embodiment, the endophyte is capable of localizing to the root, shoots, leaves and reproductive tissues of the plant. In still another embodiment, the endophyte colonizes a fruit or seed tissue of the plant. In still another embodiment, the endophyte is able to colonize the plant such that it is present in the surface of the plant (i.e., its presence is detectably present on the plant exterior, or the episphere of the plant). In still other embodiments, the endophyte is capable of localizing to substantially all, or all, tissues of the plant. In certain embodiments, the endophyte is not localized to the root of a plant. In other cases, the endophyte is not localized to the photosynthetic tissues of the plant.

Endophytes capable of altering the metabolome, epigenome, or transcriptome of plants

[0100] The endophytes useful for the invention can also be classified according to the changes conferred upon the plant. For example, the endophyte can alter the hormone status or levels of hormone production in the plant, which in turn can affect many physiological

parameters, including flowering time, water efficiency, apical dominance and/or lateral shoot branching, increase in root hair, and alteration in fruit ripening. The endophyte may also introduce other changes to the plant, including biochemical, metabolomic, proteomic, genomic, epigenomic and/or transcriptomic profiles of endophyte-associated plants can be compared with reference agricultural plants under the same conditions.

[0101] Metabolomic differences between the plants can be detected using methods known in the art. For example, a biological sample (whole tissue, exudate, phloem sap, xylem sap, root exudate, etc.) from the endophyte-associated and reference agricultural plants can be analyzed essentially as described in Fiehn et al., (2000) *Nature Biotechnol.*, 18, 1157-1161, or Roessner et al., (2001) *Plant Cell*, 13, 11-29. Such metabolomic methods can be used to detect differences in levels in hormone, nutrients, secondary metabolites, root exudates, phloem sap content, xylem sap content, heavy metal content, and the like. Such methods are also useful for detecting alterations in microbial content and status; for example, the presence and levels of bacterial/fungal signaling molecules (e.g., autoinducers and pheromones), which can indicate the status of group-based behavior of endophytes based on, for example, population of endophyte-associated and reference agricultural plants can also be performed to detect changes in expression of at least one transcript, or a set or network of genes upon endophyte association. Similarly, epigenetic changes can be detected using methylated DNA immunoprecipitation followed by high-throughput sequencing.

10 *Combinations of Endophytes*

[0102] Combinations of endophytes can be selected by any one or more of several criteria. In one embodiment, compatible endophytes are selected. As used herein, "compatibility" refers to endophyte populations that do not significantly interfere with the growth, propagation, and/or production of beneficial substances of the other. Incompatible endophyte populations can arise, for example, where one of the populations produces or secretes a compound that is toxic or deleterious to the growth of the other population(s). Incompatibility arising from production of deleterious compounds/agents can be detected using methods known in the art, and as described herein elsewhere. Similarly, the distinct populations can compete for limited resources in a way that makes co-existence difficult.

20 [0103] In another embodiment, combinations are selected on the basis of compounds produced by each population of endophytes. For example, the first population is capable of producing siderophores, and another population is capable of producing anti-fungal compounds. In an embodiment, the first population of endophytes or endophytic components

is capable of a function selected from the group consisting of auxin production, nitrogen fixation, and production of an antimicrobial compound, siderophore production, mineral phosphate solubilization, cellulase production, chitinase production, xylanase production, and acetoin production, carbon source utilization, and combinations thereof. In another embodiment, the second population of endophytes or endophytic component is capable of a function selected from the group consisting of auxin production, nitrogen fixation, production of an antimicrobial compound, siderophore production, mineral phosphate solubilization, cellulase production, chitinase production, xylanase production, and acetoin production, and combinations thereof. In still another embodiment, the first and second populations are capable of at least one different function.

[0104] In still another embodiment, the combinations of endophytes are selected for their distinct localization in the plant after colonization. For example, the first population of endophytes or endophytic components can colonize, and in some cases preferentially colonize, the root tissue, while a second population can be selected on the basis of its preferential colonization of the aerial parts of the agricultural plant. Therefore, in an embodiment, the first population is capable of colonizing one or more of the tissues selected from the group consisting of a root, shoot, leaf, flower, and seed. In another embodiment, the second population is capable of colonizing one or more tissues selected from the group consisting of root, shoot, leaf, flower, and seed. In still another embodiment, the first and second populations are capable of colonizing a different tissue within the agricultural plant.

[0105] In some embodiments, combinations of endophytes are selected for their ability to confer a benefit to the host plant at different points in the life cycle of said host plant. In one example, one endophyte can be selected to impart improved seedling vigor, and a second endophyte can be selected to improve soil nutrient acquisition by roots of the mature plant.

[0106] In still another embodiment, combinations of endophytes are selected for their ability to confer one or more distinct fitness traits on the inoculated agricultural plant, either individually or in synergistic association with other endophytes. In another embodiment, one endophyte may induce the colonization of a second endophyte. Alternatively, two or more endophytes may induce the colonization of a third endophyte. For example, the first population of endophytes or endophytic components is selected on the basis that it confers significant increase in biomass, while the second population promotes increased drought tolerance on the inoculated agricultural plant. Therefore, in one embodiment, the first population is capable of conferring at least one trait selected from the group consisting of

thermal tolerance, herbicide tolerance, drought resistance, insect resistance, fungus resistance, virus resistance, bacteria resistance, male sterility, cold tolerance, salt tolerance, increased yield, enhanced nutrient use efficiency, increased nitrogen use efficiency, increased fermentable carbohydrate content, reduced lignin content, increased antioxidant content, enhanced water use efficiency, increased vigor, increased germination efficiency, earlier or increased flowering, increased biomass, altered root-to-shoot biomass ratio, enhanced soil water retention, or a combination thereof. In another embodiment, the second population is capable of conferring a trait selected from the group consisting of thermal tolerance, herbicide tolerance, drought resistance, insect resistance, fungus resistance, virus resistance, bacteria resistance, male sterility, cold tolerance, salt tolerance, increased yield, enhanced nutrient use efficiency, increased nitrogen use efficiency, increased fermentable carbohydrate content, reduced lignin content, increased antioxidant content, enhanced water use efficiency, increased vigor, increased germination efficiency, earlier or increased flowering, increased biomass, altered root-to-shoot biomass ratio, and enhanced soil water retention. In still another embodiment, each of the first and second population is capable of conferring a different trait selected from the group consisting of thermal tolerance, herbicide tolerance, drought resistance, insect resistance, fungus resistance, virus resistance, bacteria resistance, male sterility, cold tolerance, salt tolerance, increased yield, enhanced nutrient use efficiency, increased nitrogen use efficiency, increased fermentable carbohydrate content, reduced lignin content, increased antioxidant content, enhanced water use efficiency, increased vigor, increased germination efficiency, earlier or increased flowering, increased biomass, altered root-to-shoot biomass ratio, and enhanced soil water retention.

[0107] The combinations of endophytes can also be selected based on combinations of the above criteria. For example, the first population of endophytes can be selected on the basis of the compound it produces (e.g., its ability to fix nitrogen, thus providing a potential nitrogen source to the plant), while the second population can be selected on the basis of its ability to confer increased resistance of the plant to a pathogen (e.g., a fungal pathogen).

[0108] In some embodiments of the present invention, it is contemplated that combinations of endophytes can provide an increased benefit to the host plant, as compared to that conferred by a single endophyte, by virtue of additive effects. For example, one endophyte strain that induces a benefit in the host plant may induce such benefit equally well in a plant that is also colonized with a different endophyte strain that also induces the same benefit in the host plant. The host plant thus exhibits the same total benefit from the combination of

different endophyte strains as the additive benefit to individual plants colonized with each individual endophyte of the combination. In one example, a plant is colonized with two different endophyte strains: one provides a 1X increase in biomass when associated with the plant, and the other provides a 2X increase in biomass when associated with a different plant.

5. When both endophyte strains are associated with the same plant, that plant would experience a 3X (additive of 1X + 2X single effects) increase in auxin biomass. Additive effects are a surprising embodiment of the present invention, as non-compatibility of endophytes may result in a cancelation of the beneficial effects of both endophytes.

[0109] In some embodiments of the present invention, it is contemplated that a combination of endophytes can provide an increased benefit to the host plant, as compared to that conferred by a single endophyte, by virtue of synergistic effects. For example, one endophyte strain that induces a benefit in the host plant may induce such benefit beyond additive effects in a plant that is also colonized with a different endophyte strain that also induces that benefit in the host plant. The host plant thus exhibits the greater total benefit from the combination of different endophyte strains than could be seen from the additive benefit of individual plants colonized with each individual endophyte of the combination. In one example, a plant is colonized with two different endophyte strains: one provides a 1X increase in biomass when associated with a plant, and the other provides a 2X increase in biomass when associated with a different plant. When both endophyte strains are associated with the same plant, that plant would experience a 5X (greater than an additive of 1X + 2X single effects) increase in biomass. Synergistic effects are a surprising embodiment of the present invention.

Inoculation with Multiple Endophytes

[0110] In another embodiment, the present invention contemplates methods of coating a plant element, e.g., a seed of a plant, with a plurality of endophytes, as well as synthetic compositions comprising a plurality of endophytes on and/or in the plant element. The methods according to this embodiment can be performed in a manner similar to those described herein for single endophyte coating. In one example, multiple endophytes can be prepared in a single preparation that is coated onto the plant element, e.g., a seed. The endophytes can be from a common origin (i.e., a same plant). Alternatively, the endophytes can be from different plants.

[0111] Where multiple endophytes are coated onto a plant element, each endophyte can be a bacterium. In the alternative, each endophyte can be a fungus. In still another embodiment,

a plurality of bacterial and fungal endophytes can be coated onto the surface of a plant element.

[0112] Where a plurality of endophytes are coated onto the plant element, any or all of the endophytes may be capable of conferring a beneficial trait onto the host plant. In some cases, all of the endophytes are capable of conferring a beneficial trait onto the host plant. The trait conferred by each of the endophytes may be the same (e.g., both improve the host plant's tolerance to a particular biotic stress), or may be distinct (e.g., one improves the host plant's tolerance to drought, while another improves phosphate utilization). In other cases the conferred trait may be the result of interactions between the endophytes.

[0113] In one embodiment, an agricultural plant is contacted with a formulation comprising at least two endophytic microbial entities. Specific examples of pairs of endophytic microbial entities that can be applied to an agricultural plant include, for example, a pair of endophytic microbes containing nucleic acid sequences that are each at least 97% identical to the nucleic acid sequence selected from the groups provided in Table 1, Table 2, Table 7 and Table 8.

Isolation of endophytes

[0114] According to the present invention, endophytes are isolated from a plant element, e.g., a seed of a plant. Because endophytes are capable of living and/or residing within the plant, or portion of the plant (including the seed), the endophytic nature of a microbe can be distinguished from surface associated microbes by its resistance to surface sterilization techniques. Therefore, in one embodiment, endophytes are isolated from plant elements after the surface of the plant element is sterilized by contacting with non-specific antimicrobial agents such as sodium hypochlorite, hydrogen peroxide, copper oxychloride, copper hydroxide, copper sulfate, chlorothalonil, cuprous oxide, streptomycin, copper ammonium carbonate, copper diammonia diacetate complex, copper octanoate, oxytetracycline, fosetyl-AL or chloropicrin, in an aqueous solution and also optionally including detergents such as SDS, triton X-100, tween 20, can be used. In addition, dried seeds can be soaked in organic solvents such as ethanol, for example 50% - 90% ethanol. Antibacterial or antifungal agents (e.g., captan, maneb, thiram, fludioxonil, etc.), particularly those that do not penetrate into the plant element, can also be used. In general, plant elements are soaked in an aqueous solution or commercial formulation containing one or more of these compounds for 30 seconds to 12 hours in a plastic container. After surface sterilization, the plant element is removed from the

antibacterial formulation and washed 3-5 times with sterile distilled water. In an alternative embodiment where the plant element is a seed, the seed coat can be removed under sterile conditions, and the microbes inside the seed isolated and characterized.

5 [0115] Once surface-residing microbes are removed, the surviving microbes present in the plant element are generally considered endophytes. Such endophytes can be a bacterium or fungus, and can be isolated by homogenizing the surface sterilized seeds, and placing the homogenate under conditions allowing growth of the microbe. Therefore, the loss of microbe viability upon surface sterilization indicates that the microbes are almost exclusively located on the seed surface. In contrast, resistance of the microbe population to such plant element
0 sterilization methods indicates an internal localization of the microbes. Alternatively, the presence of microbial DNA after surface sterilization with agents that cross-link or otherwise destroy DNA can be detected using sensitive detection methods such as PCR to establish the presence of the microbe within the plant element.

Growth of endophytes

5 [0116] Viability of the microbe can be tested after plant element surface sterilization, or after removal of the seed coat, by homogenizing the plant element and placing the homogenate under conditions that promote growth of the microbe. In the alternative, the presence of microbes can be detected visually or microscopically if the microbes can form a colony that is visible by such inspection. Reagents are also available for the detection of
0 microbes: the stain aniline blue can be used for detecting hyphae, other assays are known in the art.

[0117] Endophytes may require special conditions to allow for growth in isolation. A number of different growth media can be used to grow the endophytes. Additional details of endophyte growth are described within the examples sections.

5 *Functional Attributes of Endophytes*

[0118] In some cases, a single endophyte strain, a plurality of endophytes, or each individual type of endophytes of that plurality, may produce one or more compounds and/or have one or more activities, e.g., one or more of the following: production of a metabolite, production of a phytohormone such as auxin, production of acetoin, production of an
0 antimicrobial compound, production of a siderophore, production of a cellulase, production of a pectinase, production of a chitinase, production of a xylanase, nitrogen fixation, or mineral phosphate solubilization. For example, an endophyte can produce a phytohormone

selected from the group consisting of an auxin, a cytokinin, a gibberellin, ethylene, a brassinosteroid, and abscisic acid. In some embodiments, the endophyte produces auxin (e.g., indole-3-acetic acid (IAA)). Production of auxin can be assayed as described herein. Many of the microbes described herein are capable of producing the plant hormone auxin indole-3-acetic acid (IAA) when grown in culture. Auxin plays a key role in altering the physiology of the plant, including the extent of root growth. Therefore, in other embodiments, endophytes are disposed on the surface or within a tissue of the plant element in an amount effective to detectably increase production of auxin in the agricultural plant when compared with a reference agricultural plant. In some embodiments, the increased auxin production can be detected in a tissue type selected from the group consisting of the root, shoot, leaves, and flowers.

[0119] In some embodiments, a single endophyte strain, a plurality of endophytes, or each individual type of endophytes of that plurality, can produce a compound with antimicrobial properties. For example, the compound can have antibacterial properties, as determined by the growth assays provided herein. In some embodiments, the compound with antibacterial properties shows bacteriostatic or bactericidal activity against *E. coli* and/or *Bacillus sp.* In other embodiments, the endophyte produces a compound with antifungal properties, for example, fungicidal or fungistatic activity against *S. cerevisiae* and/or *Rhizoctonia*.

[0120] In some embodiments, a single endophyte strain, a plurality of endophytes, or each individual type of endophytes of that plurality, is capable of nitrogen fixation, and is thus capable of producing ammonium from atmospheric nitrogen. The ability of endophytes to fix nitrogen can be confirmed by testing for growth of the fungus in nitrogen-free growth media, for example, LGI media, as described herein.

[0121] In some embodiments, a single endophyte strain, a plurality of endophytes, or each individual type of endophytes of that plurality, can produce a compound that increases the solubility of mineral phosphate in the medium, i.e., mineral phosphate solubilization, for example, using growth assays known in the art. In some embodiments, the endophytes produce a compound that allows the bacterium to grow in growth media comprising Ca_3HPO_4 as the sole phosphate source.

[0122] In some embodiments, a single endophyte strain, a plurality of endophytes, or each individual type of endophytes of that plurality, can produce a siderophore. Siderophores are small high-affinity iron chelating agents secreted by microorganisms that increase the

bioavailability of iron. Siderophore production by the endophytes can be detected, for example, using methods known in the art.

[0123] In some embodiments, a single endophyte strain, a plurality of endophytes, or each individual type of endophytes of that plurality, can produce a hydrolytic enzyme. For example, in some embodiments, an endophytes can produce a hydrolytic enzyme selected from the group consisting of a cellulase, a pectinase, a chitinase and a xylanase. Hydrolytic enzymes can be detected using the methods known in the art.

Selection of endophytes conferring beneficial traits

[0124] The present invention contemplates inoculation of plants with microbes. As described earlier, the microbes can be derived from many different plants species, from different parts of the plants, and from plants isolated across different environments. Once a microbe is isolated, it can be tested for its ability to confer a beneficial trait. Numerous tests can be performed both *in vitro* and *in vivo* to assess what benefits, if any, are conferred upon the plant. In one embodiment, a microbe is tested *in vitro* for an activity selected from the group consisting of: liberation of complexed phosphates, liberation of complexed iron (e.g., through secretion of siderophores), production of phytohormones, production of antibacterial compounds, production of antifungal compounds, production of insecticidal compounds, production of nematocidal compounds, production and/or secretion of ACC deaminase, production and/or secretion of acetoin, production and/or secretion of pectinase, production and/or secretion of cellulase, and production and/or secretion of RNase. Exemplary *in vitro* methods for the above can be found in the Examples sections below.

[0125] It is noted that the initial test for the activities listed above can also be performed using a mixture of microbes, for example, a community of microbes isolated from a single plant. A positive activity readout using such mixture can be followed with the isolation of individual microbes within that population and repeating the *in vitro* tests for the activities to isolate the microbe responsible for the particular activity. Once validated using a single microbe isolate, then the plant can be inoculated with a microbe, and the test performed *in vivo*, either in growth chamber or greenhouse conditions, and comparing with a control plant that was not inoculated with the microbe.

Endophyte preparations

[0126] Also described herein is a preparation comprising one or more isolated modified endophytes described above. The preparation further comprises an agriculturally acceptable

carrier, and the preparation comprises an amount of endophytes sufficient to improve an agronomic trait of the population of seeds. In one embodiment, the isolated endophyte is cultured, for example, on semi-synthetic or synthetic growth medium. In one embodiment, the endophyte is provided as a powder, for example, a lyophilized powder. In another embodiment, the endophyte is applied in suspension at a suitable concentration. The preparation of microbes can be an aqueous solution, an oil-in-water emulsion or water-in-oil emulsion containing a minimum concentration of a microbe. Microbes are present as live cells, viable cells, spores, or mycelia. Typically, the concentration is at least 10^4 CFU/ml or spores/ml, for example at least 3×10^4 CFU/mL or spores/ml, at least 10^5 CFU/mL or spores/ml, at least 3×10^5 CFU/mL or spores/ml, at least 10^6 CFU/mL or spores/ml, at least 3×10^6 CFU/mL or spores/ml, at least 10^7 CFU/ml or spores/ml, at least 3×10^7 CFU/mL or spores/ml, at least 10^8 CFU/mL or spores/ml, 10^9 CFU/mL or spores/ml, or more. In one embodiment, the preparation is a solution containing a microbe at a concentration between about 10^5 CFU/mL or spores/ml and about 10^9 CFU/mL or spores/ml. In another embodiment, the preparation contains a microbe at a concentration between about 10^6 CFU/mL or spores/ml and about 10^8 CFU/mL or spores/ml.

[0127] The synthetic preparation can also contain any number of other components. In one embodiment, the synthetic preparation may contain growth media or constituents required for the growth and propagation of the microbe. In one embodiment, the growth medium is selected from the group provided in the table below.

Table 100: Exemplary growth medium

Microbe Type	Media	Organisms
Bacteria	Nutrient Peptone Agar	Heterotrophic bacteria
	MacConkey Agar + myo-inositol + Carbenicillin	Klebsiella Sp.
	J agar	Bacillus sp. and other firmicutes
	N-poor Medium (LGT)	Aerobic heterotrophic N ₂ -fixing bacteria
	Yeast Mannitol Agar	Rhizobium sp.
	King's B medium	Pseudomonas sp.
	SC medium	Fastidious bacteria
	R2A agar	Oligotrophic bacteria
	Tryptic Soy Agar	Heterotrophic bacteria
Fungi	Cornmeal agar	Fungi
	Glucose-Yeast extract agar + tetracycline	Selective enumeration of yeasts and molds.

	Potato-Dextrose agar (PDA)	Yeasts and molds
	Potato-Dextrose broth (PDB)	Yeast and molds
	Sabouraud Agar	Yeasts, molds and aciduric microorganisms
	V8 Agar	Fungi
	Malt Dextrose Agar	Identification of yeasts and moulds
	Czapek's medium	Fungi and Mold
	SPT agar	Verticillium sp.

[0128] The synthetic preparation can be of a defined pH range. In one embodiment, the pH of the preparation can be between pH 5.5 – 6.0, pH 5.75-6.25, pH 6.0 – 6.5, pH 6.25-6.75, pH 6.5-7.0, pH 6.75-7.25, and pH 7.0-7.5. The pH of the medium can be adjusted using any biologically compatible buffering agent.

[0129] The synthetic preparation can also comprise a carrier, such as diatomaceous earth, clay, or chitin, which act to complex with chemical agents, such as control agents.

[0130] The synthetic preparation can also comprise an adherent. Such agents are useful for combining the microbes of the invention with carriers that can contain other compounds (e.g., control agents that are not biologic), to yield a coating composition. Such compositions help create coatings around the plant or seed to maintain contact between the microbe and other agents with the plant or plant part. In one embodiment, adherents are selected from the group consisting of: alginate, gums, starches, lecithins, formononetin, polyvinyl alcohol, alkali formononetinate, hesperetin, polyvinyl acetate, cephalins, Gum Arabic, Xanthan Gum, Mineral Oil, Polyethylene Glycol (PEG), Polyvinyl pyrrolidone (PVP), Arabino-galactan, Methyl Cellulose, PEG 400, Chitosan, Polyacrylamide, Polyacrylate, Polyacrylonitrile, Glycerol, Triethylene glycol, Vinyl Acetate, Gellan Gum, Polystyrene, Polyvinyl, Carboxymethyl cellulose, Gum Ghatti, and polyoxyethylene-polyoxybutylene block copolymers. Other examples of adherent compositions that can be used in the synthetic preparation include those described in EP 0818135, CA 1229497, WO 2013090628, EP 0192342, WO 2008103422 and CA 1041788, each of which is incorporated by reference in its entirety.

[0131] The synthetic preparation can also contain one or more reagents that promote internalization of the microbe into the plant, and can include any one of the following classes of compounds: a surfactant, an abrasive, an osmoticum, and a plant signaling molecule.

[0132] The preparation can also contain a surfactant. Non-limiting examples of surfactants include nitrogen-surfactant blends such as Prefer 28 (Cenex), Surf-N(US), Inhance (Brandt), P-28 (Wilfarm) and Patrol (Helena); esterified seed oils include Sun-It II (AmCy), MSO (UAP), Scoil (Agasco), Hasten (Wilfarm) and Mes-100 (Drexel); and organo-silicone
5 surfactants include Silwet L77 (UAP), Silikin (Terra), Dyne-Amic (Helena), Kinetic (Helena), Sylgard 309 (Wilbur-Ellis) and Century (Precision). In one embodiment, the surfactant is present at a concentration of between 0.01% v/v to 10% v/v. In another embodiment, the surfactant is present at a concentration of between 0.1% v/v to 1% v/v.

[0133] The synthetic preparation of a defined osmolality can also be used. In one
0 embodiment, the synthetic preparation has an osmolality of less than about 100 mOsm, for example less than about 75 mOsm, less than about 50 mOsm, or less than about 25 mOsm. In another embodiment, the synthetic preparation has an osmolality of at least 250 mOsm, for example at least 300 mOsm, at least 400 mOsm, at least 500 mOsm, at least 600 mOsm, at least 700 mOsm, at least 800 mOsm, 900 mOsm or greater. The osmolality of the preparation
5 can be adjusted by addition of an osmoticum: the osmoticum can be any commonly used osmoticum, and can be selected from the group consisting of: mannitol, sorbitol, NaCl, KCl, CaCl₂, MgSO₄, sucrose, or any combination thereof.

[0134] The endophyte can be obtained from growth in culture, for example, using semi-synthetic or synthetic growth medium. In addition, the microbe can be cultured on solid
0 media, for example on petri dishes, scraped off and suspended into the preparation. Microbes at different growth phases can be used. For example, microbes at lag phase, early-log phase, mid-log phase, late-log phase, stationary phase, early death phase, or death phase can be used.

[0135] For certain microbes that exist as mycelia or mycelia-like structures, pre-treatment
5 of the microbes with enzymes (including, but not limited to, driselase, gluculase, cellulase, beta-glucanase, lysozyme, zymolyase) can be used to generate protoplasts in order to provide a suspension of microbes. After generation of protoplasts, the microbes can be allowed to partially regenerate the cell walls by leaving the protoplasts in a growth medium or solution with relatively high osmolarity for a short time (typically less than about 12 hours at room
0 temperature) to prevent bursting of protoplasts.

Detection and Quantitation of Endophytes and Other Microbes

[0136] The presence of the endophyte or other microbes can be detected and its localization in or on the host plant (including the seed) can be determined using a number of different methodologies. The presence of the microbe in the embryo or endosperm, as well as its
5 localization with respect to the plant cells, can be determined using methods known in the art, including immunofluorescence microscopy using microbe specific antibodies, or fluorescence in situ hybridization. The presence and quantity of other microbes can be established by the FISH, immunofluorescence and PCR methods using probes that are specific for the microbe. Alternatively, degenerate probes recognizing conserved sequences
10 from many bacteria and/or fungi can be employed to amplify a region, after which the identity of the microbes present in the tested tissue/cell can be determined by sequencing.

[0137] Therefore, in one embodiment, where the endophyte is coated onto the surface of a plant element of a first plant such that the endophyte is present at a higher level on the surface of the plant element than is present on the surface of an uncoated reference plant element, the
15 level of the endophyte present on the surface of the uncoated reference plant element is determined by culturing microbes that are present on the surface of the plant element. In another embodiment, the level of the endophyte present on the surface of the uncoated reference plant element is determined by PCR.

Uniformity of seeds and plants

[0138] In another aspect, the seeds according to the present invention provide a
20 substantially uniform population of seeds with a uniform endophyte composition. The uniform population of seeds can be of a predefined weight. For example, a substantially uniform population of seeds containing at least 100 g seeds, for example at least 1 kg seeds, at least 5 kg seeds, at least 10 kg seeds, can be provided by the method according to the
25 present invention that contains – as a whole product – more than 1%, for example more than 5%, more than 10%, more than 20%, more than 30%, more than 40%, especially more than 50%, of the endophytic microorganism, i.e., the strain that is coated onto the surface of the seeds. According to a preferred embodiment, the present invention provides a marketable seed product containing at least 100 g seeds, for example, at least 1 kg seeds, for example at
30 least 5 kg seeds, at least 10 kg seeds, wherein – as a whole product – more than 50%, for example, more than 60%, more than 70%, more than 80%, more than 90%, more than 95%, more than 99%, or 100% of the seeds contain the microbe, i.e., the inoculant strain. Each of

the seeds can also contain a uniform number of microbes (for example, viable endophytes): for example, at least 50% of the seeds, for example at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 99%, or more of the seeds in the population can contain at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores, at least 30,000 CFU or spores or more, of the endophytic microorganism. In some embodiments, at least 50% of the seeds, for example at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 99%, or more of the seeds in the population contains a single endophyte or a plurality of endophytes at a concentration between about 100 CFU or spores and about 30,000 CFU or spores, between about 100 CFU or spores and about 300 CFU or spores, between about 100 CFU or spores and about 1,000 CFU or spores, between about 100 CFU or spores and about 3,000 CFU or spores, between about 100 CFU or spores and about 10,000 CFU or spores, between about 100 CFU or spores and about 30,000 CFU or spores, between about 300 CFU or spores and about 1,000 CFU or spores, between about 300 CFU or spores and about 3,000 CFU or spores, between about 300 CFU or spores and about 10,000 CFU or spores, between about 300 CFU or spores and about 30,000 CFU or spores, between about 1,000 CFU or spores and about 3,000 CFU or spores, between about 1,000 CFU or spores and about 10,000 CFU or spores, between about 1,000 CFU or spores and about 30,000 CFU or spores, between about 3,000 CFU or spores and about 10,000 CFU or spores, between about 3,000 CFU or spores and about 30,000 CFU or spores, or between about 10,000 CFU or spores and about 30,000 CFU or spores. The endophyte can also be quantitated using other means, for example, using quantitative PCR, to detect the total number of endophyte present on each seed.

[0139] The uniformity of the microbes within the seed population can be measured in several different ways. In one embodiment, a substantial portion of the population of seeds, for example at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 90%, at least 95% or more of the seeds in a population, contains a viable endophyte on its surface. In another embodiment, a substantial portion of the population of seeds, for example at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 90%, at least 95% or more of the seeds in a population contain on its surface a threshold number of viable microbe that is at least 1 CFU or spore per seed, at least 10 CFU or spores per seed, for example, at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, or more, of the microbe per seed. In some

embodiments, a substantial portion of the population of seeds, for example at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 90%, at least 95% or more of the seeds in a population contain on its surface a threshold number of viable microbe that is between 1 CFU or spore per seed and about 3,000 CFU or spores per seed, between 1 CFU or spore per seed and about 10 CFU or spores per seed, between 1 CFU or spore per seed and about 100 CFU or spores per seed, between 1 CFU or spore per seed and about 300 CFU or spores per seed, between 1 CFU or spore per seed and about 1,000 CFU or spores per seed, between 1 CFU or spore per seed and about 3,000 CFU or spores per seed, between about 10 CFU or spore per seed and about 100 CFU or spores per seed, between about 10 CFU or spore per seed and about 300 CFU or spores per seed, between about 10 CFU or spore per seed and about 1,000 CFU or spores per seed, between about 10 CFU or spore per seed and about 3,000 CFU or spores per seed, between about 100 CFU or spore per seed and about 300 CFU or spores per seed, between about 100 CFU or spore per seed and about 1,000 CFU or spores per seed, between about 100 CFU or spore per seed and about 3,000 CFU or spores per seed, between about 300 CFU or spore per seed and about 1,000 CFU or spores per seed, between about 300 CFU or spore per seed and about 3,000 CFU or spores per seed, or between about 1,000 CFU or spore per seed and about 3,000 CFU or spores per seed.

[0140] In still another aspect, the present invention discloses a substantially uniform population of plants produced by growing the population of seeds described above. In one embodiment, at least 75%, at least 80%, at least 90%, at least 95% or more of the plants comprise in one or more tissues an effective amount of the endophyte or endophytes. In another embodiment, at least 1%, between 1% and 10%, for example, at least 10%, between 10% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 70%, at least 70%, between 70% and 75%, at least 75%, between 75% and 80%, at least 80%, between 80% and 90%, at least 90%, between 90% and 95%, at least 95% or more of the plants comprise a microbe population that is substantially similar.

[0141] In some cases, a substantial portion of the population of plants or seeds, for example, at least 1%, between 1% and 10%, for example, at least 10%, between 10% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 70%, at least 70%, between 70% and 75%, at least 75%, between 75% and 80%, at

least 80%, between 80% and 90%, at least 90%, between 90% and 95%, at least 95% or more of the seeds in a population, is coated with an endophyte that is able to perform one of the following functions, including: to stimulate plant growth, grow on nitrogen-free media, solubilize phosphate, sequester iron, secrete RNase, antagonize pathogens, catabolize the precursor of ethylene, produce auxin and acetoin/butanediol. In some cases, a substantial portion of the population of seeds, for example, at least 1%, between 1% and 10%, for example, at least 10%, between 10% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 70%, at least 70%, between 70% and 75%, at least 75%, between 75% and 80%, at least 80%, between 80% and 90%, at least 90%, between 90% and 95%, at least 95% or more of the seeds in a population, exhibits at least one of the endophyte community attributes listed in herein (e.g., total CFUs, presence of a taxa, absence of a taxa, spatial distribution, intercellular colonization, functional properties of endophytes; presence of monoclonal strain, presence of conserved subset of microbial plasmid repertoire, microbe isolated from habitat that is distinct from the location of seed production, etc.).

[0142] Increased uniformity of microbes in plants or seeds can also be detected by measuring the presence of non-genomic nucleic acids present in the microbes. For examples, where the microbe that is inoculated into the plant is known to harbor a plasmid or episome, the presence of the plasmid or episome can be detected in individual plants or seeds by using conventional methods of nucleic acid detection. Therefore, in one embodiment, a substantial portion of the population of seeds, for example at least example at least 1%, between 1% and 10%, for example, at least 10%, between 10% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 70%, at least 70%, between 70% and 75%, at least 75%, between 75% and 80%, at least 80%, between 80% and 90%, at least 90%, between 90% and 95%, at least 95% or more of the seeds in a population, has a detectable presence of the microbial plasmid or episome.

[0143] Increased uniformity of the microbes' epigenetic status can also be used to detect increased uniformity of a population of seeds or plants derived from such seeds. For example, where a microbe that has been inoculated by a plant is also present in the plant (for example, in a different tissue or portion of the plant), or where the introduced microbe is sufficiently similar to a microbe that is present in some of the plants (or portion of the plant, including

seeds), it is still possible to distinguish between the inoculated microbe and the native microbe, for example, by distinguishing between the two microbe types on the basis of their epigenetic status. Therefore, in one embodiment, the epigenetic status is detected in microbes across individual seeds or the plants that grow from such seeds.

5 [0144] It is also known that certain viruses are associated with endophytic fungi (such as the *Curvularia* thermal tolerance virus (CThTV) described in Márquez, L.M., et al., (2007). Science 315: 513-515). Therefore, the presence and quantity of a virus can be used to measure uniformity of seeds or plants containing the endophyte. For example, where the inoculated microbe is known to be associated with a virus, the presence of that virus can be
10 used as a surrogate indicator of uniformity. Therefore, in one embodiment, a substantial portion of the seeds, for example at least 1%, between 1% and 10%, for example, at least 10%, between 10% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 70%, at least 70%, between 70% and 75%, at least 75%,
15 between 75% and 80%, at least 80%, between 80% and 90%, at least 90%, between 90% and 95%, at least 95% or more of the seeds, contain the virus. In other embodiments, where one or more of the endogenous microbes contain associated viruses which are not found in, and not compatible with the inoculated microbe, the loss (i.e., absence) of the virus can be used to measure uniformity of the seed population. As such, in another embodiment, a substantial
20 portion of the seeds, for example at least 1%, between 1% and 10%, for example, at least 10%, between 10% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 70%, at least 70%, between 70% and 75%, at least 75%, between 75% and 80%, at least 80%, between 80% and 90%, at least 90%, between 90% and
25 95%, at least 95% or more of the seeds, do not contain the virus. In other cases, the genetic sequence of the virus can be used to measure the genetic similarity of the virus within a population. In one embodiment, a substantial proportion of the seeds, for example, at least 10%, for example at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% or more of the seeds contain the same virus, for
30 example, as determined by sequence analysis.

[0145] Such uniformity in microbial composition is unique and is extremely advantageous for high-tech and/or industrial agriculture. It allows significant standardization with respect to qualitative endophyte load of seed products. Suitable volumes or weights are those that are

currently used for plant seeds (e.g., the at least 100 g, at least 1, 5 or 10 kg; but also 25 or more, 40 or more, 50 kg or more, even 100 kg or more, 500 kg or more, 1 ton or more, etc.). Suitable containers or packages are those traditionally used in plant seed commercialization; however, also other containers with more sophisticated storage capabilities (e.g., with
5 microbiologically tight wrappings or with gas-or water-proof containments) can be used. The amount of endophytes (qualitatively and quantitatively) contained in the seeds or in the marketable seed product as a whole can be determined by standard techniques in microbiology readily available to any person skilled in the art of plant endophyte analysis.

[0146] In some cases, a sub-population of agricultural seeds can be further selected on the
10 basis of increased uniformity, for example, on the basis of uniformity of microbial population. For example, individual seeds of pools collected from individual cobs, individual plants, individual plots (representing plants inoculated on the same day) or individual fields can be tested for uniformity of microbial density, and only those pools meeting specifications (e.g., at least 80% of tested seeds have minimum density, as determined by quantitative
15 methods described elsewhere) are combined to provide the agricultural seed sub-population.

[0147] The methods described herein can also comprise a validating step. The validating step can entail, for example, growing some seeds collected from the inoculated plants into mature agricultural plants, and testing those individual plants for uniformity. Such validating step can be performed on individual seeds collected from cobs, individual plants, individual
20 plots (representing plants inoculated on the same day) or individual fields, and tested as described above to identify pools meeting the required specifications.

Agricultural Field

[0148] In another aspect, described herein is an agricultural field, including a greenhouse, comprising the population of plants described above. In one embodiment, the agricultural
25 field comprises at least 100 plants. In another embodiment, the population occupies at least about 100 square feet of space, wherein at least about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or more than 90% of the population comprises an effective amount of the microbe. In another embodiment, the population occupies at least about 100 square feet of space, wherein at least 1%, between 1% and 10%, for example, at least 10%, between 10%
30 and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 70%, at least 70%, between 70% and 75%, at least 75%, between 75% and 80%, at

least 80%, between 80% and 90%, at least 90%, between 90% and 95%, at least 95% or more of the population comprises the microbe in reproductive tissue. In still another embodiment, the population occupies at least about 100 square feet of space, wherein at least about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or more than 90% of the population comprises
5 at least 10 CFUs or spores, 100 CFUs or spores, 1,000 CFUs or spores, 10,000 CFUs or spores or more of the microbe. In still another embodiment, the population occupies at least about 100 square feet of space, wherein at least 1%, between 1% and 10%, for example, at least 10%, between 10% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and
10 60%, at least 60%, between 60% and 70%, at least 70%, between 70% and 75%, at least 75%, between 75% and 80%, at least 80%, between 80% and 90%, at least 90%, between 90% and 95%, at least 95% or more of the population comprises between about 10 CFU or spores and about 10,000 CFU or spores, between about 10 CFU or spores and about 100 CFU or spores, between about 10 CFU or spores and about 1,000 CFU or spores, between about
15 100 CFU or spores and about 1,000 CFU or spores, between about 100 CFU or spores and about 10,000 CFU or spores, or between about 1,000 CFU or spores and about 10,000 CFU or spores. In yet another embodiment, the population occupies at least about 100 square feet of space, wherein at least 1%, between 1% and 10%, for example, at least 10%, between 10% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least
20 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 70%, at least 70%, between 70% and 75%, at least 75%, between 75% and 80%, at least 80%, between 80% and 90%, at least 90%, between 90% and 95%, at least 95% or more of the population comprises a exogenous microbe (i.e., the endophyte) of monoclonal origin.

[0149] Plants can be grown individually from the seeds coated with the endophytes to
25 propagate the desired microbes in indoor or outdoor settings. An advantage of the present invention is that it allows multiple plants harboring endophytes to be grown under agricultural methods as a means of providing improved uniformity of microbe-derived benefits to farmers.

[0150] Therefore, in another aspect, provided herein are indoor arrangements of
30 populations (e.g., greenhouse) of plants generated from the methods of the present invention. Such arrangements can include at least a defined number of plants of the present invention, such as at least 1, at least 2, at least 3, between 3 and 5, at least 5, between 5 and 10, at least 10, between 10 and 15, at least 15, between 15 and 20, at least 20, between 20 and 30, at least

30, between 30 and 50, at least 50, between 50 and 100, at least 100, between 100 and 200, at least 200, between 200 and 500, at least 500, between 500 and 1000, at least 1000, between 1000 and 5000, at least 5000, between 5000 and 10000, at least 10000 or more plants.

[0151] Also provided herein are agricultural fields that contain population of plants
5 generated from the seeds of the present invention. Agricultural fields can occupy as little as 100 square feet or less, or can occupy hundreds or thousands of acres. Area of field containing a population of microbe-associated plants can be measured in square feet, such as at least 100, 500, 1000, 5000, 10,000, 50,000 or greater than 50,000 square feet, or can be measured in acres, such as least 1, at least 2, at least 3, between 3 and 5, at least 5, between 5
0 and 10, at least 10, between 10 and 15, at least 15, between 15 and 20, at least 20, between 20 and 30, at least 30, between 30 and 50, at least 50, between 50 and 100, at least 100, between 100 and 200, at least 200, between 200 and 500, at least 500, between 500 and 1000, at least 1000, between 1000 and 5000, at least 5000, between 5000 and 10000, at least 10000, between 10000 and 50000, at least 50000 or greater acres. The field can also be measured in
5 hectares, for example at least 1, at least 2, at least 3, between 3 and 5, at least 5, between 5 and 10, at least 10, between 10 and 15, at least 15, between 15 and 20, at least 20, between 20 and 30, at least 30, between 30 and 50, at least 50, between 50 and 100, at least 100, between 100 and 200, at least 200, between 200 and 500, at least 500, between 500 and 1000, at least 1000, between 1000 and 5000, at least 5000, between 5000 and 10000, at least 10000 or more
0 hectares. Additionally, a field containing a population of microbe-associated plants can be characterized by the number of plants in the population, generally a field is at least two, such as at least 3, between 3 and 5, at least 5, between 5 and 10, at least 10, between 10 and 15, at least 15, between 15 and 20, at least 20, between 20 and 30, at least 30, between 30 and 50, at least 50, between 50 and 100, at least 100, between 100 and 200, at least 200, between 200
5 and 500, at least 500, between 500 and 1000, at least 1000, between 1000 and 5000, at least 5000, between 5000 and 10000, at least 10000, between 10000 and 25000, at least 25000, between 25000 and 50000, at least 50000, between 50000 and 75000, at least 75000, between 75000 and 100000, at least 100000 or more plants. A field is generally a contiguous area but may be separated by geographical features such as roads, waterways,
0 buildings, fences, and the like known to those skilled in the art. Because the microbe-associated plants described herein benefit from an increased level of uniformity of germination and other characteristics, it is desirable to maximize the percentage of plants containing microbes. For example, at least 10% (e.g., between 10% and 20%, at least 20%,

between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 70%, at least 70%, between 70% and 75%, at least 75%, between 75% and 80%, at least 80%, between 80% and 90%, at least 90%, between 90% and 95%, between 95% and 99%, at least 99% or
5 more) of the plants contain the microbes.

Endophytes compatible with agrichemicals

[0152] In certain embodiments, the endophyte is selected on the basis of its compatibility with commonly used agrichemicals. As mentioned earlier, plants, particularly agricultural plants, can be treated with a vast array of agrichemicals, including fungicides, biocides (anti-
0 bacterial agents), herbicides, insecticides, nematocides, rodenticides, fertilizers, and other agents.

[0153] In some cases, it can be important for the endophyte to be compatible with agrichemicals, particularly those with fungicidal or antibacterial properties, in order to persist in the plant although, as mentioned earlier, there are many such fungicidal or antibacterial
5 agents that do not penetrate the plant, at least at a concentration sufficient to interfere with the endophyte. Therefore, where a systemic fungicide or antibacterial agent is used in the plant, compatibility of the endophyte to be inoculated with such agents will be an important criterion.

[0154] In one embodiment, natural isolates of endophytes that are compatible with
10 agrichemicals can be used to inoculate the plants according to the methods described herein. For example, fungal endophytes which are compatible with agriculturally employed fungicides can be isolated by plating a culture of the endophytes on a petri dish containing an effective concentration of the fungicide, and isolating colonies of the endophyte that are compatible with the fungicide. In another embodiment, an endophyte that is compatible with
5 a fungicide is used for the methods described herein. Fungicide compatible endophytes can also be isolated by selection on liquid medium. The culture of endophytes can be plated on petri dishes without any forms of mutagenesis; alternatively, the endophytes can be mutagenized using any means known in the art. For example, microbial cultures can be exposed to UV light, gamma-irradiation, or chemical mutagens such as
0 ethylmethanesulfonate (EMS) prior to selection on fungicide containing media. Finally, where the mechanism of action of a particular fungicide is known, the target gene can be specifically mutated (either by gene deletion, gene replacement, site-directed mutagenesis,

etc.) to generate an endophyte that is resilient against that particular fungicide. It is noted that the above-described methods can be used to isolate fungi that are compatible with both fungistatic and fungicidal compounds.

[0155] It will also be appreciated by one skilled in the art that a plant may be exposed to multiple types of fungicides or antibacterial compounds, either simultaneously or in succession, for example at different stages of plant growth. Where the target plant is likely to be exposed to multiple fungicidal and/or antibacterial agents, an endophyte that is compatible with many or all of these agrichemicals can be used to inoculate the plant. An endophyte that is compatible with several fungicidal agents can be isolated, for example, by serial selection. An endophyte that is compatible with the first fungicidal agent is isolated as described above (with or without prior mutagenesis). A culture of the resulting endophyte can then be selected for the ability to grow on liquid or solid media containing the second antifungal compound (again, with or without prior mutagenesis). Colonies isolated from the second selection are then tested to confirm its compatibility to both antifungal compounds.

[0156] Likewise, bacterial endophytes that are compatible to biocides (including herbicides such as glyphosate or antibacterial compounds, whether bacteriostatic or bactericidal) that are agriculturally employed can be isolated using methods similar to those described for isolating fungicide compatible endophytes. In one embodiment, mutagenesis of the microbial population can be performed prior to selection with an antibacterial agent. In another embodiment, selection is performed on the microbial population without prior mutagenesis. In still another embodiment, serial selection is performed on an endophyte: the endophyte is first selected for compatibility to a first antibacterial agent. The isolated compatible endophyte is then cultured and selected for compatibility to the second antibacterial agent. Any colony thus isolated is tested for compatibility to each, or both antibacterial agents to confirm compatibility with these two agents.

[0157] Resistance, or compatibility with an antimicrobial agent can be determined by a number of means known in the art, including the comparison of the minimal inhibitory concentration (MIC) of the unmodified and modified endophyte. Therefore, in one embodiment, the present invention discloses an isolated modified endophyte derived from an endophyte isolated from within a plant or tissue thereof, wherein the endophyte is modified such that it exhibits at least 3 fold greater, for example, at least 5 fold greater, at least 10 fold greater, at least 20 fold greater, at least 30 fold greater or more MIC to an antimicrobial agent when compared with the unmodified endophyte.

[0158] In one particular aspect, disclosed herein are bacterial endophytes with enhanced resistance to the herbicide glyphosate. In one embodiment, the bacterial endophyte has a doubling time in growth medium containing at least 1 mM glyphosate, for example, at least 2 mM glyphosate, at least 5mM glyphosate, at least 10mM glyphosate, at least 15mM glyphosate or more, that is no more than 250%, for example, no more than 200%, no more than 175%, no more than 150%, or no more than 125%, of the doubling time of the endophyte in the same growth medium containing no glyphosate. In one particular embodiment, the bacterial endophyte has a doubling time in growth medium containing 5mM glyphosate that is no more than 150% the doubling time of the endophyte in the same growth medium containing no glyphosate.

[0159] In another embodiment, the bacterial endophyte has a doubling time in a plant tissue containing at least 10 ppm glyphosate, for example, at least 15 ppm glyphosate, at least 20 ppm glyphosate, at least 30 ppm glyphosate, at least 40 ppm glyphosate or more, that is no more than 250%, for example, no more than 200%, no more than 175%, no more than 150%, or no more than 125%, of the doubling time of the endophyte in a reference plant tissue containing no glyphosate. In one particular embodiment, the bacterial endophyte has a doubling time in a plant tissue containing 40 ppm glyphosate that is no more than 150% the doubling time of the endophyte in a reference plant tissue containing no glyphosate.

[0160] The selection process described above can be repeated to identify isolates of the endophyte that are compatible with a multitude of antifungal or antibacterial agents.

[0161] Candidate isolates can be tested to ensure that the selection for agrichemical compatibility did not result in loss of a desired microbial bioactivity. Isolates of the endophyte that are compatible with commonly employed fungicides can be selected as described above. The resulting compatible endophyte can be compared with the parental endophyte on plants in its ability to promote germination.

[0162] The agrichemical compatible endophytes generated as described above can be detected in samples. For example, where a transgene was introduced to render the endophyte resistant to the agrichemical(s), the transgene can be used as a target gene for amplification and detection by PCR. In addition, where point mutations or deletions to a portion of a specific gene or a number of genes results in compatibility with the agrichemical(s), the unique point mutations can likewise be detected by PCR or other means known in the art. Such methods allow the detection of the microbe even if it is no longer viable. Thus,

commodity plant products produced using the agrichemical compatible microbes described herein can readily be identified by employing these and related methods of nucleic acid detection.

Improved traits conferred by the endophyte

5 [0163] The present invention contemplates the establishment of a microbial symbiont in a plant. In one embodiment, the microbial association results in a detectable change to the seed or plant. The detectable change can be an improvement in a number of agronomic traits (e.g., improved general health, increased response to biotic or abiotic stresses, or enhanced properties of the plant or a plant part, including fruits and grains). Alternatively, the
10 detectable change can be a physiological or biological change that can be measured by methods known in the art. The detectable changes are described in more detail in the sections below. As used herein, an endophyte is considered to have conferred an improved agricultural trait whether or not the improved trait arose from the plant, the endophyte, or the concerted action between the plant and endophyte. Therefore, for example, whether a
15 beneficial hormone or chemical is produced by the plant or endophyte, for purposes of the present invention, the endophyte will be considered to have conferred an improved agronomic trait upon the host plant.

[0164] In some embodiments, plant-endophyte combinations confer an agronomic benefit in agricultural plants. In some embodiments, the agronomic trait is selected from the group
20 consisting of altered oil content, altered protein content, altered seed carbohydrate composition, altered seed oil composition, and altered seed protein composition, chemical tolerance, cold tolerance, delayed senescence, disease resistance, drought tolerance, ear weight, growth improvement, health enhancement, heat tolerance, herbicide tolerance, herbivore resistance, improved nitrogen fixation, improved nitrogen utilization, improved
25 root architecture, improved water use efficiency, increased biomass, increased root length, increased seed weight, increased shoot length, increased yield, increased yield under water-limited conditions, kernel mass, kernel moisture content, metal tolerance, number of ears, number of kernels per ear, number of pods, nutrition enhancement, pathogen resistance, pest resistance, photosynthetic capability improvement, salinity tolerance, stay-green, vigor
30 improvement, increased dry weight of mature seeds, increased fresh weight of mature seeds, increased number of mature seeds per plant, increased chlorophyll content, increased number of pods per plant, increased length of pods per plant, reduced number of wilted leaves per plant, reduced number of severely wilted leaves per plant, and increased number of non-

wilted leaves per plant, a detectable modulation in the level of a metabolite, a detectable modulation in the level of a transcript, and a detectable modulation in the proteome relative to a reference plant. In other embodiments, at least two agronomic traits are improved in the agricultural plant.

5 [0165] For example, the endophyte may provide an improved benefit or tolerance to a plant that is of at least 3%, between 3% and 5%, at least 5%, between 5% and 10%, least 10%, between 10% and 15%, for example at least 15%, between 15% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 75%, at least
0 75%, between 75% and 100%, at least 100%, between 100% and 150%, at least 150%, between 150% and 200%, at least 200%, between 200% and 300%, or at least 300% or more, when compared with uninoculated plants grown under the same conditions.

[0166] In some aspects, provided herein, are methods for producing a seed of a plant with a heritably altered trait. The trait of the plant can be altered without known genetic
5 modification of the plant genome, and comprises the following steps. First, a preparation of an isolated endophyte that is exogenous to the seed of the plant is provided, and optionally processed to produce a microbial preparation. The microbial preparation is then contacted with the plant. The plants are then allowed to go to seed, and the seeds, which contain the endophytes on and/or in the seed are collected. The endophytes contained within the seed are
0 viably incorporated into the seed.

[0167] The method of the present invention can facilitate crop productivity by enhancing germination, seedling vigor and biomass in comparison with a non- treated control. Moreover, the introduction of the beneficial microorganisms to within the seed instead of by, e.g., seed coating, makes the endophytes less susceptible to environmental perturbation and
5 more compatible with chemical seed coatings (e.g., pesticides and herbicides). Using endophyte colonized seeds, the plant growth and biomass increases are statistically similar to those obtained using conventional inoculation methods e.g., exogenous seed soaking and soil inoculation (that are more laborious and less practicable in certain circumstances).

Improved general health

0 [0168] Also described herein are plants, and fields of plants, that are associated with beneficial endophytes, such that the overall fitness, productivity or health of the plant or a portion thereof, is maintained, increased and/or improved over a period of time. Improvement in overall plant health can be assessed using numerous physiological parameters including,

but not limited to, height, overall biomass, root and/or shoot biomass, seed germination, seedling survival, photosynthetic efficiency, transpiration rate, seed/fruit number or mass, plant grain or fruit yield, leaf chlorophyll content, photosynthetic rate, root length, or any combination thereof. Improved plant health, or improved field health, can also be demonstrated through improved resistance or response to a given stress, either biotic or abiotic stress, or a combination of one or more abiotic stresses, as provided herein.

Other abiotic stresses

[0169] Disclosed herein are endophyte-associated plants with increased resistance to an abiotic stress. Exemplary abiotic stresses include, but are not limited to: drought, salt, high metal content, low nutrients, cold stress, and heat stress.

Drought and heat tolerance

[0170] When soil water is depleted or if water is not available during periods of drought, crop yields are restricted. Plant water deficit develops if transpiration from leaves exceeds the supply of water from the roots. The available water supply is related to the amount of water held in the soil and the ability of the plant to reach that water with its root system. Transpiration of water from leaves is linked to the fixation of carbon dioxide by photosynthesis through the stomata. The two processes are positively correlated so that high carbon dioxide influx through photosynthesis is closely linked to water loss by transpiration. As water transpires from the leaf, leaf water potential is reduced and the stomata tend to close in a hydraulic process limiting the amount of photosynthesis. Since crop yield is dependent on the fixation of carbon dioxide in photosynthesis, water uptake and transpiration are contributing factors to crop yield. Plants which are able to use less water to fix the same amount of carbon dioxide or which are able to function normally at a lower water potential have the potential to conduct more photosynthesis and thereby to produce more biomass and economic yield in many agricultural systems.

[0171] In some cases, a plant resulting from seeds or other plant elements treated with a single endophyte strain or a plurality of endophytes can exhibit a physiological change, such as a compensation of the stress-induced reduction in photosynthetic activity (expressed, for example, as $\Delta F_v/F_m$) after exposure to heat shock or drought conditions as compared to a corresponding control, genetically identical plant that does not contain the endophytes grown in the same conditions. In some cases, the endophyte-associated plant as disclosed herein can exhibit an increased change in photosynthetic activity $\Delta F_v(\Delta F_v/F_m)$ after heat-shock or

drought stress treatment, for example 1, 2, 3, 4, 5, 6, 7 days or more after the heat-shock or drought stress treatment, or until photosynthesis ceases, as compared with corresponding control plant of similar developmental stage but not comprising the endophytes. For example, a plant having a plurality of the endophytes able to confer heat and/or drought-tolerance can exhibit a $\Delta Fv/Fm$ of from about 0.1 to about 0.8 after exposure to heat-shock or drought stress or a $\Delta Fv/Fm$ range of from about 0.03 to about 0.8 under one day, or 1, 2, 3, 4, 5, 6, 7, or over 7 days post heat-shock or drought stress treatment, or until photosynthesis ceases. In some embodiments, stress-induced reductions in photosynthetic activity can be compensated by at least about 0.25% (for example, at least about 0.5%, between 0.5% and 1%, at least about 1%, between 1% and 2%, at least about 2%, between 2% and 3%, at least about 3%, between 3% and 5%, at least about 5%, between 5% and 10%, at least about 8%, at least about 10%, between 10% and 15%, at least about 15%, between 15% and 20%, at least about 20%, between 20% and 25%, at least about 25%, between 25% and 30%, at least about 30%, between 30% and 40%, at least about 40%, between 40% and 50%, at least about 50%, between 50% and 60%, at least about 60%, between 60% and 75%, at least about 75%, between 75% and 80%, at least about 80%, between 80% and 85%, at least about 85%, between 85% and 90%, at least about 90%, between 90% and 95%, at least about 95%, between 95% and 99%, at least about 99%, between 99% and 100%, or at least 100%) as compared to the photosynthetic activity decrease in a corresponding reference agricultural plant following heat shock conditions. Significance of the difference between endophyte-associated and reference agricultural plants can be established upon demonstrating statistical significance, for example at $p < 0.05$ with an appropriate parametric or non-parametric statistic, e.g., Chi-square test, Student's t-test, Mann-Whitney test, or F-test based on the assumption or known facts that the endophyte-associated plant and reference agricultural plant have identical or near identical genomes (isoline comparison).

[0172] In selecting traits for improving crops, a decrease in water use, without a change in growth would have particular merit in an irrigated agricultural system where the water input costs were high. An increase in growth without a corresponding jump in water use would have applicability to all agricultural systems. In many agricultural systems where water supply is not limiting, an increase in growth, even if it came at the expense of an increase in water use also increases yield. Water use efficiency (WUE) is a parameter often correlated with drought tolerance, and is the CO_2 assimilation rate per water transpired by the plant. An increased water use efficiency of the plant relates in some cases to an increased fruit/kernel size or number. Therefore, in some embodiments, the plants described herein exhibit an

increased water use efficiency when compared with a reference agricultural plant grown under the same conditions. For example, the plants grown from the plant elements comprising the plurality of endophytes can have at least 3%, between 3% and 5%, at least 5%, between 5% and 10%, least 10%, between 10% and 15%, for example at least 15%,
5 between 15% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 75%, at least 75%, between 75% and 100%, or at least 100% higher WUE than a reference agricultural plant grown under the same conditions. Such an increase in WUE can occur under conditions without water deficit, or under conditions of water
10 deficit, for example, when the soil water content is less than or equal to 60% of water saturated soil, for example, less than or equal to 50%, less than or equal to 40%, less than or equal to 30%, less than or equal to 20%, less than or equal to 10% of water saturated soil on a weight basis. In a related embodiment, the plant comprising the plurality of endophytes can have at least 10% higher relative water content (RWC), for example, at least 3%, between 3%
15 and 5%, at least 5%, between 5% and 10%, least 10%, between 10% and 15%, for example at least 15%, between 15% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 75%, at least 75%, between 75% and 100%, or at least 100% higher RWC than a reference agricultural plant grown under the same conditions.

20 **[0173]** In some embodiments, the plants comprise a single endophyte strain or a plurality of endophytes able to increase heat and/or drought-tolerance in sufficient quantity, such that increased growth or improved recovery from wilting under conditions of heat or drought stress is observed. For example, a plurality of endophyte populations described herein can be present in sufficient quantity in a plant, resulting in increased growth as compared to a plant
25 that does not contain endophytes, when grown under drought conditions or heat shock conditions, or following such conditions. Increased heat and/or drought tolerance can be assessed with physiological parameters including, but not limited to, increased height, overall biomass, root and/or shoot biomass, seed germination, seedling survival, photosynthetic efficiency, transpiration rate, seed/fruit number or mass, plant grain or fruit yield, leaf
30 chlorophyll content, photosynthetic rate, root length, wilt recovery, turgor pressure, or any combination thereof, as compared to a reference agricultural plant grown under similar conditions. For example, the endophyte may provide an improved benefit or tolerance to a plant that is of at least 3%, between 3% and 5%, at least 5%, between 5% and 10%, least 10%, between 10% and 15%, for example at least 15%, between 15% and 20%, at least 20%,

between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 75%, at least 75%, between 75% and 100%, or at least 100%, when compared with uninoculated plants grown under the same conditions.

- 5 In various embodiments, a a single endophyte strain or plurality of endophytes introduced into altered seed microbiota can confer in the resulting plant thermal tolerance, herbicide tolerance, drought resistance, insect resistance, fungus resistance, virus resistance, bacteria resistance, male sterility, cold tolerance, salt tolerance, increased yield, enhanced nutrient use efficiency, increased nitrogen use efficiency, increased protein content, increased fermentable
10 carbohydrate content, reduced lignin content, increased antioxidant content, enhanced water use efficiency, increased vigor, increased germination efficiency, earlier or increased flowering, increased biomass, altered root-to-shoot biomass ratio, enhanced soil water retention, or a combination thereof. A difference between the endophyte-associated plant and a reference agricultural plant can also be measured using other methods known in the art.

15 *Salt Stress*

- [0174] In other embodiments, a a single endophyte strain or plurality of endophytes able to confer increased tolerance to salinity stress can be introduced into plants. The resulting plants comprising endophytes can exhibit increased resistance to salt stress, whether measured in terms of survival under saline conditions, or overall growth during, or following salt stress.
20 The physiological parameters of plant health recited above, including height, overall biomass, root and/or shoot biomass, seed germination, seedling survival, photosynthetic efficiency, transpiration rate, seed/fruit number or mass, plant grain or fruit yield, leaf chlorophyll content, photosynthetic rate, root length, or any combination thereof, can be used to measure growth, and compared with the growth rate of reference agricultural plants (e.g., isogenic
25 plants without the endophytes) grown under identical conditions. For example, the endophyte may provide an improved benefit or tolerance to a plant that is of at least 3%, between 3% and 5%, at least 5%, between 5% and 10%, least 10%, between 10% and 15%, for example at least 15%, between 15% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and
30 60%, at least 60%, between 60% and 75%, at least 75%, between 75% and 100%, or at least 100%, when compared with uninoculated plants grown under the same conditions.

[0175] In other instances, endophyte-associated plants and reference agricultural plants can be grown in soil or growth media containing different concentration of sodium to establish

the inhibitory concentration of sodium (expressed, for example, as the concentration in which growth of the plant is inhibited by 50% when compared with plants grown under no sodium stress). Therefore, in another embodiment, a plant resulting from seeds containing an endophyte able to confer salt tolerance described herein exhibits an increase in the inhibitory sodium concentration by at least 10 mM, for example at least 15 mM, at least 20 mM, at least 30 mM, at least 40 mM, at least 50 mM, at least 60 mM, at least 70 mM, at least 80 mM, at least 90 mM, at least 100mM or more, when compared with the reference agricultural plants.

High Metal Content

[0176] Plants are sessile organisms and therefore must contend with the environment in which they are placed. While plants have adapted many mechanisms to deal with chemicals and substances that may be deleterious to their health, heavy metals represent a class of toxins which are highly relevant for plant growth and agriculture. Plants use a number of mechanisms to cope with toxic levels of heavy metals (for example, nickel, cadmium, lead, mercury, arsenic, or aluminum) in the soil, including excretion and internal sequestration. For agricultural purposes, it is important to have plants that are able to tolerate otherwise hostile conditions, for example soils containing elevated levels of toxic heavy metals. Endophytes that are able to confer increased heavy metal tolerance may do so by enhancing sequestration of the metal in certain compartments. Use of such endophytes in a plant would allow the development of novel plant-endophyte combinations for purposes of environmental remediation (also known as phytoremediation). Therefore, in one embodiment, the plant containing the endophyte able to confer increased metal tolerance exhibits a difference in a physiological parameter that is at least about 5% greater, for example at least about 5%, at least about 8%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 75%, at least about 80%, at least about 80%, at least about 90%, or at least 100%, at least about 200%, at least about 300%, at least about 400% or greater than a reference agricultural plant grown under the same heavy metal concentration in the soil.

[0177] Alternatively, the inhibitory concentration of the heavy metal can be determined for the endophyte-associated plant and compared with a reference agricultural plant under the same conditions. Therefore, in one embodiment, the plants resulting from seeds containing an endophyte able to confer heavy metal tolerance described herein exhibit an increase in the inhibitory sodium concentration by at least 0.1 mM, for example at least 0.3 mM, at least 0.5 mM, at least 1 mM, at least 2 mM, at least 5 mM, at least 10 mM, at least 15 mM, at least 20

mM, at least 30 mM, at least 50mM or more, when compared with the reference agricultural plants.

[0178] Finally, plants inoculated with endophytes that are able to confer increased metal tolerance exhibits an increase in overall metal accumulation by at least 10%, for example at
5 least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 75%, at least 100%, at least 150%, at least 200%, at least 300% or more, when compared with uninoculated plants grown under the same conditions.

Low Nutrient Stress

[0179] A single endophyte strain or a plurality of endophytes described herein may also
10 confer to the plant an increased ability to grow in nutrient limiting conditions, for example by solubilizing or otherwise making available to the plants macronutrients or micronutrients that are complexed, insoluble, or otherwise in an unavailable form. In some embodiments, a plant is inoculated with a plurality of endophytes that confer increased ability to liberate and/or
15 otherwise provide to the plant with nutrients selected from the group consisting of phosphate, nitrogen, potassium, iron, manganese, calcium, molybdenum, vitamins, or other micronutrients. Such a plant can exhibit increased growth in soil comprising limiting amounts of such nutrients when compared with reference agricultural plant. Differences between the endophyte-associated plant and reference agricultural plant can be measured by comparing the biomass of the two plant types grown under limiting conditions, or by measuring the
20 physical parameters described above. Therefore, in some embodiments, the plant comprising endophytes shows increased tolerance to nutrient limiting conditions as compared to a reference agricultural plant grown under the same nutrient limited concentration in the soil, as measured for example by increased biomass or seed yield of at least 3%, between 3% and 5%, at least 5%, between 5% and 10%, least 10%, between 10% and 15%, for example at
25 least 15%, between 15% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 75%, at least 75%, between 75% and 100%, or at least 100%, when compared with uninoculated plants grown under the same conditions. In other
30 embodiments, the plant containing the plurality of endophytes is able to grown under nutrient stress conditions while exhibiting no difference in the physiological parameter compared to a plant that is grown without nutrient stress. In some embodiments, such a plant will exhibit no difference in the physiological parameter when grown with 2-5% less nitrogen than average cultivation practices on normal agricultural land, for example, at least 10%, between 10% and

15%, for example at least 15%, between 15% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 75%, at least 75%, or between 75% and 100%, less nitrogen, when compared with crop plants grown under normal conditions during an average growing season. In some embodiments, the microbe capable of providing nitrogen-stress tolerance to a plant is diazotrophic. In other embodiments, the microbe capable of providing nitrogen-stress tolerance to a plant is non-diazotrophic.

Cold Stress

[0180] In some cases, endophytes can confer to the plant the ability to tolerate cold stress. Many known methods exist for the measurement of a plant's tolerance to cold stress (as reviewed, for example, in Thomashow (2001) Plant Physiol. 125: 89-93, and Gilmour et al. (2000) Plant Physiol. 124: 1854-1865, both of which are incorporated herein by reference in their entirety). As used herein, cold stress refers to both the stress induced by chilling (0°C – 15°C) and freezing (<0°C). Some cultivars of agricultural plants can be particularly sensitive to cold stress, but cold tolerance traits may be multigenic, making the breeding process difficult. Endophytes able to confer cold tolerance would potentially reduce the damage suffered by farmers on an annual basis. Improved response to cold stress can be measured by survival of plants, the amount of necrosis of parts of the plant, or a change in crop yield loss, as well as the physiological parameters used in other examples. Therefore, in one embodiment, the plant containing the endophyte able to confer increased cold tolerance exhibits a difference in a physiological parameter that is at least about 5% greater, for example at least about 5%, at least about 8%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 75%, at least about 80%, at least about 80%, at least about 90%, or at least 100%, at least about 200%, at least about 300%, at least about 400% or greater than a reference agricultural plant grown under the same conditions of cold stress.

Biotic Stress

[0181] In other embodiments, a single endophyte strain or plurality of endophytes protects the plant from a biotic stress, for example, insect infestation, nematode infestation, complex infection, fungal infection, oomycete infection, protozoal infection, viral infection, and herbivore grazing, or a combination thereof. For example, the endophyte may provide an improved benefit or tolerance to a plant that is of at least 3%, between 3% and 5%, at least

5 5%, between 5% and 10%, least 10%, between 10% and 15%, for example at least 15%, between 15% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 75%, at least 75%, between 75% and 100%, or at least 100%, when compared with uninoculated plants grown under the same conditions.

Insect herbivory

[0182] There are an abundance of insect pest species that can infect or infest a wide variety of plants. Pest infestation can lead to significant damage. Insect pests that infest plant species are particularly problematic in agriculture as they can cause serious damage to crops and significantly reduce plant yields. A wide variety of different types of plant are susceptible to pest infestation including commercial crops such as cotton, soybean, wheat, barley, and corn.

[0183] In some embodiments, endophytes described herein confer upon the host plant the ability to repel insect herbivores. In other cases, the endophytes may produce, or induce the production in the plant of, compounds which are insecticidal or insect repellant. The insect may be any one of the common pathogenic insects affecting plants, particularly agricultural plants. Examples include, but are not limited to: *Leptinotarsa* spp. (e.g., *L. decemlineata* (Colorado potato beetle), *L. juncta* (false potato beetle), or *L. texana* (Texan false potato beetle)); *Nilaparvata* spp. (e.g., *N. lugens* (brown planthopper)); *Laodelphax* spp. (e.g., *L. striatellus* (small brown planthopper)); *Nephotettix* spp. (e.g., *N. virescens* or *N. cincticeps* (green leafhopper), or *N. nigropictus* (rice leafhopper)); *Sogatella* spp. (e.g., *S. furcifera* (white-backed planthopper)); *Chilo* spp. (e.g., *C. suppressalis* (rice striped stem borer), *C. auricilius* (gold-fringed stem borer), or *C. polychrysus* (dark-headed stem borer)); *Sesamia* spp. (e.g., *S. inferens* (pink rice borer)); *Tryporyza* spp. (e.g., *T. innotata* (white rice borer), or *T. incertulas* (yellow rice borer)); *Anthonomus* spp. (e.g., *A. grandis* (boll weevil)); *Phaedon* spp. (e.g., *P. cochleariae* (mustard leaf beetle)); *Epilachna* spp. (e.g., *E. varivetis* (Mexican bean beetle)); *Tribolium* spp. (e.g., *T. castaneum* (red floor beetle)); *Diabrotica* spp. (e.g., *D. virgifera* (western corn rootworm), *D. barberi* (northern corn rootworm), *D. undecimpunctata howardi* (southern corn rootworm), *D. virgifera zea* (Mexican corn rootworm)); *Ostrinia* spp. (e.g., *O. nubilalis* (European corn borer)); *Anaphothrips* spp. (e.g., *A. obscurus* (grass thrips)); *Pectinophora* spp. (e.g., *P. gossypiella* (pink bollworm)); *Heliothis* spp. (e.g., *H. virescens* (tobacco budworm)); *Trialeurodes* spp. (e.g., *T. abutiloneus* (banded-winged whitefly) *T. vaporariorum* (greenhouse whitefly)); *Bemisia* spp. (e.g., *B. argentifolii* (silverleaf whitefly)); *Aphis* spp. (e.g., *A. gossypii* (cotton aphid)); *Lygus* spp. (e.g., *L.*

lineolaris (tarnished plant bug) or *L. hesperus* (western tarnished plant bug)); *Euschistus* spp. (e.g., *E. conspersus* (conspersus stink bug)); *Chlorochroa* spp. (e.g., *C. sayi* (Say stinkbug)); *Nezara* spp. (e.g., *N. viridula* (southern green stinkbug)); *Thrips* spp. (e.g., *T. tabaci* (onion thrips)); *Frankliniella* spp. (e.g., *F. fusca* (tobacco thrips), or *F. occidentalis* (western flower thrips)); *Acheta* spp. (e.g., *A. domesticus* (house cricket)); *Myzus* spp. (e.g., *M. persicae* (green peach aphid)); *Macrosiphum* spp. (e.g., *M. euphorbiae* (potato aphid)); *Blissus* spp. (e.g., *B. leucopterus* (chinch bug)); *Acrosternum* spp. (e.g., *A. hilare* (green stink bug)); *Chilo* spp. (e.g., *C. polychrysa* (rice stalk borer)); *Lissorhoptrus* spp. (e.g., *L. oryzophilus* (rice water weevil)); *Rhopalosiphum* spp. (e.g., *R. maidis* (corn leaf aphid));
 10 *Anuraphis* spp. (e.g., *A. maidiradicis* (corn root aphid)), and combinations thereof.

[0184] The endophyte-associated plant can be tested for its ability to resist, or otherwise repel, pathogenic insects by measuring, for example, insect load, overall plant biomass, biomass of the fruit or grain, percentage of intact leaves, or other physiological parameters described herein, and comparing with a reference agricultural plant. In some embodiments,
 15 the endophyte-associated plant exhibits increased biomass as compared to a reference agricultural plant grown under the same conditions (e.g., grown side-by-side, or adjacent to, endophyte-associated plants). In other embodiments, the endophyte-associated plant exhibits increased fruit or grain yield as compared to a reference agricultural plant grown under the same conditions (e.g., grown side-by-side, or adjacent to, endophyte-associated plants). In
 20 any of the above, the endophyte may provide an improved benefit or tolerance to a plant that is of at least 3%, between 3% and 5%, at least 5%, between 5% and 10%, at least 10%, between 10% and 15%, for example at least 15%, between 15% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 75%, at least 75%, between
 25 75% and 100%, or at least 100%, when compared with uninoculated plants grown under the same conditions.

Nematodes

[0185] Nematodes are microscopic roundworms that feed on the roots, fluids, leaves and stems of more than 2,000 row crops, vegetables, fruits, and ornamental plants, causing an
 30 estimated \$100 billion crop loss worldwide and accounting for 13% of global crop losses due to disease. A variety of parasitic nematode species infect crop plants, including root-knot nematodes (RKN), cyst- and lesion-forming nematodes. Root-knot nematodes, which are characterized by causing root gall formation at feeding sites, have a relatively broad host

range and are therefore parasitic on a large number of crop species. The cyst- and lesion-forming nematode species have a more limited host range, but still cause considerable losses in susceptible crops.

[0186] Signs of nematode damage include stunting and yellowing of leaves, and wilting of the plants during hot periods. Nematode infestation, however, can cause significant yield losses without any obvious above-ground disease symptoms. The primary causes of yield reduction are due to underground root damage. Roots infected by SCN are dwarfed or stunted. Nematode infestation also can decrease the number of nitrogen-fixing nodules on the roots, and may make the roots more susceptible to attacks by other soil-borne plant nematodes.

[0187] In some embodiments, the endophyte-associated plant has an increased resistance to a nematode when compared with a reference agricultural plant. As before with insect herbivores, biomass of the plant or a portion of the plant, or any of the other physiological parameters mentioned elsewhere, can be compared with the reference agricultural plant grown under the same conditions. Particularly useful measurements include overall plant biomass, biomass and/or size of the fruit or grain, and root biomass. In some embodiments, the endophyte-associated plant exhibits increased biomass as compared to a reference agricultural plant grown under the same conditions (e.g., grown side-by-side, or adjacent to, the endophyte-associated plants, under conditions of nematode challenge). In other embodiments, the endophyte-associated plant exhibits increased root biomass as compared to a reference agricultural plant grown under the same conditions (e.g., grown side-by-side, or adjacent to, the endophyte-associated plants, under conditions of nematode challenge). In still another embodiment, the endophyte-associated plant exhibits increased fruit or grain yield as compared to a reference agricultural plant grown under the same conditions (e.g., grown side-by-side, or adjacent to, the endophyte-associated plants, under conditions of nematode challenge). In any of the above, the endophyte may provide an improved benefit or tolerance to a plant that is of at least 3%, between 3% and 5%, at least 5%, between 5% and 10%, least 10%, between 10% and 15%, for example at least 15%, between 15% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 75%, at least 75%, between 75% and 100%, or at least 100%, when compared with uninoculated plants grown under the same conditions.

Fungal Pathogens

[0188] Fungal diseases are responsible for yearly losses of over \$10 Billion on agricultural crops in the US, represent 42% of global crop losses due to disease, and are caused by a large variety of biologically diverse pathogens. Different strategies have traditionally been used to control them. Resistance traits have been bred into agriculturally important varieties, thus providing various levels of resistance against either a narrow range of pathogen isolates or races, or against a broader range. However, this involves the long and labor intensive process of introducing desirable traits into commercial lines by genetic crosses and, due to the risk of pests evolving to overcome natural plant resistance, a constant effort to breed new resistance traits into commercial lines is required. Alternatively, fungal diseases have been controlled by the application of chemical fungicides. This strategy usually results in efficient control, but is also associated with the possible development of resistant pathogens and can be associated with a negative impact on the environment. Moreover, in certain crops, such as barley and wheat, the control of fungal pathogens by chemical fungicides is difficult or impractical.

[0189] The present invention contemplates the use a single endophyte strain or of a plurality of endophytes that is able to confer resistance to fungal pathogens to the host plant. Increased resistance to fungal inoculation can be measured, for example, using any of the physiological parameters presented above, by comparing with reference agricultural plants. In some embodiments, the endophyte-associated plant exhibits increased biomass and/or less pronounced disease symptoms as compared to a reference agricultural plant grown under the same conditions (e.g., grown side-by-side, or adjacent to, the endophyte-associated plants, infected with the fungal pathogen). In still another embodiment, the endophyte-associated plant exhibits increased fruit or grain yield as compared to a reference agricultural plant grown under the same conditions (e.g., grown side-by-side, or adjacent to, the endophyte-associated plants, infected with the fungal pathogen). In other embodiments, the endophyte-associated plant exhibits decreased hyphal growth as compared to a reference agricultural plant grown under the same conditions (e.g., grown side-by-side, or adjacent to, the endophyte-associated plants, infected with the fungal pathogen). In any of the above, the endophyte may provide an improved benefit or tolerance to a plant that is of at least 3%, between 3% and 5%, at least 5%, between 5% and 10%, least 10%, between 10% and 15%, for example at least 15%, between 15% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 75%, at least 75%, between 75% and

100%, or at least 100%, when compared with uninoculated plants grown under the same conditions.

Viral Pathogens

[0190] Plant viruses are estimated to account for 18% of global crop losses due to disease.

5 There are numerous examples of viral pathogens affecting agricultural productivity. Examples include the American wheat striate mosaic virus (AWSMV) (wheat striate mosaic), Barley stripe mosaic virus (BSMV), Barley yellow dwarf virus (BYDV), Brome mosaic virus (BMV), Cereal chlorotic mottle virus (CCMV), Corn chlorotic vein banding virus (CCVBV), Brazilian maize mosaic virus, Corn lethal necrosis Virus complex from Maize chlorotic

10 mottle virus, (MCMV), Maize dwarf mosaic virus (MDMV), A or B Wheat streak mosaic virus (WSMV), Cucumber mosaic virus (CMV), Cynodon chlorotic streak virus (CCSV), Johnsongrass mosaic virus (JGMV), Maize bushy stunt Mycoplasma-like organism (MLO) associated virus, Maize chlorotic dwarf Maize chlorotic dwarf virus (MCDV), Maize chlorotic mottle virus (MCMV), Maize dwarf mosaic virus (MDMV), strains A, D, E and F,

15 Maize leaf fleck virus (MLFV), Maize line virus (MLV), Maize mosaic (corn leaf stripe, Maize mosaic virus (MMV), enanismo rayado), Maize mottle and chlorotic stunt virus, Maize pellucid ringspot virus (MPRV), Maize raya gruesa virus (MRGV), Maize rayado fino (fine striping) virus (MRFV), Maize red stripe virus (MRSV), Maize ring mottle virus (MRMV), Maize rio cuarto virus (MRCV), Maize rough dwarf virus (MRDV), Cereal

20 tillering disease virus, Maize sterile stunt virus, barley yellow striate virus, Maize streak virus (MSV), Maize stripe virus, Maize chlorotic stripe virus, maize hoja blanca virus, Maize stunting virus; Maize tassel abortion virus (MTAV), Maize vein enation virus (MVEV), Maize wallaby ear virus (MWEV), Maize white leaf virus, Maize white line mosaic virus (MWLMV), Millet red leaf virus (MRLV), Northern cereal mosaic virus (NCMV), Oat pseudorosette virus, (zakuklivanie), Oat sterile dwarf virus (OSDV), Rice black-streaked dwarf virus (RBSDV), Rice stripe virus (RSV), Sorghum mosaic virus (SrMV), Sugarcane mosaic virus (SCMV) strains H, 1 and M, Sugarcane Fiji disease virus (FDV), Sugarcane mosaic virus (SCMV) strains A, B, D, E, SC, BC, Sabi and MB (formerly MDMV-B), and

25 Wheat spot mosaic virus (WSMV). In one embodiment, the endophyte-associated plant

30 provides protection against viral pathogens such that there is at least 5% greater biomass, for example, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 75%, at least 100% or more biomass, than the reference agricultural plant grown under the same conditions. In still another embodiment, the endophyte-associated plant exhibits at

least 5% greater fruit or grain yield, for example, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 75%, at least 100% or more fruit or grain yield when challenged with a virus, as compared to a reference agricultural plant grown under the same conditions. In yet another embodiment, the endophyte-associated plant exhibits at least 5% lower viral titer, for example, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 75%, at least 100% lower viral titer when challenged with a virus, as compared to a reference agricultural plant grown under the same conditions.

Bacterial Pathogens

[0191] Likewise, bacterial pathogens are a significant problem negatively affecting agricultural productivity and accounting for 27% of global crop losses due to plant disease. In one embodiment, the endophyte-associated plant described herein provides protection against bacterial pathogens such that there is at least 5% greater biomass, for example, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 75%, at least 100% or more biomass, than the reference agricultural plant grown under the same conditions. In still another embodiment, the endophyte-associated plant exhibits at least 5% greater fruit or grain yield, for example, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 75%, at least 100% or more fruit or grain yield when challenged with a bacterial pathogen, than the reference agricultural plant grown under the same conditions. In yet another embodiment, the endophyte-associated plant exhibits at least 5% lower bacterial count, for example, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 75%, at least 100% lower bacterial count when challenged with a bacteria, as compared to a reference agricultural plant grown under the same conditions.

Yield and Biomass improvement

[0192] In other embodiments, the improved trait can be an increase in overall biomass of the plant or a part of the plant, including its fruit or seed. In some embodiments, a single endophyte strain or a plurality of endophytes is disposed on the surface or within a tissue of the plant element in an amount effective to increase the biomass of the plant, or a part or tissue of the plant grown from the plant element. The increased biomass is useful in the production of commodity products derived from the plant. Such commodity products include an animal feed, a fish fodder, a cereal product, a processed human-food product, a sugar or an alcohol. Such products may be a fermentation product or a fermentable product, one such

exemplary product is a biofuel. The increase in biomass can occur in a part of the plant (e.g., the root tissue, shoots, leaves, etc.), or can be an increase in overall biomass. Increased biomass production, such an increase meaning at at least 3%, between 3% and 5%, at least 5%, between 5% and 10%, least 10%, between 10% and 15%, for example at least 15%,
5 between 15% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 75%, at least 75%, between 75% and 100%, or at least 100%, when compared with uninoculated plants grown under the same conditions. Such increase in overall biomass can be under relatively stress-free conditions. In other cases, the increase in
10 biomass can be in plants grown under any number of abiotic or biotic stresses, including drought stress, salt stress, heat stress, cold stress, low nutrient stress, nematode stress, insect herbivory stress, fungal pathogen stress, bacterial pathogen stress, and viral pathogen stress. In some embodiments, a plurality of endophytes is disposed in an amount effective to increase root biomass by at least 3%, between 3% and 5%, at least 5%, between 5% and 10%,
15 least 10%, between 10% and 15%, for example at least 15%, between 15% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%, between 50% and 60%, at least 60%, between 60% and 75%, at least 75%, between 75% and 100%, or at least 100%, when compared with uninoculated plants grown under the same conditions, when compared with a reference agricultural plant.
20 In other cases, a plurality of endophytes is disposed on the plant element in an amount effective to increase the average biomass of the fruit or cob from the resulting plant at least 3%, between 3% and 5%, at least 5%, between 5% and 10%, least 10%, between 10% and 15%, for example at least 15%, between 15% and 20%, at least 20%, between 20% and 30%, at least 30%, between 30% and 40%, at least 40%, between 40% and 50%, at least 50%,
25 between 50% and 60%, at least 60%, between 60% and 75%, at least 75%, between 75% and 100%, or at least 100%, when compared with uninoculated plants grown under the same conditions.

Increase in plant growth hormones

[0193] Many of the microbes described herein are capable of producing the plant hormone
30 auxin indole-3-acetic acid (IAA) when grown in culture. Auxin may play a key role in altering the physiology of the plant, including the extent of root growth. Therefore, in other embodiments, a single endophyte strain or a plurality of endophytes is disposed on the surface or within a tissue of the plant element in an amount effective to detectably induce

production of auxin in the agricultural plant. For example, the increase in auxin production can be at least 2%, at least 3%, at least 4%, at least 5%, at least 6%, at least 7%, at least 8%, at least 9%, at least 10%, at least 15%, for example, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 75%, at least 100%, or more, when compared with a
5 reference agricultural plant. In some embodiments, the increased auxin production can be detected in a tissue type selected from the group consisting of the root, shoot, leaves, and flowers.

[0194] *Improvement of other traits.* In other embodiments, a single endophyte strain or a plurality of endophytes can confer other beneficial traits to the plant. Improved traits can
10 include an improved nutritional content of the plant or plant element used for human consumption. In some embodiments, the endophyte-associated plant is able to produce a detectable change in the content of at least one nutrient. Examples of such nutrients include amino acid, protein, oil (including any one of Oleic acid, Linoleic acid, Alpha-linoleic acid, Saturated fatty acids, Palmitic acid, Stearic acid and Trans fats), carbohydrate (including
15 sugars such as sucrose, glucose and fructose, starch, or dietary fiber), Vitamin A, Thiamine (vit. B1), Riboflavin (vit. B2), Niacin (vit. B3), Pantothenic acid (B5), Vitamin B6, Folate (vit. B9), Choline, Vitamin C, Vitamin E, Vitamin K, Calcium, Iron, Magnesium, Manganese, Phosphorus, Potassium, Sodium, Zinc. In some embodiments, the endophyte-associated plant or part thereof contains at least one increased nutrient when compared with
20 reference agricultural plants.

[0195] In other cases, the improved trait can include reduced content of a harmful or undesirable substance when compared with reference agricultural plants. Such compounds include those which are harmful when ingested in large quantities or are bitter tasting (for example, oxalic acid, amygdalin, certain alkaloids such as solanine, caffeine, nicotine,
25 quinine and morphine, tannins, cyanide). As such, in some embodiments, the endophyte-associated plant or part thereof contains less of the undesirable substance when compared with reference agricultural plant. In a related embodiment, the improved trait can include improved taste of the plant or a part of the plant, including the fruit or seed. In a related embodiment, the improved trait can include reduction of undesirable compounds produced by
30 other endophytes in plants, such as degradation of Fusarium-produced deoxynivalenol (also known as vomitoxin and a virulence factor involved in Fusarium head blight of maize and wheat) in a part of the plant, including the fruit or seed.

[0196] The endophyte-associated plant can also have an altered hormone status or altered levels of hormone production when compared with a reference agricultural plant. An alteration in hormonal status may affect many physiological parameters, including flowering time, water efficiency, apical dominance and/or lateral shoot branching, increase in root hair, and alteration in fruit ripening.

[0197] The association between the endophytes and the plant can also be detected using other methods known in the art. For example, the biochemical, genomic, epigenomic, transcriptomic, metabolomics, and/or proteomic profiles of endophyte-associated plants can be compared with reference agricultural plants under the same conditions.

[0198] Transcriptome analysis of endophyte-associated and reference agricultural plants can also be performed to detect changes in expression of at least one transcript, or a set or network of genes upon endophyte association. Similarly, epigenetic changes can be detected using methylated DNA immunoprecipitation followed by high-throughput sequencing.

[0199] Metabolomic or proteomic differences between the plants can be detected using methods known in the art. The metabolites, proteins, or other compounds described herein can be detected using any suitable method including, but not limited to gel electrophoresis, liquid and gas phase chromatography, either alone or coupled to mass spectrometry, NMR, immunoassays (enzyme-linked immunosorbent assays (ELISA)), chemical assays, spectroscopy and the like. In some embodiments, commercial systems for chromatography and NMR analysis are utilized. Such metabolomic methods can be used to detect differences in levels in hormone, nutrients, secondary metabolites, root exudates, phloem sap content, xylem sap content, heavy metal content, and the like. Such methods are also useful for detecting alterations in endophyte content and status; for example, the presence and levels of signaling molecules (e.g., autoinducers and pheromones), which can indicate the status of group-based behavior of endophytes based on, for example, population density. In some embodiments, a biological sample (whole tissue, exudate, phloem sap, xylem sap, root exudate, etc.) from endophyte-associated and reference agricultural plants can be analyzed essentially as known in the art.

[0200] In some embodiments, metabolites in plants can be modulated by making synthetic combinations of plants with pluralities of endophytes. For example, a plurality of endophytes can cause a detectable modulation (e.g., an increase or decrease) in the level of various metabolites, e.g., indole-3-carboxylic acid, trans-zeatin, abscisic acid, phaseic acid, indole-3-

acetic acid, indole-3-butyric acid, indole-3-acrylic acid, jasmonic acid, jasmonic acid methyl ester, dihydrophaseic acid, gibberellin A3, salicylic acid, upon colonization of a plant.

[0201] In some embodiments, a single endophyte strain or a plurality of endophytes modulates the level of the metabolite directly (e.g., the microbes produces the metabolite, resulting in an overall increase in the level of the metabolite found in the plant). In other cases, the agricultural plant, as a result of the association with the plurality of endophytes, exhibits a modulated level of the metabolite (e.g., the plant reduces the expression of a biosynthetic enzyme responsible for production of the metabolite as a result of the microbe inoculation). In still other cases, the modulation in the level of the metabolite is a consequence of the activity of both the microbe and the plant (e.g., the plant produces increased amounts of the metabolite when compared with a reference agricultural plant, and the endophyte also produces the metabolite). Therefore, as used herein, a modulation in the level of a metabolite can be an alteration in the metabolite level through the actions of the microbe and/or the inoculated plant.

[0202] The levels of a metabolite can be measured in an agricultural plant, and compared with the levels of the metabolite in a reference agricultural plant, and grown under the same conditions as the inoculated plant. The uninoculated plant that is used as a reference agricultural plant is a plant that has not been applied with a formulation with the plurality of endophytes (e.g., a formulation comprising a plurality of populations of purified endophytes). The uninoculated plant used as the reference agricultural plant is generally the same species and cultivar as, and is isogenic to, the inoculated plant.

[0203] The metabolite whose levels are modulated (e.g., increased or decreased) in the endophyte-associated plant may serve as a primary nutrient (i.e., it provides nutrition for the humans and/or animals who consume the plant, plant tissue, or the commodity plant product derived therefrom, including, but not limited to, a sugar, a starch, a carbohydrate, a protein, an oil, a fatty acid, or a vitamin). The metabolite can be a compound that is important for plant growth, development or homeostasis (for example, a phytohormone such as an auxin, cytokinin, gibberellin, a brassinosteroid, ethylene, or abscisic acid, a signaling molecule, or an antioxidant). In other embodiments, the metabolite can have other functions. For example, in some embodiments, a metabolite can have bacteriostatic, bactericidal, fungistatic, fungicidal or antiviral properties. In other embodiments, the metabolite can have insect-repelling, insecticidal, nematode-repelling, or nematocidal properties. In still other embodiments, the metabolite can serve a role in protecting the plant from stresses, may help

improve plant vigor or the general health of the plant. In yet another embodiment, the metabolite can be a useful compound for industrial production. For example, the metabolite may itself be a useful compound that is extracted for industrial use, or serve as an intermediate for the synthesis of other compounds used in industry. In a particular
5 embodiment, the level of the metabolite is increased within the agricultural plant or a portion thereof such that it is present at a concentration of at least 0.1 ug/g dry weight, for example, at least 0.3 ug/g dry weight, between 0.3 ug/g and 1.0 ug/g dry weight, at least 1.0 ug/g dry weight, between 1.0 ug/g and 3.0 ug/g dry weight, at least 3.0 ug/g dry weight, between 3.0
10 ug/g and 10 ug/g dry weight, at least 10 ug/g dry weight, between 10 ug/g and 30 ug/g dry weight, at least 30 ug/g dry weight, between 30 ug/g and 100 ug/g dry weight, at least 100 ug/g dry weight, between 100 ug/g and 300 ug/g dry weight, at least 300 ug/g dry weight, between 300 ug/g and 1 mg/g dry weight, or more than 1 mg/g dry weight, of the plant or portion thereof.

[0204] Likewise, the modulation can be a decrease in the level of a metabolite. The
15 reduction can be in a metabolite affecting the taste of a plant or a commodity plant product derived from a plant (for example, a bitter tasting compound), or in a metabolite which makes a plant or the resulting commodity plant product otherwise less valuable (for example, reduction of oxalate content in certain plants, or compounds which are deleterious to human and/or animal health). The metabolite whose level is to be reduced can be a compound that
20 affects quality of a commodity plant product (e.g., reduction of lignin levels).

Commodity Plant Product

[0205] The present invention provides a commodity plant product, as well as methods for producing a commodity plant product, that is derived from a plant of the present invention. As used herein, a "commodity plant product" refers to any composition or product that is
25 comprised of material derived from a plant, seed, plant cell, or plant part of the present invention. Commodity plant products may be sold to consumers and can be viable or nonviable. Nonviable commodity products include but are not limited to nonviable seeds and grains; processed seeds, seed parts, and plant parts; dehydrated plant tissue, frozen plant tissue, and processed plant tissue; seeds and plant parts processed for animal feed for
30 terrestrial and/or aquatic animal consumption, oil, meal, flour, flakes, bran, fiber, paper, tea, coffee, silage, crushed of whole grain, and any other food for human or animal consumption; and biomasses and fuel products; and raw material in industry. Industrial uses of oils derived from the agricultural plants described herein include ingredients for paints, plastics, fibers,

detergents, cosmetics, lubricants, and biodiesel fuel. Soybean oil may be split, inter-esterified, sulfurized, epoxidized, polymerized, ethoxylated, or cleaved. Designing and producing soybean oil derivatives with improved functionality and improved oliochemistry is a rapidly growing field. The typical mixture of triglycerides is usually split and separated into
5 pure fatty acids, which are then combined with petroleum-derived alcohols or acids, nitrogen, sulfonates, chlorine, or with fatty alcohols derived from fats and oils to produce the desired type of oil or fat. Commodity plant products also include industrial compounds, such as a wide variety of resins used in the formulation of adhesives, films, plastics, paints, coatings and foams.

10 [0206] In some cases, commodity plant products derived from the plants, or using the methods of the present invention can be identified readily. In some cases, for example, the presence of viable endophytes can be detected using the methods described herein elsewhere. In other cases, particularly where there are no viable endophytes, the commodity plant product may still contain at least a detectable amount of the specific and unique DNA
15 corresponding to the microbes described herein. Any standard method of detection for polynucleotide molecules may be used, including methods of detection disclosed herein.

Formulations for Agricultural Use

[0207] The present invention contemplates a synthetic combination of a plant element that is associated with a single endophyte strain or a plurality of endophytes to confer an
20 improved trait of agronomic importance to the host plant, or an improved agronomic trait potential to a plant element associated with the endophytes, that upon and after germination will confer said benefit to the resultant host plant.

[0208] In some embodiments, the plant element is associated with a single endophyte strain or a plurality of endophytes on its surface. Such association is contemplated to be via a
25 mechanism selected from the group consisting of: spraying, immersion, coating, encapsulating, dusting, dripping, aerosolizing, seed treatment, root wash, seedling soak, foliar application, soil inocula, in-furrow application, sidedress application, soil pre-treatment, wound inoculation, drip tape irrigation, vector-mediation via a pollinator, injection, osmopriming, hydroponics, aquaponics, and aeroponics.

30 [0209] In some embodiments, the plant element is a leaf, and the synthetic combination is formulated for application as a foliar treatment.

[0210] In some embodiments, the plant element is a seed, and the synthetic combination is formulated for application as a seed coating.

[0211] In some embodiments, the plant element is a root, and the synthetic combination is formulated for application as a root treatment.

5 [0212] In certain embodiments, the plant element becomes associated with a plurality of endophytes through delayed exposure. For example, the soil in which a plant element is to be introduced is first treated with a composition comprising a plurality of endophytes. In another example, the area around the plant or plant element is exposed to a formulation comprising a plurality of endophytes, and the plant element becomes subsequently associated with the
10 endophytes due to movement of soil, air, water, insects, mammals, human intervention, or other methods.

[0213] The plant element can be obtained from any agricultural plant. In some embodiments, the plant element of the first plant is from a monocotyledonous plant. For example, the plant element of the first plant is from a cereal plant. The plant element of the
15 first plant can be selected from the group consisting of a maize seed, a wheat seed, a barley seed, a rice seed, a sugarcane seed, a maize root, a wheat root, a barley root, a sugarcane root, a rice root, a maize leaf, a wheat leaf, a barley leaf, a sugarcane leaf, or a rice leaf. In an alternative embodiment, the plant element of the first plant is from a dicotyledonous plant. The plant element of the first plant can be selected from the group consisting of a cotton seed,
20 a tomato seed, a canola seed, a pepper seed, a soybean seed, a cotton root, a tomato root, a canola root, a pepper root, a soybean root, a cotton leaf, a tomato leaf, a canola leaf, a pepper leaf, or a soybean leaf. In still another embodiment, the plant element of the first plant can be from a genetically modified plant. In other embodiments, the plant element of the first plant can be a hybrid plant element.

25 [0214] The synthetic combination can comprise a plant element of the first plant which is surface-sterilized prior to combining with a plurality of endophytes. Such pre-treatment prior to coating the seed with endophytes removes the presence of other microbes which may interfere with the optimal colonization, growth and/or function of the endophytes. Surface sterilization of seeds can be accomplished without killing the seeds as described herein.

30 [0215] A single endophyte strain or a plurality of endophytes is intended to be useful in the improvement of agricultural plants, and as such, may be formulated with other compositions as part of an agriculturally compatible carrier. It is contemplated that such carriers can

include, but not be limited to: seed treatment, root treatment, foliar treatment, soil treatment. The carrier composition with a plurality of endophytes, may be prepared for agricultural application as a liquid, a solid, or a gas formulation. Application to the plant may be achieved, for example, as a powder for surface deposition onto plant leaves, as a spray to the whole plant or selected plant element, as part of a drip to the soil or the roots, or as a coating onto the seed prior to planting. Such examples are meant to be illustrative and not limiting to the scope of the invention.

[0216] In some embodiments, the present invention contemplates plant elements comprising a single endophyte strain or a plurality of endophytes, and further comprising a formulation. The formulation useful for these embodiments generally comprises at least one member selected from the group consisting of an agriculturally compatible carrier, a tackifier, a microbial stabilizer, a fungicide, an antibacterial agent, an herbicide, a nematicide, an insecticide, a plant growth regulator, a rodenticide, and a nutrient.

[0217] In some cases, a single endophyte strain or a plurality of endophytes is mixed with an agriculturally compatible carrier. The carrier can be a solid carrier or liquid carrier. The carrier may be any one or more of a number of carriers that confer a variety of properties, such as increased stability, wettability, or dispersability. Wetting agents such as natural or synthetic surfactants, which can be nonionic or ionic surfactants, or a combination thereof can be included in a composition of the invention. Water-in-oil emulsions can also be used to formulate a composition that includes a plurality of endophytes. Suitable formulations that may be prepared include wettable powders, granules, gels, agar strips or pellets, thickeners, and the like, microencapsulated particles, and the like, liquids such as aqueous flowables, aqueous suspensions, water-in-oil emulsions, etc. The formulation may include grain or legume products, for example, ground grain or beans, broth or flour derived from grain or beans, starch, sugar, or oil.

[0218] In some embodiments, the agricultural carrier may be soil or plant growth medium. Other agricultural carriers that may be used include fertilizers, plant-based oils, humectants, or combinations thereof. Alternatively, the agricultural carrier may be a solid, such as diatomaceous earth, loam, silica, alginate, clay, bentonite, vermiculite, seed cases, other plant and animal products, or combinations, including granules, pellets, or suspensions. Mixtures of any of the aforementioned ingredients are also contemplated as carriers, such as but not limited to, pesta (flour and kaolin clay), agar or flour-based pellets in loam, sand, or clay, etc. Formulations may include food sources for the cultured organisms, such as barley, rice, or

other biological materials such as seed, leaf, root, plant elements, sugar cane bagasse, hulls or stalks from grain processing, ground plant material or wood from building site refuse, sawdust or small fibers from recycling of paper, fabric, or wood. Other suitable formulations will be known to those skilled in the art.

5 [0219] In some embodiments, the formulation can comprise a tackifier or adherent. Such agents are useful for combining the microbial population of the invention with carriers that can contain other compounds (e.g., control agents that are not biologic), to yield a coating composition. Such compositions help create coatings around the plant or plant element to maintain contact between the microbe and other agents with the plant or plant part. In some
10 embodiments, adherents are selected from the group consisting of: alginate, gums, starches, lecithins, formononetin, polyvinyl alcohol, alkali formononetinate, hesperetin, polyvinyl acetate, cephalins, Gum Arabic, Xanthan Gum, carragennan, PGA, other biopolymers, Mineral Oil, Polyethylene Glycol (PEG), Polyvinyl pyrrolidone (PVP), Arabino-galactan, Methyl Cellulose, PEG 400, Chitosan, Polyacrylamide, Polyacrylate, Polyacrylonitrile,
15 Glycerol, Triethylene glycol, Vinyl Acetate, Gellan Gum, Polystyrene, Polyvinyl, Carboxymethyl cellulose, Gum Ghatti, and polyoxyethylene-polyoxybutylene block copolymers. Other examples of adherent compositions that can be used in the synthetic preparation include those described in EP 0818135, CA 1229497, WO 2013090628, EP 0192342, WO 2008103422 and CA 1041788, each of which is incorporated herein by
20 reference in its entirety.

[0220] It is also contemplated that the formulation may further comprise an anti-caking agent.

[0221] The formulation can also contain a surfactant, wetting agent, emulsifier, stabilizer, or anti-foaming agent. Non-limiting examples of surfactants include nitrogen-surfactant
25 blends such as Prefer 28 (Cenex), Surf-N(US), Inhance (Brandt), P-28 (Wilfarm) and Patrol (Helena); esterified seed oils include Sun-It II (AmCy), MSO (UAP), Scoil (Agsco), Hasten (Wilfarm) and Mes-100 (Drexel); and organo-silicone surfactants include Silwet L77 (UAP), Silikin (Terra), Dyne-Amic (Helena), Kinetic (Helena), Sylgard 309 (Wilbur-Ellis) and Century (Precision), polysorbate 20, polysorbate 80, Tween 20, Tween 80, Scattics, Alktest
30 TW20, Canarcel, Peogabsorb 80, Triton X-100, Conco NI, Dowfax 9N, Igebapl CO, Makon, Neutronyx 600, Nonipol NO, Plytergent B, Renex 600, Solar NO, Sterox, Serfonic N, T-DET-N, Tergitol NP, Triton N, IGEPAL CA-630, Nonident P-40, and Pluronic. In some embodiments, the surfactant is present at a concentration of between 0.01% v/v to 10% v/v.

In other embodiments, the surfactant is present at a concentration of between 0.1% v/v to 1% v/v. An example of an anti-foaming agent is Antifoam-C.

[0222] In certain cases, the formulation includes a microbial stabilizer. Such an agent can include a desiccant. As used herein, a "desiccant" can include any compound or mixture of compounds that can be classified as a desiccant regardless of whether the compound or compounds are used in such concentrations that they in fact have a desiccating effect on the liquid inoculant. Such desiccants are ideally compatible with the endophytes used, and should promote the ability of the microbial population to survive application on the plant elements and to survive desiccation. Examples of suitable desiccants include one or more of trehalose, sucrose, glycerol, and Methylene glycol. Other suitable desiccants include, but are not limited to, non-reducing sugars and sugar alcohols (e.g., mannitol or sorbitol). The amount of desiccant introduced into the formulation can range from about 5% to about 50% by weight/volume, for example, between about 10% to about 40%, between about 15% and about 35%, or between about 20% and about 30%.

[0223] In some cases, it is advantageous for the formulation to contain agents such as a fungicide, an antibacterial agent, an herbicide, a nematocide, an insecticide, a plant growth regulator, a rodenticide, a bactericide, a virucide, and a nutrient. Such agents are ideally compatible with the agricultural plant element or seedling onto which the formulation is applied (e.g., it should not be deleterious to the growth or health of the plant). Furthermore, the agent is ideally one which does not cause safety concerns for human, animal or industrial use (e.g., no safety issues, or the compound is sufficiently labile that the commodity plant product derived from the plant contains negligible amounts of the compound).

[0224] In the liquid form, for example, solutions or suspensions, a plurality of endophytes can be mixed or suspended in aqueous solutions. Suitable liquid diluents or carriers include aqueous solutions, petroleum distillates, or other liquid carriers.

[0225] Solid compositions can be prepared by dispersing a plurality of endophytes of the invention in and on an appropriately divided solid carrier, such as peat, wheat, bran, vermiculite, clay, talc, bentonite, diatomaceous earth, fuller's earth, pasteurized soil, and the like. When such formulations are used as wettable powders, biologically compatible dispersing agents such as non-ionic, anionic, amphoteric, or cationic dispersing and emulsifying agents can be used.

[0226] The solid carriers used upon formulation include, for example, mineral carriers such as kaolin clay, pyrophyllite, bentonite, montmorillonite, diatomaceous earth, acid white soil, vermiculite, and pearlite, and inorganic salts such as ammonium sulfate, ammonium phosphate, ammonium nitrate, urea, ammonium chloride, and calcium carbonate. Also, organic fine powders such as wheat flour, wheat bran, and rice bran may be used. The liquid carriers include vegetable oils such as soybean oil and cottonseed oil, glycerol, ethylene glycol, polyethylene glycol, propylene glycol, polypropylene glycol, etc.

[0227] In some embodiments, the formulation is ideally suited for coating of a plurality of endophytes onto plant elements. The plurality of endophytes is capable of conferring many agronomic benefits to the host plants. The ability to confer such benefits by coating the plurality of endophytes on the surface of plant elements has many potential advantages, particularly when used in a commercial (agricultural) scale.

[0228] A single endophyte strain or a plurality of endophytes can be combined with one or more of the agents described above to yield a formulation suitable for combining with an agricultural plant element or seedling. The plurality of endophytes can be obtained from growth in culture, for example, using a synthetic growth medium. In addition, the microbe can be cultured on solid media, for example on petri dishes, scraped off and suspended into the preparation. Microbes at different growth phases can be used. For example, microbes at lag phase, early-log phase, mid-log phase, late-log phase, stationary phase, early death phase, or death phase can be used. Endophytic spores may be used for the present invention, for example but not limited to: arthrospores, sporangiospores, conidia, chlamydospores, pycnidiospores, endospores, zoospores.

[0229] The formulations comprising a plurality of endophytes of the present invention typically contains between about 0.1 to 95% by weight, for example, between about 1% and 90%, between about 3% and 75%, between about 5% and 60%, between about 10% and 50% in wet weight of a plurality of endophytes. In some embodiments, the formulation contains at least about 10^2 per ml of formulation, at least about 10^3 per ml of formulation, for example, at least about 10^4 , at least about 10^5 , at least about 10^6 , at least about 10^7 CFU or spores, at least about 10^8 CFU or spores per ml of formulation. In some embodiments, the formulation be applied to the plant element at about 10^2 CFU/seed, between 10^2 and 10^3 CFU, at least about 10^3 CFU, between 10^3 and 10^4 CFU, at least about 10^4 CFU, between 10^4 and 10^5 CFU, at least about 10^5 CFU, between 10^5 and 10^6 CFU, at least

about 10^6 CFU, between 10^6 and 10^7 CFU, at least about 10^7 CFU, between 10^7 and 10^8 CFU, or even greater than 10^8 CFU per seed.

[0230] The compositions provided herein are preferably stable. The endophyte may be shelf-stable, where at least 0.01%, of the CFU or spores are viable after storage in desiccated form (i.e., moisture content of 30% or less) for 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or greater than 10 weeks at 4°C or at room temperature. Optionally, a shelf-stable formulation is in a dry formulation, a powder formulation, or a lyophilized formulation. In some embodiments, the formulation is formulated to provide stability for the population of endophytes. In one embodiment, the formulation is substantially stable at temperatures between about -20°C and about 50°C for at least about 1, 2, 3, 4, 5, or 6 days, or 1, 2, 3 or 4 weeks, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 months, or one or more years. In another embodiment, the formulation is substantially stable at temperatures between about 4°C and about 37°C for at least about 5, 10, 15, 20, 25, 30 or greater than 30 days.

[0231] As described above, in certain embodiments, the present invention contemplates the use of a single endophyte strain or a plurality of endophytes heterologously disposed on the plant, for example, the plant element. In certain cases, the agricultural plant may contain bacteria that are substantially similar to, or even genetically indistinguishable from, the bacteria that are being applied to the plant. It is noted that, in many cases, the bacteria that are being applied is substantially different from the bacteria already present in several significant ways. First, the bacteria that are being applied to the agricultural plant have been adapted to culture, or adapted to be able to grow on growth media in isolation from the plant. Second, in many cases, the bacteria that are being applied are derived from a clonal origin, rather than from a heterologous origin and, as such, can be distinguished from the bacteria that are already present in the agricultural plant by the clonal similarity. For example, where a microbe that has been inoculated by a plant is also present in the plant (for example, in a different tissue or portion of the plant), or where the introduced microbe is sufficiently similar to a microbe that is present in some of the plants (or portion of the plant, including plant elements), it is still possible to distinguish between the inoculated microbe and the native microbe by distinguishing between the two microbe types on the basis of their epigenetic status (e.g., the bacteria that are applied, as well as their progeny, would be expected to have a much more uniform and similar pattern of cytosine methylation of its genome, with respect to the extent and/or location of methylation).

[0232] It is, of course, also possible to provide a coating with additional microorganisms (either the same or different as the endophyte that was inoculated). Therefore, according to another embodiment of the present invention, the obtained plant seed containing microorganisms is therefore subjected to a further seed impregnation step.

- 5 [0233] Once coated with the endophyte formulation, the seeds can be mixed and allowed to dry before germination occurs.

Endophytes compatible with agrichemicals

[0234] In certain embodiments, the single endophyte strain or the plurality of endophytes is selected on the basis of its compatibility with commonly used agrichemicals. As mentioned
10 earlier, plants, particularly agricultural plants, can be treated with a vast array of agrichemicals, including fungicides, biocides (anti-complex agents), herbicides, insecticides, nematocides, rodenticides, fertilizers, and other agents.

[0235] In some cases, it can be important for the single endophyte strain or the plurality of endophytes to be compatible with agrichemicals, particularly those with anticomplex
15 properties, in order to persist in the plant although, as mentioned earlier, there are many such anticomplex agents that do not penetrate the plant, at least at a concentration sufficient to interfere with the endophytes. Therefore, where a systemic anticomplex agent is used in the plant, compatibility of the endophytes to be inoculated with such agents will be an important criterion.

20 *Fungicides*

[0236] In some embodiments, the control agent is a fungicide. As used herein, a fungicide is any compound or agent (whether chemical or biological) that can either inhibit the growth of a fungus or kill a fungus. In that sense, a "fungicide", as used herein, encompasses compounds that may be fungistatic or fungicidal. As used herein, the fungicide can be a
25 protectant, or agents that are effective predominantly on the seed surface, providing protection against seed surface-borne pathogens and providing some level of control of soil-borne pathogens. Non-limiting examples of protectant fungicides include captan, maneb, thiram, or fludioxonil.

[0237] The fungicide can be a systemic fungicide, which can be absorbed into the emerging
30 seedling and inhibit or kill the fungus inside host plant tissues. Systemic fungicides used for seed treatment include, but are not limited to the following: azoxystrobin, carboxin, mefenoxam, metalaxyl, thiabendazole, trifloxystrobin, and various triazole fungicides,

including difenoconazole, ipconazole, tebuconazole, and triticonazole. Mefenoxam and metalaxyl are primarily used to target the water mold fungi *Pythium* and *Phytophthora*. Some fungicides are preferred over others, depending on the plant species, either because of subtle differences in sensitivity of the pathogenic fungal species, or because of the differences in the fungicide distribution or sensitivity of the plants. In some embodiments, the endophyte is compatible with at least one of the fungicides selected from the group consisting of: 2-(thiocyanatomethylthio)-benzothiazole, 2-phenylphenol, 8-hydroxyquinoline sulfate, ametoctradin, amisulbrom, antimycin, *Ampelomyces quisqualis*, azaconazole, azoxystrobin, *Bacillus subtilis*, benalaxyl, benomyl, benthiavalicarb-isopropyl, benzylaminobenzene-sulfonate (BABS) salt, bicarbonates, biphenyl, bismethiazol, bitertanol, bixafen, blasticidin-S, borax, Bordeaux mixture, boscalid, bromuconazole, bupirimate, calcium polysulfide, captafol, captan, carbendazim, carboxin, carpropamid, carvone, chloroneb, chlorothalonil, chlozolinate, *Coniothyrium minitans*, copper hydroxide, copper octanoate, copper oxychloride, copper sulfate, copper sulfate (tribasic), cuprous oxide, cyazofamid, cyflufenamid, cymoxanil, cyproconazole, cyprodinil, dazomet, debacarb, diammonium ethylenebis-(dithiocarbamate), dichlofluanid, dichlorophen, diclocymet, diclomezine, dichloran, diethofencarb, difenoconazole, difenzoquat ion, diflumetorim, dimethomorph, dimoxystrobin, diniconazole, diniconazole-M, dinobuton, dinocap, diphenylamine, dithianon, dodemorph, dodemorph acetate, dodine, dodine free base, edifenphos, enestrobin, epoxiconazole, ethaboxam, ethoxyquin, etridiazole, famoxadone, fenamidone, fenarimol, fenbuconazole, fenfuram, fenhexamid, fenoxanil, fenpiclonil, fenpropidin, fenpropimorph, fentin, fentin acetate, fentin hydroxide, ferbam, ferimzone, fluazinam, fludioxonil, flumorph, fluopicolide, fluopyram, fluoroimide, fluoxastrobin, fluquinconazole, flusilazole, flusulfamide, flutianil, flutolanil, flutriafol, fluxapyroxad, folpet, formaldehyde, fosetyl, fosetyl-aluminium, fuberidazole, furalaxyl, furametpyr, guazatine, guazatine acetates, GY-81, hexachlorobenzene, hexaconazole, hymexazol, imazalil, imazalil sulfate, imibenconazole, iminoctadine, iminoctadine triacetate, iminoctadine tris(albesilate), ipconazole, iprobenfos, iprodione, iprovalicarb, isoprothiolane, isopyrazam, isotianil, kasugamycin, kasugamycin hydrochloride hydrate, kresoxim-methyl, mancozeb, mandipropamid, maneb, mepanipyrim, mepronil, mercuric chloride, mercuric oxide, mercurous chloride, metalaxyl, mefenoxam, metalaxyl-M, metam, metam-ammonium, metam-potassium, metam-sodium, metconazole, methasulfocarb, methyl iodide, methyl isothiocyanate, metiram, metominostrobin, metrafenone, mildiomyacin, myclobutanil, nabam, nitrothal-isopropyl, nuarimol, octhilinone, ofurace, oleic acid (fatty acids), orysastrobin, oxadixyl, oxine-copper,

oxpoconazole fumarate, oxycarboxin, pefurazoate, penconazole, pencycuron, penflufen, pentachlorophenol, pentachlorophenyl laurate, penthiopyrad, phenylmercury acetate, phosphonic acid, phthalide, picoxystrobin, polyoxin B, polyoxins, polyoxorim, potassium bicarbonate, potassium hydroxyquinoline sulfate, probenazole, prochloraz, procymidone, propamocarb, propamocarb hydrochloride, propiconazole, propineb, proquinazid, prothioconazole, pyraclostrobin, pyrametostrobin, pyraoxystrobin, pyrazophos, pyribencarb, pyributicarb, pyrifenox, pyrimethanil, pyroquilon, quinoxamine, quinoxifen, quintozone, Reynoutria sachalinensis extract, sedaxane, silthiofam, simeconazole, sodium 2-phenylphenoxide, sodium bicarbonate, sodium pentachlorophenoxide, spiroxamine, sulfur, SYP-Z071, SYP-Z048, tar oils, tebuconazole, tebufloquin, tecnazene, tetraconazole, thiabendazole, thifluzamide, thiophanate-methyl, thiram, tiadinil, tolclofos-methyl, tolylfluanid, triadimefon, triadimenol, triazoxide, tricyclazole, tridemorph, trifloxystrobin, triflumizole, triforine, triticonazole, validamycin, valifenalate, valiphenal, vinclozolin, zineb, ziram, zoxamide, *Candida oleophila*, *Fusarium oxysporum*, *Gliocladium* spp., *Phlebiopsis gigantea*, *Streptomyces griseoviridis*, *Trichoderma* spp., (RS)—N-(3,5-dichlorophenyl)-2-(methoxymethyl)-succinimide, 1,2-dichloropropane, 1,3-dichloro-1,1,3,3-tetrafluoroacetone hydrate, 1-chloro-2,4-dinitronaphthalene, 1-chloro-2-nitropropane, 2-(2-heptadecyl-2-imidazolin-1-yl)ethanol, 2,3-dihydro-5-phenyl-1,4-dithiane 1,1,4,4-tetraoxide, 2-methoxyethylmercury acetate, 2-methoxyethylmercury chloride, 2-methoxyethylmercury silicate, 3-(4-chlorophenyl)-5-methylrhodanine, 4-(2-nitroprop-1-enyl)phenyl thiocyanate, ampropylfos, anilazine, azithiram, barium polysulfide, Bayer 32394, benodanil, benquinox, bentazon, benzamyl, benzamyl-isobutyl, benzamyl, binapacryl, bis(methylmercury) sulfate, bis(tributyltin) oxide, buthiobate, cadmium calcium copper zinc chromate sulfate, carbamorph, CECA, chlobenthiazole, chloranilmethane, chlorfenazole, chlorquinox, climbazole, cyclafuramid, cypendazole, cyproflumuron, decafentin, dichloro, dichlozoline, diclobutrazol, dimethirimol, dinocron, dinosulfon, dinoterbon, dipyrithione, ditalimfos, dodicin, drazoxolon, EBP, ESBP, etaconazole, etem, ethirim, fenaminosulf, fenapanil, fenitropan, 5-fluorocytosine and fungicides thereof, fluotrimazole, furcarbanil, furconazole, furconazole-cis, furmecyclox, furophanate, glyodine, griseofulvin, halacrinat, Hercules 3944, hexylthiofos, ICIA0858, isopamphos, isovaldione, mebenil, mecarbinzid, metazoxolon, methfuroxam, methylmercury dicyandiamide, metsulfovax, milneb, mucochloric anhydride, myclozolin, N-3,5-dichlorophenyl-succinimide, N-3-nitrophenylitaconimide, natamycin, N-ethylmercurio-4-toluenesulfonanilide, nickel bis(dimethyldithiocarbamate), OCH, phenylmercury dimethyldithiocarbamate,

phenylmercury nitrate, phosdiphen, picolinamide UK-2A and derivatives thereof, prothiocarb; prothiocarb hydrochloride, pyracarbolid, pyridinitril, pyroxychlor, pyroxyfur, quinacetol; quinacetol sulfate, quinazamid, quinconazole, rabenzazole, salicylanilide, SSF-109, sultropen, tecoram, thiadifluor, thicyofen, thiochlorfenphim, thiophanate, thioquinox, 5 tioxymid, triamiphos, triarimol, triazbutil, trichlamide, urbacid, XRD-563, and zarilamide, IK-1140. In still another embodiment, an endophyte that is compatible with an antibacterial compound is used for the methods described herein. For example, the endophyte is compatible with at least one of the antibiotics selected from the group consisting of: Amikacin, Gentamicin, Kanamycin, Neomycin, Netilmicin, Tobramycin, Paromomycin, 10 Spectinomycin, Geldanamycin, Herbimycin, Rifaximin, streptomycin, Loracarbef, Ertapenem, Doripenem, Imipenem/Cilastatin, Meropenem, Cefadroxil, Cefazolin, Cefalotin or Cefalothin, Cefalexin, Cefaclor, Cefamandole, Cefoxitin, Cefprozil, Cefuroxime, Cefixime, Cefdinir, Cefditoren, Cefoperazone, Cefotaxime, Cefpodoxime, Ceftazidime, Ceftibuten, Ceftizoxime, Ceftriaxone, Cefepime, Ceftaroline fosamil, Ceftobiprole, 15 Teicoplanin, Vancomycin, Telavancin, Clindamycin, Lincomycin, Daptomycin, Azithromycin, Clarithromycin, Dirithromycin, Erythromycin, Roxithromycin, Troleandomycin, Telithromycin, Spiramycin, Aztreonam, Furazolidone, Nitrofurantoin, Linezolid, Posizolid, Radezolid, Torezolid, Amoxicillin, Ampicillin, Azlocillin, Carbenicillin, Cloxacillin, Dicloxacillin, Flucloxacillin, Mezlocillin, Methicillin, Nafcillin, 20 Oxacillin, Penicillin G, Penicillin V, Piperacillin, Penicillin G, Temocillin, Ticarcillin, Amoxicillin/clavulanate, Ampicillin/sulbactam, Piperacillin/tazobactam, Ticarcillin/clavulanate, Bacitracin, Colistin, Polymyxin B, Ciprofloxacin, Enoxacin, Gatifloxacin, Levofloxacin, Lomefloxacin, Moxifloxacin, Nalidixic acid, Norfloxacin, Ofloxacin, Trovafloxacin, Grepafloxacin, Sparfloxacin, Temafloxacin, Mafenide, 25 Sulfacetamide, Sulfadiazine, Silver sulfadiazine, Sulfadimethoxine, Sulfamethizole, Sulfamethoxazole, Sulfanilimide (archaic), Sulfasalazine, Sulfisoxazole, Trimethoprim-Sulfamethoxazole (Co-trimoxazole) (TMP-SMX), Sulfonamidochrysoidine (archaic), Demeclocycline, Doxycycline, Minocycline, Oxytetracycline, Tetracycline, Clofazimine, Dapsone, Capreomycin, Cycloserine, Ethambutol, Ethionamide, Isoniazid, Pyrazinamide, 30 Rifampicin (Rifampin in US), Rifabutin, Rifapentine, Streptomycin, Arsphenamine, Chloramphenicol, Fosfomycin, Fusidic acid, Metronidazole, Mupirocin, Platensimycin, Quinupristin/Dalfopristin, Thiamphenicol, Tigecycline, Tinidazole, and Trimethoprim.

[0238] A fungicide can be a biological control agent, such as a bacterium or fungus. Such organisms may be parasitic to the pathogenic fungi, or secrete toxins or other substances which can kill or otherwise prevent the growth of fungi. Any type of fungicide, particularly ones that are commonly used on plants, can be used as a control agent in a seed composition.

5 *Antibacterial agents*

[0239] In some cases, the seed coating composition comprises a control agent which has antibacterial properties. In some embodiments, the control agent with antibacterial properties is selected from the compounds described herein elsewhere. In other embodiments, the compound is Streptomycin, oxytetracycline, oxolinic acid, or gentamicin.

10 *Plant growth regulators*

[0240] The seed coat composition can further comprise a plant growth regulator. In some embodiments, the plant growth regulator is selected from the group consisting of: Absciscic acid, amidochlor, ancymidol, 6-benzylaminopurine, brassinolide, butralin, chlormequat (chlormequat chloride), choline chloride, cyclanilide, daminozide, dikegulac, dimethipin, 2,6-
 15 dimethylpuridine, ethephon, flumetralin, flurprimidol, fluthiacet, forchlorfenuron, gibberellic acid, inabenfide, indole-3-acetic acid, maleic hydrazide, mefluidide, mepiquat (mepiquat chloride), naphthaleneacetic acid, N-6-benzyladenine, paclobutrazol, prohexadione (prohexadione- calcium), prohydrojasmon, thidiazuron, triapenthenol, tributyl phosphorotrithioate, 2,3,5-tri-iodobenzoic acid, trinexapac-ethyl and uniconazole. Other
 20 examples of antibacterial compounds which can be used as part of a seed coating composition include those based on dichlorophene and benzylalcohol hemi formal (Proxel® from ICI or Acticide® RS from Thor Chemie and Kathon® MK from Rohm & Haas) and isothiazolinone derivatives such as alkylisothiazolinones and benzisothiazolinones (Acticide® MBS from Thor Chemie). Other plant growth regulators that can be incorporated seed coating
 25 compositions are described in US 2012/0108431, which is incorporated by reference in its entirety.

Nematicides

[0241] Preferred nematode-antagonistic biocontrol agents include ARF18; *Arthrobotrys* spp.; *Chaetomium* spp.; *Cylindrocarpon* spp.; *Exophilia* spp.; *Fusarium* spp.; *Gliocladium* spp.; *Hirsutella* spp.; *Lecanicillium* spp.; *Monacrosporium* spp.; *Myrothecium* spp.; *Neocosmospora* spp.; *Paecilomyces* spp.; *Pochonia* spp.; *Stagonospora* spp.; vesicular-arbuscular mycorrhizal fungi, *Burkholderia* spp.; *Pasteuria* spp., *Brevibacillus* spp.;

Pseudomonas spp.; and *Rhizobacteria*. Particularly preferred nematode-antagonistic biocontrol agents include ARF18, *Arthrobotrys oligospora*, *Arthrobotrys dactyloides*, *Chaetomium globosum*, *Cylindrocarpon heteronema*, *Exophiala jeanselmei*, *Exophiala pisciphila*, *Fusarium aspergillus*, *Fusarium solani*, *Gliocladium catenulatum*, *Gliocladium roseum*, *Gliocladium virens*, *Hirsutella rhossiliensis*, *Hirsutella minnesotensis*, *Lecanicillium lecanii*, *Monacrosporium drechsleri*, *Monacrosporium geophyropagum*, *Myrothecium verrucaria*, *Neocosmospora vasinfecta*, *Paecilomyces lilacinus*, *Pochonia chlamydosporia*, *Stagonospora heteroderae*, *Stagonospora phaseoli*, vesicular-arbuscular mycorrhizal fungi, *Burkholderia cepacia*, *Pasteuria penetrans*, *Pasteuria thornei*, *Pasteuria nishizawae*, *Pasteuria ramosa*, *Pastrueia usage*, *Brevibacillus laterosporus* strain G4, *Pseudomonas fluorescens* and *Rhizobacteria*.

Nutrients

[0242] In other embodiments, the seed coating composition can comprise a nutrient. The nutrient can be selected from the group consisting of a nitrogen fertilizer including, but not limited to Urea, Ammonium nitrate, Ammonium sulfate, Non-pressure nitrogen solutions, Aqua ammonia, Anhydrous ammonia, Ammonium thiosulfate, Sulfur-coated urea, Urea-formaldehydes, IBDU, Polymer-coated urea, Calcium nitrate, Ureaform, and Methylene urea, phosphorous fertilizers such as Diammonium phosphate, Monoammonium phosphate, Ammonium polyphosphate, Concentrated superphosphate and Triple superphosphate, and potassium fertilizers such as Potassium chloride, Potassium sulfate, Potassium-magnesium sulfate, Potassium nitrate. Such compositions can exist as free salts or ions within the seed coat composition. Alternatively, nutrients/fertilizers can be complexed or chelated to provide sustained release over time.

Rodenticides

[0243] Rodents such as mice and rats cause considerable economical damage by eating and soiling planted or stored seeds. Moreover, mice and rats transmit a large number of infectious diseases such as plague, typhoid, leptospirosis, trichinosis and salmonellosis. Anticoagulants such as coumarin and indandione derivatives play an important role in the control of rodents. These active ingredients are simple to handle, relatively harmless to humans and have the advantage that, as the result of the delayed onset of the activity, the animals being controlled identify no connection with the bait that they have ingested, therefore do not avoid it. This is an important aspect in particular in social animals such as rats, where individuals act as

tasters. In some embodiments, the seed coating composition comprises a rodenticide selected from the group of substances consisting of 2-isovalerylindan- 1,3-dione, 4-(quinoxalin-2-ylamino)benzenesulfonamide, alpha-chlorohydrin, aluminum phosphide, antu, arsenous oxide, barium carbonate, bithiosemi, brodifacoum, bromadiolone, bromethalin, calcium cyanide, chloralose, chlorophacinone, cholecalciferol, coumachlor, coumafuryl, coumatetralyl, crimidine, difenacoum, difethialone, diphacinone, ergocalciferol, flocoumafen, fluoroacetamide, flupropadine, flupropadine hydrochloride, hydrogen cyanide, iodomethane, lindane, magnesium phosphide, methyl bromide, norbormide, phosacetim, phosphine, phosphorus, pindone, potassium arsenite, pyrinuron, scilliroside, sodium arsenite, sodium cyanide, sodium fluoroacetate, strychnine, thallium sulfate, warfarin and zinc phosphide.

Compatibility

[0244] In some embodiments, a single endophyte strain or a plurality of endophytes that are compatible with agrichemicals can be used to inoculate the plants according to the methods described herein. In each case below, each single endophyte strain or each type of endophyte used in a plurality of endophytes can be tested for compatibility on their own or as the plurality. Endophytes that are compatible with agriculturally employed anticomplex agents can be isolated by plating a culture of endophytes on a petri dish comprising an effective concentration of the anticomplex agent, and isolating colonies of endophytes that are compatible with the anticomplex agent. In other embodiments, a plurality of endophytes that are compatible with an anticomplex agent are used for the methods described herein.

[0245] In some embodiments, the endophytes of the present invention display tolerance to an agrichemical selected from the group consisting of: Aeris®, Avicta® DuoCot 202, Cruiser®, Syntenta CCB ® (A), Clariva®, Albaugh, Dynasty®, Apron®, Maxim®, Gaucho®, Provoke® ST, Syngenta CCB®, Trilex®, WG Purple, WG Silver, Azoxystrobin, Carboxin, Difenconazole, Fludioxonil, fluxapyroxad, Ipconazole, Mefenoxam, Metalaxyl, Myclobutanil, Penflufen, pyraclostrobin, Sedaxane, TCMTB, Tebuconazole, Thiram, Triadimenol (Baytan®), Trifloxystrobin, Triticonazole, Tolclofos-methyl, PCNB, Abamectin, Chlorpyrifos, Clothianidin, Imidacloprid, Thiamethoxam, and Thiodicarb.

[0246] Bactericide-compatible endophytes can also be isolated by selection on liquid medium. The culture of endophytes can be plated on petri dishes without any forms of mutagenesis; alternatively, endophytes can be mutagenized using any means known in the art. For example, endophyte cultures can be exposed to UV light, gamma-irradiation, or

chemical mutagens such as ethylmethanesulfonate (EMS), ethidium bromide (EtBr) dichlovos (DDVP, methyl methane sulphonale (MMS), triethylphosphate (TEP), trimethylphosphate (TMP), nitrous acid, or DNA base analogs, prior to selection on fungicide comprising media. Finally, where the mechanism of action of a particular bactericide is known, the target gene can be specifically mutated (either by gene deletion, gene replacement, site-directed mutagenesis, etc.) to generate a plurality of endophytes that are resilient against that particular chemical. It is noted that the above-described methods can be used to isolate endophytes that are compatible with both bacteriostatic and bactericidal compounds.

[0247] It will also be appreciated by one skilled in the art that a plant may be exposed to multiple types of anticomplex compounds, either simultaneously or in succession, for example at different stages of plant growth. Where the target plant is likely to be exposed to multiple anticomplex agents, a plurality of endophytes that are compatible with many or all of these agrichemicals can be used to inoculate the plant. Endophytes that are compatible with several agents can be isolated, for example, by serial selection. Endophytes that are compatible with the first agent can be isolated as described above (with or without prior mutagenesis). A culture of the resulting endophytes can then be selected for the ability to grow on liquid or solid media comprising the second agent (again, with or without prior mutagenesis). Colonies isolated from the second selection are then tested to confirm its compatibility to both agents.

[0248] Likewise, endophytes that are compatible to biocides (including herbicides such as glyphosate or anticomplex compounds, whether bacteriostatic or bactericidal) that are agriculturally employed can be isolated using methods similar to those described for isolating compatible endophytes. In some embodiments, mutagenesis of the endophytes can be performed prior to selection with an anticomplex agent. In other embodiments, selection is performed on the endophytes without prior mutagenesis. In still another embodiment, serial selection is performed on endophytes: the endophytes are first selected for compatibility to a first anticomplex agent. The isolated compatible endophytes are then cultured and selected for compatibility to the second anticomplex agent. Any colony thus isolated is tested for compatibility to each, or both anticomplex agents to confirm compatibility with these two agents.

[0249] Compatibility with an antimicrobial agent can be determined by a number of means known in the art, including the comparison of the minimal inhibitory concentration (MIC) of

the unmodified and modified endophytes. Therefore, in some embodiments, the present invention discloses modified endophytes, wherein the endophytes are modified such that they exhibits at least 3 fold greater, for example, at least 5 fold greater, between 5 and 10 fold greater, at least 10 fold greater, between 10 and 20 fold greater, at least 20 fold greater, between 20 and 30 fold greater, at least 30 fold greater or more MIC to an antimicrobial agent when compared with the unmodified endophytes.

[0250] In some embodiments, disclosed herein are endophytes with enhanced compatibility to the herbicide glyphosate. In some embodiments, the endophytes have a doubling time in growth medium comprising least 1 mM glyphosate, for example, between 1 mM and 2mM glyphosate, at least 2 mM glyphosate, between 2 mM and 5 mM glyphosate, at least 5mM glyphosate, between 5 mM and 10 mM glyphosate, at least 10mM glyphosate, between 10 mM and 15 mM glyphosate, at least 15mM glyphosate or more, that is no more than 250%, between 250% and 100%, for example, no more than 200%, between 200% and 175%, no more than 175%, between 175% and 150%, no more than 150%, between 150% and 125%, or no more than 125%, of the doubling time of the endophytes in the same growth medium comprising no glyphosate. In some embodiments, the endophytes have a doubling time in growth medium comprising 5mM glyphosate that is no more than 150% the doubling time of the endophytes in the same growth medium comprising no glyphosate.

[0251] In other embodiments, the endophytes have a doubling time in a plant tissue comprising at least 10 ppm glyphosate, for example, between 10 and 15 ppm, at least 15 ppm glyphosate, between 15 and 10 ppm, at least 20 ppm glyphosate, between 20 and 30 ppm, at least 30 ppm glyphosate, between 30 and 40 ppm, at least 40 ppm glyphosate or more, that is no more than 250%, between 250% and 200%, for example, no more than 200%, between 200% and 175%, no more than 175%, between 175% and 150%, no more than 150%, between 150% and 125%, of the doubling time of the endophytes in a reference plant tissue comprising no glyphosate. In some embodiments, the endophytes have a doubling time in a plant tissue comprising 40 ppm glyphosate that is no more than 150% the doubling time of the endophytes in a reference plant tissue comprising no glyphosate.

[0252] The selection process described above can be repeated to identify isolates of endophytes that are compatible with a multitude of agents.

[0253] Candidate isolates can be tested to ensure that the selection for agrichemical compatibility did not result in loss of a desired bioactivity. Isolates of endophytes that are

compatible with commonly employed agents can be selected as described above. The resulting compatible endophytes can be compared with the parental endophytes on plants in its ability to promote germination.

5 [0254] The agrichemical compatible endophytes generated as described above can be detected in samples. For example, where a transgene was introduced to render the endophytes compatible with the agrichemical(s), the transgene can be used as a target gene for amplification and detection by PCR. In addition, where point mutations or deletions to a portion of a specific gene or a number of genes results in compatibility with the agrichemical(s), the unique point mutations can likewise be detected by PCR or other means
10 known in the art. Such methods allow the detection of the endophytes even if they is no longer viable. Thus, commodity plant products produced using the agrichemical compatible endophytes described herein can readily be identified by employing these and related methods of nucleic acid detection.

Populations of Plant Elements

15 [0255] The synthetic combinations of the present invention may be confined within an object selected from the group consisting of: bottle, jar, ampule, package, vessel, bag, box, bin, envelope, carton, container, silo, shipping container, truck bed, and case. In a particular embodiment, the population of plant elements is packaged in a bag or container suitable for commercial sale. For example, a bag contains a unit weight or count of the plant elements
20 comprising a plurality of endophytes as described herein, and further comprises a label. In one embodiment, the bag or container contains at least 100 plant elements, between 100 and 1,000 plant elements, 1,000 plant elements, between 1,000 and 5,000 plant elements, for example, at least 5,000 plant elements, between 5,000 and 10,000 plant elements, at least 10,000 plant elements, between 10,000 and 20,000 plant elements, at least 20,000 plant
25 elements, between 20,000 and 30,000 plant elements, at least 30,000 plant elements, between 30,000 and 50,000 plant elements, at least 50,000 plant elements, between 50,000 and 70,000 plant elements, at least 70,000 plant elements, between 70,000 and 80,000 plant elements, at least 80,000 plant elements, between 80,000 and 90,000, at least 90,000 plant elements or more. In another embodiment, the bag or container can comprise a discrete weight of plant
30 elements, for example, at least 1 lb, between 1 and 2 lbs, at least 2 lbs, between 2 and 5 lbs, at least 5 lbs, between 5 and 10 lbs, at least 10 lbs, between 10 and 30 lbs, at least 30 lbs, between 30 and 50 lbs, at least 50 lbs, between 50 and 70 lbs, at least 70 lbs or more. The label can contain additional information, for example, the information selected from the

group consisting of: net weight, lot number, geographic origin of the plant elements, test date, germination rate, inert matter content, and the amount of noxious weeds, if any. Suitable containers or packages include those traditionally used in plant plant element commercialization. The invention also contemplates other containers with more sophisticated storage capabilities (e.g., with microbiologically tight wrappings or with gas-or water-proof containments).

[0256] In some cases, a sub-population of plant elements comprising a plurality of endophytes is further selected on the basis of increased uniformity, for example, on the basis of uniformity of microbial population. For example, individual plant elements of pools collected from individual cobs, individual plants, individual plots (representing plants inoculated on the same day) or individual fields can be tested for uniformity of microbial density, and only those pools meeting specifications (e.g., at least 80% of tested plant elements have minimum density, as determined by quantitative methods described elsewhere) are combined to provide the agricultural plant element sub-population.

[0257] The methods described herein can also comprise a validating step. The validating step can entail, for example, growing some plant elements collected from the inoculated plants into mature agricultural plants, and testing those individual plants for uniformity. Such validating step can be performed on individual plant elements collected from cobs, individual plants, individual plots (representing plants inoculated on the same day) or individual fields, and tested as described above to identify pools meeting the required specifications.

[0258] In some embodiments, methods described herein include planting a synthetic composition described herein. Suitable planters include an air seeder and/or fertilizer apparatus used in agricultural operations to apply particulate materials including one or more of the following, seed, fertilizer and/or inoculants, into soil during the planting operation. Seeder/fertilizer devices can include a tool bar having ground-engaging openers thereon, behind which is towed a wheeled cart that includes one or more containment tanks or bins and associated metering means to respectively contain and meter therefrom particulate materials.

[0259] In certain embodiments, a composition described herein may be in the form of a liquid, a slurry, a solid, or a powder (wetable powder or dry powder). In another embodiment, a composition may be in the form of a seed coating. Compositions in liquid, slurry, or powder (e.g., wettable powder) form may be suitable for coating plant elements.

When used to coat plant elements, the composition may be applied to the plant elements and allowed to dry. In embodiments wherein the composition is a powder (e.g., a wettable powder), a liquid, such as water, may need to be added to the powder before application to a seed.

5 [0260] In still another embodiment, the methods can include introducing into the soil an inoculum of one or more of the endophyte populations described herein. Such methods can include introducing into the soil one or more of the compositions described herein. The inoculum(s) or compositions may be introduced into the soil according to methods known to those skilled in the art. Non-limiting examples include in-furrow introduction, spraying,
10 coating seeds, foliar introduction, etc. In a particular embodiment, the introducing step comprises in-furrow introduction of the inoculum or compositions described herein.

[0261] In one embodiment, plant elements may be treated with composition(s) described herein in several ways but preferably via spraying or dripping. Spray and drip treatment may be conducted by formulating compositions described herein and spraying or dripping the
15 composition(s) onto a seed(s) via a continuous treating system (which is calibrated to apply treatment at a predefined rate in proportion to the continuous flow of seed), such as a drum-type of treater. Batch systems, in which a predetermined batch size of seed and composition(s) as described herein are delivered into a mixer, may also be employed.

[0262] In another embodiment, the treatment entails coating plant elements. One such
20 process involves coating the inside wall of a round container with the composition(s) described herein, adding plant elements, then rotating the container to cause the plant elements to contact the wall and the composition(s), a process known in the art as "container coating". Plant elements can be coated by combinations of coating methods. Soaking typically entails using liquid forms of the compositions described. For example, plant
25 elements can be soaked for about 1 minute to about 24 hours (e.g., for at least 1 min, between 1 and 5 min, 5 min, between 5 and 10 min, 10 min, between 10 and 20 min, 20 min, between 20 and 40 min, 40 min, between 40 and 80 min, 80 min, between 80 min and 3 hrs, 3 hrs, between 3 hrs and 6 hrs, 6 hr, between 6 hrs and 12 hrs, 12 hr, between 12 hrs and 24 hrs, or at least 24 hrs).

30 [0263] Throughout the specification, the word "comprise," or variations such as "comprises" or "comprising," will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers.

[0264] Although the present invention has been described in detail with reference to examples below, it is understood that various modifications can be made without departing from the spirit of the invention. For instance, while the particular examples below may illustrate the methods and embodiments described herein using a specific plant, the principles
5 in these examples may be applied to any agricultural crop. Therefore, it will be appreciated that the scope of this invention is encompassed by the embodiments of the inventions recited herein and the specification rather than the specific examples that are exemplified below.

EXAMPLES

Example 1: Cultivation-independent analysis of microbial taxa in agriculturally relevant seed communities based on marker gene high-throughput sequencing

Example Description

Microbial taxa found in agriculturally relevant communities were identified using high-throughput marker gene sequencing across several crops and numerous varieties of seeds.

Experimental description

To identify core (i.e. ubiquitous) microbial taxa across seeds, we used high-throughput sequencing of marker genes for bacteria, archaea, and fungi.

Cereals

2 inbred, 10 landrace, 4 teosinte corn seeds, and 4 modern and 4 wild wheat seeds were obtained. Accessions were categorized into landrace, wild, and inbred varieties based on their assessment of improvement status. In order to extract microbial DNA, the seeds were first sterilized in one of four different manners. Some of the seeds were surface sterilized using 95% ethanol to reduce superficial contaminant microbes, then rinsed in water. Others were first soaked in sterile, DNA-free water for 48 hours to soften them, and they were surface sterilized using 95% ethanol to reduce superficial contaminant microbes, then rinsed in water. Others were rinsed in deionized water, immersed in 95% ethanol for 5 seconds, 0.5% NaOCl for 2 minutes, 70% ethanol for 2 minutes, and then washed three times in deionized water for 1 minute each.

Grasslands

To identify microbial taxa from seeds of wild grassland plants, we used high-throughput sequencing of marker genes for bacteria, archaea, and fungi. Seeds from the following wild grassland species were obtained: Big bluestem, Side oats grama, Bicknell's sedge, Short beak sedge, Canada wild rye, Virginia wild rye, June grass, Leafy satin grass, Switch grass, Little bluestem, Prairie cord grass, Prairie dropseed, Nodding wild onion, Meadow/Canada anemone, Common milkweed, Butterfly weed, Whorled milkweed, New England aster, False boneset, Tall coreopsis, Shooting star, Pale purple coneflower, Rattlesnake master, Tall boneset, Purple joe pye weed, Biennial gaure, Prairie smoke, False sunflower, Rough blazing star, Wild bergamot, Horse mint, Common evening primrose, Wild quinine, Beardtongue, Yellow

coneflower, Black-eyed Susan, Sweet black-eyed susan, Compass plant, Prairie dock, Stiff goldenrod, Showy goldenrod, Hairy aster, Hoary vervain, Culver's root, Golden alexanders, Dogtooth daisy, Wild blue iris, Pointed broom sedge, Dark green bulrush, and Blue vervain. In order to extract microbial DNA, the seeds were first soaked in sterile, DNA-free water for 48 h to soften them, and they were surface sterilized using 95% ethanol to reduce superficial contaminant microbes, then rinsed in water.

Fruits and Vegetables

Seeds from 22 different varieties of cabbage were obtained, including broccoli, cauliflower, and collards. In addition, seeds from 8 different varieties of lettuce, 9 varieties of melon (including cantaloupe and honeydew), 7 varieties of onions (including cippolini, shallots, and vidalia), 4 varieties of tomatoes, one variety of toria, 4 varieties of turnip, 7 varieties of watermelon, and one variety of yellow sarcon were obtained. For strawberries, the seeds or runner plant tissue of 9 varieties were obtained. For sterilization, the seeds were first soaked in sterile, DNA-free water for 48 h to soften them, and they were surface sterilized using 95% ethanol to reduce superficial contaminant microbes, then rinsed in water. Strawberry tissue was surface sterilized using 95% ethanol, then rinsed in water.

Oilseed

Seeds from 1 wild and 3 modern cultivars of *Brassica Napus* were also obtained. In order to extract microbial DNA, the seeds were first soaked in sterile, DNA-free water for 48 h to soften them, and they were surface sterilized using 95% ethanol to reduce superficial contaminant microbes, then rinsed in water.

The seeds or tissues from all of the plants described above were then ground using a mortar and pestle treated with 95% ethanol and RNase Away (Life Technologies, Inc., Grand Island, NY) to remove contaminant DNA. DNA was extracted from the ground seeds using the PowerPlant Pro DNA extraction kit (Mo Bio Laboratories, Inc., Carlsbad, CA) according to the manufacturer's instructions. The surface wash off from certain sterilization treatments of cereal seeds was also collected and DNA was extracted as above.

Marker genes were amplified and sequenced from the extracted DNA. For the bacterial and archaeal analyses, the V4 hypervariable region of the 16S rRNA gene was targeted (primers

515f/806r), and for fungi, the first internal transcribed spacer (ITS1) region of the rRNA operon (primers ITS1f/ITS2r) was targeted. The two marker genes were PCR amplified separately using 35 cycles, and error-correcting 12-bp barcoded primers specific to each sample were used to facilitate combining of samples. To reduce the amplification of chloroplast and mitochondrial DNA, PNA clamps specific to the rRNA genes in these organelles were used. PCR reactions to amplify 16S rRNA genes followed the protocol of (Lundberg et al. 2013), and those to amplify ITS regions followed the protocol of (Fierer et al. 2012). PCR products were quantified using the PicoGreen assay (Life Technologies, Inc., Grand Island, NY), pooled in equimolar concentrations, and cleaned using the UltraClean kit (Mo Bio Laboratories, Inc., Carlsbad, CA). Cleaned DNA pools were sequenced on an Illumina MiSeq instrument at the University of Colorado Next Generation Sequencing Facility.

OTU assignment

For both 16S rRNA and ITS1 sequences, the raw sequence data were reassigned to distinct samples using a custom Python script, and quality filtering and OTU (i.e. operational taxonomic unit) clustering was conducted using the UPARSE pipeline (Edgar 2013). Briefly, a *de novo* sequence database with representative sequences for each OTU was created using a 97% similarity threshold, and raw reads were mapped to this database to calculate sequence counts per OTU per sample. Prior to creating the database, sequences were quality filtered using an expected error frequency threshold of 0.5 errors per sequence. In addition, sequences were dereplicated and singletons were removed prior to creating the database. OTUs were provided taxonomic classifications using the RDP classifier (Wang et al. 2007) trained with the Greengenes (McDonald et al. 2012) and UNITE (Abarenkov et al. 2010) databases for 16S rRNA and ITS sequences, respectively. To account for differences in the variable number of sequences per sample, each sample was rarefied to 1000 16S rRNA and 1000 ITS sequences per sample. OTUs classified as chloroplasts or mitochondria were discarded prior to rarefaction.

Overall differences in bacterial community composition between the control and inoculated plants were evaluated using non-metric multidimensional scaling based on Bray-Curtis dissimilarities in order to visualize pairwise differences between sample communities. Permutational analysis of variance (PERMANOVA) was used to statistically test the significance of these differences. Analyses were conducted using the vegan package in R (R Core Team 2013). To determine the OTUs contributing to overall differences among crop types, mean

relative abundances were calculated for each OTU within each crop type. Only OTUs with a mean relative abundance of 0.1% in either group were included in this analysis.

Results

Across seeds from all plants analyzed herein, a total of 144 bacterial and 145 fungal OTUs were detected and evaluated (Table 3 and Table 4) following stringent sequence quality filtering approach. Among all OTUs, 28 bacterial OTUs and 20 fungal OTUs were found to be core taxa within seeds across plants (Table 1 and Table 2).

Table 3. Exemplary bacterial endophytes present in all plants.

OTU ID	SEQ ID NO	Phylum	Class	Order	Family	Genus	Species
OTU 558	1	OD1	ABY1				
OTU 762	2	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae		
OTU 136	3	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces	
OTU 161	4	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	
OTU 309	5	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	
OTU 63	6	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae		
OTU 67	7	Actinobacteria	Actinobacteria	Actinomycetales	Sanguibacteraceae	Sanguibacter	
OTU 1203	8	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Rathayibacter	caricis
OTU 364	9	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Microbispora	rosea
OTU 130	10	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus	fascians
OTU 74	11	Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae	Kineococcus	
OTU 41	12	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae		
OTU 24	13	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae		
OTU 1230	14	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae		
OTU 30	15	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Mycoplana	
OTU 799	16	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	
OTU 101	17	Proteobacteria	Alphaproteobacteria	Rhizobiales	Aurantimonadaceae		
OTU 572	18	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	Mesorhizobium	
OTU 153	19	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia	
OTU 140	20	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	
OTU 194	21	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae		
OTU 158	22	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae		
OTU 124	23	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	wittichii
OTU 188	24	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae		
OTU 1287	25	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	
OTU 971	26	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodobacter	
OTU 20	27	Proteobacteria	Alphaproteobacteria	Rhizobiales	Aurantimonadaceae		
OTU 57	28	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	
OTU 49	29	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae		
OTU 1222	30	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	
OTU 80	31	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	
OTU 436	32	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	
OTU 1077	33	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	adhaesivum
OTU 510	34	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Azospirillum	
OTU 43	35	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	adhaesivum
OTU 65	36	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae		
OTU 64	37	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	wittichii
OTU 27	38	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	
OTU 47	39	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	

OTU 15	40	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	
OTU 956	41	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	adhaesivum
OTU 21	42	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	
OTU 14	43	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	
OTU 6	44	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	
OTU 1436	45	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	
OTU 61	46	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	
OTU 77	47	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	Leuconostoc	
OTU 358	48	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	badius
OTU 353	49	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	
OTU 1250	50	Firmicutes	Bacilli	Bacillales	Planococcaceae	Sporosarcina	ginsengi
OTU 84	51	Firmicutes	Bacilli	Bacillales	Bacillaceae		
OTU 34	52	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	cereus
OTU 98	53	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	
OTU 152	54	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	
OTU 1178	55	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planomicrobium	
OTU 299	56	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	Leuconostoc	
OTU 241	57	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Carnobacterium	
OTU 203	58	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Lactococcus	
OTU 25	59	Firmicutes	Bacilli	Bacillales	Paenibacillaceae		
OTU 17	60	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	
OTU 330	61	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae		
OTU 211	62	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	
OTU 108	63	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	
OTU 19	64	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	amylyticus
OTU 16	65	Firmicutes	Bacilli	Bacillales	[Exiguobacteraceae]	Exiguobacterium	
OTU 372	66	Firmicutes	Bacilli	Bacillales	Sporolactobacillaceae	Bacillus	racemilacti
OTU 222	67	Firmicutes	Bacilli	Bacillales	Bacillaceae	Geobacillus	
OTU 653	68	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	endophytic
OTU 11	69	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	
OTU 71	70	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Saccharibacillus	kuertensis
OTU 13	71	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	flexus
OTU 10	72	Firmicutes	Bacilli	Bacillales	Planococcaceae	Sporosarcina	ginsengi
OTU 118	73	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Comamonas	
OTU 676	74	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Limnhabitans	
OTU 1014	75	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium	
OTU 26	76	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae		
OTU 182	77	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	Pigmentiphaga	
OTU 980	78	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium	lividum
OTU 35	79	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Polaromonas	
OTU 1226	80	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae		
OTU 1068	81	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae		
OTU 1252	82	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae		
OTU 113	83	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium	
OTU 39	84	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae		
OTU 345	85	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Ralstonia	
OTU 168	86	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae		
OTU 7	87	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium	
OTU 1344	88	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae		
OTU 87	89	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	butyricum
OTU 206	90	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	intestinale
OTU 258	91	Firmicutes	Clostridia	Clostridiales	Clostridiaceae		
OTU 342	92	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Thermoanaerobacterium	saccharolyticum
OTU 259	93	Firmicutes	Clostridia	Thermoanaerobacterales	Caldicellulosiruptoraceae	Caldicellulosiruptor	saccharolyticus
OTU 428	94	Firmicutes	Clostridia	Thermoanaerobacterales	Carboxydodecaceae	Carboxydodecella	
OTU 485	95	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Hymenobacter	
OTU 1306	96	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Hymenobacter	
OTU 735	97	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Hymenobacter	
OTU 37	98	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Hymenobacter	
OTU 775	99	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Hymenobacter	
OTU 141	100	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Hymenobacter	

OTU 149	101	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacterineae		
OTU 70	102	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]	Chryseobacterium	
OTU 23	103	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]	Chryseobacterium	
OTU 236	104	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]	Chryseobacterium	
OTU 148	105	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]	Chryseobacterium	
OTU 181	106	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]	Chryseobacterium	
OTU 347	107	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae		
OTU 1190	108	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Yersinia	
OTU 1201	109	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Enterobacter	hormaechei
OTU 679	110	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	fragi
OTU 234	111	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae		
OTU 46	112	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	lwoffii
OTU 1274	113	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Xanthomonadaceae	Stenotrophomonas	malophilia
OTU 1303	114	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae		
OTU 401	115	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae		
OTU 1261	116	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae		
OTU 548	117	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	
OTU 132	118	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	veronii
OTU 1343	119	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae		
OTU 22	120	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae		
OTU 163	121	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	
OTU 771	122	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	
OTU 826	123	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	
OTU 166	124	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Xanthomonas	
OTU 1441	125	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae		
OTU 1158	126	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Serratia	marcescens
OTU 1083	127	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae		
OTU 8	128	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae		
OTU 18	129	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Xanthomonas	axonopodis
OTU 51	130	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	Halomonas	
OTU 72	131	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	viridiflava
OTU 9	132	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	
OTU 696	133	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia	coli
OTU 53	134	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Enterobacter	
OTU 4	135	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Pantoea	agglomerans
OTU 220	136	Tenericutes	Mollicutes	Anaeroplasmatales	Anaeroplasmataceae	Asteroleplasma	
OTU 343	137	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae		
OTU 82	138	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	
OTU 69	139	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae		
OTU 36	140	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	
OTU 1386	141	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	
OTU 1165	142	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	cryoconitis
OTU 368	143	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	
OTU 91	144	Cyanobacteria					

Table 4. Exemplary fungal endophytes present in all plants

OTU ID	SEQ ID NO	Phylum	Class	Order	Family	Genus	Species
OTU 288	145	Basidiomycota	Agaricomycetes	Corticiales	Corticaceae	Waitea	circinata var circinata
OTU 327	146	Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Thanatephorus	cucumeris
OTU 1	147	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	sp MY 2011
OTU 2	148	Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Cladosporium	
OTU 12	149	Ascomycota	Dothideomycetes	Capnodiales	Davidiellaceae	Davidiella	tassiana
OTU 9	150	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Lewia	infectoria
OTU 29	151	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Epicoccum	nigrum
OTU 15	152	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Ulocladium	
OTU 55	153	Ascomycota	Dothideomycetes	Capnodiales	Davidiellaceae	Cladosporium	
OTU 10	154	Ascomycota	Dothideomycetes	Pleosporales	Incertae sedis	Phoma	sp P48E5

OTU 133	155	Ascomycota	Dothideomycetes	Capnodiales	Davidiellaceae	Cladosporium	sp ascomyc1
							Phaeosphaeriaceae sp MJ23
OTU 26	156	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	unidentified	
OTU 47	157	Ascomycota	Dothideomycetes				
OTU 24	158	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae		
OTU 522	159	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Ampelomyces	quisqualis
OTU 66	160	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Dendryphiella	arenaria
OTU 23	161	Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Septoria	phalaridis
OTU 71	162	Ascomycota	Dothideomycetes	Pleosporales			
OTU 27	163	Ascomycota	Dothideomycetes	Pleosporales	Incertae sedis		
OTU 32	164	Ascomycota	Dothideomycetes	Dothideales	Dothioraceae	Aureobasidium	
							Phaeosphaeriaceae sp MJ23
OTU 20	165	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	unidentified	
OTU 16	166	Ascomycota	Dothideomycetes	Pleosporales	Incertae sedis	Phoma	
OTU 44	167	Ascomycota	Dothideomycetes	Capnodiales	Davidiellaceae	Cladosporium	sp 234B
OTU 38	168	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae		
OTU 104	169	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	brassicicola
							Phaeosphaeriaceae sp MJ23
OTU 1123	170	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	unidentified	
OTU 90	171	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Ampelomyces	quisqualis
OTU 48	172	Ascomycota	Dothideomycetes	Incertae sedis	Incertae sedis	Leptospora	rubella
OTU 73	173	Ascomycota	Dothideomycetes	Pleosporales	Incertae sedis	Phoma	rhei
							uncultured Epicoccum
OTU 1432	174	Ascomycota	Dothideomycetes	Pleosporales	Leptosphaeriaceae	unidentified	
OTU 1095	175	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Lewia	infectoria
OTU 486	176	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Parastagonospora	caricis
OTU 110	177	Ascomycota	Dothideomycetes	Capnodiales	Davidiellaceae	Cladosporium	sp ascomyc1
OTU 78	178	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Phaeosphaeria	
							Dothideomycetes sp
OTU 83	179	Ascomycota	Dothideomycetes	unidentified	unidentified	unidentified	
OTU 815	180	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	sp MY 2011
							sphaerospermum
OTU 244	181	Ascomycota	Dothideomycetes	Capnodiales	Davidiellaceae	Cladosporium	
OTU 775	182	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	sp MY 2011
OTU 259	183	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Lewia	infectoria
OTU 447	184	Ascomycota	Dothideomycetes	Pleosporales	Incertae sedis	Phoma	macrostoma
OTU 1429	185	Ascomycota	Dothideomycetes	Pleosporales	Incertae sedis	Phoma	sp P48E5
OTU 122	186	Ascomycota	Dothideomycetes	Pleosporales	Incertae sedis	Phoma	macrostoma
							Phaeosphaeriaceae sp
OTU 82	187	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	unidentified	
OTU 324	188	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Lewia	infectoria
OTU 60	189	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Cochliobolus	
OTU 142	190	Ascomycota	Dothideomycetes	Incertae sedis	Pseudeurotiaceae	Pseudeurotium	
OTU 92	191	Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Cercospora	nicotianae
OTU 87	192	Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Mycosphaerella	punctiformis
OTU 99	193	Ascomycota	Dothideomycetes	Pleosporales	Leptosphaeriaceae		
OTU 1316	194	Ascomycota	Dothideomycetes	Pleosporales	Incertae sedis	Phoma	
OTU 138	195	Ascomycota	Dothideomycetes	Capnodiales	Davidiellaceae	Cladosporium	
OTU 992	196	Ascomycota	Dothideomycetes	Dothideales	Dothioraceae	Aureobasidium	pullulans
OTU 378	197	Ascomycota	Dothideomycetes	Pleosporales	Incertae sedis	Phoma	
OTU 353	198	Ascomycota	Dothideomycetes	Pleosporales	Incertae sedis	Phoma	
OTU 227	199	Ascomycota	Dothideomycetes	Pleosporales	Incertae sedis		
OTU 68	200	Ascomycota	Dothideomycetes	Pleosporales	Incertae sedis	Phoma	paspali
OTU 680	201	Ascomycota	Dothideomycetes				
							Phaeosphaeriaceae sp MJ23
OTU 97	202	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	unidentified	
OTU 115	203	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Phaeosphaeria	
OTU 22	204	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	
OTU 262	205	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	citrinum
OTU 17	206	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Aspergillus	niger
							bialowiezensis
OTU 28	207	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	

OTU 21	208	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	<i>unidentified</i>	uncultured Eurotium
OTU 938	209	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	
OTU 64	210	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	spinulosum
OTU 105	211	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Emericella	nidulans
OTU 527	212	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	bialowiezens e
OTU 121	213	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	
OTU 77	214	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Aspergillus	flavus
OTU 340	215	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	
OTU 186	216	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	
OTU 131	217	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Emericella	nidulans
OTU 18	218	Zygomycota	Uncertae sedis	Mucorales	Rhizopodaceae	Rhizopus	oryzae
OTU 6	219	Ascomycota	Leotiomycetes	Helotiales	Helotiaceae		
OTU 42	220	Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Erysiphe	cruciferarum
OTU 125	221	Ascomycota	Leotiomycetes	Helotiales	Sclerotiniaceae	Botrytis	sp CID95
OTU 50	222	Basidiomycota	Microbotryomycetes	Sporidiobolales	Uncertae sedis	Sporobolomyces	oryzicola
OTU 37	223	Basidiomycota	Microbotryomycetes	Sporidiobolales	Uncertae sedis	Sporobolomyces	roseus
OTU 1406	224	Basidiomycota	Microbotryomycetes	Sporidiobolales	Uncertae sedis	Sporobolomyces	
OTU 72	225	Basidiomycota	Microbotryomycetes	Sporidiobolales	Uncertae sedis	Sporobolomyces	ruberrimus
OTU 1184	226	Basidiomycota	Microbotryomycetes	Sporidiobolales	Uncertae sedis	Sporobolomyces	roseus
OTU 70	227	Basidiomycota	Microbotryomycetes	Sporidiobolales	Uncertae sedis	<i>unidentified</i>	Sporidiobola les sp
OTU 65	228	Basidiomycota	Microbotryomycetes	Sporidiobolales	Uncertae sedis	Rhodospodium	diobovatum
OTU 103	229	Basidiomycota	Microbotryomycetes	Sporidiobolales	Uncertae sedis	Sporobolomyces	symmetricus
OTU 53	230	Ascomycota	Saccharomycetes	Saccharomycetales	Pichiaceae	Pichia	fermentans
OTU 94	231	Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycodaceae	Hanseniaspora	uvarum
OTU 86	232	Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycodaceae	Hanseniaspora	thailandica
OTU 5	233	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium	
OTU 11	234	Ascomycota	Sordariomycetes	Xylariales	Uncertae sedis	Monographella	sp 68
OTU 13	235	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium	culmorum
OTU 25	236	Ascomycota	Sordariomycetes	Sordariales			
OTU 120	237	Ascomycota	Sordariomycetes	Hypocreales	Uncertae sedis	Acremonium	sp 2 J12
OTU 1072	238	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	intricans
OTU 58	239	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	intricans
OTU 62	240	Ascomycota	Sordariomycetes	Hypocreales			
OTU 30	241	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	baccata
OTU 56	242	Ascomycota	Sordariomycetes	Hypocreales	Uncertae sedis	Acremonium	sp 4053
OTU 209	243	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium	petroliphilum
OTU 34	244	Ascomycota	Sordariomycetes	Uncertae sedis	Plectosphaerellaceae	Gibellulopsis	sp YH 2012
OTU 45	245	Ascomycota	Sordariomycetes	Xylariales	Uncertae sedis	Monographella	cucumerina
OTU 100	246	Ascomycota	Sordariomycetes	Hypocreales	<i>unidentified</i>	<i>unidentified</i>	
OTU 877	247	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium	sporotrichoides
OTU 682	248	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		
OTU 81	249	Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Phomopsis	sp MAFF 239532
OTU 238	250	Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	<i>unidentified</i>	Lasiosphaeriaceae sp
OTU 85	251	Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Chaetomium	globosum
OTU 525	252	Ascomycota	Sordariomycetes				
OTU 106	253	Ascomycota	Sordariomycetes	Uncertae sedis	Glomerellaceae	Colletotrichum	acutatum
OTU 150	254	Ascomycota	Sordariomycetes	Hypocreales	Uncertae sedis	Acremonium	dichromosporum
OTU 1278	255	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium	sporotrichoides
OTU 1403	256	Ascomycota	Sordariomycetes	Xylariales	Uncertae sedis	Monographella	sp 68
OTU 160	257	Ascomycota	Sordariomycetes	Uncertae sedis	Plectosphaerellaceae	Lectera	longa
OTU 1214	258	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	intricans
OTU 181	259	Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	Engyodontium	album
OTU 172	260	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium	poae
OTU 19	261	Basidiomycota	Tremellomycetes	<i>unidentified</i>	<i>unidentified</i>	<i>unidentified</i>	uncultured Cryptococcus
OTU 40	262	Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Cryptococcus	
OTU 74	263	Basidiomycota	Tremellomycetes	Tremellales	Uncertae sedis	Cryptococcus	victoriae

OTU 163	264	Basidiomycota	Tremellomycetes	Tremellales	unidentified	<i>unidentified</i>	Tremellales sp TG05
OTU 52	265	Basidiomycota	Tremellomycetes	Tremellales	Incertae sedis	Cryptococcus	victoriae
OTU 325	266	Basidiomycota	Tremellomycetes	Tremellales	Incertae sedis	Hannaella	
OTU 128	267	Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Cryptococcus	wieringae
OTU 180	268	Basidiomycota	Tremellomycetes	Tremellales	Incertae sedis	Cryptococcus	laurentii
OTU 46	269	Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Cryptococcus	oeirensis
OTU 174	270	Basidiomycota	Tremellomycetes	Tremellales	Incertae sedis	Cryptococcus	sp VP 2009b
OTU 69	271	Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Cryptococcus	oeirensis
OTU 80	272	Basidiomycota	Tremellomycetes	Cystofilobasidiales	Cystofilobasidiaceae	Udeniomyces	puniceus
OTU 96	273	Basidiomycota	Tremellomycetes	Cystofilobasidiales	Cystofilobasidiaceae	Udeniomyces	pyricola
OTU 51	274	Basidiomycota	Tremellomycetes	Tremellales	Incertae sedis	Bullera	Bullera unica
OTU 109	275	Basidiomycota	Tremellomycetes	Tremellales	Incertae sedis	Dioszegia	fristingensis
OTU 222	276	Basidiomycota	Tremellomycetes	Cystofilobasidiales	Cystofilobasidiaceae	Cystofilobasidium	infirmominia tum
OTU 1054	277	Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Cryptococcus	oeirensis
OTU 971	278	Basidiomycota	Tremellomycetes	<i>unidentified</i>	<i>unidentified</i>	<i>unidentified</i>	Tremellomyc etes sp
OTU 79	279	Basidiomycota	Tremellomycetes	Tremellales	Incertae sedis	Hannaella	luteola
OTU 135	280	Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Cryptococcus	albidus
OTU 166	281	Basidiomycota	Tremellomycetes	Tremellales	Incertae sedis	Cryptococcus	victoriae
OTU 111	282	Basidiomycota	Tremellomycetes	<i>unidentified</i>	<i>unidentified</i>	<i>unidentified</i>	Tremellomyc etes sp
OTU 158	283	Basidiomycota	Tremellomycetes	<i>unidentified</i>	<i>unidentified</i>	<i>unidentified</i>	Tremellomyc etes sp
OTU 91	284	Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Cryptococcus	albidus
OTU 127	285	Basidiomycota	Tremellomycetes	Tremellales	Incertae sedis	Hannaella	
OTU 1103	286	Basidiomycota	Wallemiomycetes	Wallemiales	Wallemiaceae	Wallemia	sebi
OTU 54	287	Basidiomycota	Wallemiomycetes	Wallemiales	Wallemiaceae	Wallemia	muriae
OTU 114	288	Basidiomycota	Wallemiomycetes	Wallemiales	Wallemiaceae	Wallemia	sebi
OTU 1326	289	Basidiomycota	Wallemiomycetes	Wallemiales	Wallemiaceae	Wallemia	muriae

Table 1: Exemplary core bacterial endophytes

OTU ID	SEQ ID NO	Phylum	Class	Order	Family	Genus	Species
OTU 47	39		Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	
OTU 14	43		Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	
OTU 6	44		Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	
OTU 25	59		Bacilli	Bacillales	Paenibacillaceae		
OTU 19	64		Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	amylolyticus
OTU 16	65		Bacilli	Bacillales	[Exiguobacteraceae]	Exiguobacterium	
OTU 222	67		Bacilli	Bacillales	Bacillaceae	Geobacillus	
OTU 653	68		Bacilli	Bacillales	Bacillaceae	Bacillus	endophyticus
OTU 11	69		Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	
OTU 71	70		Bacilli	Bacillales	Paenibacillaceae	Saccharibacillus	kuerlensis
OTU 13	71		Bacilli	Bacillales	Bacillaceae	Bacillus	flexus
OTU 1014	75		Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium	
OTU 168	86		Betaproteobacteria	Burkholderiales	Comamonadaceae		
OTU 7	87		Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium	
OTU 1344	88		Betaproteobacteria	Burkholderiales	Oxalobacteraceae		
OTU 1303	114		Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae		
OTU 401	115		Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae		
OTU 1261	116		Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae		
OTU 771	122		Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	
OTU 1441	125		Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae		
OTU 1158	126		Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Serratia	marcescens
OTU 8	128		Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae		
OTU 18	129		Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Xanthomonas	axonopodis
OTU 51	130		Gammaproteobacteria	Oceanospirillales	Halomonadaceae	Halomonas	

OTU 9	132		Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	
OTU 696	133		Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia	coli
OTU 53	134		Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Enterobacter	
OTU 4	135		Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Pantoea	agglomerans

Table 2: Exemplary core fungal endophytes

OTU ID	SEQ ID NO	Phylum	Class	Order	Family	Genus	Species
OTU 1	147		Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	sp MY 2011
OTU 2	148		Dothideomycetes	Capnodiales	Mycosphaerellaceae	unidentified	uncultured Cladosporium
OTU 12	149		Dothideomycetes	Capnodiales	Davidiellaceae	Davidiella	tassiana
OTU 9	150		Dothideomycetes	Pleosporales	Pleosporaceae	Lewia	infectoria
OTU 815	180		Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	sp MY 2011
OTU 775	182		Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	sp MY 2011
OTU 22	204		Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	
OTU 6	219		Leotiomycetes	Helotiales	Helotiaceae		
OTU 50	222		Microbotryomycetes	Sporidiobolales	Incertae sedis	Sporobolomyces	oryzicola
OTU 37	223		Microbotryomycetes	Sporidiobolales	Incertae sedis	Sporobolomyces	roseus
OTU 1406	224		Microbotryomycetes	Sporidiobolales	Incertae sedis	Sporobolomyces	
OTU 1184	226		Microbotryomycetes	Sporidiobolales	Incertae sedis	Sporobolomyces	roseus
OTU 5	233		Sordariomycetes	Hypocreales	Nectriaceae	Fusarium	
OTU 1072	238		Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	intricans
OTU 58	239		Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	intricans
OTU 682	248		Sordariomycetes	Hypocreales	Nectriaceae		
OTU 19	261		Tremellomycetes	unidentified	unidentified	unidentified	uncultured Cryptococcus
OTU 40	262		Tremellomycetes	Filobasidiales	Filobasidiaceae	Cryptococcus	
OTU 52	265		Tremellomycetes	Tremellales	Incertae sedis	Cryptococcus	victoriae
OTU 166	281		Tremellomycetes	Tremellales	Incertae sedis	Cryptococcus	victoriae

Example 2 – Identification and characterization of culturable bacterial and fungal endophytes belonging to core OTUs

In order to better understand the role played by core seed-derived endophytic microbes in improving the vigor, general health and stress resilience of agricultural plants, we initiated a systematic screen to isolate and characterize endophytic microbes from seeds and tissues of commercially significant agricultural plants.

Seeds from diverse types of cereals, fruits, vegetables, grasses, oilseed, and other seeds were acquired and screened for cultivatable microbes, as described below. Culturable microbes (i.e., SYM strains) belonging to the same OTUs as the core OTUs described in **Table 1** and **Table 2** were isolated and identified.

Isolation of bacteria and fungi from the interior of seeds

Isolation of fungi and bacteria (including endophytes) from the interior of surface-sterilized seeds was performed using techniques known in the art. Surface sterilized seeds were ground, diluted in liquid media, and the suspension used to inoculate solid media plates. These were incubated under different conditions at room temperature.

Experiment description

Approximately fifty surface-sterilized seeds were transferred aseptically to a sterile blender and ground. The ground seeds were resuspended in 50mL of sterile R2A broth, and incubated for 4h at room temperature. Ten 1mL aliquots of the seed homogenates were collected and centrifuged, their supernatants discarded and the pellets gently resuspended in 1mL of sterile 0.05 phosphate buffer; 0.5mL of 50% glycerol is added to each of five tubes. These were stored at -80C for further characterization. The remaining aliquots were diluted down twice in hundred-fold dilutions to 10^{-4} . 100 microliters of the 1, 10^{-2} , and 10^{-4} dilutions were used to inoculate three Petri dishes containing the following media in order to isolate of bacteria and/or fungi:

1. Tryptic Soy agar
2. R2A agar
3. Potato dextrose agar
4. Sabouraud Agar
5. Other media depending on target microorganism

The plates were divided into three sets comprising each media type and incubated in different environments. The first set was incubated aerobically, the second under anaerobic conditions, and the third under microaerophilic conditions and all were inspected daily for up to 5 days. 1-2 individual colonies per morphotype were isolated and streaked for purity onto fresh plates of the same media/environment from which the microorganism was isolated. Plates were incubated at room temperature for 2-5 days. After an isolate grew it was streaked once more onto a fresh plate of the same media to ensure purity and incubated under the same environmental conditions.

From the second streaked plate, isolates were stored in Tryptic soy broth +15% glycerol at -80°C for further characterization, by first scraping 2-3 colonies (about 10μL) from the plate into a cryogenic tube containing 1.5mL of the above-mentioned media and gently resuspending the cells. Alternatively, isolates were propagated in specialized media as recommended for the

particular taxon of microorganism. The microbes obtained represent those that live in the seeds of the plant accession.

Isolation of bacteria and fungi from plant interior tissues

Isolation of fungi and bacteria (including endophytes) from surface-sterilized plant tissues was performed using techniques known in the art. Surface sterilized plant tissues were ground, diluted in liquid media, and then this suspension was used to inoculate solid media plates. These were incubated under different environmental conditions at room temperature.

Experiment description

Approximately fifty grams of surface-sterilized plant tissue were transferred aseptically to a sterile blender and ground. The ground tissue was resuspended in 50mL of sterile R2A broth, and incubated for 4h at room temperature. Ten 1mL aliquots of the plant tissue homogenates were collected and centrifuged, their supernatants discarded and the pellets gently resuspended in 1mL of sterile 0.05 phosphate buffer. 0.5mL of 50% Glycerol was added to each of five tubes. These were stored at -80°C for possible further characterization. The remaining aliquots were diluted down twice in hundred-fold dilutions to 10^{-4} . One hundred microliters of the 1 , 10^{-2} , and 10^{-4} dilutions were used to inoculate three Petri dishes containing the following media in order to isolate of bacteria and/or fungi:

1. Tryptic Soy agar
2. R2A agar
3. Potato dextrose agar
4. Sabouraud Agar
5. Other media depending on target microorganism

Plates were divided into three sets comprising each media type and incubated in different environments. The first set was incubated aerobically, the second under anaerobic conditions, and the third under microaerophilic conditions and all were inspected daily for up to 5 days. 1-2 individual colonies per morphotype were isolated and streaked for purity onto fresh plates of the same media/environment from which the microorganism was isolated. Plates were incubated at room temperature for 2-5 days. After an isolate grew it was streaked once more onto a fresh plate of the same media to ensure purity and incubated under the same environmental conditions.

[0001] From the second streaked plate, isolates were stored in Tryptic soy broth +15% glycerol at -80°C for further characterization, by first scraping 2-3 colonies (about 10µL) from the plate into a cryogenic tube containing 1.5mL of the above-mentioned media and gently resuspending the cells. Alternatively, isolates were propagated in specialized media as recommended for the particular taxon of microorganism.

Isolation of bacteria and fungi from plant or seed surfaces

[0002] To collect phyllosphere, rhizosphere, or spermosphere material for culturing of microbes, unwashed shoot, roots or seeds were shaken free/cleaned of any attached soil and stuffed into sterile 50 mL Falcon tubes. To these, 10 mL of sterile 0.1 M sodium phosphate buffer was added and shaken, followed by 5 minutes of sonication to dislodge microbes from plant surfaces, with the resulting cloudy or muddy wash collected in a separate 15 mL Falcon tube. 100 µL of this microbe filled wash was directly spread onto agar plates or nutrient broth for culturing and enrichment, or it was further diluted with sterile 0.1 M sodium phosphate buffer by 10X, 100X, 1,000X, 10,000X and even 100,000X, before microbial culturing on agar plates or nutrient broth. Glycerol stock preparations of the plant surface wash solution were made at this point by mixing 1 mL of the soil wash solution and 0.5 mL of sterile, 80% glycerol, flash freezing the preparation in a cryotube dipped in liquid nitrogen, and storing at -80°C. Nutrient broth inoculated with a mixture of plant surface bacteria forms a stable, mixed community of microbes which was used in plant inoculation experiments described herein, subcultured in subsequent broth incubations, or spread on agar plates and separated into individual colonies which were tested via methods described herein.

Characterization of fungal and bacterial isolates

[0003] Characterization of fungi and bacteria isolated from surface-sterilized or non-sterilized plant or seed tissues was performed using techniques known in the art. These techniques take advantage of differential staining of microorganisms, morphological characteristics of cells, spores, or colonies, biochemical reactions that provide differential characterization, and DNA amplification and sequencing of diagnostic regions of genes, among other methods.

Experimental description

[0004] Isolates of bacteria and/or fungi isolated as described herein (including endophytic bacteria and fungi) were categorized into three types: bacterial isolates, fungal isolates, and unknown isolates (since yeast colonies can resemble bacterial colonies in some cases) based on colony morphology, formation of visible mycelia, and/or formation of spores. To determine if an unknown isolate was bacterial or fungal, microscopic analysis of the isolates was performed. Some of the analyses known to the art to differentiate microorganisms include, but are not limited to: the 10% KOH test, positive staining with Lactophenol cotton blue, Gram staining, and growth on media with selective agents. The distinguishing features observed by these tests are relative cell size (yeast size is much larger than bacterial size), formation of hyphae and spores (filamentous bacteria form smaller hyphae than fungi, and do not form structures containing spores), or growth under selection agents (most bacteria can grow in the presence of antifungal compounds like nystatin, while most fungi cannot; likewise, most fungi are unaffected by the presence of broad-spectrum antibiotics like chloramphenicol and spectinomycin).

[0005] To identify the isolates, DNA sequence analysis of conserved genomic regions like the ribosomal DNA loci was performed. To obtain DNA to perform PCR amplifications, some cellular growth from solid media (approximately 5-10 μ L) was resuspended in 30 μ L of sterile Tris/EDTA buffer (pH 8.0). Samples were heated to 98°C for 10 minutes followed by cooling down to 4°C for 1 minute in a thermocycler. This cycle was repeated twice. Samples were then centrifuged at ~13,000 RCF for 1-5 minutes and used as DNA template for PCR reactions. Below is a series of exemplary primer combinations used to identify isolates to a genus level.

Table 5: Exemplary primer combinations for isolate identification at a genus level

Primer 1	Primer 2	Target
V4_515F (5' – GTGCCAGCMGCCGCGGTAA-3') (SEQ ID NO:453)	V4_806R (5'-GGACTACHVGGGTWTCTAAT-3') (SEQ ID NO:454)	The 4 th Variable region of the bacterial 16S rDNA
27F (5'-AGAGTTTGATCCTGGCTCAG-3') (SEQ ID NO:455)	1492R (5'-GGTTACCTTGTTACGACTT-3') (SEQ ID NO:456)	Full length of the bacterial 16S rDNA, from position 8-1507.
ITS1 (5'-TCCGTAGGTGAACCTGCGG-3') (SEQ ID NO:457)	ITS2 (5' -GCTGCGTTCTTCATCGATGC- 3') (SEQ ID NO:458)	~240 bp ITS1 region of fungal genome
SR1R (5' – TACCTGGTTGATQCTGCCAGT -3') (SEQ ID NO:459)	SR6 (5' –TGTTACGACTTTTACTT-3') (SEQ ID NO:460)	Small subunit (18s) of the fungal rDNA gene
ITS1F (5'-	ITS4 (5'-	~600-1000 bp ITS region of

CTTGGTCATTTAGAGGAAGTA A-3') (SEQ ID NO:461)	TCCTCCGCTTATTGATATGC-3') (SEQ ID NO:462)	fungus genomes
ITS5 (Universal) (5'- GGAAGTAAAAGTCGTAACAA GG-3') (SEQ ID NO:463)	• ITS4Asco (Ascomycota-specific): 5' CGTTACTRRGGCAATCCCTGTTG3' (SEQ ID NO:464) or • ITS4Basidio (Basidiomycota-specific): 5' GCRCGGAARACGCTTCTC3' (SEQ ID NO:465); or • ITS4Chytrid (Chytridiomycota-specific): 5' TTTTCCCGTTTCATTGCGCA 3' (SEQ ID NO:466); or • ITS4Oo (Oomycota-specific): 5' ATAGACTACAATTCGCC 3' (SEQ ID NO:467); or • ITS4Zygo (Zygomycota-specific): 5' AAAACGTWTCTTCAAA 3' (SEQ ID NO:468).	~500 bp fragment from different fungal Phyla
SSUmAf - (equimolar mix of 2 degenerate primers) and SSUmCf (equimolar mix of 3 degenerate primers)	LSUmAr (equimolar mix of 4 degenerate primers) and LSUmBr (equimolar mix of 5 degenerate primers)	1000-1600 bp fragment of the Glomerycota (arbuscular mycorrhizae) genome comprising partial SSU, whole internal transcribed spacer (ITS) rDNA region and partial LSU.
Arch 340F (5'- CCCTAYGGGGYGCASCAG-3') (SEQ ID NO:469)	Arch 1000R (5'- GAGARGWRGTGCATGGCC-3') (SEQ ID NO:470)	~660 bp product of the 18S from Archaea
27F-Degen (5'- AGRRTTYGATYMTGGYTYAG- 3') (SEQ ID NO:471) and 799f (5'- AACMGGATTAGATACCKG- 3') (SEQ ID NO:473)	27F-Degen (5'- HGGHTACCTTGTTACGACTT-3') (SEQ ID NO:472)	Full length of the bacterial 16S rDNA, from position 8-1507.

[0006] To decrease background noise due to the non-specific binding of primers to DNA, the thermocycler was programmed for a touchdown-PCR, which increased specificity of the reaction at higher temperatures and increased the efficiency towards the end by lowering the annealing temperature. Exemplary conditions for performing Touchdown PCR are shown in Table 6.

Table 6: Exemplary conditions for performing Touchdown PCR

Step #	Cycle	Temperature	Time
1	Initial Denaturalization	98°C*	5m
2	Denaturalization	98°C*	30s
3	Annealing	Predicted optimal T _m for the primer set +10°C, minus 1°C/cycle	30s

4	Elongation	72°C*	1m/1Kb
5	GoTo Step 2 x 10 times		
6	Denaturalization	98°C*	30s
7	Annealing	Predicted optimal T _m for the primer set	30s
8	Elongation	72°C*	1m/1Kb
9	GoTo Step 6 x 20 times		
10	Final Elongation	72°C*	5m
11	Cool Down	4°C	5m

* Or the temperature specified by the DNA polymerase manufacturer for this step.

[0007] PCR reactions were purified to remove primers, dNTPs, and other components by methods known in the art, for example by the use of commercially available PCR clean-up kits.

[0008] The resulting sequences were aligned as query sequences with the publicly available databases GenBank nucleotide, RDP, UNITE and PlutoF. RDP was specifically compiled and used for bacterial 16s classification. UNITE and PlutoF were specifically compiled and used for identification of fungi. In all the cases, the strains were identified to species level if their sequences were more than 95% similar to any identified accession from all databases analyzed. When the similarity percentage was between 90–97%, the strain was classified at genus, family, order, class, subdivision or phylum level depending on the information displayed in databases used. Isolates with lower similarity values (from 30–90%) were classified as “*unknown*” or “*uncultured*” depending on the information displayed after BLAST analysis. To compliment the molecular identification, fungal taxa were confirmed by inducing sporulation on PDA or V8 agar plates and using reported morphological criteria for identification of fruiting bodies structure and shape. Bacterial taxa were confirmed by using reported morphological criteria in specialized differential media for the particular taxon, or by biochemical differentiation tests, as described by the Bergey’s Manual of Systematic Microbiology (Whitman, William B., et al., eds. Bergey’s manual® of systematic bacteriology. Vols. 1-5. Springer, 2012).

Culture-independent characterization of fungal and bacterial communities in seeds or plants

[0009] To understand the diversity of culturable and unculturable microbial (e.g., bacterial and fungal) taxa that reside inside of seeds or plants of agriculturally-relevant cultivars, landraces, and ancestral wild varieties, microbial DNA was extracted from surface sterilized seed or plant parts, as described herein, followed by amplification of conserved genomic regions, for example the ribosomal DNA loci. Amplified DNA represented a “snapshot” of the full microbial community inside seeds or plants.

Experimental Description

[0010] To obtain microbial DNA from seeds, plants or plant parts, the seeds, plants or plant parts were surface sterilized under aseptic conditions as described herein. Microbial DNA from seeds, plants, or plant parts was extracted using methods known in the art, for example using commercially available Seed-DNA or plant DNA extraction kits, or the following method.

1. A sample of each kind of seed or plant tissue is placed in a cold-resistant container and 10-50mL of liquid nitrogen is applied. The seeds or plant tissues are then macerated to a powder.
2. Genomic DNA is extracted from each seed or plant tissue preparation, following a chloroform:isoamyl alcohol 24:1 protocol (Sambrook et al. 1989).

[0011] Fungal-specific primers were used to amplify the ITS (Internal Transcribed Spacer) region of nuclear ribosomal DNA. Bacterial specific primers were used to amplify region of the 16s rDNA gene of the bacterial genome. Sequences obtained through NGS platforms were analyzed against databases, such as the ones mentioned herein.

[0012] Exemplary primer pairs used for this analysis are listed in **Table 5**.

[0013] As an alternative to next generation sequencing, Terminal Restriction Fragment Length Polymorphism, (TRFLP) can be performed. Group specific, fluorescently labeled primers are used to amplify diagnostic regions of genes in the microbial population. This fluorescently labeled PCR product is cut by a restriction enzyme chosen for heterogeneous distribution in the PCR product population. The enzyme cut mixture of fluorescently labeled and unlabeled DNA fragments is then submitted for sequence analysis on a Sanger sequence platform such as the Applied Biosystems 3730 DNA Analyzer.

Determination of the plant pathogenic potential of microbial isolates

[0014] Since a microbe that confers positive traits to one cultivar might be a pathogenic agent in a different plant species, a general assay was used to determine the pathogenic potential of microbial isolates. Surface and interior-sterilized seeds are germinated in water agar, and once the plant develops its first set of leaves, are inoculated with the isolate. Alternatively, the plants are inoculated as seeds. For inoculation the microbial isolate is grown on solid media, and inoculated into a plant or onto a seed via any of the methods described herein. Plants are

allowed to grow under ideal conditions for 2-3 weeks and any pathogenic effect of the introduced microbe is evaluated against uninoculated control plants.

Identification of culturable microbial isolates that correspond to core OTUs

[0015] To accurately characterize the isolated microbial endophytes, colonies were submitted for marker gene sequencing, and the sequences were analyzed to provide taxonomic classifications. Among the cultured microbes (SYM strains), those with at least 97% 16S or ITS sequence similarity to OTUs of **Table 1** and **Table 2** were identified. Exemplary isolated microbes that correspond to core OTUs are listed in **Table 7** (bacteria) and **Table 8** (fungi).

Table 7: Exemplary bacterial endophytes

SEQ ID NO	SYM	Taxonomic Classification
290	SYM00003	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; <i>Ralstonia pickettii</i>
291	SYM00009	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; <i>Ralstonia pickettii</i>
292	SYM00013	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; <i>Pseudomonas oryzae</i>
293	SYM00017A	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; <i>Agrobacterium larrymoorei</i>
294	SYM00018	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; <i>Pantoea dispersa</i>
295	SYM00020	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; <i>Pantoea dispersa</i>
296	SYM00021b	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; <i>Escherichia hermannii</i>
297	SYM00025	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; <i>Pantoea dispersa</i>
298	SYM00033	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; <i>Enterobacter ludwigii</i>
300	SYM00043	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; <i>Pantoea dispersa</i>
301	SYM00044	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; <i>Enterobacter hormaechei</i>
302	SYM00050	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; <i>Enterobacter cloacae</i>
303	SYM00053	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; <i>Escherichia hermannii</i>
305	SYM00062c	Bacteria; Firmicutes; Bacilli; Bacillales; Paenibacillaceae; <i>Saccharibacillus kuerlensis</i>

306	SYM00065	Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas sanguinis
308	SYM00068	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas psychrotolerans
309	SYM00070	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Pantoea agglomerans
310	SYM00074	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Enterobacter cloacae
311	SYM00103	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; Ralstonia pickettii
321	SYM00170	Bacteria; Firmicutes; Bacilli; Bacillales; Paenibacillaceae; Paenibacillus hunanensis
322	SYM00183	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas maltophilia
323	SYM00184	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas maltophilia
324	SYM00207	Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus pumilus
325	SYM00212	Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus sp.
326	SYM00219	Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus sp.
327	SYM00234	Bacteria; Firmicutes; Bacilli; Bacillales; Paenibacillaceae; Paenibacillus sp.
328	SYM00236	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium sp.
329	SYM00248	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Pantoea sp.
330	SYM00249	Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus sp.
331	SYM00506c	Bacteria; Firmicutes; Bacilli; Bacillales; Paenibacillaceae; Paenibacillus sp.
332	SYM00507	Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus sp.
333	SYM00508	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Enterobacter asburiae
334	SYM00525	Bacteria; Actinobacteria; incertae sedis; Actinomycetales; Microbacteriaceae; Curtobacterium sp.
335	SYM00538A	Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas aquatilis
336	SYM00538B	Bacteria; Firmicutes; Bacilli; Bacillales; Paenibacillaceae; Paenibacillus sp.
337	SYM00538i	Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales; [Weeksellaceae]; Chryseobacterium sp.
338	SYM00543	Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus sp.
339	SYM00545	Bacteria; Firmicutes; Bacilli; Bacillales; Paenibacillaceae; Paenibacillus sp.
340	SYM00549	Bacteria; Firmicutes; Bacilli; Bacillales; Paenibacillaceae; Paenibacillus sp.

341	SYM00563	Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus sp.
343	SYM00574	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia gladioli
347	SYM00617	Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus sp.
348	SYM00620	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Enterobacter sp.
350	SYM00627	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Enterobacter sp.
351	SYM00628	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Enterobacter sp.
353	SYM00646	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas sp.
354	SYM00650	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas sp.
355	SYM00662	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas putida
358	SYM00714	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium sp.
365	SYM00905	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas sp.
366	SYM00924	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium sp.
367	SYM00963	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia coli
368	SYM00982	Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales; [Weeksellaceae]; Chryseobacterium sp.
369	SYM00987	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia coli
370	SYM00978	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium aquaticum
371	SYM00991	Bacteria; Proteobacteria; Beta Proteobacteria; Burkholderiales; Comamonadaceae; Acidovorax avenae
372	SYM00999	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium sp.
373	SYM01049	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Enterobacter sp.
426	SYM00057B	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia caledonica
427	SYM00091	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium sp.
428	SYM00092D	Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales; Caulobacteraceae; Brevundimonas sp.
430	SYM00290	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Acinetobacter lwoffii
433	SYM00576	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Pantoea dispersa

434	SYM00607	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Pantoea stewartii
435	SYM00619	Bacteria; Firmicutes; Bacilli; Bacillales; [Exiguobacteraceae]; Exiguobacterium acetylicum
436	SYM00786	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Pantoea dispersa
437	SYM00879	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium populi
438	SYM00879B	Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas aquatilis
439	SYM00906	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas rhizophila
440	SYM00965	Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Erythrobacteraceae; Luteibacter yejuensis
441	SYM01004	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium larrymoorei
442	SYM01022	Bacteria; Actinobacteria; incertae sedis; Actinomycetales; Microbacteriaceae; Curtobacterium flaccumfaciens;
451	SYM00865	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas rhizophila
452	SYM01158	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Pantoea agglomerans

Table 8: Exemplary fungal endophytes

SEQ ID NO	SYM	Taxonomic Classification
299	SYM00034	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Incertae sedis; Acremonium zeae
304	SYM00061A	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Incertae sedis; Acremonium zeae
307	SYM00066	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Incertae sedis; Acremonium zeae
312	SYM00120	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae; Alternaria alternata
313	SYM00122	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae; Epicoccum nigrum
314	SYM00123	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae; Epicoccum nigrum
315	SYM00124	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; Fusarium graminearum
316	SYM00129	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; Fusarium proliferatum
317	SYM00135	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae;

		<i>Fusarium proliferatum</i>
318	SYM00136	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; <i>Fusarium proliferatum</i>
319	SYM00151	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; <i>Fusarium proliferatum</i>
320	SYM00154	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; <i>Fusarium</i> sp.
342	SYM00566B	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Incertae sedis; <i>Acremonium zeae</i>
344	SYM00577	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Incertae sedis; <i>Acremonium zeae</i>
345	SYM00590	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Incertae sedis; <i>Acremonium zeae</i>
346	SYM00603	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Incertae sedis; <i>Acremonium zeae</i>
349	SYM00622	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Incertae sedis; <i>Acremonium strictum</i>
352	SYM00629	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Incertae sedis; <i>Acremonium strictum</i>
356	SYM00663	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae; <i>Alternaria alternata</i>
357	SYM00696	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae; <i>Alternaria tenuissima</i>
359	SYM00741a	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Incertae sedis; <i>Phoma herbarum</i>
360	SYM00741b	Fungi; Ascomycota; Dothideomycetes; Capnodiales; Davidiellaceae; <i>Cladosporium tenuissimum</i>
361	SYM00793	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; <i>Fusarium verticillioides</i>
362	SYM00795	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Incertae sedis; <i>Acremonium zeae</i>
363	SYM00854	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae; <i>Epicoccum sorghinum</i>
364	SYM00880	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae; <i>Alternaria tenuissima</i>
374	SYM01300	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Incertae sedis; <i>Acremonium zeae</i>
375	SYM01303	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; <i>Fusarium</i> sp.
376	SYM01310	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; <i>Fusarium proliferatum</i>
377	SYM01311	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; <i>Fusarium</i> sp.
378	SYM01314	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Incertae sedis; <i>Acremonium zeae</i>
379	SYM01315	Fungi; Ascomycota; Dothideomycetes; Capnodiales; Davidiellaceae;

		Cladosporium sp.
380	SYM01325	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae; Alternaria sp.
381	SYM01326	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae; Alternaria alternata
382	SYM01327	Fungi; Ascomycota; Dothideomycetes; Capnodiales; Davidiellaceae; Cladosporium sp.
383	SYM01328	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae; Alternaria sp.
384	SYM01333	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae; Alternaria infectoria
385	SYM15811	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae; Alternaria sp.
386	SYM15820	Fungi; Ascomycota; Sordariomycetes; Trichosphaeriales; incertae sedis; Nigrospora oryzae
387	SYM15821	Fungi; Ascomycota; Sordariomycetes; Trichosphaeriales; incertae sedis; Nigrospora oryzae
388	SYM15825	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; Fusarium sp.
389	SYM15828	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; Fusarium sp.
390	SYM15831	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; Fusarium sp.
391	SYM15837	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; Fusarium sp.
392	SYM15839	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; Fusarium sp.
393	SYM15847	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; Fusarium udum
394	SYM15870	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; Fusarium sp.
395	SYM15872	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; Fusarium sp.
396	SYM15890	Fungi; Ascomycota; Dothideomycetes; Capnodiales; Davidiellaceae; Cladosporium sp.
397	SYM15901	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; Fusarium sp.
398	SYM15920	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; Fusarium equiseti
399	SYM15926	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae; Alternaria sp.
400	SYM15928	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae; Alternaria sp.
401	SYM15932	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; Fusarium sp.
402	SYM15939	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae;

		Fusarium sp.
429	SYM00157	Fungi; Ascomycota; Dothideomycetes; incertae sedis; incertae sedis; Leptosphaerulina chartarum
431	SYM00299	Fungi; Ascomycota; Dothideomycetes; Capnodiales; Davidiellaceae; Cladosporium tenuissimum
432	SYM00301	Fungi; Ascomycota; Eurotiomycetes; Eurotiales; Trichocomaceae; Penicillium chrysogenum
443	SYM01324	Fungi; Ascomycota; Eurotiomycetes; Eurotiales; Trichocomaceae; Aspergillus pseudoglaucus
444	SYM01329	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Didymellaceae; Peyronellaea glomerata
445	SYM01330	Fungi; Zygomycota; incertae sedis; Mucorales; Rhizopodaceae; Rhizopus oryzae
446	SYM12462	Fungi; Ascomycota; Dothideomycetes; Capnodiales; Davidiellaceae; Cladosporium sphaerospermum
447	SYM15774	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Incertae sedis; Phoma medicaginis
448	SYM15783	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae; Alternaria macrospora
449	SYM00300	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Incertae sedis; Acremonium strictum
450	SYM01331	Fungi; Ascomycota; Dothideomycetes; Pleosporales; Incertae sedis; Phoma pedaeiae
453	SYM15810	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; Fusarium sp.
454	SYM15879	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; Fusarium torulosum
455	SYM15880	Fungi; Ascomycota; Eurotiomycetes; Eurotiales; Trichocomaceae; Penicillium chrysogenum
299	SYM00034	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Incertae sedis; Acremonium zeae

Example 2: Synthetic Compositions Comprising Plant seeds and a Single Endophyte Strain or a Plurality of Endophytes confer Benefits to Agricultural Plants

[0016] This example describes the ability of synthetic compositions comprising plant seeds and a single endophyte strain or a plurality of endophyte strains described herein, to confer one or more benefits to a host plant. Among other things, this Example describe the ability of endophytes (e.g., bacterial and fungal endophytes described herein) to confer beneficial traits on a variety of host plants, including but not limited to, dicots (e.g., soy, peanut) and monocots (e.g., corn, soy, wheat, cotton, sorghum), and combinations thereof. Endophyte-inoculated seeds (e.g., seeds described herein) were tested under water-limited conditions (e.g., drought stress) in seed

germination assays and seedling root vigor assays to test whether one or more endophytes confer an increase in tolerance to these stresses. These growth tests were performed using growth assays (e.g., germination assays and seedling root vigor assays) on sterile filter papers. Seeds were treated either with a single bacterial or fungal strain, or with a combination of two bacterial or two fungal strains. In some embodiments, seeds were treated with a combination of at least one bacterial and at least one fungal strain.

Experimental Description

Growth & scale-up of bacteria for inoculation

[0017] Each bacterial endophyte was streaked out onto 20% Tryptic Soy Agar, forming a lawn on regular Petri dishes (9 cm in diameter). Once the bacteria grew to high density, which happened after one or two days depending on the bacterial growth rate, a plate per bacterial strain was scraped with the aid of a sterile loop (filling the entire hole of the loop and producing a droplet of bacterial biomass of about 20 mg). The bacteria collected in this way were transferred into 1 ml of sterile 50mM Phosphate Buffer Saline (PBS) in a microcentrifuge tube and fully resuspended by vortexing for ~20 sec at maximum speed. This method achieves highly concentrated (~0.5-1 optical density, corresponding to about 10^8 CFU/mL) and viable bacteria pre-adapted to live coating a surface.

Growth & scale-up of fungi for inoculation

[0018] Fungal isolates were grown from a frozen stock on Petri dishes containing potato dextrose agar and the plates were incubated at room temperature for about a week. After mycelia and spore development, four agar plugs (1 cm in diameter) were used to inoculate erlenmeyers containing 150 ml of potato dextrose broth. Liquid cultures were grown at room temperature and agitation on an orbital shaker at 115 rpm for 4 days. Then, the cultures were transferred to 50 ml sterile test tubes with conical bottoms. Mycelium mats were disrupted by pulse sonication at 75% setting and 3 pulses of 20 seconds each, using a Fisher Scientific sonicator (Model FB120) with a manual probe (CL-18). The sonicated cultures were used in the same manner as the bacterial suspensions for seed inoculation.

Surface sterilization of seeds

[0019] Un-treated seeds (e.g., soy seeds or wheat seeds) were sterilized overnight with chlorine gas as follows: 200g of seeds were weighed and placed in a 250mL glass bottle. The opened bottle and its cap were placed in a dessicator jar in a fume hood. A beaker containing 100mL of commercial bleach (8.25% sodium hypochlorite) was placed in the dessicator jar. Immediately prior to sealing the jar, 3mL of concentrated hydrochloric acid (34-37.5%) were carefully added to the bleach. The sterilization was left to proceed for 17-24h. After sterilization, the bottle was closed with its sterilized cap, and reopened in a sterile flow hood. The opened bottle was left in the sterile hood for a couple hours to air out the seeds and remove chlorine gas leftover. The bottle was then closed and the seeds stored at room temperature in the dark until use.

Preparation of synthetic compositions comprising plant seeds and endophytes

[0020] The following procedure was used to coat seeds with a plurality of fungal endophyte inocula for planting in greenhouse and field trials. First, 3% Sodium alginate (SA) was prepared and autoclaved in the following manner. Erlenmeyer flasks were filled with the appropriate amount of deionized water and warmed to about 50 degrees C on a heat plate with agitation using a stirring bar. SA powder was poured slowly into the water until it all dissolved. The solution was autoclaved (121°C @15PSI for 30 minutes). Talcum powder was autoclaved in dry cycle (121°C @15PSI for 30 minutes) and aliquoted in Ziploc bags or 50 ml falcon tubes at a ratio of 15g per kg of seed to be treated for formulation controls and 10g per kg of seed for actual treatments.

[0021] The next day, seeds were treated with either powdered or liquid formulations.

[0022] For powdered formulations, 10 g per kg of seed was allocated to the seeds to be treated, according to the following procedure. Seeds were placed in large plastic container. 16.6 ml of 2% SA per Kg of seeds to be treated were poured on the seeds. The container was covered and shaken slowly in orbital motion for about 20 seconds to disperse the SA. Endophyte powder was mixed with an equal amount of talcum powder. The mix of endophytes and talc was added on top of the seeds, trying to disperse it evenly. The container was covered and seeds are shaken slowly in orbital motion for about 20 seconds. 13.3 ml of Flo-rite per kg of seed to be treated was poured on the seeds. Seeds were shaken again, slowly and in orbital motion.

[0023] For liquid formulations, 8.5 mL per seed was allocated to the seeds to be treated, according to the following procedure. Seeds were placed in large plastic container. 8.3 ml of 2%

SA per kg of seed and the same amount of bacterial culture (8.3 ml per kg of seed) was poured on the seeds. The container was covered and shaken slowly in orbital motion for about 20 seconds to disperse the SA. 15 g of talcum powder per kg of seed was added, trying to disperse it evenly. The container was covered and seeds were shaken slowly in orbital motion for about 20 seconds. 13.3 ml of Flo-rite per kg of seed to be treated are poured on the seeds. Seeds were shaken again, slowly and in orbital motion. For soy seeds, 10 μ L of sodium alginate and inoculum were applied for every one gram of seeds. For wheat seeds, the amount of SA and bacterial suspension or fungal inoculum was adjusted to 15 ml/kg to account for the larger surface to volume ratio of these small seeds.

Testing for germination enhancement under drought stress

[0024] Polyethylene glycol (PEG) is an inert, water-binding polymer with a non-ionic and virtually impermeable long chain that accurately mimics drought stress under dry-soil conditions. The higher the concentration of PEG, the lower the water potential achieved, thus inducing higher water stress in a watery medium. To determine germination enhancement in seeds, the interiors of which are colonized by microbial strains, the effect of osmotic potential on germination is tested at a range of water potential representative of drought conditions following Perez-Fernandez et al. [J. Environ. Biol. 27: 669-685 (2006)]. The range of water potentials simulates those that are known to cause drought stress in a range of cultivars and wild plants, (-0.05 MPa to -5 MPa). The appropriate concentration of polyethylene glycol (6000) required to achieve a particular water potential was determined following Michel and Kaufmann (Plant Physiol., 51: 914-916 (1973)) and further modifications by Hardegree and Emmerich (Plant Physiol., 92, 462-466 (1990)). The final equation used to determine amounts of PEG is: $\Psi = 0.130 [\text{PEG}]^2 T - 13.7 [\text{PEG}]^2$; where the osmotic potential (Ψ) is a function of temperature (T).

Soy seedling germination assay in drought conditions

[0025] For each SYM tested in the germination assay, ten (10) SYM-coated soy seeds were placed on a 150mm Petri plate that contained a single heavy germination paper (SD5-1/4 76# heavy weight seed germination paper, Anchor Paper Co., St. Paul, MN). To each petri plate, 10 mL 8% polyethylene glycol (PEG 6000) was added for germination screening assays in drought conditions. Plates were covered and incubated at in the dark at 22° Celcius and 60% relative humidity for four days for bacterial SYM strains) or five days for fungal SYM strains. All

experiments were done in triplicate under sterile conditions. Seedlings were scored based on germination percentage relative to formulation only and non-treated seedling controls at the end of the incubation period. Exemplary soy germination results under drought conditions are shown in Table A.

Table A: Soy germination assay results

Crop	SYM1	SYM2	Ave (%toNT)	Type
soy	SYM00057B		155.83	bacteria
soy	SYM00074		283.33	bacteria
soy	SYM00091	SYM00092D	120.00	bacterial plurality
soy	SYM00092D		175.83	bacteria
soy	SYM00590		141.18	bacteria
soy	SYM00603		135.29	bacteria
soy	SYM00607	SYM00091	115.00	bacterial plurality
soy	SYM00607	SYM00092D	135.00	bacterial plurality
soy	SYM00619		212.50	bacteria
soy	SYM00092D	SYM15879	140.00	Bacterium-Fungus plurality
soy	SYM00092D	SYM15880	115.00	Bacterium-Fungus plurality
soy	SYM00092D	SYM15934	115.00	Bacterium-Fungus plurality
soy	SYM00299		115.51	fungi
soy	SYM00301		123.02	fungi
soy	SYM00577		141.18	fungi
soy	SYM01310		135.29	fungi
soy	SYM01311		135.29	fungi
soy	SYM01314		135.29	fungi
soy	SYM01330		325.00	fungi
soy	SYM15774		115.98	fungi
soy	SYM15783		141.18	fungi
soy	SYM15879	SYM15934	110.00	fungal plurality
soy	SYM15880	SYM15884	158.82	fungal plurality

Soy seedling root vigor assay in drought conditions

[0026] For each SYM tested in the root vigor assay, ten (10) soy seeds were placed equidistant to each other on moistened heavy weight germination paper sandwiches. Each layer of the germination paper was pre-soaked in 25 mL of sterile distilled water. The germination paper sandwich was rolled, taped using surgical tape, placed in glass bottles and incubated at 22° Celcius with 60% relative humidity in dark for four (4) days to allow seed germination. On day five (5), bottle lids were removed and seed samples were placed in a growth chamber set to 25°

Celcius, 70% RH, 250-300 microEinstein light for 12 hours and 18° Celcius, 60% RH dark 12 hours for five (5) days. Placement of bottles were randomized daily to reduce any positional effect throughout the incubation period. At the end of the experiment, each soy seedling was measured for total root length and compared relative to formulation only and non-treated seedling controls. Exemplary soy root vigor results under drought conditions are shown in Table B.

Table B: Soy root vigor assay results

Crop	SYM1	SYM2	Ave(%toNT)	SE(%toNT)	Type
soy	SYM00057B		98.0	11.9	bacteria
soy	SYM00074		99.0	10.8	bacteria
soy	SYM00091	SYM00092 D	96.7	5.9	bacterial plurality
soy	SYM00092 D		87.9	12.9	bacteria
soy	SYM00590		100.6	11.8	bacteria
soy	SYM00603		118.2	9.3	bacteria
soy	SYM00607	SYM00091	82.3	5.1	bacterial plurality
soy	SYM00607	SYM00092 D	92.1	8.1	bacterial plurality
soy	SYM00619		99.0	12.4	bacteria
soy	SYM00092 D	SYM15879	72.6	8.7	Bacterium - Fungus plurality
soy	SYM00092 D	SYM15880	111.2	2.2	Bacterium - Fungus plurality
soy	SYM00092 D	SYM15934	82.8	9.7	Bacterium - fungus plurality
soy	SYM00299		92.5	10.0	fungi
soy	SYM00301		111.3	8.5	fungi
soy	SYM00577		132.4	3.3	fungi
soy	SYM01310		91.2	15.7	fungi
soy	SYM01311		97.6	12.3	fungi
soy	SYM01314		107.1	12.3	fungi
soy	SYM01330		97.6	16.0	fungi
soy	SYM15774		153.7	7.6	fungi
soy	SYM15783		137.1	7.6	fungi
soy	SYM15879	SYM15934	95.0	12.3	fungal plurality
soy	SYM15880	SYM15884	104.7	12.3	fungal plurality

Wheat seedling germination assay in drought conditions

[0027] For each SYM tested, 25 uL of sonicated, 7-day old fungal culture or 3-day old bacteria culture was added into 15 mL of semi-solid solution [12.5% polyethylene glycol (PEG 6000) and 0.3% of agar] pre-aliquoted in a 90 mm deep well petri dish. After adding the SYM biomass, the petri dishes were horizontally shaken for even distribution of SYM biomass. Fifteen (15) surface-steriled wheat seeds were placed onto each petri dish. Plates were covered and incubated in the dark at 24° Celcius and 60% relative humidity for three days in a Conviron chamber. All experiments were done in triplicate under sterile conditions. Seedlings were scored by counting the number of germinated seedlings per dish and the performance of each SYM normalized as germination percentage relative to formulation only and non-treated seedling controls at the end of the incubation period. Exemplary wheat germination results under drought conditions are shown in Table C.

Table C: Wheat germination assay results

Crop	SYM1	SYM2	Ave(%toNT)	SE(%toNT)	Type
wheat	SYM00044		126.9	5.5	bacteria
wheat	SYM00044	SYM00021B	150.0	0.0	bacterial plurality
wheat	SYM00044	SYM00074	136.4	7.9	bacterial plurality
wheat	SYM00044	SYM00879	145.5	18.2	bacterial plurality
wheat	SYM00044	SYM00879B	136.4	7.9	bacterial plurality
wheat	SYM00057B		107.4	11.5	bacteria
wheat	SYM00057B	SYM00906	154.5	16.4	bacterial plurality
wheat	SYM00057B	SYM01004	136.4	20.8	bacterial plurality
wheat	SYM00074		109.4	11.0	bacteria
wheat	SYM00074	SYM00092D	131.8	9.1	bacterial plurality
wheat	SYM00074	SYM00290	131.8	12.0	bacterial plurality
wheat	SYM00074	SYM00879	131.8	12.0	bacterial plurality
wheat	SYM00074	SYM01004	136.4	7.9	bacterial plurality
wheat	SYM00074	SYM01022	154.5	16.4	bacterial plurality
wheat	SYM00092D		118.6	7.4	bacteria

wheat	SYM00092D	SYM00021B	136.4	13.6	bacterial plurality
wheat	SYM00092D	SYM00865	135.0	8.7	bacterial plurality
wheat	SYM00092D	SYM00965	150.0	17.3	bacterial plurality
wheat	SYM00212		157.9	0.0	bacteria
wheat	SYM00290		119.6	6.8	bacteria
wheat	SYM00290	SYM00906	131.8	27.6	bacterial plurality
wheat	SYM00290	SYM01022	145.5	24.1	bacterial plurality
wheat	SYM00696		108.3	10.1	bacteria
wheat	SYM00786	SYM00865	140.0	18.0	bacterial plurality
wheat	SYM00879		111.4	7.2	bacteria
wheat	SYM00879	SYM01004	172.7	4.5	bacterial plurality
wheat	SYM00879B		105.2	17.3	bacteria
wheat	SYM00906		125.0	7.2	bacteria
wheat	SYM00906	SYM01004	136.4	7.9	bacterial plurality
wheat	SYM00965	SYM00865	150.0	17.3	bacterial plurality
wheat	SYM01004		115.2	12.5	bacteria
wheat	SYM01004	SYM01022	140.9	16.4	bacterial plurality
wheat	SYM01022		115.5	9.3	bacteria
wheat	SYM01158		142.1	24.1	bacteria
wheat	SYM01326		103.8	8.5	bacteria
wheat	SYM00157		115.6	10.1	fungi
wheat	SYM00157	SYM15783	141.7	11.0	fungus plurality
wheat	SYM00299		121.4	10.6	fungi
wheat	SYM00299	SYM00696	145.8	11.0	fungus plurality
wheat	SYM00299	SYM01324	133.3	25.3	fungus plurality
wheat	SYM00299	SYM15783	137.5	0.0	fungus plurality
wheat	SYM00301		112.7	10.1	fungi
wheat	SYM00301	SYM01326	133.3	15.0	fungus plurality
wheat	SYM00301	SYM15774	145.8	11.0	fungus plurality
wheat	SYM01324		114.2	8.8	fungi
wheat	SYM01326	SYM12462	129.2	11.0	fungus plurality
wheat	SYM12462	SYM15774	133.3	18.2	fungus plurality
wheat	SYM12462	SYM15783	141.7	16.7	fungus plurality
wheat	SYM15774		122.4	9.5	fungi
wheat	SYM15774	SYM01324	137.5	12.5	fungus plurality

wheat	SYM15783		120.0	5.4	fungi
wheat	SYM15783	SYM01324	129.2	8.3	fungal plurality
wheat	SYM15879		99.4	8.5	fungi
wheat	SYM15880	SYM15888	159.1	12.0	fungal plurality

Wheat seedling root vigor assay in drought conditions

[0028] For each SYM tested, twelve (12) SYM-coated wheat seeds were placed onto a 125 mm filter paper pre-wet with 5 mL of 12.5% polyethylene glycol (PEG 6000). The seeds were arranged in a circular formation and with embryo facing toward the center of the filter paper. Plates were covered and incubated in the dark at 24° Celcius and 60% relative humidity for three days in a Conviron chamber. All experiments were done in triplicate under sterile conditions. At the end of the incubation period, images were taken for each plate and root length were measured (in pixel) on the images using ImageJ and the pixel was finally converted into cm based on an internal standard. The performance of each SYM was normalized as root length percentage relative to formulation only and non-treated seedling controls. Exemplary wheat root vigor results under drought conditions are shown in **Table D**.

Table D: Wheat root vigor assay results

Crop	SYM1	SYM2	Ave(%toNT)	SE(%toNT)	Type
wheat	SYM00021B		104.0	4.4	bacteria
wheat	SYM00044		101.4	4.0	bacteria
wheat	SYM00044	SYM00021B	111.7	3.7	bacterial plurality
wheat	SYM00044	SYM00074	101.9	5.1	bacterial plurality
wheat	SYM00044	SYM00879	105.4	4.6	bacterial plurality
wheat	SYM00044	SYM00879B	107.6	5.0	bacterial plurality
wheat	SYM00057B		102.8	4.6	bacteria
wheat	SYM00057B	SYM00906	118.7	5.4	bacterial plurality
wheat	SYM00057B	SYM01004	104.1	4.8	bacterial plurality
wheat	SYM00074		111.2	5.6	bacteria
wheat	SYM00074	SYM00092D	99.5	4.4	bacterial plurality
wheat	SYM00074	SYM00290	103.5	4.3	bacterial plurality

wheat	SYM00074	SYM00879	107.8	4.6	bacterial plurality
wheat	SYM00074	SYM01004	110.8	4.7	bacterial plurality
wheat	SYM00074	SYM01022	102.9	4.7	bacterial plurality
wheat	SYM00092D		112.1	3.8	bacteria
wheat	SYM00092D	SYM00021B	103.5	5.8	bacterial plurality
wheat	SYM00092D	SYM00865	105.2	5.5	bacterial plurality
wheat	SYM00092D	SYM00965	119.2	4.5	bacterial plurality
wheat	SYM00212		117.7	5.6	bacteria
wheat	SYM00290		103.2	6.3	bacteria
wheat	SYM00290	SYM00906	103.1	5.5	bacterial plurality
wheat	SYM00290	SYM01022	112.7	4.0	bacterial plurality
wheat	SYM00696		162.0	19.6	bacteria
wheat	SYM00786	SYM00865	111.3	4.3	bacterial plurality
wheat	SYM00879		102.0	4.9	bacteria
wheat	SYM00879	SYM01004	111.5	5.3	bacterial plurality
wheat	SYM00879B		102.3	5.8	bacteria
wheat	SYM00906		118.3	5.2	bacteria
wheat	SYM00906	SYM01004	111.1	5.3	bacterial plurality
wheat	SYM00965	SYM00865	111.3	5.5	bacterial plurality
wheat	SYM01004		111.6	4.9	bacteria
wheat	SYM01004	SYM01022	108.2	5.6	bacterial plurality
wheat	SYM01022		102.1	6.3	bacteria
wheat	SYM01158		117.0	5.6	bacteria
wheat	SYM00157		128.1	17.9	fungi
wheat	SYM00157	SYM15783	234.4	13.5	fungal plurality
wheat	SYM00299		140.3	11.2	fungi
wheat	SYM00299	SYM00696	47.4	11.5	fungal plurality
wheat	SYM00299	SYM01324	72.6	15.9	fungal plurality
wheat	SYM00299	SYM15783	90.2	14.2	fungal plurality
wheat	SYM00301		183.7	17.0	fungi
wheat	SYM00301	SYM01326	28.9	8.2	fungal plurality
wheat	SYM00301	SYM15774	226.9	17.2	fungal plurality

wheat	SYM01324		181.9	18.5	fungi
wheat	SYM01326		62.4	14.1	fungi
wheat	SYM01326	SYM12462	60.4	10.6	fungal plurality
wheat	SYM01329		195.7	15.0	fungi
wheat	SYM01330		102.7	8.2	fungi
wheat	SYM12462		96.3	15.7	fungi
wheat	SYM12462	SYM15774	17.6	7.8	fungal plurality
wheat	SYM12462	SYM15783	198.2	16.3	fungal plurality
wheat	SYM15774		143.4	5.2	fungi
wheat	SYM15774	SYM01324	102.5	16.2	fungal plurality
wheat	SYM15783		119.0	14.8	fungi
wheat	SYM15783	SYM01324	61.5	13.2	fungal plurality
wheat	SYM15879		158.9	15.2	fungi
wheat	SYM15880	SYM15888	148.6	13.3	fungal plurality

Discussion

[0029] Plant vigor and improved stress resilience are important components of providing fitness to a plant in an agricultural setting. These were measured in germination assays and seedling root vigor assays to test the improvement on plant phenotype as conferred by microbial inoculation. The collection of seed-derived endophytes produced a measurable response in soy and wheat when inoculated as compared to non-inoculated controls, as shown in **Table A, Table B, Table C and Table D**. For example, most of the strains tested were found to produce a favorable phenotype in any of the measured multiple parameters such as germination efficiency, root length, or shoot length, suggesting that the strains play an intimate role modulating and improving plant vigor and conferring stress resilience to the host plant. The stress responses in the strain collection can be seen by the ability of a subgroup to confer a beneficial response under different conditions such as water stress. These can be applicable to products for arid and marginal lands. In a large proportion of cases for the tested strains, the beneficial effect was measurable in several crops. In one aspect of the invention, it is understood that beneficial strains described herein are capable of colonizing multiple varieties and plant species.

Example 3: Synthetic Compositions Comprising Plant Seeds and a Single Endophyte Strain or a Plurality of Endophyte Strains Confer Benefits to Agricultural Plants

[0030] This Example describes the ability of synthetic compositions comprising plant seeds and a single endophyte strain or a plurality of endophyte strains described herein, to confer beneficial traits to a host plant. Among other things, this Example describe the ability of

endophytes (e.g., bacterial and fungal endophytes described herein) to confer beneficial traits on a variety of host plants, including but not limited to, dicots (e.g., soy, peanuts) and monocots (e.g., corn, soy, wheat, cotton, sorghum), and combinations thereof. Endophyte-inoculated seeds (e.g., seeds described herein) are tested under normal conditions, biotic stress, heat stress, cold stress, high salt stress, soil with high metal content, and combinations thereof, in seed germination assays and seedling root vigor assays to test whether one or more endophytes confer an increase in tolerance to one or more stresses. Growth tests are performed using growth assays (e.g., germination assays and seedling root vigor assays) on sterile filter papers. In some embodiments, seeds are treated either with a single bacterial or fungal strain, or with a combination of two bacterial or two fungal strains. In some embodiments, seeds are treated with two or more bacterial or fungal strains. In some embodiments, seeds are treated with a combination of at least one bacterial and at least one fungal strain.

[0031] Growth and scale-up of bacteria and fungi for inoculation, surface sterilization of seeds, and seed coating are performed as described herein.

Testing for germination enhancement in normal conditions

[0032] Standard Germination Tests are used to assess the ability of the endophyte to enhance the seeds' germination and early growth. Briefly, 400 seeds (e.g., seeds described herein) are coated with one or more endophytes described herein, and are placed in between wet brown paper towels (8 replicates with 50 seeds each). An equal number of seeds are treated with formulation only. Paper towels are placed on top of 1 X 2 feet plastic trays and maintained in a growth chamber set at 25°C and 70% humidity for 7 days. Seedlings are scored based on germination percentage relative to formulation only and non-treated seedling controls

Testing for germination enhancement under biotic stress

[0033] A modification of the method developed by Hodgson [Am. Potato. J. 38: 259-264 (1961)] is used to test germination enhancement in microbe-colonized seeds under biotic stress. Biotic stress is understood as a concentration of inocula in the form of cell (bacteria) or spore suspensions (fungus) of a known pathogen for a particular crop (e.g., *Pantoea stewartii* or *Fusarium graminearum* for *Zea mays* L.). Briefly, for each level of biotic stress, 400 seeds (e.g., seeds described herein), the interiors of which are colonized by microbial strains, and 400 seed controls (lacking the microbial strains), are placed in between brown paper towels: 8 replicates

with 50 seeds each for each treatment (microbe-colonized and control). Each one of the replicates is placed inside a large petri dish (150 mm in diameter). The towels are then soaked with 10 mL of pathogen cell or spore suspension at a concentration of 10^4 to 10^8 cells/spores per mL. Each level corresponds with an order of magnitude increment in concentration (thus, 5 levels). The petri dishes are maintained in a growth chamber set at 25°C and 70% humidity for 7 days. The proportion of seeds that germinate successfully is compared between the seeds coming from microbe-colonized plants with those coming from controls for each level of biotic stress.

Testing for germination enhancement in heat conditions

[0034] Standard Germination Tests are used to determine if a microbe colonizing the interior of a seed protects maize against heat stress during germination. Briefly, 400 seeds (e.g, seeds described herein), the interiors of which are colonized by microbial strains are placed in between wet brown paper towels (8 replicates with 50 seeds each). An equal number of seeds obtained from control plants that lack the microbe is treated in the same way. The paper towels are placed on top of 1 X 2 ft plastic trays and maintained in a growth chamber set at 16:8 hour light:dark cycle, 70% humidity, and at least 120 $\mu\text{E}/\text{m}^2/\text{s}$ light intensity for 7 days. A range of high temperatures (from 35 °C to 45 °C, with increments of 2 degrees per assay) is tested to assess the germination of microbe-colonized seeds at each temperature. The proportion of seeds that germinate successfully is compared between the seeds coming from microbe-colonized plants and those coming from controls.

Testing for germination enhancement in cold conditions

[0035] Standard Germination Tests are used to determine if a microbe colonizing the interior of a seed protects maize against cold stress during germination. Briefly, 400 seeds (e.g., seeds described herein), the interiors of which are colonized by microbial strains are placed in between wet brown paper towels (8 replicates with 50 seeds each). An equal number of seeds obtained from control plants that lack the microbe is treated in the same way. The paper towels are placed on top of 1 X 2 ft plastic trays and maintained in a growth chamber set at 16:8 hour light:dark cycle, 70% humidity, and at least 120 $\mu\text{E}/\text{m}^2/\text{s}$ light intensity for 7 days. A range of low temperatures (from 0°C to 10 °C, with increments of 2 degrees per assay) is tested to assess the germination of microbe-colonized seeds at each temperature. The proportion of seeds that

germinate successfully is compared between the seeds coming from microbe-colonized plants and those coming from controls.

Testing for germination enhancement in high salt concentrations

[0036] Germination experiments are conducted in 90 mm diameter petri dishes. Replicates consist of a Petri dish, watered with 10 mL of the appropriate solution and 20 seeds floating in the solution. 400 seeds (e.g., seeds described herein), the interiors of which are colonized by microbial strains, and 400 seed controls (lacking the microbial strains) are tested in this way (40 petri dishes total). To prevent large variations in salt concentration due to evaporation, dishes are sealed with parafilm and the saline solutions are renewed weekly by pouring out the existing saline solution in the petri dish and adding the same amount of fresh solution. A range of saline solutions (100–500 mM NaCl) is tested for to assess the germination of microbe-colonized seeds at varying salt levels. Petri dishes are maintained in a growth chamber set at 25°C, 16:8 hour light:dark cycle, 70% humidity, and at least 120 $\mu\text{E}/\text{m}^2/\text{s}$ light intensity. The proportion of seeds that germinates successfully after two weeks is compared between the seeds coming from inoculated plants and those coming from controls.

Testing for germination enhancement in soils with high metal content

[0037] Standard Germination Tests are used to determine if a microbe colonizing the interior of a seed protects maize against stress due to high soil metal content during germination. Briefly, 400 seeds (e.g., seeds described herein), the interiors of which are colonized by microbial strains, are placed in between wet brown paper towels (8 replicates with 50 seeds each). An equal number of seeds obtained from control plants that lack the microbe (microbe-free) is treated in the same way. The paper towels are placed on top of 1 X 2 ft plastic trays with holes to allow water drainage. The paper towels are covered with an inch of sterile sand. For each metal to be tested, the sand needs to be treated appropriately to ensure the release and bioavailability of the metal. For example, in the case of aluminum, the sand is watered with pH 4.0 + ~1 g/Kg soil Al^{+3} (-621 μM). The trays are maintained in a growth chamber set at 25°C and 70% humidity for 7 days. The proportion of seeds that germinates successfully is compared between the seeds coming from microbe-colonized plants and those coming from controls.

Testing for growth promotion in growth chamber in normal conditions

[0038] Soil is made from a mixture of 60% Sunshine Mix #5 (Sun Gro; Bellevue, Wash., USA) and 40% vermiculite. To determine if a particular microbe colonizing the interior of seeds is capable of promoting plant growth under normal conditions, 24 pots are prepared in two 12-pot no-hole flat trays with 28 grams of dry soil in each pot, and 2 L of filtered water is added to each tray. The water is allowed to soak into the soil and the soil surface is misted before seeding. For each seed-microbe combination, 12 pots are seeded with 3-5 seeds colonized by the microbe and 12 pots are seeded with 3-5 seeds lacking the microbe (microbe-free plants). The seeded pots are covered with a humidity dome and kept in the dark for 3 days, after which the pots are transferred to a growth chamber set at 25°C, 16:8 hour light:dark cycle, 70% humidity, and at least 120 $\mu\text{E}/\text{m}^2/\text{s}$ light intensity. The humidity domes are removed on day 5, or when cotyledons are fully expanded. After removal of the domes, each pot is irrigated to saturation with 0.5 X Hoagland's solution, then allowing the excess solution to drain. Seedlings are then thinned to 1 per pot. In the following days, the pots are irrigated to saturation with filtered water, allowing the excess water to drain after about 30 minutes of soaking, and the weight of each 12-pot flat tray is recorded weekly. Canopy area is measured at weekly intervals. Terminal plant height, average leaf area and average leaf length are measured at the end of the flowering stage. The plants are allowed to dry and seed weight is measured. Significance of difference in growth between microbe-colonized plants and controls lacking the microbe is assessed with the appropriate statistical test depending on the distribution of the data at $p < 0.05$.

Testing for growth promotion in growth chamber under biotic stress

[0039] Soil is made from a mixture of 60% Sunshine Mix #5 (Sun Gro; Bellevue, Wash., USA) and 40% vermiculite. To determine if a particular microbe colonizing the interior of seeds is capable of promoting plant growth in the presence of biotic stress, 24 pots are prepared in two 12-pot no-hole flat trays with 28 grams of dry soil in each pot, and 2 L of filtered water is added to each tray. The water is allowed to soak into the soil before planting. For each seed-microbe combination test, 12 pots are seeded with 3-5 seeds colonized by the microbe and 12 pots are seeded with 3-5 seeds lacking the microbe (microbe-free plants). The seeded pots are covered with a humidity dome and kept in the dark for 3 days, after which the pots are transferred to a growth chamber set at 25°C, 16:8 hour light:dark cycle, 70% humidity, and at least 120 $\mu\text{E}/\text{m}^2/\text{s}$ light intensity. The humidity domes are removed on day 5, or when cotyledons are fully expanded. After removal of the domes, each pot is irrigated to saturation with 0.5 X Hoagland's

solution, allowing the excess solution to drain. Seedlings are then thinned to 1 per pot. In the following days, the pots are irrigated to saturation with filtered water, allowing the excess water to drain after about 30 minutes of soaking.

[0040] Several methods of inoculation are used depending on the lifestyle of the pathogen. For leaf pathogens (e.g., *Pseudomonas syringae* or *Colletotrichum graminicola*), a suspension of cells for bacteria (10^8 cell/mL) or spores for fungi (10^7 spores/mL) is applied with an applicator on the adaxial surface of each of the youngest fully expanded leaves. Alternatively for fungal pathogens that do not form conidia easily, two agar plugs containing mycelium (~4 mm in diameter) are attached to the adaxial surface of each of the youngest leaves on each side of the central vein. For vascular pathogens (e.g., *Pantoea stewartii* or *Fusarium moniliforme*), the suspension of cells or spores is directly introduced into the vasculature (5-10 μ L) through a minor injury inflicted with a sterile blade. Alternatively, the seedlings can be grown hydroponically in the cell/spore or mycelium suspension. To test the resilience of the plant-microbe combination against insect stresses, such as thrips or aphids, plants are transferred to a specially-designated growth chamber containing the insects. Soil-borne insect or nematode pathogens are mixed into or applied topically to the potting soil. In all cases, care is taken to contain the fungal, insect, nematode or other pathogen and prevent release outside of the immediate testing area.

[0041] The weight of each 12-pot flat tray is recorded weekly. Canopy area is measured at weekly intervals. Terminal plant height, average leaf area and average leaf length are measured at the cease of flowering. The plants are allowed to dry and seed weight is measured. Significance of difference in growth between microbe-colonized plants and controls lacking the microbe is assessed with the appropriate statistical test depending on the distribution of the data at $p < 0.05$.

Example 4 – Functional Characterization of Endophytes

Auxin production assay

[0042] Auxin is an important plant hormone, which can promote cell enlargement and inhibit branch development (meristem activity) in above ground plant tissues, while below ground it has the opposite effect, promoting root branching and growth. Interestingly, plant auxin is manufactured above ground and transported to the roots. It thus follows that plant, and especially

root inhabiting microbes which produce significant amounts of auxin, will be able to promote root branching and development even under conditions where the plant reduces its own production of auxin. Such conditions can exist for example when soil is flooded and roots encounter an anoxic environment.

[0043] Indole containing IAA is able to generate a pinkish chromophore under acidic conditions in the presence of ferric chloride. For auxin measurement, 1 µl of overnight-grown cultures of endophytic bacterial strains were inoculated into 750 µl of R2A broth supplemented with L-TRP (5 mM) in 2-mL 96 well culture plates. The plates were sealed with a breathable membrane and incubated at 23°C with constant shaking at 200 rpm for 4 days. To measure auxin production by fungal strains, 3 µl of 5-day old liquid fungal cultures were inoculated into 1 ml R2A broth supplemented with L-TRP (5 mM) in 24-well culture plates. The plates were sealed with breathable tape and incubated at 23°C with constant shaking at 130 rpm for 4 days. After 4 days, 100 µL of each culture was transferred to a 96 well plate. 25 µL of Salkowski reagent (1 mL of FeCl₃ 0.5 M solution to 50 mL of 35% HClO₄) was added into each well and the plates were incubated in the dark for 30 minutes before taking picture and measuring 540 nm absorption using the SpectraMax M5 plate reader (Molecular Devices). Dark pink halos around colonies are visualized in the membrane by background illumination using a light table.

[0044] Endophytes were screened for their ability to produce auxins as possible root growth promoting agents. Four replicates were performed for each strain assayed. Exemplary auxin production results for endophytes belonging to core OTUs are presented below in **Table E**, **Table F**, and **Table G**.

Acetoin and diacetyl production assay

[0045] For acetoin measurements, microbial strains were cultured as described above in R2A broth supplemented with 5% glucose. After 4 days, 100 µL of each culture was transferred to a 96 well plate and mixed with 25 µL Barritt's Reagents A and B and 525 nm absorption was measured. Barritt's Reagents A and B were prepared by mixing 5 g/L creatine mixed 3:1 (v/v) with freshly prepared alpha-naphthol (75 g/L in 2.5 M sodium hydroxide). After 15 minutes, plates are scored for red or pink colouration against a copper coloured negative control. Four replicates were performed for each strain assayed. Exemplary acetoin production results for endophytes belonging to core OTUs are presented below in **Table E**, **Table F**, and **Table G**.

Siderophore production assay

[0046] To ensure no contaminating iron is carried over from previous experiments, all glassware is deferrated with 6 M HCl and water prior to media preparation. For siderophore measurements, microbial strains were cultured as described above in R2A broth. After 3 days of incubation at 25°C, plates are overlaid with O-CAS overlay. Again using the cleaned glassware, 1 liter of O-CAS overlay is made by mixing 60.5 mg of Chrome azurol S (CAS), 72.9 mg of hexadecyltrimethyl ammonium bromide (HDTMA), 30.24 g of finely crushed Piperazine-1,4-bis-2-ethanesulfonic acid (PIPES) with 10 mL of 1 mM $\text{FeCl}_3 \cdot 6\text{H}_2\text{O}$ in 10 mM HCl solvent. The PIPES had to be finely powdered and mixed gently with stirring (not shaking) to avoid producing bubbles, until a dark blue colour is achieved. Melted 1% agarose is then added to pre-warmed O-CAS just prior pouring the overlay in a proportion of 1:3 (v/v). After 15 minutes, colour change is scored by looking for purple halos (catechol type siderophores) or orange colonies (hydroxamate siderophores). Four replicates were performed for each strain assayed.

[0047] In many environments, iron is a limiting nutrient for growth. A coping mechanism which many microbes have developed is to produce and secrete iron chelating compounds called siderophores which often only that particular species or strain has the means to re-uptake and interact with to release the bound iron, making it available for metabolism. A fringe effect of siderophore production and secretion is that a siderophore secreting microbes can remove all the bio-available iron in its environment, making it difficult for a competing species to invade and grow in that micro-environment.

[0048] Siderophore production by microbes on a plant surface or inside a plant may both show that a microbe is equipped to grow in a nutrient limited environment, and perhaps protect the plant environment from invasion by other, perhaps undesirable microbes. Exemplary siderophore production results for endophytes belonging to core OTUs are presented below in Table E, Table F, and Table G.

Table E: Auxin, siderophore, and acetoin production by bacterial endophytes belonging to core OTUs; Legend: 0 = no production; 1= low production; 2 = medium production; 3 = high production

Strain	SEQ ID NO.	Secretes siderophores	Produces Auxin/Indoles	Produces Acetoin
SYM00003	290	2	1	0

SYM00009	291	1	1	0
SYM00013	292	0	1	0
SYM00017A	293	1	3	0
SYM00018	294	0	3	2
SYM00020	295	0	2	2
SYM00021b	296	0	2	3
SYM00025	297	1	3	2
SYM00043	300	1	3	2
SYM00044	301	1	1	3
SYM00050	302	1	2	3
SYM00053	303	1	1	2
SYM00062C	305	1	2	1
SYM00068	308	2	2	0
SYM00070	309	2	2	0
SYM00074	310	2	3	0
SYM00103	311	2	2	2
SYM00183	322	0	2	1
SYM00184	323	0	2	0
SYM00207	324	1	2	2
SYM00212	325	2	2	3
SYM00219	326	3	2	3
SYM00234	327	2	2	2
SYM00236	328	0	2	0
SYM00248	329	1	2	0
SYM00249	330	2	2	2
SYM00506c	331	0	2	2
SYM00507	332	1	2	2
SYM00508	333	0	3	2
SYM00525	525	2	2	3
SYM00538A	335	3	2	3
SYM00538B	336	2	2	2
SYM00538i	337	0	1	0
SYM00543	338	0	3	1
SYM00545	339	2	2	2
SYM00549	340	2	2	2
SYM00563	341	2	2	1
SYM00574	343	3	1	0
SYM00617	347	1	3	1
SYM00620	348	1	3	0
SYM00627	350	0	1	3
SYM00628	351	2	2	3

SYM00646	353	3	2	3
SYM00650	354	2	2	0
SYM00662	355	1	1	1
SYM00714	358	1	2	2
SYM00905	365	3	2	2
SYM00924	366	2	2	2
SYM00963	367	2	2	1
SYM00978	370	2	2	1
SYM00982	368	0	2	3
SYM00987	369	1	3	2
SYM00991	371	1	2	2
SYM00999	372	1	1	3
SYM01049	373	1	1	0

Table F: Auxin, siderophore, and acetoin production by fungal endophytes belonging to core OTUs; Legend: 0 = no production; 1 = low production; 2 = medium production; 3 = high production

Strain	SEQ NO.	ID	Secretes siderophores	Produces Auxin/Indoles	Produces Acetoin
SYM00034	299		1	0	0
SYM00061A	304		1	0	2
SYM00066	307		1	0	0
SYM00120	312		1	0	0
SYM00122	313		0	0	0
SYM00123	314		1	0	3
SYM00124	315		1	1	0
SYM00129	316		0	1	0
SYM00135	317		0	1	0
SYM00136	318		0	0	1
SYM00151	319		1	1	0
SYM00154	320		0	0	0
SYM00566B	342		3	0	0
SYM00577	344		0	0	1
SYM00590	345		0	1	2
SYM00603	346		2	1	0
SYM00622	349		1	0	2
SYM00629	352		0	1	2
SYM00663	356		2	1	2
SYM00696	357		2	0	0
SYM00741b	360		0	0	0
SYM00793	361		1	0	0

SYM00795	362	1	0	1
SYM00854	363	2	0	2
SYM00880	364	2	1	2
SYM01300	374	2	1	0
SYM01310	376	0	2	0
SYM01311	377	0	0	0
SYM01314	378	2	1	0
SYM01315	379	0	0	0
SYM01325	380	0	0	2
SYM01326	381	0	0	2
SYM01327	382	2	1	2
SYM01328	383	1	0	0
SYM01333	384	0	0	0
SYM15811	385	3	1	0
SYM15820	386	1	0	0
SYM15821	387	1	0	0
SYM15825	388	0	0	2
SYM15828	389	0	0	2
SYM15831	390	2	1	2
SYM15837	391	1	0	0
SYM15839	392	2	0	0
SYM15847	393	0	0	0
SYM15870	394	0	0	0
SYM15872	395	0	0	1
SYM15890	396	0	0	2
SYM15901	397	0	0	2
SYM15920	398	2	0	2
SYM15926	399	1	2	0
SYM15928	400	0	0	0
SYM15932	401	0	0	0
SYM15939	402	0	1	0

Table G: Exemplary siderophore, auxin, and acetoin production of microbial endophytes belonging to core OTUs; Legend: 0 = no production; 1= low production; 2 = medium production; 3 = high production

SYM	Taxonomy	Type	SEQ ID NO.	Secretes siderophores	Produces Auxin/Indoles	Produces Acetoin
SYM00021B	Escherichia sp.	bacteria	296	1	1	3
SYM00044	Escherichia sp.	bacteria	301	1	1	3
SYM00057b	Burkholderia sp.	bacteria	426	1	2	3

SYM00074	Enterobacter sp.	bacteria	310	0	3	0
SYM00091	Agrobacterium sp.	bacteria	427	2	2	0
SYM00092D	Brevundimonas sp.	bacteria	428	3	3	3
SYM00157	Leptosphaerulina sp.	fungi	429	3	1	0
SYM00212	Bacillus sp.	bacteria	325	0	0	3
SYM00290	Acinetobacter sp.	bacteria	430	1	0	0
SYM00300	Acremonium sp.	fungi	449	2	0	2
SYM00301	Penicillium sp.	fungi	432	0	0	2
SYM00577	Acremonium sp.	fungi	344	0	0	0
SYM00619	Exiguobacterium sp.	bacteria	435	0	0	0
SYM00865	Stenotrophomonas sp.	bacteria	451	2	1	1
SYM00879	Methylobacterium sp.	bacteria	437	0	0	0
SYM00879B	Sphingomonas sp.	bacteria	438	3	1	0
SYM00906	Stenotrophomonas sp.	bacteria	439	1	1	1
SYM00965	Luteibacter sp.	bacteria	440	2	3	3
SYM01004	Agrobacterium sp.	bacteria	441	1	2	2
SYM01022	Curtobacterium sp.	bacteria	442	3	2	3
SYM01158	Pantoea sp.	bacteria	452	1	1	1
SYM01314	Fusarium sp.	fungi	378	2	1	0
SYM01324	Aspergillus sp.	fungi	443	2	1	0
SYM01326	Alternaria sp.	fungi	381	0	0	0
SYM01329	Phoma sp.	fungi	444	1	0	2
SYM01330	Rhizopus sp.	fungi	445	0	0	0
SYM01331	Phoma sp.	fungi	450	0	0	1
SYM12462	Cladosporium sp.	fungi	446	0	0	2
SYM15774	Phoma sp.	fungi	447	0	0	1
SYM15783	Alternaria sp.	fungi	448	0	0	2
SYM15810	Fusarium sp.	fungi	453	0	2	1
SYM15879	Fusarium sp.	fungi	454	0	0	0
SYM15880	Penicillium sp.	fungi	455	0	0	1

Assay for growth on nitrogen free LGI media

[0049] All glassware is cleaned with 6 M HCl before media preparation. A new 96 deep-well plate (2 mL well volume) is filled with 250 ul /well of sterile LGI broth [per L, 50 g Sucrose, 0.01 g FeCl₃-6H₂O, 0.8 g K₃PO₄, 0.2 g MgSO₄-7H₂O, 0.002 g Na₂MoO₄-2H₂O, pH 7.5]. Microbes are inoculated into the 96 wells simultaneously with a flame-sterilized 96 pin

replicator. The plate is sealed with a breathable membrane, incubated at 28°C without shaking for 3 days, and OD₆₀₀ readings taken with a 96 well plate reader.

[0050] A nitrogen fixing plant associated bacterium is able theoretically to add to the host's nitrogen metabolism, and the most famous beneficial plant associated bacteria, rhizobia, are able to do this within specially adapted organs leguminous plant grows for them to be able to do this. In some embodiments, seed associated microbes described herein are able to fix nitrogen in association with developing seedling, regardless of whether they colonize the plant's surfaces or interior, and thereby add to the plant's nitrogen nutrition.

ACC deaminase activity assay

[0051] Microbes are assayed for growth with ACC as their sole source of nitrogen. Prior to media preparation all glassware is cleaned with 6 M HCl. A 2 M filter sterilized solution of ACC (#1373A, Research Organics, USA) is prepared in water. 1 µl/mL of this is added to autoclaved LGI broth (see above), and 1 mL aliquots are placed in a new 96 well plate. The plate is sealed with a breathable membrane, incubated at 25°C with gentle shaking for 5 days, and OD₆₀₀ readings taken. Only wells that are significantly more turbid than their corresponding nitrogen free LGI wells are considered to display ACC deaminase activity.

[0052] Plant stress reactions are strongly impacted by the plant's own production and overproduction of the gaseous hormone ethylene. Ethylene is metabolized from its precursor 1-aminocyclopropane-1-carboxylate (ACC) which can be diverted from ethylene metabolism by microbial and plant enzymes having ACC deaminase activity. As the name implies, ACC deaminase removes molecular nitrogen from the ethylene precursor, removing it as a substrate for production of the plant stress hormone and providing for the microbe a source of valuable nitrogen nutrition.

Mineral phosphate solubilization assay

[0053] Microbes are plated on tricalcium phosphate media. This is prepared as follows: 10 g/L glucose, 0.373 g/L NH₄NO₃, 0.41 g/L MgSO₄, 0.295 g/L NaCl, 0.003 FeCl₃, 0.7 g/L Ca₃HPO₄ and 20 g/L Agar, pH 6, then autoclaved and poured into 150 mm plates. After 3 days of growth at 25°C in darkness, clear halos are measured around colonies able to solubilize the tricalcium phosphate.

RNAse activity assay

[0054] 1.5 g of torula yeast RNA (#R6625, Sigma) is dissolved in 1 mL of 0.1 M Na₂HPO₄ at pH 8, filter sterilized and added to 250 mL of autoclaved R2A agar media which is poured into 150 mm plates. The bacteria from a glycerol stock plate are inoculated using a flame-sterilized 96 pin replicator, and incubated at 25°C for 3 days. On day three, plates are flooded with 70% perchloric acid (#311421, Sigma) for 15 minutes and scored for clear halo production around colonies.

Pectinase activity assay

[0055] Adapting a previous protocol 0.2%(w/v) of citrus pectin (#76280, Sigma) and 0.1% triton X-100 are added to R2A media, autoclaved and poured into 150 mm plates. Bacteria are inoculated using a 96 pin plate replicator. After 3 days of culturing in the darkness at 25°C, pectinase activity is visualized by flooding the plate with Gram's iodine. Positive colonies are surrounded by clear halos.

Cellulase activity assay

[0056] Adapting a previous protocol, 0.2% carboxymethylcellulose (CMC) sodium salt (#C5678, Sigma) and 0.1% triton X-100 are added to R2A media, autoclaved and poured into 150 mm plates. Bacteria are inoculated using a 96 pin plate replicator. After 3 days of culturing in the darkness at 25°C, cellulose activity is visualized by flooding the plate with Gram's iodine. Positive colonies are surrounded by clear halos.

Antibiosis assay

[0057] Bacteria or fungi are inoculated using a 96 pin plate replicator onto 150 mm Petri dishes containing R2A agar, then grown for 3 days at 25°C. At this time, colonies of either *E. coli* DH5α (gram negative tester), *Bacillus subtilis* ssp. *Subtilis* (gram positive tester), or yeast strain AH109 (fungal tester) are resuspended in 1 mL of 50 mM Na₂HPO₄ buffer to an OD₆₀₀ of 0.2, and 30 µl of this is mixed with 30 mL of warm LB agar. This is quickly poured completely over a microbe array plate, allowed to solidify and incubated at 37°C for 16 hours. Antibiosis is scored by looking for clear halos around microbial colonies.

BIOLOG characterization of endophyte substrate metabolism

[0058] In addition to the auxin, acetoin, and siderophore assays described above, endophytes described herein were characterized for their ability to metabolize a variety of carbon substrates. Liquid cultures of microbe were first sonicated to achieve homogeneity. 1 mL culture of each strain was harvested by centrifugation for 10 minutes at 4500 RPM and subsequently washed three times with sterile distilled water to remove any traces of residual media. Microbial samples were resuspended in sterile distilled water to a final OD₅₉₀ of 0.2. Measurements of absorbance were taken using a SpectraMax M microplate reader (Molecular Devices, Sunnyvale, CA).

[0059] Sole carbon substrate assays were done using BIOLOG Phenotype MicroArray (PM) 1 and 2A MicroPlates (Hayward, CA). An aliquot of each bacterial cell culture (2.32 mL) were inoculated into 20 mL sterile IF-0a GN/GP Base inoculating fluid (IF-0), 0.24 mL 100X Dye F obtained from BIOLOG, and brought to a final volume of 24 mL with sterile distilled water. Negative control PM1 and PM2A assays were also made similarly minus bacterial cells to detect abiotic reactions. An aliquot of fungal culture (0.05 mL) of each strain were inoculated into 23.95 mL FF-IF medium obtained from BIOLOG. Microbial cell suspensions were stirred in order to achieve uniformity. One hundred microliters of the microbial cell suspension was added per well using a multichannel pipettor to the 96-well BIOLOG PM1 and PM2A MicroPlates that each contained 95 carbon sources and one water-only (negative control) well.

[0060] MicroPlates were sealed in paper surgical tape (Dynarex, Orangeburg, NY) to prevent plate edge effects, and incubated stationary at 24°C in an enclosed container for 70 hours. Absorbance at 590 nm was measured for all MicroPlates at the end of the incubation period to determine carbon substrate utilization for each strain and normalized relative to the negative control (water only) well of each plate (Garland and Mills, 1991; Barua et al., 2010; Siemens et al., 2012; Blumenstein et al., 2015). The bacterial assays were also calibrated against the negative control (no cells) PM1 and PM2A MicroPlates data to correct for any biases introduced by media on the colorimetric analysis (Borglin et al., 2012). Corrected absorbance values that were negative were considered as zero for subsequent analysis (Garland and Mills, 1991; Blumenstein et al., 2015) and a threshold value of 0.1 and above was used to indicate the ability of a particular microbial strain to use a given carbon substrate (Barua et al., 2010; Blumenstein et al., 2015). Additionally, bacterial MicroPlates were visually examined for the irreversible formation of violet color in wells indicating the reduction of the tetrazolium redox dye to formazan that result from cell respiration (Garland and Mills, 1991). Fungal PM tests were

measured as growth assays and visual observation of mycelial growth in each well was made. Exemplary BIOLOG substrate utilization by endophytes described herein are presented in Table H, Table I, Table J, Table K, Table L, Table M, Table N, Table O, Table P, Table Q, Table R, Table S, Table T, and Table U.

Table H: Substrate utilization as determined by BIOLOG PM1 MicroPlates by bacterial endophytes belonging to OTUs present in landrace and wild corn and wheat seeds that are present in lower levels in modern corn and wheat seeds.

Strain/Substrate	SYM00013	SYM00018	SYM000183	SYM000184	SYM000219	SYM000043	SYM000050	SYM000508	SYM000617	SYM000620	SYM000668	SYM000905
D-Serine	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
D-Glucose-6-Phosphate	NO	NO	NO	NO	NO	YES	YES	YES	NO	YES	NO	NO
L-Asparagine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-glutamine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Glycyl-L-Aspartic acid	YES	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO
Glycyl-L-Glutamic acid	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	YES	NO
Glycyl-L-Proline	NO	NO	YES	YES	NO	NO	YES	NO	NO	NO	YES	YES
L-Arabinose	YES	YES	NO	YES	NO	YES	YES	NO	NO	NO	YES	NO
D-Sorbitol	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO
D-Galactonic acid-?-lactone	YES	YES	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO
D-Aspartic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
m-Tartaric acid	YES	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
Citric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
Tricarballic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
p-Hydroxy Phenyl acetic acid	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
N-Acetyl-D-Glucosamine	YES	YES	YES	YES	YES	YES	YES	NO	NO	NO	NO	NO
Glycerol	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO
D-L-Malic acid	NO	NO	NO	YES	NO	YES	NO	YES	YES	NO	YES	NO
D-Glucosaminic acid	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO
D-Glucose-1-Phosphate	NO	YES	NO	NO	NO	YES	YES	YES	NO	NO	NO	NO
m-Inositol	NO	YES	NO	YES	NO	YES	YES	NO	NO	NO	NO	NO
L-Serine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
m-Hydroxy Phenyl Acetic acid	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO
D-Saccharic acid	NO	NO	NO	YES	NO	YES	YES	YES	NO	NO	NO	NO
L-Fucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Ribose	NO	YES	YES	YES	NO	YES	NO	NO	NO	NO	YES	NO
1,2-Propanediol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Fructose-6-Phosphate	NO	YES	NO	NO	NO	NO	YES	YES	NO	YES	NO	NO
D-Threonine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Threonine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Tyramine	YES	YES	YES	NO	YES	NO	NO	NO	NO	NO	YES	NO
Succinic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Glucuronic acid	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
Tween 20	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
Tween 40	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
Tween 80	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES
Fumaric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Alanine	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES
D-Psicose	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
D-Galactose	YES	YES	NO	YES	YES	YES	YES	YES	NO	NO	NO	NO
D-Gluconic acid	NO	YES	NO	NO	NO	YES	YES	YES	NO	YES	NO	NO
L-Rhamnose	NO	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	NO
a-Keto-Glutaric acid	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	YES	NO
a-Hydroxy Glutaric acid-?-lactone	YES	NO	NO	YES	NO	NO	YES	NO	NO	NO	YES	NO
Bromo succinic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Alanyl-Glycine	YES	YES	YES	YES	NO	NO	YES	NO	NO	NO	YES	NO

L-Lyxose	NO	YES	NO	NO	NO	YES	YES	YES	NO	NO	YES	NO
L-Aspartic acid	NO	NO	YES	NO	NO	NO	YES	YES	NO	NO	NO	NO
D-L-a-Glycerol phosphate	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Fructose	NO	NO	NO	YES	NO	YES	YES	NO	NO	NO	YES	NO
a-Keto-Butyric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
a-Hydroxy Butyric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Propionic acid	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
Acetoacetic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Glucuronamide	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Proline	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO
D-Xylose	YES	YES	YES	YES	NO	YES	YES	NO	NO	NO	YES	NO
Acetic acid	NO	YES	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO
a-Methyl-D-Galactoside	NO	NO	NO	NO	YES	NO	YES	NO	NO	YES	NO	NO
B-Methyl-D-glucoside	NO	YES	NO	YES	YES	YES	YES	YES	NO	NO	NO	NO
Mucic acid	YES	YES	YES	NO	NO	YES	YES	YES	NO	NO	YES	NO
N-acetyl- B-D-Mannosamine	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO
Pyruvic acid	NO	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	NO
D-Alanine	YES	YES	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO
L-Lactic acid	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO
a-D-Glucose	NO	YES	YES	YES	NO	YES	YES	NO	YES	NO	NO	NO
a-D-Lactose	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO
Adonitol	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
Glycolic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Mono Methyl Succinate	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Galactonic-acid-?-lactone	NO	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO
D-Trehalose	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO
Formic acid	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
Maltose	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES
Lactulose	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO
Maltotriose	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES
Glyoxylic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Methyl Pyruvate	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	YES	NO
D-Galacturonic acid	NO	NO	YES	NO	NO	YES	YES	NO	NO	YES	NO	NO
D-Mannose	NO	YES	YES	YES	NO	YES	YES	NO	NO	NO	NO	YES
D-Mannitol	NO	YES	NO	YES	NO	YES	YES	NO	NO	NO	NO	NO
D-Melibiose	NO	YES	YES	YES	YES	YES	YES	NO	YES	NO	NO	NO
Sucrose	NO	NO	YES	YES	NO	YES	YES	NO	NO	NO	NO	NO
2-Deoxy adenosine	NO	YES	NO	NO	NO	YES	YES	YES	NO	YES	NO	NO
D-Cellulobiose	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES
D-Malic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
Phenylethyl-amine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Dulcitol	NO	NO	NO	NO	YES	YES	NO	NO	YES	NO	NO	NO
L-Glutamic acid	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
Thymidine	NO	YES	NO	NO	NO	YES	YES	YES	NO	NO	NO	NO
Uridine	YES	YES	YES	YES	NO	NO	YES	YES	NO	NO	NO	NO
Adenosine	NO	YES	NO	NO	YES	YES	NO	YES	NO	YES	NO	NO
Inosine	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
L-Malic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
2-Aminoethanol	NO	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO

Table I: Substrate utilization as determined by BIOLOG PM2A MicroPlates by bacterial endophytes belonging to OTUs present in landrace and wild corn and wheat seeds that are present in lower levels in modern corn and wheat seeds.

Strain/Substrate	SYM00013	SYM00018	SYM00183	SYM00184	SYM00219	SYM00043	SYM00050	SYM00058	SYM00067	SYM000620	SYM00068	SYM000905
N-acetyl-D-Galactosamine	NO	NO	YES	YES	NO	NO	YES	NO	NO	NO	NO	YES
Gentiobiose	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES
D-Raffinose	NO	NO	NO	YES	NO	YES	NO	NO	YES	YES	NO	NO
Capric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO

D-lactic acid methyl ester	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
Acetamide	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
L-Ornithine	YES	YES	NO	YES	YES	NO	YES	NO	NO	NO	YES	NO
Chondroitin sulfate C	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
N-acetyl-neuraminic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
L-glucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Salicin	NO	NO	YES	YES	YES	NO	YES	YES	YES	NO	NO	YES
Caproic acid	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
Malonic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Alaninamide	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES
L-Phenylalanine	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
α -Cyclodextrin	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
β -D-allose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Lactitol	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES
Sedoheptulosan	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Citraconic acid	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
Melibionnic acid	NO	NO	NO	NO	YES	NO	YES	NO	NO	YES	YES	NO
N-Acetyl-L-Glutamic acid	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO
L-Pyrroglutamic acid	YES	YES	YES	YES	YES	NO	NO	YES	NO	NO	YES	NO
β -Cyclodextrin	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO
Amygdalin	NO	NO	YES	YES	NO	NO	NO	NO	YES	NO	NO	NO
D-Melezitose	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO
L-Sorbose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Citramalic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Oxalic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Arginine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Valine	YES	YES	NO	YES	YES	NO	NO	NO	NO	NO	YES	NO
γ -Cyclodextrin	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO
D-arabinose	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
Maltitol	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES
Stachyose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Glucosamine	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES
Oxalomalic acid	YES	YES	YES	YES	NO	YES	NO	NO	YES	NO	YES	YES
Glycine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D,L-Carnitine	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Dextrin	NO	NO	NO	YES	YES	NO	NO	YES	YES	YES	NO	NO
D-arabitol	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
α -Methyl-D-Glucoside	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Tagatose	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
2-Hydroxy benzoic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Quinic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Histidine	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO
Sec-Butylamine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Gelatin	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES
L-arabitol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
β -Methyl-D-Galactoside	NO	NO	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO
Turanose	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO
4-Hydroxy benzoic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Ribono-1,4-Lactone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Homoserine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D,L-Octopamine	YES	YES	YES	YES	YES	NO	NO	NO	YES	NO	YES	YES
Glycogen	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
Arbutin	NO	NO	YES	YES	YES	NO	YES	YES	YES	NO	NO	YES
3-Methyl Glucose	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
Xylitol	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
β -Hydroxy butyric acid	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO
Sebacic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Hydroxy-L-Proline	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
Putrescine	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
Inulin	NO	NO	YES	YES	YES	YES	NO	NO	NO	NO	NO	NO
2-Deoxy-D-Ribose	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO
β -Methyl-D-Glucuronic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
N-Acetyl-D-glucosaminitol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
γ -Hydroxy butyric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Sorbic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Isoleucine	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO

Dihydroxy acetone	NO	NO	NO	YES	NO	NO	YES	YES	NO	NO	NO	NO
Laminarin	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
i-Erythritol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
α -Methyl-D-Mannoside	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
γ -amino butyric acid	YES	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
α -Keto-valeric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Succinamic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Leucine	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
2,3-Butanediol	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Mannan	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Fucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
β -Methyl-D-Xyloside	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
d-amino valeric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Itaconic acid	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO
D-Tartaric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Lysine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
2,3-Butanone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Pectin	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
3-O- β -D-Galactopyranosyl-D-arabinose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Palatinose	NO	NO	YES	YES	YES	NO	NO	NO	NO	NO	NO	YES
Butyric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
5-Keto-D-Gluconic acid	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO
L-Tartaric acid	YES	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO
L-Methionine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
3-Hydroxy 2-Butanone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO

[0061] Twelve SYM strains of culturable bacteria belonging to OTUs present in landrace and wild corn and wheat seeds that are present in lower levels in modern corn and wheat seeds were tested for sole carbon substrate utilization using BIOLOG PM1 and PM2A MicroPlates. The most utilized substrates by these strains are L-alanine, L-galactonic-acid- γ -lactone, maltose, maltotriose, D-cellobiose, gentiobiose, and D-glucosamine. The least utilized substrates by these strains are L-asparagine, L-glutamine, D-aspartic acid, tricarballic acid, L-serine, L-fucose, 1,2-propanediol, D-threonine, L-threonine, succinic acid, fumaric acid, bromo succinic acid, D-L-a-glycerol phosphate, α -keto-butyric acid, α -hydroxy butyric acid, acetoacetic acid, glucuronamide, glycolic acid, mono methyl succinate, glyoxylic acid, phenylethyl-amine, and L-malic acid.

[0062] The substrates most utilized by a large number of the culturable bacteria belonging to core OTUs are mucic acid, L-arabinose, L-galactonic-acid- γ -lactone, N-acetyl-D-glucosamine, maltose, maltotriose, and D-cellobiose. These core bacteria did not utilize sedoheptulosan, oxalic acid, 2-hydroxy benzoic acid, quinic acid, mannan, L-methionine, N-acetyl-D-glucosaminitol, sorbic acid, 2,3-butanone, succinic acid, phenylethyl-amine, and 3-hydroxy 2-butanone as sole carbon sources. Results for the culturable fungi belonging to core OTUs indicate that D-sorbitol, L-arabinose, N-acetyl-D-glucosamine, glycerol, tween 40, tween 80, D-gluconic acid, L-proline, α -D-glucose, D-trehalose, maltose, lactulose, D-mannose, D-mannitol, sucrose, D-cellobiose, L-

glutamic acid, L-ornithine, and L-pyroglutamic acid are carbon substrates that are utilized by a large number of the endophyte strains examined here. The carbon substrate that seemed to be not utilized by fungi in these assays is 2-deoxy-D-ribose. All other substrates could be utilized as a sole carbon nutrient by at least one fungal SYM strain.

Table J: Substrate utilization as determined by BIOLOG PM1 MicroPlates by bacterial endophytes belonging to core OTUs.

Strain/Substrate	SYM00103	SYM01049	SYM00013	SYM00017A	SYM00018	SYM00183	SYM00184	SYM00020	SYM00207	SYM00212	SYM00219	SYM00234	SYM00236	SYM00248	SYM00249	SYM00260
D-Serine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
D-Glucose-6-Phosphate	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	YES	NO
L-Asparagine	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES
L-glutamine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
Glycyl-L-Aspartic acid	NO	YES	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
Glycyl-L-Glutamic acid	YES	NO	NO	NO	NO	YES	YES	NO	YES	YES	NO	NO	NO	NO	NO	YES
Glycyl-L-Proline	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Arabinose	NO	YES	YES	YES	YES	NO	YES	YES	NO	YES	NO	YES	YES	YES	YES	YES
D-Sorbitol	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Galactonic acid-?-lactone	NO	YES	YES	NO	YES	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO
D-Aspartic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
m-Tartaric acid	NO	YES	YES	NO	YES	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO
Citric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES
Tricarballic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
p-Hydroxy Phenyl acetic acid	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
N-Acetyl-D-Glucosamine	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO
Glycerol	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	YES	NO	YES	NO	YES
D-L-Malic acid	NO	NO	NO	YES	YES	NO	YES	NO	YES	YES	NO	YES	NO	NO	NO	YES
D-Glucosaminic acid	NO	NO	NO	YES	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
D-Glucose-1-Phosphate	NO	NO	NO	YES	YES	NO	NO	YES	NO	YES	NO	NO	NO	NO	YES	NO
m-Inositol	NO	NO	NO	YES	YES	NO	YES	YES	NO	YES	NO	NO	NO	YES	YES	YES
L-Serine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
m-Hydroxy Phenyl Acetic acid	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO
D-Saccharic acid	NO	NO	NO	YES	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	YES
L-Fucose	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
D-Ribose	NO	YES	NO	YES	YES	YES	YES	NO	NO	YES	NO	NO	NO	NO	YES	NO
1,2-Propanediol	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES
D-Fructose-6-Phosphate	NO	NO	NO	YES	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO
D-Threonine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Threonine	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES
Tyramine	NO	NO	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	NO
Succinic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Glucuronic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
Tween 20	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES
Tween 40	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
Tween 80	YES	YES	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES
Fumaric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES
L-Alanine	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES
D-Psicose	NO	NO	NO	YES	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
D-Galactose	NO	YES	YES	YES	YES	NO	YES	YES	NO	NO	YES	NO	NO	YES	YES	NO
D-Gluconic acid	YES	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO	YES
L-Rhamnose	NO	NO	NO	YES	YES	NO	NO	YES	NO	YES	YES	YES	NO	YES	YES	NO
a-Keto-Glutaric acid	YES	NO	NO	YES	NO	YES	NO	NO	YES	YES	NO	NO	YES	NO	NO	YES
a-Hydroxy Glutaric acid-?-lactone	NO	NO	YES	YES	NO	NO	YES	NO	NO	YES	NO	NO	YES	NO	NO	YES
Bromo succinic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES

L-Alanyl-Glycine	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	NO	YES
L-Lyxose	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO
L-Aspartic acid	YES	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	YES	YES	YES	YES
D-L-a-Glycerol phosphate	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
D-Fructose	NO	NO	NO	YES	NO	NO	YES	YES	NO	YES	NO	YES	NO	YES	NO	NO	NO
a-Keto-Butyric acid	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO
a-Hydroxy Butyric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES
Propionic acid	NO	NO	NO	YES	YES	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	YES
Acetoacetic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
Glucuronamide	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Proline	NO	NO	NO	NO	YES	YES	NO	NO	YES	YES	NO	YES	YES	YES	YES	NO	YES
D-Xylose	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	YES	YES	YES	NO	YES
Acetic acid	NO	NO	NO	YES	YES	NO	YES	NO	YES	YES	NO	YES	YES	YES	NO	NO	YES
a-Methyl-D-Galactoside	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	YES	YES	YES	NO	YES	NO	NO
B-Methyl-D-glucoside	NO	NO	NO	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES	NO	YES	YES	YES
Mucic acid	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	NO	YES	NO	YES	NO	YES	YES
N-acetyl- B-D-Mannosamine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES
Pyruvic acid	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES
D-Alanine	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	NO	NO	NO	YES
L-Lactic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
a-D-Glucose	NO	YES	NO	YES	YES	YES	YES	NO	NO	YES	NO	YES	NO	YES	NO	NO	NO
a-D-Lactose	NO	NO	NO	NO	NO	YES	YES	NO	NO	YES	NO	YES	NO	YES	NO	NO	NO
Adonitol	NO	NO	NO	YES	YES	YES	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO
Glycolic acid	YES	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	YES
Mono Methyl Succinate	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	YES
L-Galactonic-acid-?-lactone	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	NO	YES
D-Trehalose	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO
Formic acid	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	YES
Maltose	NO	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	NO	YES	YES	YES
Lactulose	NO	NO	NO	YES	NO	YES	YES	YES	NO	YES	NO	YES	YES	NO	NO	NO	NO
Maltotriose	NO	NO	NO	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	NO	YES	YES
Glyoxylic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
Methyl Pyruvate	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	YES
D-Galacturonic acid	YES	NO	NO	YES	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES
D-Mannose	NO	YES	NO	YES	YES	YES	YES	YES	NO	NO	NO	NO	YES	NO	YES	NO	NO
D-Mannitol	NO	NO	NO	YES	YES	NO	YES	NO	NO	NO	NO	YES	NO	YES	YES	YES	YES
D-Melibiose	NO	NO	NO	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	NO	YES	NO	NO
Sucrose	NO	NO	NO	YES	NO	YES	YES	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO
2-Deoxy adenosine	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES
D-Cellobiose	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES
D-Malic acid	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	YES
Phenylethyl-amine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Dulcitol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
L-Glutamic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Thymidine	NO	NO	NO	NO	YES	NO	NO	NO	YES	YES	NO	YES	NO	NO	NO	YES	YES
Uridine	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	NO	NO	YES	YES
Adenosine	YES	NO	NO	YES	YES	NO	NO	NO	NO	YES	YES	YES	YES	NO	YES	NO	YES
Inosine	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO
L-Malic acid	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES
2-Aminoethanol	YES	NO	NO	YES	YES	YES	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES

Table K: Substrate utilization as determined by BIOLOG PM1 MicroPlates by bacterial endophytes belonging to core OTUs.

Strain/Substrate	SYM00290	SYM00292	SYM00003	SYM00043	SYM00050	SYM05066	SYM00508	SYM00525	SYM00053	SYM00538A	SYM00538B	SYM00538i	SYM00543	SYM00563	SYM00574	SYM00057B	SYM00617
D-Serine	NO	YES	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO
D-Glucose-6-Phosphate	NO	NO	NO	YES	YES	NO	YES	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO
L-Asparagine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO

L-glutamine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Glycyl-L-Aspartic acid	NO	NO	NO	YES	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
Glycyl-L-Glutamic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO
Glycyl-L-Proline	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO
L-Arabinose	YES	YES	YES	YES	YES	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	NO
D-Sorbitol	NO	NO	NO	NO	YES	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO
D-Galactonic acid-?-lactone	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Aspartic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
m-Tartaric acid	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Citric acid	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	YES	NO	NO
Tricarballic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
p-Hydroxy Phenyl acetic acid	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
N-Acetyl-D-Glucosamine	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	YES	YES	NO	YES	NO	NO
Glycerol	YES	YES	NO	YES	YES	NO	NO	NO	NO	NO	YES	NO	YES	NO	YES	NO	NO
D-L-Malic acid	YES	YES	NO	YES	NO	NO	YES	YES	NO	YES	YES	YES	YES	NO	YES	NO	YES
D-Glucosaminic acid	NO	NO	YES	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Glucose-1-Phosphate	NO	NO	NO	YES	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
m-Inositol	NO	YES	NO	YES	YES	NO	NO	YES	YES	NO	YES	YES	YES	NO	YES	NO	NO
L-Serine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO
m-Hydroxy Phenyl Acetic acid	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO
D-Saccharic acid	NO	YES	NO	YES	YES	NO	YES	NO	NO	NO	NO	YES	YES	NO	YES	NO	NO
L-Fucose	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO
D-Ribose	YES	YES	YES	YES	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO
1,2-Propanediol	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
D-Fructose-6-Phosphate	NO	NO	NO	NO	YES	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
D-Threonine	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Threonine	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO
Tyramine	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
Succinic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Glucuronic acid	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Tween 20	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	YES	NO
Tween 40	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
Tween 80	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO
Fumaric acid	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
L-Alanine	YES	YES	YES	YES	YES	NO	NO	YES	YES	NO	NO	NO	YES	NO	YES	NO	NO
D-Psicose	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Galactose	YES	YES	NO	YES	YES	NO	YES	YES	NO	NO	YES	NO	NO	NO	NO	YES	NO
D-Gluconic acid	YES	YES	NO	YES	YES	NO	YES	NO	YES	NO	YES	NO	YES	NO	YES	NO	NO
L-Rhamnose	YES	YES	NO	YES	YES	NO	YES	YES	YES	NO	YES	NO	NO	YES	NO	YES	YES
a-Keto-Glutaric acid	NO	YES	NO	NO	YES	NO	NO	NO	YES	YES	YES	YES	YES	YES	NO	YES	NO
a-Hydroxy Glutaric acid-?-lactone	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO
Bromo succinic acid	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO
L-Alanyl-Glycine	YES	YES	YES	NO	YES	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO	YES	NO
L-Lyxose	NO	NO	NO	YES	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Aspartic acid	NO	YES	NO	NO	YES	NO	YES	YES	NO	NO	YES	YES	YES	NO	YES	NO	NO
D-L-a-Glycerol phosphate	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
D-Fructose	YES	YES	NO	YES	YES	NO	NO	YES	YES	NO	YES	NO	YES	NO	NO	NO	NO
a-Keto-Butyric	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO

acid																	
α-Hydroxy Butyric acid	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
Propionic acid	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO
Acetoacetic acid	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO
Glucuronamide	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Proline	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	YES	NO	NO
D-Xylose	YES	YES	YES	YES	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO	YES	NO	NO
Acetic acid	YES	YES	NO	YES	NO	NO	NO	YES	NO	NO	YES	YES	YES	NO	YES	YES	NO
α-Methyl-D-Galactoside	YES	YES	NO	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO
β-Methyl-D-glucoside	YES	YES	NO	YES	YES	NO	YES	YES	YES	NO	YES	NO	YES	NO	YES	NO	NO
Mucic acid	NO	YES	YES	YES	YES	NO	YES	YES	YES	NO	NO	YES	YES	NO	YES	YES	NO
N-acetyl-β-D-Mannosamine	YES	YES	NO	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO	YES	NO	YES
Pyruvic acid	YES	YES	YES	YES	YES	NO	YES	NO	NO	NO	YES	NO	YES	NO	YES	NO	NO
D-Alanine	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
L-Lactic acid	NO	YES	NO	YES	YES	NO	NO	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO
α-D-Glucose	YES	YES	NO	YES	YES	NO	NO	NO	YES	NO	YES	NO	YES	NO	NO	YES	YES
α-D-Lactose	YES	YES	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO
Adonitol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Glycolic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
Mono Methyl Succinate	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO
L-Galactonic acid-2-lactone	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	NO	YES	NO	NO	YES	NO	NO
D-Trehalose	YES	YES	NO	YES	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO
Formic acid	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	YES	NO
Maltose	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	YES	NO	YES
Lactulose	YES	YES	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO
Maltotriose	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	YES	NO	YES
Glyoxylic acid	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
Methyl Pyruvate	YES	YES	NO	NO	YES	NO	YES	NO	NO	YES	YES	NO	YES	NO	YES	NO	NO
D-Galacturonic acid	NO	YES	NO	YES	YES	NO	NO	NO	NO	NO	YES	YES	NO	NO	YES	NO	NO
D-Mannose	NO	YES	NO	YES	YES	NO	NO	NO	YES	YES	YES	NO	NO	YES	NO	NO	NO
D-Mannitol	YES	YES	NO	YES	YES	NO	NO	YES	YES	NO	YES	YES	NO	NO	YES	NO	NO
D-Melibiose	YES	YES	NO	YES	YES	NO	NO	YES	YES	NO	YES	NO	NO	NO	NO	NO	YES
Sucrose	YES	YES	NO	YES	YES	NO	NO	YES	YES	NO	YES	YES	NO	NO	NO	NO	NO
2-Deoxy adenosine	NO	YES	NO	YES	YES	NO	YES	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO
D-Cellobiose	YES	YES	NO	YES	YES	NO	YES	YES	YES	NO	YES	NO	YES	YES	YES	NO	YES
D-Malic acid	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
Phenylethyl-amine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Dulcitol	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
L-Glutamic acid	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Thymidine	YES	YES	NO	YES	YES	NO	YES	NO	YES	NO	YES	NO	YES	NO	YES	NO	NO
Uridine	YES	YES	YES	NO	YES	NO	YES	YES	YES	NO	YES	YES	YES	NO	YES	NO	NO
Adenosine	YES	YES	YES	YES	NO	NO	YES	NO	NO	NO	YES	NO	YES	NO	YES	NO	NO
Inosine	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	YES	NO	NO	NO	NO
L-Malic acid	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO
2-Aminoethanol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	YES	NO	NO

Table L: Substrate utilization as determined by BIOLOG PM1 MicroPlates by bacterial endophytes belonging to core OTUs.

Strain/Substrate	SYN00620	SYN00627	SYN00628	SYN0062C	SYN00650	SYN00668	SYN00670	SYN00714	SYN00809	SYN00905	SYN00924	SYN00963	SYN00978	SYN00982	SYN00987	SYN00991	SYN00999

D-Serine	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO
D-Glucose-6-Phosphate	YES	YES	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
L-Asparagine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-glutamine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Glycyl-L-Aspartic acid	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Glycyl-L-Glutamic acid	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Glycyl-L-Proline	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
L-Arabinose	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO	NO	NO	NO	NO	NO	YES	NO	YES
D-Sorbitol	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Galactonic acid-?-lactone	NO	YES	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Aspartic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
m-Tartaric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Citric acid	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Tricarballic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
p-Hydroxy Phenyl acetic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
N-Acetyl-D-Glucosamine	NO	YES	YES	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
Glycerol	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-L-Malic acid	NO	NO	NO	NO	NO	YES	YES	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
D-Glucosaminic acid	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Glucose-1-Phosphate	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
m-Inositol	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Serine	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
m-Hydroxy Phenyl Acetic acid	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Saccharic acid	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES
L-Fucose	NO	NO	YES	NO	NO	NO	YES	YES	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO
D-Ribose	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
1,2-Propanediol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Fructose-6-Phosphate	YES	YES	YES	NO	NO	NO	YES	YES	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO
D-Threonine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Threonine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Tyramine	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Succinic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Glucuronic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Tween 20	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Tween 40	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Tween 80	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	YES	NO	NO	YES	NO	NO	NO
Fumaric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Alanine	YES	NO	YES	NO	NO	YES	YES	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
D-Psicose	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Galactose	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO

D-Gluconic acid	YES	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Rhamnose	YES	YES	YES	NO	YES	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
α -Keto-Glutaric acid	NO	NO	NO	NO	NO	YES	YES	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO
α -Hydroxy Glutaric acid- γ -lactone	NO	NO	NO	NO	NO	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
Bromo succinic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Alanyl-Glycine	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Lyxose	NO	NO	NO	NO	NO	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Aspartic acid	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO
D-L-a-Glycerol phosphate	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Fructose	NO	NO	NO	NO	NO	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
α -Keto-Butyric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
α -Hydroxy Butyric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Propionic acid	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO
Acetoacetic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Glucuronamide	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Proline	NO	NO	YES	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Xylose	NO	YES	YES	NO	YES	YES	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO
Acetic acid	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO
α -Methyl-D-Galactoside	YES	YES	YES	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO
β -Methyl-D-glucoside	NO	YES	YES	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
Mucic acid	NO	YES	YES	NO	YES	YES	YES	YES	YES	NO	NO	YES	NO	NO	YES	NO	YES
N-acetyl- β -D-Mannosamine	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO
Pyruvic acid	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Alanine	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Lactic acid	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO
α -D-Glucose	NO	NO	NO	NO	YES	NO	YES	YES	NO	NO	NO	NO	NO	NO	YES	YES	NO
α -D-Lactose	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO
Adonitol	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
Glycolic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Mono Methyl Succinate	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES
L-Galactonic-acid- γ -lactone	YES	YES	YES	NO	NO	YES	YES	YES	YES	NO	NO	NO	NO	NO	YES	NO	NO
D-Trehalose	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
Formic acid	NO	YES	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
Maltose	NO	YES	YES	YES	YES	NO	YES	YES	NO	YES	NO	YES	NO	NO	NO	YES	NO
Lactulose	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	YES	NO	NO
Maltotriose	NO	YES	YES	NO	NO	NO	YES	YES	NO	YES	NO	YES	NO	NO	NO	NO	NO
Glyoxylic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES
Methyl Pyruvate	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES
D-Galacturonic acid	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Mannose	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO

D-Mannitol	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Melibiose	NO	YES	YES	YES	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
Sucrose	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO
2-Deoxy adenosine	YES	YES	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Cellobiose	NO	YES	YES	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO
D-Malic acid	NO	NO	NO	NO	YES	YES	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO
Phenylethyl-amine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Dulcitol	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
L-Glutamic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Thymidine	NO	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
Uridine	NO	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
Adenosine	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Inosine	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Malic acid	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
2-Aminoethanol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO

Table M: Substrate utilization as determined by BIOLOG PM2A MicroPlates by bacterial endophytes belonging to core OTUs.

Strain/Substrate	SYN00103	SYN01049	SYN00013	SYN00017A	SYN00018	SYN000183	SYN000184	SYN00020	SYN000207	SYN000212	SYN000219	SYN000234	SYN000236	SYN000248	SYN000249
N-acetyl-D-Galactosamine	NO	NO	NO	YES	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO
Gentiobiose	NO	NO	NO	YES	YES	YES	YES	YES	NO	YES	YES	YES	NO	YES	YES
D-Raffinose	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	YES	YES	NO	YES	YES
Capric acid	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
D-lactic acid methyl ester	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Acetamide	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Ornithine	YES	NO	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	NO	NO
Chondroitin sulfate C	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
N-acetyl-neuraminic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-glucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
Salicin	NO	NO	NO	YES	NO	YES	YES	NO	NO	YES	YES	YES	NO	NO	YES
Caproic acid	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
Malonic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Alaninamide	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	YES	NO	YES
L-Phenylalanine	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
α -Cyclodextrin	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO
β -D-allose	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Lactitol	NO	NO	NO	YES	NO	YES	YES	NO	NO	NO	NO	YES	NO	YES	NO
Sedoheptulosan	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO

Citraconic acid	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Melibionc acid	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	YES	NO	NO	YES	NO
N-Acetyl-L-Glutamic acid	YES	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO
L-Pyrogutamic acid	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO
B-Cyclodextrin	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	YES
Amygdalin	NO	NO	NO	NO	NO	YES	YES	NO	NO	YES	NO	YES	NO	YES	YES
D-Melezitose	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	YES	YES
L-Sorbose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Citramalic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Oxalic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Arginine	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Valine	YES	NO	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	NO	NO	NO
γ-Cyclodextrin	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO
D-arabinose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Maltitol	NO	NO	NO	YES	NO	YES	YES	NO	NO	YES	NO	YES	NO	YES	YES
Stachyose	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO
D-Glucosamine	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES
Oxalomalic acid	YES	NO	YES	YES	YES	YES	YES	YES	NO	NO	NO	YES	YES	YES	YES
Glycine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
D,L-Carnitine	YES	YES	YES	YES	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES
Dextrin	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	YES	NO	NO	NO
D-arabitol	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
α-Methyl-D-Glucoside	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	YES
D-Tagatose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
2-Hydroxy benzoic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Quinic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Histidine	NO	YES	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO
Sec-Butylamine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
Gelatin	NO	NO	NO	NO	NO	YES	YES	NO	YES	NO	NO	YES	NO	NO	YES
L-arabitol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
β-Methyl-D-Galactoside	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO
Turanose	NO	YES	NO	YES	NO	YES	YES	NO	NO	YES	NO	YES	NO	NO	YES
4-Hydroxy benzoic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Ribono-1,4-Lactone	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Homoserine	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
D,L-Octopamine	YES	NO	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	NO	NO
Glycogen	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO
Arbutin	NO	NO	NO	YES	NO	YES	YES	NO	NO	YES	YES	YES	NO	YES	YES
3-Methyl Glucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Xylitol	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO

β -Hydroxy butyric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Sebacic acid	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
Hydroxy-L-Proline	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES
Putrescine	YES	NO	NO	YES	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
Inulin	NO	NO	NO	YES	NO	YES	YES	NO	NO	NO	YES	NO	NO	YES	YES
2-Deoxy-D-Ribose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
β -Methyl-D-Glucuronic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
N-Acetyl-D-glucosaminitol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
γ -Hydroxy butyric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Sorbic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Isoleucine	YES	NO	YES	YES	NO	NO	NO	NO	YES	YES	NO	YES	NO	NO	NO
Dihydroxy acetone	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
Laminarin	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO
i-Erythritol	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
α -Methyl-D-Mannoside	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
γ -amino butyric acid	YES	YES	YES	YES	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES
α -Keto-valeric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Succinamic acid	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
L-Leucine	YES	NO	YES	YES	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO
2,3-Butanediol	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO
Mannan	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Fucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
β -Methyl-D-Xyloside	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO
d-amino valeric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
Itaconic acid	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO
D-Tartaric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Lysine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
2,3-Butanone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Pectin	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO
3-O- β -D-Galactopyranosyl-D-arabinose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO
Palatinose	NO	NO	NO	YES	NO	YES	YES	NO	NO	YES	YES	YES	NO	NO	NO
Butyric acid	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
5-Keto-D-Gluconic acid	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO
L-Tartaric acid	YES	NO	YES	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO
L-Methionine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
3-Hydroxy 2-Butanone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO

Table N: Substrate utilization as determined by BIOLOG PM2A MicroPlates by bacterial endophytes belonging to core OTUs.

Strain/Substrate	SYM00260	SYM00290	SYM00292	SYM00003	SYM00043	SYM00050	SYM00506	SYM00508	SYM00525	SYM00053	SYM00538A	SYM00538B	SYM00538i	SYM00543	SYM00563	SYM00574
N-acetyl-D-Galactosamine	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
Gentiobiose	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	NO	YES	YES	NO	YES	NO
D-Raffinose	YES	YES	YES	NO	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO
Capric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-lactic acid methyl ester	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
Acetamide	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
L-Ornithine	YES	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Chondroitin sulfate C	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
N-acetyl-neuraminic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-glucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Salicin	YES	YES	YES	NO	NO	YES	NO	YES	YES	YES	NO	YES	YES	NO	YES	NO
Caproic acid	YES	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
Malonic acid	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO
L-Alaninamide	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	YES	NO	NO	YES
L-Phenylalanine	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
α -Cyclodextrin	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO
β -D-allose	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Lactitol	NO	YES	YES	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO
Sedoheptulosan	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Citraconic acid	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
Melibionc acid	YES	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
N-Acetyl-L-Glutamic acid	YES	NO	YES	NO	NO	YES	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO
L-Pyrogutamic acid	YES	NO	YES	YES	NO	NO	NO	YES	YES	NO	YES	NO	YES	YES	NO	YES
β -Cyclodextrin	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO
Amygdalin	NO	YES	YES	NO	NO	NO	NO	NO	YES	NO	NO	YES	YES	NO	YES	NO
D-Melezitose	NO	YES	YES	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO
L-Sorbose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Citramalic acid	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Oxalic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Arginine	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES
L-Valine	YES	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
γ -Cyclodextrin	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO
D-arabinose	NO	YES	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES
Maltitol	NO	YES	YES	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO
Stachyose	YES	YES	YES	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO

D-Glucosamine	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Oxalomalic acid	YES	YES	YES	YES	YES	NO	YES	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES
Glycine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D,L-Carnitine	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
Dextrin	YES	YES	YES	NO	NO	NO	NO	YES	YES	NO	YES	YES	NO	YES	NO	NO	NO
D-arabitol	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
α -Methyl-D-Glucoside	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
D-Tagatose	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
2-Hydroxy benzoic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Quinic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Histidine	YES	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	YES
Sec-Butylamine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Gelatin	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	YES	NO	NO	NO
L-arabitol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
β -Methyl-D-Galactoside	NO	YES	YES	NO	NO	NO	NO	YES	YES	NO	NO	YES	NO	NO	NO	NO	YES
Turanose	NO	YES	YES	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO
4-Hydroxy benzoic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
D-Ribono-1,4-Lactone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
L-Homoserine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
D,L-Octopamine	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Glycogen	YES	YES	YES	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO
Arbutin	NO	YES	YES	NO	NO	YES	NO	YES	YES	YES	YES	NO	YES	NO	YES	NO	NO
3-Methyl Glucose	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
Xylitol	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES
β -Hydroxy butyric acid	YES	NO	NO	NO	NO	YES	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	YES
Sebacic acid	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
Hydroxy-L-Proline	YES	NO	YES	NO	NO	YES	NO	NO	YES	YES	NO	NO	NO	YES	NO	YES	YES
Putrescine	YES	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO
Inulin	YES	YES	YES	YES	YES	NO	NO	NO	NO	NO	YES	YES	YES	NO	NO	YES	YES
2-Deoxy-D-Ribose	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
β -Methyl-D-Glucuronic acid	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
N-Acetyl-D-glucosaminitol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
γ -Hydroxy butyric acid	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Sorbic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Isoleucine	YES	NO	YES	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
Dihydroxy acetone	NO	NO	YES	NO	NO	YES	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	YES
Laminarin	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES
i-Erythritol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
α -Methyl-D-Mannoside	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
γ -amino butyric acid	YES	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES

a-Keto-valeric acid	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Succinamic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Leucine	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
2,3-Butanediol	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
Mannan	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Fucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
B-Methyl-D-Xyloside	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
d-amino valeric acid	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Itaconic acid	YES	NO	YES	NO	NO	YES	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO
D-Tartaric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
L-Lysine	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
2,3-Butanone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Pectin	NO	YES	YES	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO
3-O-β-D-Galactopyranosyl-D-arabinose	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
Palatinose	NO	YES	YES	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO
Butyric acid	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
5-Keto-D-Gluconic acid	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES
L-Tartaric acid	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES
L-Methionine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
3-Hydroxy 2-Butanone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO

Table O: Substrate utilization as determined by BIOLOG PM2A MicroPlates by bacterial endophytes belonging to core OTUs.

Strain/Substrate	SYN00057B	SYN000617	SYN000620	SYN000627	SYN000628	SYN00062C	SYN000650	SYN000668	SYN00070	SYN000714	SYN000009	SYN000905	SYN000924	SYN000963	SYN000978	SYN000982	SYN000987	SYN000991	SYN000999
N-acetyl-D-Galactosamine	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	YES	NO
Gentiobiose	NO	YES	YES	YES	YES	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO
D-Raffinose	NO	NO	YES	YES	YES	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO
Capric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-lactic acid methyl ester	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Acetamide	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Ornithine	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
Chondroitin sulfate C	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
N-acetyl-neuraminic acid	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-glucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Salicin	NO	YES	NO	YES	YES	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	YES	NO
Caproic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Malonic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO

L-Alaninamide	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	YES	NO	NO	NO	NO	NO
L-Phenylalanine	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
α -Cyclodextrin	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO
β -D-allose	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
Lactitol	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO
Sedoheptulosan	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Citraconic acid	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO
Melibionc acid	NO	NO	YES	YES	YES	NO	NO	YES	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO
N-Acetyl-L-Glutamic acid	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
L-Pyrogutamic acid	NO	NO	NO	NO	NO	YES	NO	YES	YES	YES	YES	NO	NO	NO	NO	YES	YES	NO	NO
β -Cyclodextrin	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO
Amygdalin	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
D-Melezitose	NO	YES	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	YES	NO	NO
L-Sorbose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO
Citramalic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Oxalic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Arginine	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Valine	NO	NO	NO	NO	NO	NO	NO	YES	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO
γ -Cyclodextrin	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-arabinose	NO	NO	NO	NO	YES	NO	YES	NO	NO	YES	NO	NO	YES	YES	NO	NO	NO	NO	NO
Maltitol	NO	NO	NO	YES	YES	NO	NO	NO	NO	YES	NO	YES	NO	YES	NO	NO	NO	NO	NO
Stachyose	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
D-Glucosamine	YES	YES	NO	YES	YES	YES	NO	YES	YES	YES	YES	YES	NO	NO	YES	NO	YES	YES	YES
Oxalomalic acid	YES	YES	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO	NO	YES	NO	YES	NO	YES
Glycine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D,L-Carnitine	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
Dextrin	NO	YES	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
D-arabitol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
α -Methyl-D-Glucoside	NO	NO	NO	YES	YES	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO
D-Tagatose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
2-Hydroxy benzoic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Quinic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Histidine	YES	NO	YES	NO	NO	NO	YES	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
Sec-Butylamine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Gelatin	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO
L-arabitol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
β -Methyl-D-Galactoside	NO	NO	YES	YES	YES	YES	NO	NO	NO	YES	NO	NO	NO	YES	YES	NO	YES	NO	NO
Turanose	NO	NO	NO	YES	NO	YES	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	YES	NO	NO
4-Hydroxy benzoic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Ribono-1,4-Lactone	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO

L-Homoserine	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D,L-Octopamine	NO	YES	NO	NO	NO	YES	NO	YES	YES	NO	YES	YES	NO	YES	NO	NO	YES	YES	NO
Glycogen	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Arbutin	NO	YES	NO	YES	YES	YES	NO	NO	YES	YES	NO	YES	NO	NO	YES	NO	NO	YES	NO
3-Methyl Glucose	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Xylitol	YES	NO	NO	NO	NO	NO	NO	NO	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO
β -Hydroxy butyric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Sebacic acid	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
Hydroxy-L-Proline	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	YES
Putrescine	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Inulin	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES
2-Deoxy-D-Ribose	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
β -Methyl-D-Glucuronic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
N-Acetyl-D-glucosaminitol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
γ -Hydroxy butyric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
Sorbic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Isoleucine	NO	NO	NO	NO	NO	YES	NO	YES	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO
Dihydroxy acetone	YES	NO	NO	YES	YES	NO	YES	NO	NO	NO	NO	NO	YES	YES	NO	NO	YES	NO	NO
Laminarin	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO
i-Erythritol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
α -Methyl-D-Mannoside	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
γ -amino butyric acid	YES	NO	NO	NO	NO	NO	YES	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
α -Keto-valeric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Succinamic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
L-Leucine	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO
2,3-Butanediol	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Mannan	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Fucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
β -Methyl-D-Xyloside	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
d-amino valeric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Itaconic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
D-Tartaric acid	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Lysine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
2,3-Butanone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Pectin	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
3-O- β -D-Galactopyranosyl-D-arabinose	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
Palatinose	NO	NO	NO	YES	YES	YES	NO	NO	NO	YES	NO	YES	NO	YES	YES	NO	YES	NO	NO
Butyric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
5-Keto-D-Gluconic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Tartaric acid	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO

L-Methionine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
3-Hydroxy 2-Butanone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO

Table P: Substrate utilization as determined by BIOLOG PM1 MicroPlates by fungal endophytes belonging to core OTUs.

Strain/Substrate	SYM00120	SYM00122	SYM00123	SYM00124	SYM00129	SYM01300	SYM01310	SYM01311	SYM01314	SYM01315	SYM01325	SYM01326	SYM01327	SYM01328	SYM01333	SYM0135	SYM0136
D-Serine	NO	NO	YES	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO
D-Glucose-6-Phosphate	NO	NO	NO	YES	YES	NO	NO	NO	YES	NO	NO	NO	YES	YES	NO	NO	NO
L-Asparagine	NO	NO	NO	YES	NO	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	NO	NO
L-glutamine	NO	NO	NO	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	NO	YES	YES	NO
Glycyl-L-Aspartic acid	NO	NO	NO	NO	NO	YES	NO	YES	NO	YES	NO	YES	n/a	NO	NO	NO	NO
Glycyl-L-Glutamic acid	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO	NO	YES	YES	NO	NO	NO
Glycyl-L-Proline	NO	NO	NO	YES	NO	YES	NO	YES	YES	NO	NO	YES	YES	YES	NO	NO	NO
L-Arabinose	YES	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Sorbitol	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Galactonic acid-?-lactone	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO
D-Aspartic acid	NO	NO	YES	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
m-Tartaric acid	NO	NO	NO	YES	NO	YES	NO	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO
Citric acid	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO	YES	n/a	NO	YES	NO	NO
Tricarballic acid	NO	NO	NO	YES	NO	YES	NO	YES	YES	NO	YES	NO	YES	YES	NO	YES	NO
p-Hydroxy Phenyl acetic acid	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	YES	YES	NO	NO	NO	NO
N-Acetyl-D-Glucosamine	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES
Glycerol	YES	NO	NO	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	NO	NO
D-L-Malic acid	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	NO	NO
D-Glucosaminic acid	NO	NO	NO	YES	NO	YES	NO	NO	YES	NO	NO	YES	YES	NO	NO	NO	NO
D-Glucose-1-Phosphate	NO	NO	YES	YES	NO	YES	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO
m-Inositol	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	n/a	NO	YES	NO	NO
L-Serine	NO	NO	NO	YES	NO	YES	YES	YES	YES	NO	NO	YES	YES	NO	YES	NO	NO
m-Hydroxy Phenyl Acetic acid	NO	NO	NO	YES	NO	YES	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO
D-Saccharic acid	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	NO
L-Fucose	NO	NO	NO	YES	NO	YES	NO	YES	YES	YES	NO	NO	YES	NO	NO	NO	NO
D-Ribose	NO	NO	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	NO	YES	NO
1,2-Propanediol	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Fructose-6-Phosphate	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Threonine	NO	NO	YES	YES	NO	NO	NO	YES	NO	NO	NO	NO	n/a	YES	NO	NO	NO
L-Threonine	NO	YES	NO	YES	NO	YES	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO
Tyramine	YES	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	NO	NO
Succinic acid	NO	NO	NO	YES	NO	YES	YES	YES	NO	NO	NO	YES	YES	NO	YES	NO	NO

D-Glucuronic acid	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	NO
Tween 20	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES
Tween 40	NO	NO	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Tween 80	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Fumaric acid	NO	NO	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	n/a	YES	YES	NO	NO
L-Alanine	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO
D-Psicose	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
D-Galactose	YES	NO	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Gluconic acid	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES
L-Rhamnose	NO	NO	NO	YES	YES	YES	NO	YES	YES	YES	YES	YES	NO	YES	NO	NO	NO	NO
α -Keto-Glutaric acid	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	NO	NO
α -Hydroxy Glutaric acid- γ -lactone	NO	NO	YES	YES	NO	YES	YES	YES	YES	YES	NO	NO	NO	YES	YES	YES	NO	NO
Bromo succinic acid	NO	NO	YES	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	n/a	NO	NO	NO	NO
L-Alanyl-Glycine	NO	NO	YES	YES	NO	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	NO	NO
L-Lyxose	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Aspartic acid	NO	NO	YES	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	NO	NO
D-L-a-Glycerol phosphate	NO	NO	NO	YES	NO	NO	YES	NO	YES	YES	NO	NO	YES	NO	NO	NO	NO	NO
D-Fructose	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO
α -Keto-Butyric acid	NO	NO	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO
α -Hydroxy Butyric acid	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Propionic acid	NO	NO	YES	YES	NO	YES	YES	YES	YES	YES	NO	NO	NO	n/a	NO	NO	NO	NO
Acetoacetic acid	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
Glucuronamide	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Proline	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	NO
D-Xylose	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	NO	YES	YES	NO
Acetic acid	NO	NO	YES	YES	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
α -Methyl-D-Galactoside	NO	NO	NO	YES	YES	NO	YES	YES	NO	NO	YES	YES	YES	YES	YES	NO	YES	YES
β -Methyl-D-glucoside	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	NO	YES	YES
Mucic acid	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	n/a	YES	YES	NO	NO
N-acetyl- β -D-Mannosamine	NO	NO	YES	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO
Pyruvic acid	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	NO	YES	NO	NO
D-Alanine	NO	NO	YES	YES	NO	YES	YES	YES	YES	YES	NO	NO	YES	YES	NO	YES	NO	NO
L-Lactic acid	NO	NO	YES	NO	NO	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	NO	NO
α -D-Glucose	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
α -D-Lactose	NO	NO	YES	YES	YES	YES	NO	YES	YES	NO	NO	YES	YES	YES	YES	YES	NO	NO
Adonitol	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	NO	NO
Glycolic acid	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	n/a	NO	NO	NO	NO	NO
Mono Methyl Succinate	NO	NO	NO	YES	NO	YES	NO	YES	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO
L-Galactonic-acid- γ -lactone	NO	NO	NO	NO	NO	YES	YES	YES	YES	YES	NO	YES	YES	YES	NO	YES	YES	NO
D-Trehalose	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO

Formic acid	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO
Maltose	YES	NO	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES
Lactulose	YES	NO	NO	YES	NO	YES	NO	YES	NO	YES	NO	NO	YES	YES	NO	NO	NO
Maltotriose	NO	NO	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES
Glyoxylic acid	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	n/a	NO	NO	NO	NO
Methyl Pyruvate	NO	NO	YES	YES	NO	YES	YES	YES	NO	NO	NO	YES	YES	NO	NO	NO	NO
D-Galacturonic acid	NO	NO	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	NO	YES	NO	NO
D-Mannose	NO	NO	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES
D-Mannitol	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES
D-Melibiose	NO	NO	YES	YES	YES	YES	YES	YES	NO	NO	YES	NO	YES	YES	NO	YES	YES
Sucrose	NO	NO	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES
2-Deoxy adenosine	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Cellobiose	NO	NO	YES	YES	NO	YES	YES	YES	YES	NO	YES	YES	n/a	YES	NO	YES	NO
D-Malic acid	NO	NO	NO	YES	NO	YES	YES	YES	YES	NO	NO	NO	YES	NO	NO	NO	NO
Phenylethyl-amine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Dulcitol	NO	NO	YES	YES	YES	YES	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO
L-Glutamic acid	NO	NO	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES
Thymidine	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO
Uridine	NO	NO	YES	YES	NO	YES	YES	YES	YES	NO	NO	YES	YES	NO	YES	NO	YES
Adenosine	NO	NO	YES	YES	NO	YES	NO	NO	YES	YES	NO	NO	YES	NO	YES	NO	NO
Inosine	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	NO	YES	n/a	NO	YES	NO	NO
L-Malic acid	YES	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	NO
2-Aminoethanol	NO	NO	YES	YES	NO	YES	YES	YES	YES	NO	YES	NO	YES	NO	YES	NO	NO

Table Q: Substrate utilization as determined by BIOLOG PM1 MicroPlates by fungal endophytes belonging to core OTUs.

Strain/Substrate	SYM00151	SYM00154	SYM015811	SYM15820	SYM15825	SYM15828	SYM15831	SYM15837	SYM15839	SYM15847	SYM15872	SYM15890	SYM15901	SYM15920	SYM15926	SYM15928
D-Serine	NO	NO	NO	NO	YES	NO	NO	NO	YES	YES	NO	NO	NO	YES	NO	NO
D-Glucose-6-Phosphate	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Asparagine	YES	NO	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES
L-glutamine	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO
Glycyl-L-Aspartic acid	NO	YES	YES	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
Glycyl-L-Glutamic acid	NO	YES	NO	YES	YES	YES	NO	YES	NO	YES	YES	YES	YES	YES	NO	NO
Glycyl-L-Proline	YES	YES	NO	YES	YES	YES	YES	NO	NO	YES	YES	NO	YES	YES	NO	YES
L-Arabinose	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES
D-Sorbitol	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES
D-Galactonic acid-?-lactone	NO	YES	YES	YES	NO	NO	NO	YES	YES	NO	NO	NO	NO	YES	YES	NO
D-Aspartic acid	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	YES

m-Tartaric acid	YES	NO	NO	NO	YES	NO	YES	NO	YES	NO	YES	NO	YES	YES	NO	NO
Citric acid	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	NO	NO	NO	NO
Tricarballic acid	YES	NO	NO	NO	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	NO	NO
p-Hydroxy Phenyl acetic acid	YES	YES	YES	YES	NO	YES	NO	YES	YES	NO	NO	NO	NO	YES	NO	NO
N-Acetyl-D-Glucosamine	YES	YES	NO	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
Glycerol	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
D-L-Malic acid	NO	YES	NO	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES	NO	NO
D-Glucosaminic acid	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
D-Glucose-1-Phosphate	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
m-Inositol	YES	YES	NO	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	NO	NO
L-Serine	NO	NO	NO	YES	YES	YES	NO	YES	NO	NO	YES	NO	YES	YES	NO	NO
m-Hydroxy Phenyl Acetic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Saccharic acid	YES	NO	NO	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	NO	YES
L-Fucose	NO	YES	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Ribose	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES
1,2-Propanediol	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Fructose-6-Phosphate	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Threonine	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO
L-Threonine	NO	NO	YES	YES	YES	NO	NO	YES	NO	NO	YES	NO	YES	YES	NO	NO
Tyramine	YES	YES	NO	NO	YES	YES	NO	YES	YES	YES	YES	NO	YES	YES	YES	NO
Succinic acid	YES	YES	NO	YES	YES	YES	NO	YES	NO	NO	NO	YES	YES	YES	NO	NO
D-Glucuronic acid	NO	YES	NO	YES	YES	YES	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES
Tween 20	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES
Tween 40	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	NO	YES
Tween 80	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES
Fumaric acid	NO	NO	YES	YES	YES	YES	YES	NO	NO	NO	YES	NO	YES	YES	NO	YES
L-Alanine	YES	NO	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	YES	YES	NO
D-Psicose	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Galactose	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	NO
D-Gluconic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES
L-Rhamnose	YES	YES	NO	NO	YES	NO	NO	YES	YES	YES	YES	NO	YES	YES	NO	NO
α -Keto-Glutaric acid	NO	NO	YES	YES	NO	YES	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO
α -Hydroxy Glutaric acid- lactone	NO	YES	NO	YES	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
Bromo succinic acid	NO	YES	NO	NO	YES	YES	NO	NO	YES	YES	YES	NO	YES	YES	NO	NO
L-Alanyl-Glycine	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES
L-Lyxose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO
L-Aspartic acid	YES	NO	NO	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	NO	YES
D-L- α -Glycerol phosphate	NO	YES	YES	YES	NO	YES	NO	YES	YES	NO	YES	NO	NO	NO	YES	NO
D-Fructose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO
α -Keto-Butyric acid	NO	YES	NO	NO	YES	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO

a-Hydroxy Butyric acid	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Propionic acid	NO	YES	NO	NO	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	NO	NO
Acetoacetic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
Glucuronamide	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Proline	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Xylose	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES
Acetic acid	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	NO
a-Methyl-D-Galactoside	YES	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	NO
B-Methyl-D-glucoside	YES	YES	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES
Mucic acid	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO
N-acetyl- B-D-Mannosamine	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
Pyruvic acid	YES	YES	NO	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	NO	YES
D-Alanine	YES	NO	YES	YES	NO	YES	YES	YES	NO	NO	NO	NO	NO	NO	YES	YES	NO
L-Lactic acid	YES	NO	NO	YES	YES	YES	YES	NO	YES	YES	YES	YES	NO	YES	YES	NO	YES
a-D-Glucose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
a-D-Lactose	YES	NO	NO	NO	YES	NO	NO	YES	NO	YES	YES	NO	YES	YES	NO	NO	NO
Adonitol	YES	YES	YES	YES	YES	YES	NO	YES	NO	NO	YES	NO	YES	YES	NO	NO	NO
Glycolic acid	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Mono Methyl Succinate	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES
L-Galactonic-acid-?-lactone	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Trehalose	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES
Formic acid	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	YES	YES	YES	NO	NO	NO
Maltose	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Lactulose	YES	YES	NO	NO	YES	NO	YES	YES	NO	NO	YES	NO	YES	YES	NO	NO	NO
Maltotriose	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES
Glyoxylic acid	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO
Methyl Pyruvate	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES
D-Galacturonic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	NO
D-Mannose	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES
D-Mannitol	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES
D-Melibiose	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES
Sucrose	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES
2-Deoxy adenosine	YES	NO	NO	NO	YES	NO	NO	NO	YES	NO	YES	NO	YES	NO	NO	NO	NO
D-Cellobiose	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES
D-Malic acid	YES	YES	YES	NO	YES	NO	NO	YES	YES	NO	YES	NO	YES	YES	YES	NO	NO
Phenylethyl-amine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Dulcitol	YES	YES	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES
L-Glutamic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO
Thymidine	NO	YES	NO	NO	YES	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO
Uridine	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES	YES	NO	NO	NO

Adenosine	NO	YES	YES	YES	NO	YES	YES	YES	NO	YES	YES	NO	YES	NO	NO	NO	NO
Inosine	YES	NO	YES	YES	NO	YES	YES	YES	NO	NO	NO	YES	YES	YES	YES	YES	NO
L-Malic acid	YES	YES	NO	YES	NO	YES	YES	NO	NO	YES	YES	NO	YES	YES	NO	YES	YES
2-Aminoethanol	YES	YES	NO	YES	YES	YES	NO	YES	NO	YES	YES	NO	YES	YES	YES	YES	YES

Table R: Substrate utilization as determined by BIOLOG PM1 MicroPlates by fungal endophytes belonging to core OTUs.

Strain/Substrate	SYM15932	SYM00160	SYM00034	SYM00566B	SYM00577	SYM00590	SYM00603	SYM0061A	SYM00622	SYM00629	SYM00666	SYM00663	SYM00696	SYM00741A	SYM00741B	SYM00854	SYM00880
D-Serine	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Glucose-6-Phosphate	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Asparagine	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES
L-glutamine	NO	YES	YES	YES	YES	NO	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	NO
Glycyl-L-Aspartic acid	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
Glycyl-L-Glutamic acid	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	YES	NO	NO	NO	YES	NO	NO
Glycyl-L-Proline	NO	YES	NO	YES	YES	NO	YES	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO
L-Arabinose	YES	NO	YES	NO	YES	YES	YES	YES	YES	NO	NO	NO	YES	NO	YES	YES	NO
D-Sorbitol	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	NO	NO	NO	YES	YES	NO	NO
D-Galactonic acid-γ-lactone	NO	NO	NO	YES	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO
D-Aspartic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO
m-Tartaric acid	NO	NO	NO	YES	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
Citric acid	NO	NO	NO	YES	YES	NO	YES	YES	YES	YES	NO	YES	NO	YES	YES	YES	NO
Tricarballic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
p-Hydroxy Phenyl acetic acid	NO	NO	NO	YES	YES	NO	YES	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO
N-Acetyl-D-Glucosamine	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	NO	YES	YES	NO
Glycerol	NO	NO	YES	YES	NO	NO	YES	YES	NO	YES	YES	YES	YES	YES	YES	NO	NO
D-L-Malic acid	NO	YES	NO	NO	YES	NO	YES	YES	YES	YES	NO	YES	NO	NO	YES	YES	YES
D-Glucosaminic acid	NO	NO	YES	YES	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO
D-Glucose-1-Phosphate	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
m-Inositol	NO	NO	NO	YES	YES	NO	YES	YES	YES	YES	NO	NO	NO	NO	YES	NO	NO
L-Serine	NO	NO	NO	YES	YES	NO	YES	YES	YES	NO	NO	YES	NO	YES	YES	YES	NO
m-Hydroxy Phenyl Acetic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
D-Saccharic acid	NO	NO	NO	YES	YES	NO	YES	YES	YES	NO	NO	NO	YES	NO	YES	YES	NO
L-Fucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Ribose	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	NO	NO	YES	NO	NO
1,2-Propanediol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
D-Fructose-6-Phosphate	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Threonine	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Threonine	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO

Tyramine	YES	NO	NO	NO	YES	NO	YES	NO	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO
Succinic acid	NO	NO	YES	NO	NO	NO	YES	YES	YES	YES	YES	YES	NO	NO	NO	YES	YES	NO
D-Glucuronic acid	YES	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO	YES	NO	YES	YES	NO	NO
Tween 20	NO	NO	YES	NO	YES	YES	YES	YES	NO	YES	NO	NO	NO	NO	NO	YES	YES	NO
Tween 40	NO	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	NO	YES	NO	NO	YES	YES	NO
Tween 80	NO	NO	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	NO
Fumaric acid	NO	YES	YES	YES	NO	NO	YES	YES	YES	YES	YES	NO	NO	NO	YES	YES	YES	NO
L-Alanine	NO	NO	NO	NO	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	NO
D-Psicose	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO
D-Galactose	NO	NO	YES	NO	YES	NO	YES	YES	YES	NO	NO	NO	YES	NO	YES	YES	YES	NO
D-Gluconic acid	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	NO	YES	YES	YES	NO
L-Rhamnose	NO	NO	YES	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
α -Keto-Glutaric acid	NO	NO	YES	NO	NO	NO	YES	NO	NO	YES	NO	YES	NO	YES	NO	YES	YES	NO
α -Hydroxy Glutaric acid- γ -lactone	NO	NO	NO	YES	YES	NO	YES	YES	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO
Bromo succinic acid	NO	NO	YES	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO
L-Alanyl-Glycine	NO	NO	NO	NO	NO	NO	YES	YES	YES	YES	NO	YES	NO	NO	NO	YES	YES	NO
L-Lyxose	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
L-Aspartic acid	NO	NO	YES	YES	YES	NO	YES	YES	YES	YES	NO	YES	NO	NO	NO	YES	YES	NO
D-L-a-Glycerol phosphate	NO	NO	NO	YES	NO	NO	YES	NO	YES	YES	NO	YES	NO	NO	NO	YES	NO	NO
D-Fructose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	NO
α -Keto-Butyric acid	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
α -Hydroxy Butyric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
Propionic acid	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO
Acetoacetic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Glucuronamide	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Proline	NO	NO	YES	NO	YES	NO	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	NO
D-Xylose	NO	NO	NO	YES	YES	NO	YES	YES	YES	YES	NO	NO	YES	NO	YES	YES	YES	NO
Acetic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
α -Methyl-D-Galactoside	YES	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
β -Methyl-D-glucoside	YES	YES	YES	YES	YES	YES	NO	YES	NO	NO	YES	NO	YES	NO	NO	YES	YES	YES
Mucic acid	NO	NO	NO	YES	YES	NO	YES	YES	YES	YES	NO	YES	NO	YES	YES	YES	YES	NO
N-acetyl- β -D-Mannosamine	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Pyruvic acid	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO
D-Alanine	NO	NO	NO	YES	YES	NO	YES	YES	YES	YES	NO	NO	NO	NO	NO	YES	YES	NO
L-Lactic acid	NO	NO	NO	NO	NO	NO	YES	YES	YES	NO	NO	YES	YES	NO	YES	NO	NO	NO
α -D-Glucose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO
α -D-Lactose	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	YES	NO	NO	YES	NO	NO
Adonitol	NO	NO	NO	NO	YES	NO	YES	YES	YES	YES	NO	YES	NO	NO	YES	YES	YES	NO
Glycolic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Mono Methyl Succinate	YES	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO

L-Galactonic-acid-?-lactone	NO	NO	NO	NO	YES	NO	YES	YES	NO	YES	NO	NO	YES	NO	YES	YES	NO
D-Trehalose	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	NO
Formic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Maltose	YES	YES	YES	NO	YES	YES	NO	YES	NO	NO	YES	YES	YES	YES	NO	YES	YES
Lactulose	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	YES	NO	NO	YES	NO
Maltotriose	YES	YES	YES	NO	YES	YES	NO	YES	NO	NO	YES	YES	YES	NO	NO	YES	YES
Glyoxylic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Methyl Pyruvate	NO	YES	NO	NO	NO	NO	NO	YES	NO	YES	NO	YES	NO	NO	YES	NO	NO
D-Galacturonic acid	NO	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	YES	NO
D-Mannose	YES	YES	YES	YES	YES	NO	YES	YES	YES	NO	NO	YES	YES	NO	YES	YES	NO
D-Mannitol	YES	NO	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	NO	NO	YES	YES	NO
D-Melibiose	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	YES	NO	YES	NO	NO	YES	NO
Sucrose	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES
2-Deoxy adenosine	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Cellobiose	YES	YES	YES	NO	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES	NO	YES	YES
D-Malic acid	NO	NO	NO	NO	YES	NO	YES	YES	NO	YES	NO	NO	NO	NO	NO	YES	NO
Phenylethyl-amine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Dulcitol	NO	NO	YES	YES	YES	YES	NO	YES	NO	NO	YES	NO	YES	NO	NO	YES	NO
L-Glutamic acid	NO	NO	YES	NO	NO	NO	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	NO
Thymidine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Uridine	NO	NO	NO	NO	YES	NO	YES	YES	YES	YES	NO	NO	NO	NO	YES	YES	NO
Adenosine	NO	YES	NO	NO	NO	NO	YES	NO	YES	YES	NO	NO	NO	NO	YES	NO	NO
Inosine	NO	NO	NO	YES	YES	NO	YES	YES	YES	YES	NO	YES	YES	NO	YES	NO	NO
L-Malic acid	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	YES	NO
2-Aminoethanol	NO	NO	NO	NO	YES	NO	YES	YES	YES	YES	NO	NO	NO	NO	YES	NO	NO

Table S: Substrate utilization as determined by BIOLOG PM2A MicroPlates by fungal endophytes belonging to core OTUs.

Strain/Substrate	SYN00120	SYN00122	SYN00123	SYN00124	SYN00129	SYN00130	SYN001310	SYN001311	SYN001314	SYN001315	SYN001324	SYN001325	SYN001326	SYN001327	SYN001333
N-acetyl-D-Galactosamine	NO	NO	YES	NO	NO	YES	NO	NO	YES	YES	NO	NO	NO	YES	NO
Gentiobiose	NO	NO	YES	YES	YES	NO	NO	YES	NO	YES	YES	YES	NO	NO	NO
D-Raffinose	NO	NO	YES	YES	YES	NO	NO	YES	NO	NO	NO	YES	YES	NO	NO
Capric acid	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	YES	YES	YES
D-lactic acid methyl ester	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Acetamide	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Ornithine	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES
Chondroitin sulfate C	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
N-acetyl-neuraminic acid	NO	YES	YES	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	YES	NO

L-glucose	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Salicin	YES	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	YES	YES	NO	NO	NO
Caproic acid	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO
Malonic acid	NO	NO	YES	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Alaninamide	NO	NO	YES	NO	NO	YES	NO	NO	YES	NO	NO	YES	YES	YES	YES	YES
L-Phenylalanine	YES	NO	NO	NO	NO	YES	NO	YES	YES	NO	NO	NO	NO	YES	NO	NO
α -Cyclodextrin	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
β -D-allose	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
Lactitol	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO
Sedoheptulosan	YES	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Citraconic acid	NO	YES	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
Melibionc acid	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO
N-Acetyl-L-Glutamic acid	NO	NO	NO	NO	NO	YES	YES	NO	YES	NO	NO	NO	YES	YES	YES	YES
L-Pyroglutamic acid	NO	NO	YES	NO	NO	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES
β -Cyclodextrin	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Amygdalin	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO
D-Melezitose	NO	YES	YES	NO	YES	NO	NO	YES	NO	NO	YES	YES	NO	NO	NO	NO
L-Sorbose	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Citramalic acid	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
Oxalic acid	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Arginine	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES
L-Valine	NO	YES	YES	NO	NO	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	YES
γ -Cyclodextrin	NO	NO	YES	YES	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	YES	YES
D-arabinose	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
Maltitol	NO	NO	YES	YES	YES	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO
Stachyose	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	YES	YES	NO	NO	NO	NO
D-Glucosamine	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO
Oxalomalic acid	NO	NO	YES	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
Glycine	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
D,L-Carnitine	NO	YES	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	YES	YES	NO	NO
Dextrin	NO	NO	YES	NO	YES	NO	NO	YES	NO	YES	NO	YES	NO	NO	NO	NO
D-arabitol	NO	YES	NO	YES	NO	NO	NO	YES	NO	YES	YES	YES	NO	NO	YES	YES
α -Methyl-D-Glucoside	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
D-Tagatose	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
2-Hydroxy benzoic acid	NO	YES	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	YES	NO	NO	NO
Quinic acid	NO	NO	NO	NO	NO	YES	NO	YES	YES	NO	YES	YES	NO	NO	NO	NO
L-Histidine	NO	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES
Sec-Butylamine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Gelatin	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-arabitol	NO	YES	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO

β-Methyl-D-Galactoside	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
Turanose	NO	YES	YES	YES	YES	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO
4-Hydroxy benzoic acid	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
D-Ribono-1,4-Lactone	NO	YES	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO
L-Homoserine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D,L-Octopamine	NO	NO	YES	NO	NO	YES	YES	YES	YES	NO	NO	NO	YES	YES	YES	YES
Glycogen	YES	YES	YES	YES	NO	YES	NO	YES	NO	YES	YES	YES	YES	YES	NO	NO
Arbutin	NO	NO	YES	YES	NO	NO	NO	YES	NO	YES	YES	YES	YES	NO	NO	NO
3-Methyl Glucose	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Xylitol	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
β-Hydroxy butyric acid	NO	NO	YES	NO	NO	YES	NO	YES	NO	YES	YES	YES	YES	NO	YES	YES
Sebacic acid	YES	YES	YES	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
Hydroxy-L-Proline	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES
Putrescine	NO	YES	NO	YES	YES	YES	YES	YES	NO	YES	NO	YES	NO	NO	NO	NO
Inulin	NO	YES	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO
2-Deoxy-D-Ribose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
β-Methyl-D-Glucuronic acid	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
N-Acetyl-D-glucosaminitol	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
γ-Hydroxy butyric acid	NO	YES	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
Sorbic acid	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Isoleucine	NO	NO	NO	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	YES
Dihydroxy acetone	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Laminarin	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
i-Erythritol	NO	NO	YES	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	YES
α-Methyl-D-Mannoside	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
γ-amino butyric acid	NO	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
α-Keto-valeric acid	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
Succinamic acid	NO	NO	YES	NO	NO	YES	NO	NO	YES	YES	NO	YES	YES	YES	YES	NO
L-Leucine	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES
2,3-Butanediol	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Mannan	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Fucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
β-Methyl-D-Xyloside	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
d-amino valeric acid	NO	YES	YES	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO
Itaconic acid	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
D-Tartaric acid	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
L-Lysine	NO	NO	YES	NO	NO	NO	NO	YES	NO	YES	NO	YES	NO	NO	NO	NO
2,3-Butanone	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO
Pectin	NO	YES	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO
3-O-β-D-Galactopyranosyl-D-arabinose	NO	NO	YES	NO	NO	NO	YES	NO	NO	YES	YES	NO	NO	NO	NO	YES

Palatinose	NO	NO	YES	YES	YES	NO	NO	YES	NO	YES	YES	YES	NO	NO	NO
Butyric acid	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO
5-Keto-D-Gluconic acid	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	YES	NO	NO	NO
L-Tartaric acid	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO
L-Methionine	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
3-Hydroxy 2-Butanone	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO

Table T: Substrate utilization as determined by BIOLOG PM2A MicroPlates by fungal endophytes belonging to core OTUs.

Strain/Substrate	SYM00135	SYM00136	SYM00151	SYM00154	SYM15811	SYM15820	SYM15825	SYM15828	SYM15831	SYM15837	SYM15839	SYM15847	SYM15872	SYM15890	SYM15901	SYM15920	SYM15926
N-acetyl-D-Galactosamine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Gentiobiose	NO	YES	YES	NO	NO	NO	YES	NO	NO	NO	YES	YES	YES	NO	YES	YES	NO
D-Raffinose	YES	YES	YES	YES	YES	NO	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	NO
Capric acid	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-lactic acid methyl ester	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Acetamide	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Ornithine	YES	NO	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Chondroitin sulfate C	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
N-acetyl-neuraminic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-glucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Salicin	NO	NO	YES	NO	YES	NO	YES	NO	YES	NO	YES	YES	YES	NO	YES	YES	NO
Caproic acid	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Malonic acid	NO	NO	YES	NO	NO	NO	YES	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO
L-Alaninamide	NO	NO	YES	NO	YES	NO	YES	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO
L-Phenylalanine	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	YES	YES	YES	NO	YES	YES	NO
α -Cyclodextrin	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
β -D-allose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Lactitol	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Sedoheptulosan	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO
Citraconic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Melibionc acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
N-Acetyl-L-Glutamic acid	NO	NO	NO	NO	NO	YES	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	YES
L-Pyrogutamic acid	NO	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO
β -Cyclodextrin	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Amygdalin	NO	NO	YES	NO	NO	NO	YES	NO	NO	YES	YES	YES	YES	NO	YES	YES	NO
D-Melezitose	YES	YES	YES	NO	YES	NO	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	NO
L-Sorbose	NO	YES	YES	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	YES	NO	NO
Citramalic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO

Oxalic acid	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES
L-Arginine	NO	NO	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO
L-Valine	NO	NO	NO	NO	NO	YES	YES	YES	NO	YES	YES	NO	YES	NO	YES	YES	YES	YES
γ -Cyclodextrin	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	YES	NO	YES	YES	NO	NO
D-arabinose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
Maltitol	NO	YES	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	YES	YES	YES	YES
Stachyose	YES	YES	YES	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	NO	NO
D-Glucosamine	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO
Oxalomalic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Glycine	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	YES	YES	NO	YES	NO	NO	NO
D,L-Carnitine	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO
Dextrin	YES	NO	YES	NO	YES	NO	YES	NO	YES	YES	YES	NO	YES	NO	YES	YES	YES	YES
D-arabitol	YES	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	YES	YES	NO	NO
α -Methyl-D-Glucoside	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	YES	NO	NO
D-Tagatose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
2-Hydroxy benzoic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Quinic acid	NO	NO	YES	NO	YES	NO	YES	NO	NO	NO	YES	NO	YES	NO	NO	YES	NO	NO
L-Histidine	NO	YES	NO	NO	YES	YES	YES	YES	NO	NO	YES	NO	YES	NO	YES	YES	YES	YES
Sec-Butylamine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
Gelatin	NO	NO	YES	NO	NO	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-arabitol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
β -Methyl-D-Galactoside	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO
Turanose	YES	YES	YES	YES	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	NO	NO
4-Hydroxy benzoic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
D-Ribono-1,4-Lactone	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Homoserine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D,L-Octopamine	NO	NO	NO	NO	YES	YES	NO	YES	NO	YES	NO	NO	YES	YES	NO	NO	NO	NO
Glycogen	NO	YES	YES	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	NO	NO
Arbutin	NO	YES	YES	NO	NO	NO	YES	NO	NO	YES	YES	YES	YES	NO	YES	YES	NO	NO
3-Methyl Glucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Xylitol	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
β -Hydroxy butyric acid	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	YES	NO	NO
Sebacic acid	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO
Hydroxy-L-Proline	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Putrescine	YES	YES	YES	NO	NO	NO	YES	YES	NO	NO	YES	YES	YES	NO	YES	YES	NO	NO
Inulin	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO
2-Deoxy-D-Ribose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
β -Methyl-D-Glucuronic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	YES
N-Acetyl-D-glucosaminitol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
γ -Hydroxy butyric acid	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO

Sorbic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Isoleucine	NO	NO	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO
Dihydroxy acetone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Laminarin	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	YES	NO
D-Erythritol	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO
α-Methyl-D-Mannoside	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
γ-amino butyric acid	NO	YES	YES	NO	YES	NO	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	YES
α-Keto-valeric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	YES	NO	NO	NO
Succinamic acid	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	YES	YES	YES	NO	YES	NO	NO
L-Leucine	NO	NO	YES	YES	NO	NO	YES	NO	NO	YES	YES	YES	YES	NO	YES	YES	NO
2,3-Butanediol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
Mannan	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Fucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
β-Methyl-D-Xyloside	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-amino valeric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	YES	NO	YES
Itaconic acid	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES
D-Tartaric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Lysine	NO	NO	YES	NO	NO	NO	YES	NO	YES	YES	NO	YES	YES	NO	YES	NO	NO
2,3-Butanone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Pectin	NO	NO	YES	NO	NO	NO	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	YES
3-O-β-D-Galactopyranosyl-D-arabinose	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
Palatinose	YES	YES	YES	NO	YES	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO
Butyric acid	NO	NO	NO	NO	YES	NO	YES	YES	NO	YES	NO	NO	YES	NO	YES	YES	NO
5-Keto-D-Gluconic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
L-Tartaric acid	NO	NO	YES	NO	YES	NO	YES	NO	NO	NO	NO	NO	YES	NO	YES	YES	NO
L-Methionine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
3-Hydroxy 2-Butanone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO

Table U: Substrate utilization as determined by BIOLOG PM2A MicroPlates by fungal endophytes belonging to core OTUs.

Strain/Substrate	SYM15928	SYM15932	SYM00160	SYM00034	SYM00566B	SYM00577	SYM00590	SYM00603	SYM0061A	SYM00622	SYM00629	SYM00666	SYM00663	SYM00696	SYM00741A	SYM00741B	SYM00854	SYM00880
N-acetyl-D-Galactosamine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
Gentiobiose	YES	YES	YES	YES	NO	YES	YES	NO	YES	NO	NO	NO	NO	YES	YES	NO	NO	NO
D-Raffinose	YES	YES	YES	NO	NO	YES	NO	NO	YES	NO	NO	YES	NO	YES	YES	NO	YES	NO
Capric acid	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-lactic acid methyl ester	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Acetamide	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES

L-Ornithine	YES	YES	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	NO	NO
Chondroitin sulfate C	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO
N-acetyl-neuraminic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
L-glucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
Salicin	YES	YES	YES	YES	NO	YES	YES	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
Caproic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
Malonic acid	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Alaninamide	NO	NO	NO	YES	NO	YES	NO	YES	YES	NO	NO	NO	NO	NO	YES	NO	YES	NO	YES
L-Phenylalanine	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
α -Cyclodextrin	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	NO	YES	NO	NO	NO	YES	NO	YES	YES
β -D-allose	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES
Lactitol	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	YES	NO	NO	YES
Sedoheptulosan	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES
Citraconic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES
Melibionc acid	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
N-Acetyl-L-Glutamic acid	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	YES	NO	NO	YES	NO	YES	NO	YES	YES
L-Pyrroglutamic acid	YES	NO	NO	YES	YES	YES	NO	YES	YES	YES	NO	NO	YES	NO	YES	YES	YES	YES	YES
β -Cyclodextrin	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	YES
Amygdalin	NO	YES	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	YES	YES
D-Melezitose	YES	YES	YES	YES	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	YES	YES	NO	NO	YES
L-Sorbose	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
Citramalic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
Oxalic acid	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES
L-Arginine	YES	YES	NO	YES	NO	YES	NO	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES
L-Valine	NO	NO	NO	YES	NO	YES	NO	YES	NO	YES	YES	NO	NO	YES	YES	YES	YES	NO	YES
γ -Cyclodextrin	YES	YES	YES	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO
D-arabinose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
Maltitol	YES	YES	YES	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	YES	YES	NO	YES	YES
Stachyose	YES	YES	YES	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	YES	YES	NO	YES	YES
D-Glucosamine	NO	NO	NO	YES	NO	YES	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
Oxalomalic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Glycine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	YES
D,L-Carnitine	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO
Dextrin	YES	YES	YES	YES	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	YES	YES	NO	YES	YES
D-arabitol	YES	NO	NO	YES	NO	YES	NO	NO	YES	NO	YES	NO	NO	YES	YES	NO	YES	NO	NO
α -Methyl-D-Glucoside	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO
D-Tagatose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
2-Hydroxy benzoic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO
Quinic acid	NO	YES	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES
L-Histidine	NO	NO	NO	NO	YES	YES	NO	YES	YES	YES	NO	NO	NO	NO	YES	NO	YES	NO	NO

Sec-Butylamine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Gelatin	YES	YES	NO	YES	NO	YES	YES	NO	YES	NO	NO	NO	NO	YES	YES	YES	YES	NO	NO
L-arabitol	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	YES	YES
β-Methyl-D-Galactoside	NO	YES	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
Turanose	YES	YES	YES	YES	NO	YES	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	YES	YES	YES
4-Hydroxy benzoic acid	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	YES	YES
D-Ribono-1,4-Lactone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	YES	YES	YES
L-Homoserine	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D,L-Octopamine	NO	NO	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO	NO	NO	YES	YES	YES	NO
Glycogen	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	NO	NO	YES	YES	YES	NO	YES	YES	YES
Arbutin	YES	YES	YES	YES	NO	YES	YES	NO	YES	NO	NO	NO	NO	YES	YES	YES	YES	YES	YES
3-Methyl Glucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO
Xylitol	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
β-Hydroxy butyric acid	YES	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO
Sebacic acid	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO
Hydroxy-L-Proline	NO	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	YES	YES	YES
Putrescine	YES	NO	NO	YES	NO	YES	NO	YES	YES	NO	NO	NO	NO	YES	YES	NO	NO	YES	YES
Inulin	YES	NO	NO	NO	NO	NO	YES	NO	NO	YES	YES	NO	NO	YES	YES	YES	NO	YES	YES
2-Deoxy-D-Ribose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
β-Methyl-D-Glucuronic acid	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
N-Acetyl-D-glucosaminitol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	YES
γ-Hydroxy butyric acid	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
Sorbic acid	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Isoleucine	NO	YES	NO	YES	NO	YES	NO	YES	NO	YES	YES	NO	NO	YES	YES	YES	NO	YES	YES
Dihydroxy acetone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Laminarin	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Erythritol	YES	NO	NO	YES	NO	NO	YES	NO	NO	NO	YES	NO	NO	YES	NO	YES	YES	NO	NO
α-Methyl-D-Mannoside	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
γ-amino butyric acid	YES	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	YES
α-Keto-valeric acid	NO	YES	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	YES	YES
Succinamic acid	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES	YES	NO	YES	YES	YES
L-Leucine	NO	NO	NO	YES	NO	YES	NO	YES	NO	YES	YES	NO	NO	NO	YES	YES	NO	NO	NO
2,3-Butanediol	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	NO	NO	YES	YES
Mannan	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	YES
D-Fucose	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	YES
β-Methyl-D-Xyloside	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-amino valeric acid	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Itaconic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
D-Tartaric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
L-Lysine	NO	NO	NO	YES	YES	NO	NO	NO	YES	NO	NO	NO	NO	YES	YES	NO	NO	YES	YES

2,3-Butanone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Pectin	YES	YES	YES	YES	NO	YES	NO	NO	YES	NO	NO	NO	NO	YES	YES	NO	YES	YES	YES
3-O-β-D-Galactopyranosyl-D-arabinose	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES	YES	YES	NO	YES	YES
Palatinose	YES	YES	YES	YES	NO	YES	YES	NO	NO	NO	NO	NO	YES	YES	YES	NO	YES	YES	YES
Butyric acid	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
5-Keto-D-Gluconic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO
L-Tartaric acid	NO	YES	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Methionine	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
3-Hydroxy 2-Butanone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO

Characterization of culturable microbes: substrate use

[0063] Additional BIOLOG analyses were performed. For additional biolog analyses, microbes were cultivated in three biological replicates for each strain. Each bacterium was initially streaked on Reasoner's 2A (R2A) agar, distinct CFUs selected and cultured in 6 mL R2A broth for 4 days. Fungal strains were streaked on potato dextrose (PD) agar and individual plugs containing spores and mycelial tissues were used to initiate growth in 6 mL PD broth for 6 days. All strains were grown with agitation at room temperature. One mL liquid cultures of each sample were harvested by centrifugation for 15 minutes at 4500 RPM and subsequently washed at least four times with sterile distilled water to remove any traces of residual media. Additionally, fungal cultures were first sonicated to achieve homogeneity after the growth period. Microbes were resuspended in 500 µL sterile distilled water and measurements of absorbance were taken using a SpectraMax M microplate reader (Molecular Devices, Sunnyvale, CA).

[0064] Sole carbon substrate assays were done using BIOLOG Phenotype MicroArray (PM) 1 and 2A MicroPlates (Hayward, CA). An aliquot of each bacterial cell culture corresponding to a final absorbance of 0.2 were inoculated into 20 mL sterile IF-0a GN/GP Base inoculating fluid (IF-0), 0.24 mL 100X Dye B obtained from BIOLOG, and brought to a final volume of 24 mL with sterile distilled water in 50 mL Falcon tubes. Negative control PM1 and PM2A assays were done similarly for each dye minus bacterial cells to detect abiotic reactions. Fungal culture of each strain with a final absorbance of 0.2 (~ 63% turbidity) was brought to a final volume of 24 mL with the FF-IF medium (BIOLOG). Microbial cell suspensions in tubes were gently shaken to achieve uniformity. One hundred microliters of the microbial cell suspension was added per well using a multichannel pipettor to the 96-well BIOLOG PM1 and PM2A MicroPlates that

each contained 95 carbon sources and one water-only (negative control) well. All steps were performed under sterile conditions using biosafety cabinets.

[0065] MicroPlates were sealed in paper surgical tape (Dynarex, Orangeburg, NY) to minimize plate edge effects, and incubated stationary at 24°C in an enclosed container for a minimum of 72 hours. Absorbance at 590 nm was measured for all MicroPlates at least every 24 hours or at a defined interval (72 hours post-assay) to determine carbon substrate utilization for each strain. Measurements were normalized relative to the negative control (water only) well of each plate (Garland and Mills, 1991; Barua et al., 2010; Siemens et al., 2012; Blumenstein et al., 2015). Bacterial MicroPlates were also visually examined for the irreversible formation of violet color in wells indicating the reduction of the tetrazolium redox dye to formazan that result from cell respiration (Garland and Mills, 1991), and assessed against the negative control (no cells) PM1 and PM2A MicroPlates to detect any abiotic color changes potentially introduced by the medium and/or dyes (Borglin et al., 2012). Normalized absorbance values that were negative were considered as zero for subsequent analysis (Garland and Mills, 1991; Blumenstein et al., 2015) and a threshold value of 0.1 and above was used to indicate the ability of a particular microbial strain to use a given carbon substrate (Barua et al., 2010; Blumenstein et al., 2015). Fungal PM tests were measured as growth assays and visual observation of mycelial growth in each well was made.

Table V: Substrate utilization as determined by BIOLOG PM1 MicroPlates by bacterial endophytes belonging to OTUs present in cereal seeds, fruit seeds, vegetable seeds, and oil seeds.

Strain/Substrate	SYM00021b	SYM00044	SYM00057b	SYM00074	SYM00091	SYM00092d	SYM00212	SYM00290	SYM00619	SYM00865	SYM00879	SYM00879b	SYM00906	SYM00965	SYM01004	SYM01022	SYM01158
1,2-Propanediol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
2-Aminoethanol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES
2'-Deoxyadenosine	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES	YES	NO
a-D-Glucose	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES
a-D-Lactose	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	NO
a-Hydroxybutyric acid	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	YES	YES	YES	YES	NO	YES
a-Hydroxyglutaric acid-g-Lactone	NO	NO	NO	NO	YES	NO	NO	NO	YES	YES	NO	YES	NO	YES	YES	YES	NO
a-Ketobutyric acid	NO	NO	NO	NO	YES	NO	NO	YES	YES	NO	NO	YES	YES	YES	YES	NO	YES
a-Ketoglutaric acid	YES	NO	NO	NO	YES	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES
a-Methyl-D-Galactoside	YES	YES	YES	YES	YES	NO	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	NO
Acetic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Acetoacetic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Adenosine	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES	YES	NO
Adonitol	YES	YES	YES	YES	YES	NO	YES	NO	YES	YES	NO	YES	NO	YES	YES	NO	YES
Ala-Gly	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES	YES	YES

b-Methyl-D-Glucoside	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO
Bromosuccinic acid	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Citric acid	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES
D-Alanine	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES
D-Aspartic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Cellobiose	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Fructose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Fructose-6-Phosphate	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO
D-Galactonic acid-g-Lactone	YES	YES	YES	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES	YES	YES	YES
D-Galactose	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	YES	YES	YES	YES	YES
D-Galacturonic acid	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	NO	YES	YES	YES	NO
D-Gluconic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES
D-Glucosaminic acid	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	NO	YES	NO	YES	YES	YES	YES
D-Glucose-1-Phosphate	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	NO	YES	NO	YES	YES	YES	NO
D-Glucose-6-Phosphate	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	NO	YES	YES	YES	NO
D-Glucuronic acid	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES	YES	YES
D-Malic acid	NO	NO	NO	NO	YES	NO	NO	YES	YES	YES	NO	YES	NO	YES	YES	YES	YES
D-Mannitol	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO
D-Mannose	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
D-Melibiose	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO
D-Psicose	YES	NO	NO	NO	YES	YES	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	NO
D-Ribose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Saccharic acid	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	NO	YES	YES	YES	NO
D-Serine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Sorbitol	YES	YES	YES	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	YES	NO
D-Threonine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
D-Trehalose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Xylose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES
DL-α-Glycerol Phosphate	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	NO
DL-Malic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Dulcitol	YES	YES	YES	YES	NO	YES	NO	YES	NO	YES	NO	YES	NO	YES	YES	NO	YES
Formic acid	YES	YES	YES	NO	YES	YES	NO	NO	NO	YES	YES	YES	NO	YES	YES	YES	NO
Fumaric acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Glucuronamide	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Gly-Asp	NO	YES	YES	YES	NO	YES	YES	NO	NO	YES	NO	YES	NO	YES	YES	NO	YES
Gly-Glu	NO	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Gly-Pro	NO	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES
Glycerol	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	NO
Glycolic acid	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	YES
Glyoxylic acid	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO
Inosine	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES	YES	NO
L-Alanine	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	YES	YES	YES	YES	YES
L-Arabinose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-Asparagine	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES
L-Aspartic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-Fucose	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	YES	YES	YES	YES	YES	YES
L-Galactonic acid-g-Lactone	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-Glutamic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES
L-Glutamine	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-Lactic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-Lyxose	NO	NO	NO	YES	YES	YES	YES	YES	NO	NO	YES	NO	YES	YES	YES	NO	NO
L-Malic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-Proline	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-Rhamnose	YES	YES	YES	YES	YES	YES	YES	NO	NO	NO	NO	YES	NO	YES	YES	NO	YES
L-Serine	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES	YES	YES

L-Threonine	NO	NO	NO	YES	YES	NO	NO	NO	NO	YES	NO	NO	YES	YES	YES	NO	NO
Lactulose	NO	NO	NO	NO	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO
m-Hydroxyphenyl Acetic acid	NO	YES	YES	YES	NO	NO	YES	NO	YES	YES	NO	YES	YES	YES	YES	YES	NO
m-Inositol	YES	NO	NO	NO	YES	YES	NO	NO	NO	YES	NO	YES	NO	YES	YES	YES	YES
m-Tartaric acid	YES	NO	NO	NO	YES	YES	NO	NO	NO	YES	NO	YES	NO	YES	YES	YES	NO
Maltose	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	YES
Maltotriose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Methylpyruvate	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Mono-Methylsuccinate	NO	NO	NO	NO	YES	NO	NO	YES	YES	YES	NO	YES	YES	YES	YES	YES	NO
Mucic acid	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	NO	YES	NO	YES	YES	YES	NO
N-Acetyl-D-Glucosamine	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
N-Acetyl-D-Mannosamine	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO
Negative Control	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
p-Hydroxyphenyl Acetic acid	NO	YES	YES	YES	YES	NO	YES	NO	YES	NO	NO	YES	YES	YES	NO	YES	NO
Phenylethylamine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO
Propionic acid	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES
Pyruvic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Succinic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Sucrose	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES
Thymidine	YES	YES	YES	YES	NO	YES	YES	NO	YES	NO	YES	NO	YES	NO	YES	NO	YES
Tricarballic acid	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	YES	NO	YES	NO
Tween 20	NO	NO	NO	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO
Tween 40	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO
Tween 80	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Tyramine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO
Uridine	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES

Table W: Substrate utilization as determined by BIOLOG PM1 MicroPlates by fungal endophytes belonging to OTUs present in cereal seeds, fruit seeds, vegetable seeds, and oil seeds.

	SYM00157	SYM00300	SYM00301	SYM00577	SYM01314	SYM01324	SYM01326	SYM01329	SYM01330	SYM01331	SYM12462	SYM15774	SYM15783	SYM15810	SYM15879	SYM15880
1,2-Propanediol	YES	YES	NO	YES	YES	NO	NO	YES	NO	NO	YES	NO	NO	YES	YES	NO
2-Aminoethanol	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	NO	NO	YES	YES	YES	YES
2'-Deoxyadenosine	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	NO	YES	YES	YES	YES
a-D-Glucose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
a-D-Lactose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
a-Hydroxybutyric acid	NO	YES	YES	NO	YES	YES	NO	NO	YES	NO	NO	NO	YES	YES	YES	NO
a-Hydroxyglutaric acid-g-Lactone	YES	NO	NO	NO	YES	YES	YES	NO	YES	NO	YES	YES	YES	NO	YES	NO
a-Ketobutyric acid	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	YES	YES	YES	YES	YES
a-Ketoglutaric acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
a-Methyl-D-Galactoside	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES
Acetic acid	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES
Acetoacetic acid	YES	NO	YES	NO	YES	NO	YES	NO	NO	NO	YES	YES	YES	NO	YES	NO
Adenosine	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	NO	YES	YES	YES	YES
Adonitol	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES
Ala-Gly	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
b-Methyl-D-Glucoside	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Bromosuccinic acid	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES

Citric acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	NO	YES	YES
D-Alanine	YES	YES	YES	YES	YES	NO	YES	NO	NO	NO	NO	NO	NO	YES	YES	YES	YES
D-Aspartic acid	NO	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO
D-Cellobiose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Fructose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Fructose-6-Phosphate	NO	YES	NO	NO	YES	NO	YES	YES	YES	YES	NO	NO	YES	NO	YES	YES	NO
D-Galactonic acid-g-Lactone	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO
D-Galactose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Galacturonic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Gluconic acid	YES	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Glucosaminic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	NO	NO	NO
D-Glucose-1-Phosphate	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	YES	YES	NO	NO	NO	NO	NO
D-Glucose-6-Phosphate	NO	YES	NO	NO	YES	NO	YES	NO	YES	NO	YES	YES	YES	YES	YES	YES	NO
D-Glucuronic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Malic acid	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	NO	YES	YES	YES	YES
D-Mannitol	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES
D-Mannose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Melibiose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Psicose	YES	YES	YES	NO	NO	YES	YES	YES	NO	YES	NO	NO	YES	YES	YES	YES	YES
D-Ribose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Saccharic acid	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES
D-Serine	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	NO	NO	NO	YES	YES	YES	NO
D-Sorbitol	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES
D-Threonine	YES	NO	NO	NO	YES	NO	YES	YES	NO	YES	YES	YES	YES	YES	NO	YES	NO
D-Trehalose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Xylose	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	NO	YES	YES	YES	YES
DL-α-Glycerol Phosphate	NO	NO	NO	NO	YES	NO	YES	NO	YES	NO	NO	YES	YES	YES	YES	YES	YES
DL-Malic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES
Dulcitol	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES
Formic acid	YES	NO	YES	NO	YES	YES	YES	YES	NO	NO	NO	NO	YES	NO	YES	YES	NO
Fumaric acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES
Glucuronamide	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
Gly-Asp	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES
Gly-Glu	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Gly-Pro	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Glycerol	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	YES	YES	YES	YES	YES
Glycolic acid	NO	NO	NO	NO	YES	YES	NO	NO	YES	NO	NO	YES	YES	YES	YES	NO	YES
Glyoxylic acid	YES	NO	NO	NO	YES	YES	NO	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES
Inosine	YES	YES	YES	NO	YES	YES	YES	NO	NO	YES	YES	NO	NO	YES	YES	YES	YES
L-Alanine	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-Arabinose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES
L-Asparagine	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
L-Aspartic acid	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES
L-Fucose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	YES	YES	NO
L-Galactonic acid-g-Lactone	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-Glutamic acid	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
L-Glutamine	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-Lactic acid	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES
L-Lyxose	YES	YES	YES	YES	YES	NO	YES	NO	YES	YES	NO	NO	YES	YES	YES	YES	YES
L-Malic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-Proline	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES
L-Rhamnose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-Serine	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-Threonine	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES
Lactulose	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	NO
m-Hydroxyphenyl Acetic acid	YES	YES	YES	NO	YES	YES	NO	YES	NO	NO	YES	YES	YES	NO	NO	YES	YES

m-Inositol	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES
m-Tartaric acid	YES	YES	YES	NO	YES	YES	YES	YES	YES	NO	YES	NO	NO	YES	YES	YES	NO
Maltose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Maltotriose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Methylpyruvate	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
Mono-Methylsuccinate	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
Mucic acid	YES	YES	YES	NO	YES	YES	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
N-Acetyl-D-Glucosamine	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
N-Acetyl-D-Mannosamine	NO	YES	NO	NO	YES	NO	YES	NO	YES	NO	NO	NO	YES	YES	NO	NO	NO
Negative Control	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
p-Hydroxyphenyl Acetic acid	YES	NO	YES	YES	YES	YES	NO	NO	YES	YES	YES	NO	YES	YES	YES	YES	YES
Phenylethylamine	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
Propionic acid	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	NO	YES	YES	YES	YES	YES	YES
Pyruvic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES
Succinic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES
Sucrose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Thymidine	YES	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	YES	NO	NO	YES	YES	NO
Tricarballic acid	NO	NO	YES	YES	YES	YES	NO	NO	NO	NO	NO	YES	YES	YES	YES	NO	NO
Tween 20	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
Tween 40	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Tween 80	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Tyramine	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES
Uridine	YES	NO	YES	YES	YES	NO	YES	YES	NO	NO	NO	NO	NO	NO	YES	YES	YES

Table X: Substrate utilization as determined by BIOLOG PM2 MicroPlates by bacterial endophytes belonging to OTUs present in cereal seeds, fruit seeds, vegetable seeds, and oil seeds.

Strain/Substrate	SYM00021b	SYM00044	SYM00057b	SYM00074	SYM00091	SYM00092d	SYM00212	SYM00290	SYM00619	SYM00865	SYM00879	SYM00879b	SYM00906	SYM00965	SYM01004	SYM01022	SYM01158
2-Deoxy-D-Ribose	NO	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES
2-Hydroxybenzoic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
2,3-Butanediol	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	YES	NO	YES
2,3-Butanedione	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
3-Hydroxy-2-butanone	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES
3-Methylglucose	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	YES	YES	YES	YES
3-O-b-D-Galactopyranosyl-D-Arabinose	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
4-Hydroxybenzoic acid	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES
5-Keto-D-Gluconic acid	YES	YES	YES	NO	NO	YES	YES	YES	NO	YES	YES	YES	NO	YES	YES	YES	YES
a-Cyclodextrin	NO	NO	NO	YES	YES	YES	NO	NO	YES	YES	NO	YES	NO	YES	YES	YES	NO
a-Keto-Valeric acid	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	YES	YES
a-Methyl-D-Glucoside	NO	NO	NO	NO	YES	YES	NO	NO	YES	NO	NO	NO	YES	YES	YES	YES	YES
a-Methyl-D-Mannoside	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO

Acetamide	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO
Amygdalin	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Arbutin	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES
b-Cyclodextrin	NO	NO	NO	NO	YES	YES	NO	YES	YES	NO	NO	YES	NO	YES	YES	YES	NO
b-D-Allose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO
b-Hydroxybutyric acid	YES	NO	NO	NO	YES	NO	NO	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES
b-Methyl-D-Galactoside	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES
b-Methyl-D-Glucuronic acid	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES
b-Methyl-D-Xyloside	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	YES	NO	YES
Butyric acid	NO	NO	NO	YES	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
Capric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Caproic acid	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES
Chondroitin Sulfate C	YES	NO	NO	YES	YES	NO	NO	NO	NO	YES	YES	YES	YES	YES	NO	YES	YES
Citraconic acid	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO	YES	YES	NO	YES
Citramalic acid	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	YES	YES	YES
d-Amino Valeric acid	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	YES
D-Arabinose	NO	NO	NO	NO	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	YES	NO	YES
D-Arabitol	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	NO	YES	YES	YES	YES
D-Fucose	YES	YES	YES	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	YES
D-Glucosamine	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Lactic acid Methyl Ester	NO	NO	NO	YES	NO	NO	NO	YES	NO	YES	YES	NO	NO	NO	YES	YES	YES
D-Lactitol	NO	NO	NO	YES	YES	NO	NO	NO	NO	YES	YES	NO	YES	YES	YES	YES	YES
D-Melezitose	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES	YES	YES	YES	YES	YES
D-Raffinose	YES	YES	YES	YES	YES	NO	YES	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES
D-Ribono-1,4-Lactone	YES	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	YES	YES	YES	NO	YES
D-Tagatose	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	YES	YES	NO	YES
D-Tartaric acid	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES
D,L-Carnitine	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	YES
D,L-Octopamine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO
Dextrin	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Dihydroxyacetone	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
g-Amino-N-Butyric acid	YES	NO	NO	NO	YES	YES	NO	NO	NO	YES	NO	YES	NO	YES	YES	YES	YES
g-Cyclodextrin	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	YES	NO	YES	YES
g-Hydroxybutyric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	YES	YES	YES	YES
Gelatin	NO	NO	NO	YES	YES	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
Gentiobiose	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES
Glycine	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	YES

Glycogen	NO	YES	YES	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES
Hydroxy-L-Proline	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	YES	NO	YES	YES	YES	YES
i-Erythritol	YES	NO	NO	NO	YES	YES	YES	NO	NO	NO	YES	NO	NO	YES	YES	NO	YES
Inulin	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	YES
Itaconic acid	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES	YES	YES	NO	YES	YES
L-Alaninamide	YES	NO	NO	YES	YES	YES	NO	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES
L-Arabitol	NO	NO	NO	NO	YES	YES	NO	NO	NO	NO	NO	YES	NO	YES	YES	NO	YES
L-Arginine	YES	YES	YES	YES	YES	YES	NO	NO	NO	YES	NO	YES	NO	YES	YES	YES	YES
L-Glucose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Histidine	YES	NO	NO	YES	YES	YES	YES	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES
L-Homoserine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO
L-Isoleucine	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES
L-Leucine	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES
L-Lysine	NO	NO	NO	NO	YES	NO	NO	NO	NO	YES	NO	YES	NO	YES	YES	YES	YES
L-Methionine	NO	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Ornithine	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	YES	YES	YES	YES	YES
L-Phenylalanine	YES	NO	NO	YES	NO	NO	YES	NO	NO	YES	NO	YES	YES	YES	NO	YES	NO
L-Pyrogutamic acid	YES	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	YES	YES	YES	YES	YES	YES
L-Sorbose	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
L-Tartaric acid	YES	YES	YES	NO	NO	YES	YES	NO	NO	NO	YES	NO	NO	NO	NO	YES	YES
L-Valine	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	YES	YES	YES	NO	YES
Laminarin	NO	NO	NO	NO	YES	NO	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
Malonic acid	YES	NO	NO	YES	NO	NO	YES	NO	NO	YES	YES	NO	YES	YES	YES	NO	YES
Maltitol	YES	NO	NO	NO	YES	NO	NO	NO	NO	YES	YES	NO	YES	YES	YES	YES	YES
Mannan	NO	NO	NO	YES	NO	YES	YES	YES	NO	NO	NO	NO	YES	YES	YES	NO	YES
Melibiononic acid	YES	YES	YES	YES	YES	NO	NO	YES	NO	YES	NO	YES	NO	YES	YES	YES	YES
N-Acetyl-D-Galactosamine	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES
N-Acetyl-D-Glucosaminol	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES
N-Acetyl-L-Glutamic acid	NO	NO	NO	YES	NO	YES	NO	NO	NO	YES	NO	YES	YES	YES	NO	YES	YES
N-Acetyl-Neuraminic acid	NO	YES	YES	YES	NO	NO	YES	NO	NO	NO	NO	YES	YES	YES	NO	NO	YES
Negative Control. 1	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Oxalic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO
Oxalomalic acid	NO	NO	NO	NO	YES	YES	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
Palatinose	YES	NO	NO	NO	YES	NO	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES
Pectin	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
Putrescine	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES	YES	YES	YES	YES	YES
Quinic acid	YES	NO	NO	NO	YES	YES	NO	NO	NO	YES	NO	YES	NO	YES	YES	YES	YES
Salicin	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES

Sebacic acid	YES	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	YES	NO	YES	NO	YES	YES
sec-Butylamine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Sedoheptulosan	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Sorbic acid	NO	NO	NO	NO	NO	NO	NO	YES	NO	YES	NO	YES	YES	YES	NO	YES	YES
Stachyose	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	YES	YES
Succinamic acid	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
Turanose	YES	NO	NO	NO	YES	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES
Xylitol	NO	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	YES	NO	YES	YES	NO	NO

Table Y: Substrate utilization as determined by BIOLOG PM2 MicroPlates by fungal endophytes belonging to OTUs present in cereal seeds, fruit seeds, vegetable seeds, and oil seeds.

Strain/Substrate	SYM00157	SYM00300	SYM00301	SYM00577	SYM01314	SYM01324	SYM01326	SYM01329	SYM01330	SYM01331	SYM12462	SYM15774	SYM15783	SYM15810	SYM15879	SYM15880
2-Deoxy-D-Ribose	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO	YES	YES	YES	NO
2-Hydroxybenzoic acid	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
2,3-Butanediol	NO	NO	YES	NO	NO	YES	NO	NO	YES	YES	NO	YES	NO	YES	NO	NO
2,3-Butanedione	NO	NO	YES	NO	NO	YES	NO	NO	YES	YES	NO	NO	NO	YES	NO	NO
3-Hydroxy-2-butanone	NO	NO	NO	NO	NO	YES	NO	NO	YES	NO	NO	NO	NO	NO	NO	NO
3-Methylglucose	YES	NO	YES	YES	NO	NO	NO	YES	YES	YES	NO	NO	YES	NO	YES	NO
3-O-b-D-Galactopyranosyl-D-Arabinose	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	YES	YES	YES	YES	NO	YES
4-Hydroxybenzoic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES
5-Keto-D-Gluconic acid	NO	NO	YES	NO	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
a-Cyclodextrin	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
a-Keto-Valeric acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
a-Methyl-D-Glucoside	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES
a-Methyl-D-Mannoside	YES	NO	YES	NO	NO	YES	YES	NO	YES	YES	NO	NO	YES	YES	YES	NO
Acetamide	YES	YES	YES	NO	NO	NO	NO	NO	YES	YES	NO	YES	NO	NO	NO	NO
Amygdalin	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Arbutin	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
b-Cyclodextrin	YES	YES	YES	NO	NO	YES	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES
b-D-Allose	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	YES	YES	YES	YES	YES
b-Hydroxybutyric acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO
b-Methyl-D-Galactoside	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
b-Methyl-D-Glucuronic acid	YES	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	NO	NO	YES	NO
b-Methyl-D-Xyloside	NO	NO	YES	NO	YES	YES	YES	NO	NO	NO	NO	NO	YES	YES	NO	NO
Butyric acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES
Capric acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Caproic acid	NO	YES	YES	YES	YES	YES	YES	NO	NO	YES	NO	NO	YES	YES	YES	YES
Chondroitin Sulfate C	YES	NO	YES	NO	YES	YES	NO	NO	YES	YES	YES	NO	NO	YES	YES	NO
Citraconic acid	YES	NO	YES	NO	YES	YES	NO	NO	YES	YES	YES	NO	YES	YES	NO	NO
Citramalic acid	YES	NO	NO	NO	YES	YES	NO	YES	YES	YES	NO	NO	YES	YES	YES	YES
d-Amino Valeric acid	NO	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	NO	YES	YES	YES	YES
D-Arabinose	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES
D-Arabitol	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Fucose	YES	NO	YES	NO	YES	YES	NO	NO	NO	YES	NO	YES	YES	YES	YES	YES

D-Glucosamine	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	NO	NO	YES	YES	YES
D-Lactic acid Methyl Ester	YES	NO	YES	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	YES	NO	NO
D-Lactitol	YES	YES	YES	YES	NO	NO	YES	YES	NO	YES	YES	YES	YES	YES	YES	NO
D-Melezitose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Raffinose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
D-Ribono-1,4-Lactone	YES	NO	YES	YES	YES	NO	YES	NO	YES	YES	NO	NO	YES	NO	NO	YES
D-Tagatose	NO	YES	YES	NO	YES	NO	YES	NO	YES	NO	NO	NO	YES	YES	YES	YES
D-Tartaric acid	YES	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	YES	YES	YES	NO
D,L-Carnitine	YES	NO	YES	NO	NO	NO	NO	NO	YES	YES	YES	NO	NO	NO	NO	NO
D,L-Octopamine	YES	NO	YES	NO	YES	YES	NO	NO	NO	YES	NO	YES	YES	YES	YES	NO
Dextrin	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Dihydroxyacetone	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	NO	YES	YES	YES	NO
g-Amino-N-Butyric acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES
g-Cyclodextrin	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
g-Hydroxybutyric acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO
Gelatin	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO
Gentiobiose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Glycine	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	NO	YES	YES	YES	YES
Glycogen	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Hydroxy-L-Proline	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	NO	YES	YES	YES
i-Erythritol	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES
Inulin	YES	YES	YES	YES	YES	NO	NO	NO	YES	NO	YES	YES	NO	YES	YES	YES
Itaconic acid	NO	NO	YES	NO	NO	NO	NO	YES	NO	YES	NO	NO	NO	NO	NO	NO
L-Alaninamide	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO
L-Arabitol	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES
L-Arginine	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-Glucose	NO	NO	YES	NO	NO	NO	YES	NO	NO	YES	NO	NO	YES	YES	YES	NO
L-Histidine	YES	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	YES	YES	YES	YES	YES
L-Homoserine	YES	YES	YES	YES	NO	YES	YES	NO	NO	YES	NO	NO	YES	NO	YES	NO
L-Isoleucine	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-Leucine	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES	NO
L-Lysine	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
L-Methionine	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	YES	YES	NO	NO	NO
L-Ornithine	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
L-Phenylalanine	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES
L-Pyrogutamic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES
L-Sorbose	NO	YES	YES	YES	YES	YES	YES	NO	YES	NO	YES	NO	YES	YES	YES	YES
L-Tartaric acid	YES	NO	YES	NO	YES	YES	YES	YES	NO	YES	NO	YES	NO	YES	YES	NO
L-Valine	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES
Laminarin	YES	YES	YES	YES	YES	YES	YES	NO	NO	YES	YES	YES	YES	YES	YES	NO
Malonic acid	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	NO	YES	YES	YES	YES	NO
Maltitol	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES
Mannan	YES	NO	YES	NO	YES	NO	NO	NO	YES	NO	YES	YES	NO	NO	NO	NO
Melibionid acid	YES	NO	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	NO	YES	YES	NO
N-Acetyl-D-Galactosamine	YES	NO	NO	NO	NO	NO	YES	NO	YES	NO	NO	YES	NO	YES	NO	NO
N-Acetyl-D-Glucosaminitol	NO	NO	NO	NO	YES	YES	NO	YES	NO	NO	NO	NO	NO	YES	YES	NO
N-Acetyl-L-Glutamic acid	NO	NO	YES	NO	NO	YES	NO	NO	YES	YES	NO	YES	NO	NO	NO	NO
N-Acetyl-Neuraminic acid	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Negative Control.1	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Oxalic acid	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	NO	YES	YES	YES	NO
Oxalomalic acid	NO	NO	NO	NO	YES	NO	NO	NO	YES	NO	NO	NO	YES	YES	YES	NO
Palatinose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Pectin	YES	NO	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES

Putrescine	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES
Quinic acid	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES
Salicin	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Sebacic acid	YES	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	NO	YES	YES	YES	YES
sec-Butylamine	NO	YES	YES	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Sedoheptulosan	YES	YES	NO	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Sorbic acid	YES	YES	YES	YES	YES	YES	YES	NO	YES	YES	NO	NO	YES	YES	YES	YES	NO
Stachyose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Succinamic acid	YES	YES	YES	YES	YES	YES	NO	YES	YES	YES	YES	YES	YES	YES	YES	YES	NO
Turanose	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES
Xylitol	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES

[0066] Seventeen (17) bacterial SYM strains and sixteen (16) fungal SYM strains were tested in biological triplicate for sole carbon substrate utilization using BIOLOG PM1 and PM2A MicroPlates. The most utilized substrates overall by these strains are a-D-Glucose, Arbutin, b-Methyl-D-Galactoside, b-Methyl-D-Glucoside, D-Arabitol, D-Cellobiose, Dextrin, D-Fructose, D-Galactose, D-Gluconic acid, D-Glucosamine, Dihydroxyacetone, DL-Malic acid, D-Mannitol, D-Mannose, D-Melezitose, D-Melibiose, D-Raffinose, D-Ribose, D-Trehalose, D-Xylose, g-Amino-N-Butyric acid, g-Cyclodextrin, Gelatin, Gentiobiose, Glycogen, i-Erythritol, L-Alanine, L-Arabinose, L-Galactonic acid-g-Lactone, L-Histidine, L-Proline, L-Rhamnose, Maltitol, Maltose, Maltotriose, N-Acetyl-D-Glucosamine, Palatinose, Pectin, Salicin, Stachyose, Sucrose, and Turanose. Overall, these strains did not utilize 2,3-Butanediol, 2,3-Butanedione, b-Methyl-D-Glucuronic acid, b-Methyl-D-Xyloside, Capric acid, D,L-Carnitine, Glucuronamide, Itaconic acid, L-Methionine, N-Acetyl-D-Glucosaminitol, N-Acetyl-Neuraminic acid, Phenylethylamine, or sec-Butylamine as sole carbon sources.

[0067] The most utilized substrates by these seventeen bacterial endophytes are 2-Deoxy-D-Ribose, a-D-Glucose, a-Methyl-D-Galactoside, Arbutin, b-Methyl-D-Galactoside, b-Methyl-D-Glucoside, D-Arabitol, D-Cellobiose, Dextrin, D-Fructose, D-Galactose, D-Galacturonic acid, D-Gluconic acid, D-Glucosamine, Dihydroxyacetone, DL-Malic acid, D-Mannitol, D-Mannose, D-Melibiose, D-Raffinose, D-Ribose, D-Trehalose, D-Xylose, Gelatin, Gentiobiose, L-Arabinose, L-Aspartic acid, L-Galactonic acid-g-Lactone, L-Glutamic acid, L-Glutamine, L-Histidine, L-Ornithine, L-Proline, Maltose, Maltotriose, N-Acetyl-D-Glucosamine, Pyruvic acid, Salicin, Sucrose, and Turanose. These bacterial endophytes did not utilize 1,2-Propanediol, 2,3-Butanediol, 2,3-Butanedione, 2-Aminoethanol, 2-Hydroxybenzoic acid, 3-Hydroxy-2-butanone, 3-Methylglucose, 4-Hydroxybenzoic acid, Acetamide, Acetoacetic acid, a-Hydroxybutyric acid,

a-Hydroxyglutaric acid-g-Lactone, a-Ketobutyric acid, a-Keto-Valeric acid, a-Methyl-D-Glucoside, a-Methyl-D-Mannoside, b-D-Allose, b-Methyl-D-Glucuronic acid, b-Methyl-D-Xyloside, Capric acid, Caproic acid, Citraconic acid, Citramalic acid, D,L-Carnitine, D,L-Octopamine, d-Amino Valeric acid, D-Aspartic acid, D-Melezitose, D-Serine, D-Tagatose, D-Tartaric acid, D-Threonine, g-Cyclodextrin, g-Hydroxybutyric acid, Glucuronamide, Glycine, Glycolic acid, Glyoxylic acid, Hydroxy-L-Proline, i-Erythritol, Inulin, Itaconic acid, L-Arabitol, L-Fucose, L-Glucose, L-Homoserine, L-Methionine, L-Sorbose, L-Threonine, L-Valine, m-Tartaric acid, N-Acetyl-D-Glucosaminitol, N-Acetyl-D-Mannosamine, N-Acetyl-Neuraminic acid, Oxalic acid, Phenylethylamine, Sebamic acid, sec-Butylamine, Sedoheptulosan, Stachyose, Tricarballic acid, Tyramine, or Xylitol as sole carbon sources.

[0068] The most utilized substrates by these sixteen fungal endophytes are a-D-Glucose, a-Methyl-D-Glucoside, Amygdalin, Arbutin, b-Methyl-D-Galactoside, b-Methyl-D-Glucoside, D-Arabitol, D-Cellobiose, Dextrin, D-Fructose, D-Galactose, D-Mannitol, D-Mannose, D-Melezitose, D-Melibiose, D-Raffinose, D-Trehalose, D-Xylose, g-Amino-N-Butyric acid, g-Cyclodextrin, Gentiobiose, Glycogen, i-Erythritol, L-Alanine, L-Arabinose, L-Arginine, L-Ornithine, L-Rhamnose, Maltitol, Maltose, Maltotriose, N-Acetyl-D-Glucosamine, Palatinose, Pectin, Putrescine, Quinic acid, Salicin, Stachyose, Sucrose, and Turanose. These fungal endophytes did not utilize 2,3-Butanediol, 2,3-Butanedione, 2-Deoxy-D-Ribose, b-Methyl-D-Glucuronic acid, b-Methyl-D-Xyloside, Capric acid, D,L-Carnitine, D-Galactonic acid-g-Lactone, D-Glucose-1-Phosphate, Glucuronamide, Itaconic acid, L-Methionine, N-Acetyl-D-Galactosamine, N-Acetyl-D-Glucosaminitol, N-Acetyl-L-Glutamic acid, N-Acetyl-Neuraminic acid, Phenylethylamine, or sec-Butylamine as sole carbon sources.

Example 5: Transcriptomic Characterization of Host Plant Response to Synthetic Compositions Comprising Plant Seeds and an Endophyte (Soy RNA-SEQ Experiments)

[0069] This Example describes the ability of synthetic compositions comprising plant seeds a single endophyte strain or a plurality of endophyte strains described herein, to confer beneficial traits to a host plant. Among other things, this Example describe the ability of endophytes (e.g., endophytes described herein) to confer beneficial traits on a variety of host plants by modulating the transcriptome of the host plant. In some embodiments, host plants include, but are not limited to, dicots (e.g., soy, peanuts) and monocots (e.g., plants described herein, e.g., corn, soy, wheat, cotton, sorghum), and combinations thereof.

[0070] Among other things, this Example describes surprising and unexpected modulations in the transcriptome of a host plant in response to synthetic compositions comprising plant seeds and a beneficial fungal endophyte strain, compared to a neutral fungal strain of the same genus.

Plant seedling

[0071] Untreated soy seeds were surface sterilized using chlorine fumes. Briefly, Erlenmyer flasks containing seeds and a bottle with 100 mL of fresh bleach solution were placed in a desiccation jar located in a fume hood. Immediately prior to closing the lid of the desiccation jar, 3 mL hydrochloric acid was carefully pipetted into the bleach. Sterilization was done for 17 hours, and upon completion the flasks with seeds were removed, sealed in sterile foil, and opened in a sterile biosafety cabinet or laminar flow hood for subsequent work.

Soy seedling assay

[0072] Seeds were first coated with 3% sodium alginate, and gently shaken to obtain homogenous coverage. SYM strain fungal inoculum grown as described previously was added to the sodium alginate coated seeds and gently mixed. For every one gram of seeds, 10 μ L of sodium alginate and inoculum were applied. Formulation only soybean seeds were coated with 3% sodium alginate and fresh PDB.

[0073] Ten seeds were placed on a 150mm Petri plate that contained a single heavy germination paper (SD5-1/4 76# heavy weight seed germination paper, Anchor Paper Co., St. Paul, MN) added with 10 mL 8% polyethylene glycol (PEG 6000). Plates were incubated at 22° Celsius in dark and 60% relative humidity for five days. Seedlings were harvested at the end of

the incubation period and stored in -80 °C until total RNA isolation using standard extraction method using TriReagent (Sigma-Aldrich, St. Louis, MO, USA) and purification with RNeasy Mini Kit (Qiagen, Hilden, Germany). All experiments (beneficial, neural, formulation) were done in triplicate under sterile conditions resulting in a total of nine samples.

Soy RNA-SEQ

[0074] Initial quality control was performed using Agilent Bioanalyzer and Tapestation.

polyA cDNA preparation

[0075] For each of the 9 soybean RNAs, polyA cDNA was prepared using a Clontech cDNA synthesis kit. Briefly, after initial QC passed, 500ng of total RNA was used to generate 1-2ug of cDNA using Clontech SMARTer PCR cDNA kit (Clontech Laboratories, Inc., Mountain View, CA USA, catalog# 634925). Manufacturer's instructions were strictly followed to perform polyA cDNA construction; 14 PCR cycles were performed.

Fragmentation

[0076] Briefly, cDNA was fragmented using Bioruptor (Diagenode, Inc., Denville, NJ USA). Fragmented cDNAs were tested for size distribution and concentration using an Agilent Bioanalyzer 2100 or Tapestation 2200 and Nanodrop.

DNA library construction

[0077] For each the 9 soybean samples, Illumina libraries were made from qualified fragmented cDNA using Beckman Coulter SPRIworks HT Reagent Kit (Beckman Coulter, Inc. Indianapolis, IN USA, catalog# B06938) on the Biomek FXp liquid handler.

[0078] Beckman Biomek FXp (Biomek 6000, Beckman Coulter) fully automatic workstation and a Beckman HT library kit were used to generate fragment libraries. The instructions were strictly followed to perform library construction. Briefly, after fragmentation the ends were repaired and 'A' bases were added to the 3' end of the fragments. Adapters were then ligated to both ends. The adaptor-ligated templates were further purified using Agencourt AMPure SPRI beads. The adaptor-ligated library was amplified by ligation-mediated PCR which consisted of 10 cycles of amplification, and the PCR product was purified using Agencourt AMPure SPRI

beads again. After the library construction procedure was completed, QC was performed using a Nanodrop and Agilent Bioanalyzer to ensure the library quality and quantity.

RNA sequencing

[0079] Sequencing was performed on an Illumina HiSeq 2500, using Rapid run v2.0 chemistry which generated paired-end reads of 106 nucleotides (nt.) according to Illumina manufacturer's instructions. The initial data analysis was started directly on the HiSeq 2500 System during the run. The HiSeq Control Software 2.2.58 in combination with RTA 1.18.64 (real time analysis) performed the initial image analysis and base calling. In addition, bcl2fastq1.8.4 generated and reported run statistics. Data was analyzed using FASTQC (Babraham Institute, Cambridge, UK) comprising the sequence information which was used for all subsequent bioinformatics analyses. Sequences were de-multiplexed according to the 6bp index code with 1 mismatch allowed.

Analysis

[0080] Differential analysis of the soy transcriptome in the presence of neutral vs beneficial fungi was performed using standard RNA-seq analysis methods. Briefly, mapped reads overlapping with exon features were counted and aggregated by gene. These gene-level counts were analyzed with the DESeq2 R package, available through the Bioconductor software repository. All possible comparisons of the three groups (control, neutral, beneficial) were performed, and the false discovery rate method was used to adjust p-values for multiple testing. High- and low-confidence differential gene lists were created using false discovery rate thresholds of 0.1 and 0.05, and log2 fold-change thresholds of 1 and 2, respectively. Set differences were extracted, e.g., genes differentially expressed in beneficial vs control but not in neutral vs control. Gene Ontology (GO) enrichment analysis was performed for all differential gene lists.

Table 500: This table shows the genes that are up-regulated (negative log FC) or down-regulated (positive log FC) in soybean as a result of treatment with a beneficial endophyte, as compared to formulation control.

The genes described in this table show significant (fdr adjusted p-value ≤ 0.05) differences in expression in soybean seedlings treated with a *Acremonium zeae* sp. with beneficial effects on soybean growth and soybean seedlings treated with a formulation ("Beneficial v Formulation"). "Median Exp. Beneficial" and "Median Exp. Formulation" represent the median expression value in cpm across biological replicates of soy seedlings treated with the beneficial *Acremonium* and formulation, respectively. "Log FC" represents the estimate of the log2-fold-change of the contrast. "Adj. p-value" represents the false discovery rate (Benjamini & Hochberg, 1995) adjusted p-values.

SEQ ID	Gene	Annotation	log FC	Adj. p-value	Median Exp. Beneficial	Median Exp. Formulation
4127	GLYMA01G31730	GO:0006952, GO, defense response	-1.369956983	3.89E-08	12.63236736	3.673553109
4128	GLYMA01G31921	NA	-1.238022219	1.45E-06	8.528180493	2.738466863
4129	GLYMA01G38630	GO:0055114, GO, oxidation-reduction process	-1.099323189	0.000263359	4.903703783	1.347924708
4130	GLYMA01G41070	GO:0008150, GO, biological_process	-1.568722399	1.04E-14	13.25341979	3.395530442
4131	GLYMA01G43420	GO:0006355, GO, regulation of transcription, DNA-dependent	-1.253171009	1.81E-09	22.27987154	8.177409896
4132	GLYMA01G44660	GO:0008150, GO, biological_process	-1.163160876	1.25E-05	7.245224059	1.797232944
4133	GLYMA02G01400	GO:0008152, GO, metabolic process	-1.1051522	1.17E-05	5.985185092	2.156679533
4134	GLYMA02G03420	GO:0019761, GO, glucosinolate biosynthetic process	-1.015176361	4.96E-05	24.06891956	9.008550154
4135	GLYMA02G04000	GO:0080167, GO, response to karrikin	-1.070349401	8.30E-10	27.49585031	12.58063061

4136	GLYMA02G061 50	GO:0008150, GO, biological_process	-1.034377122	2.01E-05	49.3568446	19.85942403
4137	GLYMA02G097 50	GO:0006468, GO, protein phosphorylation	-1.109501892	1.06E-05	18.65539483	5.75161279
4138	GLYMA02G142 60	GO:0008150, GO, biological_process	-1.251479824	4.10E-10	30.38164301	12.49076896
4139	GLYMA02G367 00	GO:0006457, GO, protein folding	1.234514786	1.70E-08	5.983985525	17.25483837
4140	GLYMA02G409 90	GO:0010200, GO, response to chitin	-1.627009953	7.37E-22	34.59243212	10.33408943
4141	GLYMA02G422 51	NA	-1.411718736	9.82E-18	83.37686498	28.48614217
4142	GLYMA02G454 20	GO:0006508, GO, proteolysis	-1.424759326	7.78E-14	51.01901733	15.27648003
4143	GLYMA03G005 40	GO:0006468, GO, protein phosphorylation	-1.349391458	2.98E-07	9.405290859	1.803380617
4144	GLYMA03G018 20	GO:0008150, GO, biological_process	-1.012023704	0.00095219 7	3.464573325	0.988478119
4145	GLYMA03G018 35	NA	-1.259097901	1.11E-08	22.70628056	8.626718132
4146	GLYMA03G018 40	GO:0008150, GO, biological_process	-1.407747152	6.51E-15	50.47616829	19.58983909
4147	GLYMA03G034 80	GO:0009733, GO, response to auxin stimulus	-1.008891294	3.93E-06	14.00695871	5.543723171
4148	GLYMA03G052 20	GO:0006355, GO, regulation of transcription, DNA-dependent	-1.368776464	5.33E-08	11.67294705	3.873928733
4149	GLYMA03G304 10	GO:0006499, GO, N-terminal protein myristoylation	-1.076960853	0.00035478 5	4.230130817	1.068669995
4150	GLYMA03G347 80	GO:0006979, GO, response to oxidative stress	1.536202396	9.85E-09	0.576235643	3.953912477
4151	GLYMA03G359	GO:0005575, GO, cellular_component	-1.037941628	6.65E-05	5.718030613	2.27092374

4152	50 GLYMA03G359 80	GO:0010150, GO, leaf senescence	-1.093799446	2.45E-08	27.18357532	9.618029959
4153	30 GLYMA03G363	GO:0009870, GO, defense response signaling pathway, resistance gene-dependent	-1.456183569	7.05E-14	14.35544394	3.606761235
4154	90 GLYMA03G423	GO:0008270, GO, zinc ion binding	-1.155489867	7.37E-09	20.94734334	7.6919159
4155	90 GLYMA04G004	GO:0008150, GO, biological_process	-1.066752001	0.00013450 ₁	5.490016192	2.066817886
4156	90 GLYMA04G008	GO:0009409, GO, response to cold	-1.23197541	1.83E-05	2.97009185	0.667918747
4157	80 GLYMA04G022	GO:0008150, GO, biological_process	-1.129891407	1.65E-07	27.07697307	12.08932932
4158	60 GLYMA04G047	GO:0006979, GO, response to oxidative stress	-1.145087639	1.78E-13	110.3884138	47.53681137
4159	10 GLYMA04G091	GO:0006108, GO, malate metabolic process	-1.023288707	6.87E-08	62.46892211	27.71861586
4160	70 GLYMA04G097	GO:0006810, GO, transport	-1.067742926	9.20E-06	7.225108449	2.785711064
4161	40 GLYMA04G111	GO:0006810, GO, transport	-1.034043016	0.00073192 ₇	3.411272197	0.667918747
4162	00 GLYMA04G126	GO:0003824, GO, catalytic activity	-1.311303393	8.14E-10	40.34895396	12.12689444
4163	10 GLYMA04G126	GO:0003824, GO, catalytic activity	-1.283734962	9.78E-06	1.652334971	0
4164	50 GLYMA04G176	GO:0010193, GO, response to ozone	-1.384727165	3.29E-11	12.87039802	3.594465888
4165	30 GLYMA04G375	GO:0008150, GO, biological_process	1.196382319	7.27E-06	2.216290935	8.800660535
4166	GLYMA04G407	NA	-1.056299293	8.46E-11	67.64119934	32.350193

4167	00	GLYMA04G407 10	GO:0008150, GO, biological_process	-1.564590555	2.15E-18	24.55650356	7.278793424
4168	61	GLYMA04G408	NA	-1.006211746	7.60E-06	19.61481513	7.146730595
4169	01	GLYMA04G417	NA	-1.201080148	1.28E-05	5.170209424	1.247337714
4170	43	GLYMA05G032	NA	-1.226133282	7.41E-08	14.53544951	5.476933727
4171	60	GLYMA05G227	PF05678, PFAM, VQ motif	-1.058133573	0.00013828 9	7.995169212	2.217489269
4172	20	GLYMA05G259	GO:0008150, GO, biological_process	-1.461542925	7.05E-14	22.86618395	7.368655071
4173	40	GLYMA05G333	GO:0008150, GO, biological_process	1.371586716	5.70E-09	2.475076542	8.038398599
4174	60	GLYMA05G347	GO:0010112, GO, regulation of systemic acquired resistance	-1.093610202	3.89E-08	18.28228693	8.348984339
4175	90	GLYMA05G376	GO:0006813, GO, potassium ion transport	-1.152485783	4.56E-13	64.84867276	29.1151737
4176	40	GLYMA06G023	GO:0008150, GO, biological_process	-1.000797368	1.73E-07	50.90257732	23.63361322
4177	50	GLYMA06G104	GO:0008150, GO, biological_process	-1.442423906	2.55E-11	10.54954485	2.771861586
4178	80	GLYMA06G105	GO:0008150, GO, biological_process	-1.333680454	9.34E-11	13.65235216	3.774189183
4179	90	GLYMA06G130	GO:0006355, GO, regulation of transcription, DNA-dependent	-1.099137285	0.00013450 1	7.195652291	2.938842487
4180	90	GLYMA06G140	GO:0008150, GO, biological_process	-1.147251562	5.98E-13	143.6465402	58.94924057
4181	20	GLYMA06G450	NA	-1.262217964	3.80E-15	53.83413936	18.7100657

4182	GLYMA06G450 43	NA	1.138574305	3.09E-10	3928.774615	8118.418788
4183	GLYMA07G063 20	GO:0006355, GO, regulation of transcription, DNA-dependent	-1.006619206	2.17E-07	33.46599312	13.89270994
4184	GLYMA07G119 60	GO:0010200, GO, response to chitin	-1.161974193	8.23E-07	43.02133043	12.67049226
4185	GLYMA07G158 00	GO:0008150, GO, biological_process	1.009903371	2.03E-06	5127.965314	11633.54157
4186	GLYMA07G297 30	GO:0006499, GO, N-terminal protein myristoylation	-1.193477886	7.29E-05	2.437920029	0.400751248
4187	GLYMA08G019 00	GO:0006813, GO, potassium ion transport	-1.203154273	2.80E-12	62.30901873	28.12669558
4188	GLYMA08G025 80	GO:0006355, GO, regulation of transcription, DNA-dependent	-1.102088699	1.08E-07	59.11095104	27.85221176
4189	GLYMA08G083 60	GO:0006952, GO, defense response	-1.107144375	4.96E-05	6.556038754	1.870172492
4190	GLYMA08G104 35	NA	1.27926219	6.52E-06	1.305040358	4.642868156
4191	GLYMA08G112 60	GO:0008150, GO, biological_process	-1.031833196	3.58E-09	51.55092715	23.63361322
4192	GLYMA08G168 10	GO:0009061, GO, anaerobic respiration	-1.153355774	1.13E-09	32.75678002	14.02629369
4193	GLYMA08G171 40	GO:0007275, GO, multicellular organismal development	1.013378053	0.00163564 2	0.479710153	1.803380617
4194	GLYMA08G226 30	GO:0009408, GO, response to heat	1.167051089	1.64E-05	1.950336023	6.144852474
4195	GLYMA09G007 20	GO:0008150, GO, biological_process	-1.297617667	9.76E-07	6.023027473	1.335837494
4196	GLYMA09G068 40	NA	1.043842712	0.00023051 5	1.980061233	6.236688568
4197	GLYMA09G124	GO:0008168, GO, methyltransferase	-1.110391457	0.00013828	4.637198143	0.868294371

	40	activity		9		
4198	GLYMA09G210 40	NA	-1.129686949	0.00019171 8	3.015093242	0.449308236
4199	GLYMA09G302 50	GO:0010200, GO, response to chitin	-1.480411528	3.22E-16	37.95040319	10.04799825
4200	GLYMA09G389 30	GO:0009611, GO, response to wounding	-1.114614822	3.43E-05	5.809822961	2.00959965
4201	GLYMA09G416 70	GO:0006355, GO, regulation of transcription, DNA-dependent	-1.282700181	1.93E-09	17.21626437	5.127943934
4202	GLYMA10G042 10	GO:0006355, GO, regulation of transcription, DNA-dependent	-1.021042996	1.99E-05	9.380998542	4.672805655
4203	GLYMA10G221 00	GO:0055114, GO, oxidation-reduction process	-1.184360983	7.75E-05	1.595729473	0.179723294
4204	GLYMA10G379 20	GO:0004497, GO, monooxygenase activity	-1.440645295	3.88E-10	13.27198089	3.339593736
4205	GLYMA10G399 71	NA	-1.199223405	2.01E-05	5.223510552	1.87100657
4206	GLYMA10G441 60	GO:0006355, GO, regulation of transcription, DNA-dependent	-1.469325378	1.70E-11	28.40950127	8.549359964
4207	GLYMA11G066 60	GO:0055114, GO, oxidation-reduction process	-1.013056688	6.65E-05	40.40225509	14.96137994
4208	GLYMA11G132 90	NA	-1.186249968	1.08E-06	34.87607854	13.47924708
4209	GLYMA11G138 00	GO:0005975, GO, carbohydrate metabolic process	-1.212845405	8.71E-11	32.35378475	12.62366432
4210	GLYMA11G138 10	GO:0005975, GO, carbohydrate metabolic process	-1.025842415	0.00023018 4	5.330112808	2.204131866
4211	GLYMA11G161 20	NA	-1.343091922	6.61E-11	16.52334971	4.313359066
4212	GLYMA11G212 50	GO:0006468, GO, protein phosphorylation	-1.06809702	0.00049506 7	2.77165866	0.718893178

4213	GLYMA11G256 70	GO:0010193, GO, response to ozone	-1.137836997	1.03E-05	8.634782749	2.695849416
4214	GLYMA11G334 50	GO:0010200, GO, response to chitin	-1.387745046	4.11E-19	57.82678829	19.16926804
4215	GLYMA12G004 60	GO:0006468, GO, protein phosphorylation	-1.042089407	1.75E-09	35.01739678	15.63592661
4216	GLYMA12G007 80	GO:0005975, GO, carbohydrate metabolic process	1.075138028	0.000616457	0.443258187	1.536213118
4217	GLYMA12G014 20	GO:0006952, GO, defense response	-1.02645451	1.87E-07	30.36318581	14.73731014
4218	GLYMA12G057 70	GO:0005975, GO, carbohydrate metabolic process	1.235797291	3.38E-07	9.663028477	25.91524739
4219	GLYMA12G058 00	GO:0005975, GO, carbohydrate metabolic process	-1.014997151	7.90E-06	29.83592268	13.15799932
4220	GLYMA12G080 20	GO:0006887, GO, exocytosis	-1.088877462	8.78E-06	7.18078263	2.494675427
4221	GLYMA12G098 30	GO:000289, GO, nuclear-transcribed mRNA poly(A) tail shortening	-1.038592224	5.61E-09	269.4683333	120.4146073
4222	GLYMA12G122 60	NA	-1.305617284	9.36E-18	48.29082204	15.69609056
4223	GLYMA12G156 20	GO:0005975, GO, carbohydrate metabolic process	-1.21921729	2.12E-08	28.83591029	10.41953246
4224	GLYMA12G363 10	GO:0006814, GO, sodium ion transport	-1.417198792	1.03E-07	6.076328601	1.335837494
4225	GLYMA13G096 90	GO:0006071, GO, glycerol metabolic process	-1.091584652	1.88E-07	29.58212608	11.0874512
4226	GLYMA13G098 40	GO:0006071, GO, glycerol metabolic process	-1.048336234	2.07E-07	45.73236789	20.63868929
4227	GLYMA13G100 10	GO:0006468, GO, protein phosphorylation	-1.18204335	2.97E-06	7.515459059	2.286785808
4228	GLYMA13G195	GO:0006355, GO, regulation of	-1.2382138	5.37E-07	6.870501899	2.078896189

4229	60	transcription, DNA-dependent							
	GLYMA13G225	NA		-1.055564007	1.97E-08	31.66087008	13.47924708		
4230	40								
	GLYMA13G353	GO:0006952, GO, defense response		1.440915562	2.97E-12	52.07520214	149.0804727		
4231	20								
	GLYMA13G357	GO:0008150, GO, biological_process		1.011655056	0.00062530	0.045001392	1.61750965		
4232	10				6				
	GLYMA14G057	PTHR10499:SF51, Panther, VON WILLEBRAND FACTOR A3		-1.079821764	0.00030877	1.935059842	0.138593079		
4233	10				7				
	GLYMA14G066	GO:0006979, GO, response to oxidative stress		-1.215771987	1.16E-08	20.25689915	6.791060885		
4234	40								
	GLYMA14G069	GO:0009408, GO, response to heat		1.019854223	0.00021457	3.195098808	9.684821834		
4235	00								
	GLYMA14G095	NA		-1.007062495	0.00124968	2.925090458	0.868294371		
4236	71				1				
	GLYMA14G324	GO:0009414, GO, response to water deprivation		1.002316095	1.01E-06	10.62032843	22.59067192		
4237	30								
	GLYMA14G393	GO:0010200, GO, response to chitin		-1.134859314	4.96E-09	71.15700599	29.02531205		
4238	00								
	GLYMA14G399	GO:0008150, GO, biological_process		-1.057047859	1.33E-08	19.72141739	7.553322821		
4239	50								
	GLYMA15G111	GO:0009651, GO, response to salt stress		-1.008285337	1.31E-05	28.83591029	14.15987744		
4240	40								
	GLYMA15G135	GO:0006979, GO, response to oxidative stress		-1.4392098	9.46E-11	19.88132077	5.543723171		
4241	10								
	GLYMA16G065	GO:0008150, GO, biological_process		-1.436684015	1.57E-08	5.625173959	0.988478119		
4242	20								
	GLYMA16G314	NA		-1.106530815	1.52E-05	9.270286684	3.118344284		
4243	01								
	GLYMA17G015	GO:0008150, GO, biological_process		-1.037614878	0.00112929	1.773032748	0.400751248		
4243	30				8				

4244	GLYMA17G033 40	GO:0006952, GO, defense response	-1.220260866	1.01E-10	372.1615091	135.9882569
4245	GLYMA17G052 40	GO:0006355, GO, regulation of transcription, DNA-dependent	-1.407526282	2.79E-13	17.00305986	5.8108931
4246	GLYMA17G113 40	GO:0008150, GO, biological_process	-1.27822077	1.25E-09	20.03527005	7.368655071
4247	GLYMA17G114 90	GO:0008150, GO, biological_process	-1.298456505	3.81E-06	3.411272197	0.623668857
4248	GLYMA17G354 30	GO:0006979, GO, response to oxidative stress	-1.083557924	1.71E-10	130.7740442	53.1082335
4249	GLYMA18G030 66	NA	-1.022521386	2.16E-08	84.85539591	34.95618076
4250	GLYMA18G047 70	GO:0010200, GO, response to chitin	-1.328972157	1.26E-22	78.45926054	28.58692238
4251	GLYMA18G204 70	GO:0010193, GO, response to ozone	-1.03304461	0.00026752 2	6.875845522	2.137339991
4252	GLYMA18G288 30	GO:0015995, GO, chlorophyll biosynthetic process	-1.360956021	6.62E-07	4.850402655	1.001878121
4253	GLYMA18G440 30	GO:0006355, GO, regulation of transcription, DNA-dependent	-1.121912469	5.61E-06	14.60450909	5.682316251
4254	GLYMA18G491 58	NA	-1.354034842	4.58E-07	4.635143342	0.801502497
4255	GLYMA18G506 91	NA	-1.039325485	9.07E-05	6.715942138	2.40450749
4256	GLYMA18G532 50	GO:0008150, GO, biological_process	1.250925416	2.68E-08	2.878260916	9.255749663
4257	GLYMA19G014 40	GO:0009408, GO, response to heat	1.091071017	3.48E-13	33.43603401	78.48045279
4258	GLYMA19G344 90	NA	-1.064397801	0.00016410 4	5.265162825	1.536213118
4259	GLYMA19G357	GO:0006355, GO, regulation of	-1.062085765	4.69E-05	7.225108449	2.516126122

4260	40	transcription, DNA-dependent	NA	-1.105970011	0.00010177 1	3.89098235	1.078339767
	GLYMA19G371 61						
4261	70	GO:0010150, GO, leaf senescence		-1.11397824	4.23E-09	34.91223889	14.4677252
	GLYMA19G385						
4262	90	GO:0010150, GO, leaf senescence		-1.295108361	8.98E-07	5.540727338	1.707371297
	GLYMA19G385						
4263	10	GO:0005975, GO, carbohydrate metabolic process		1.336821707	2.59E-06	0.132977456	2.003756241
	GLYMA19G414						
4264	70	GO:0006499, GO, N-terminal protein myristoylation		-1.124709392	4.41E-06	6.715942138	2.156679533
	GLYMA20G011						
4265	50	NA		-1.027846502	0.00069154 9	4.05012525	1.247337714
	GLYMA20G038						
4266	90	GO:0006499, GO, N-terminal protein myristoylation		-1.110406177	1.18E-09	60.21186205	26.50918593
	GLYMA20G259						
4267	00	GO:0006952, GO, defense response		-1.008944076	7.29E-07	46.74508933	17.03192805
	GLYMA20G266						
4268	20	GO:0008150, GO, biological_process		-1.092005979	2.85E-10	42.46413432	18.10059805
	GLYMA20G270						
4269	80	GO:0006355, GO, regulation of transcription, DNA-dependent		-1.034170042	9.83E-09	21.94128026	9.751613708
	GLYMA20G351						
4270	00	GO:0042545, GO, cell wall modification		1.646163821	2.88E-09	0.213204512	2.426264
	GLYMA03G374						
4271	40	GO:0005975, GO, carbohydrate metabolic process		2.018195916	1.64E-15	0.576235643	5.391699
	GLYMA03G388						
4272	80	GO:0009693, GO, ethylene biosynthetic process		1.14033694	9.07E-05	0.900027833	4.133636
	GLYMA07G153						
4273	50	GO:0005975, GO, carbohydrate metabolic process		2.028493959	7.27E-15	0.310280731	3.684328
	GLYMA08G464						
4274	40	GO:0005975, GO, carbohydrate metabolic process		3.395302467	6.40E-68	1.152471286	24.89168
	GLYMA09G358						

4275	GLYMA10G303 40	GO:0008150, GO, biological_process	-2.087505841	1.42E-27	35.23204566	5.032252
4276	GLYMA11G023 50	GO:0005975, GO, carbohydrate metabolic process	2.628824882	2.44E-30	1.012721434	13.47925
4277	GLYMA12G015 10	GO:0005975, GO, carbohydrate metabolic process	3.161170918	8.63E-48	0.5400167	13.1198
4278	GLYMA13G304 40	GO:0008150, GO, biological_process	-2.347970113	7.37E-22	7.195652291	0.467543
4279	GLYMA15G077 00	PF00264, PFAM, Common central domain of tyrosinase	0.824086029	0.01860205 4	3.102807309	19.05067
4281	GLYMA17G084 00	GO:0006032, GO, chitin catabolic process	-2.054291387	1.57E-22	16.26757546	2.066818
4283	GLYMA17G148 90	GO:0006869, GO, lipid transport	1.278386816	1.57E-08	25.8419523	62.159
4284	GLYMA18G473 90	GO:0009611, GO, response to wounding	-2.306445262	6.24E-19	3.900672046	0.089862
4285	GLYMA18G534 40	GO:0008150, GO, biological_process	0.105360923	0.99200749 9	16.84315647	19.54162

Table 501: This table shows the genes that are up-regulated (positive log FC) or down-regulated (negative log FC) in soybean as a result of treatment with a beneficial endophyte, as compared to a soybean treated with a reference microorganism.

This table describes soybean genes differentially expressed in soybean seedlings treated with an Acremonium zea sp. with neutral effects on soybean growth and soybean seedlings treated with an Acremonium zea sp. with beneficial effects on soybean growth. "Median Exp. Neutral" and "Median Exp. Beneficial" represent the median expression value in cpm across biological replicates of soy seedlings treated with the neutral Acremonium and beneficial Acremonium, respectively. "Log FC" represents the estimate of the log2-fold-change of the contrast. "Adj. p-value" represents the false discovery rate (Benjamini & Hochberg, 1995) adjusted p-values.

SEQ ID	Gene	Annotation	log FC	Adj. p-value	Median Exp. Neutral	Median Exp. Beneficial
4162	GLYMA04G12600	GO:0003824, GO, catalytic activity	1.206357	9.85E-08	13.26698	40.34895
4201	GLYMA09G41670	GO:0006355, GO, regulation of transcription, DNA-dependent	1.221864	1.58E-06	5.909453	17.21626
4153	GLYMA03G36330	GO:0009870, GO, defense response signaling pathway, resistance gene-dependent	0.856536	0.000672	6.648135	14.35544
4253	GLYMA18G44030	GO:0006355, GO, regulation of transcription, DNA-dependent	0.998764	0.001135	5.793248	14.60451
4181	GLYMA06G45020	NA	0.657628	0.003708	31.22163	53.83414
4195	GLYMA09G00720	GO:0008150, GO, biological_process	0.90306	0.003708	2.788204	6.023027
4206	GLYMA10G44160	GO:0006355, GO, regulation of transcription, DNA-dependent	0.819527	0.009033	13.67119	28.4095
4269	GLYMA20G35180	GO:0006355, GO, regulation of transcription, DNA-dependent	0.663267	0.009033	13.62622	21.94128
4167	GLYMA04G40710	GO:0008150, GO, biological_process	0.829353	0.010992	12.55759	24.5565
4140	GLYMA02G40990	GO:0010200, GO, response to chitin	0.795223	0.01505	17.04244	34.59243
4183	GLYMA07G06320	GO:0006355, GO, regulation of transcription, DNA-dependent	0.748416	0.015784	18.20323	33.46599
4142	GLYMA02G45420	GO:0006508, GO, proteolysis	0.894101	0.016107	21.73835	51.01902
4199	GLYMA09G30250	GO:0010200, GO, response to chitin	0.819331	0.017054	15.30126	37.9504
4250	GLYMA18G04770	GO:0010200, GO, response to chitin	0.787911	0.019874	39.88881	78.45926
4213	GLYMA11G25670	GO:0010193, GO, response to ozone	0.897841	0.02031	3.00749	8.634783
4150	GLYMA03G34780	GO:0006979, GO, response to oxidative stress	-0.91553	0.022156	2.078494	0.576236
4222	GLYMA12G12260	NA	0.730565	0.02231	26.27596	48.29082
4184	GLYMA07G11960	GO:0010200, GO, response to chitin	0.881315	0.026957	16.19823	43.02133

4131	GLYMA01G43420	GO:0006355, GO, regulation of transcription, DNA-dependent	0.792195	0.0384	11.50233	22.27987
4223	GLYMA12G15620	GO:0005975, GO, carbohydrate metabolic process	0.802313	0.040823	13.75344	28.83591
4270	GLYMA03G37400	GO:0042545, GO, cell wall modification	0.166032	NA	0.05276297	0.21320451
4271	GLYMA03G38840	GO:0005975, GO, carbohydrate metabolic process	-0.91714	0.022324	1.79394116	0.57623564
4272	GLYMA07G15380	GO:0009693, GO, ethylene biosynthetic process	0.727432	0.132533	0.26533960	0.90002783
4273	GLYMA08G46450	GO:0005975, GO, carbohydrate metabolic process	-0.44339	0.684951	0.84420760	0.31028073
4274	GLYMA09G35840	GO:0005975, GO, carbohydrate metabolic process	-1.28626	1.70E-05	4.04739281	1.15247128
4275	GLYMA10G30340	GO:0008150, GO, biological_process	0.531076	0.317217	17.0440208	35.2320456
4276	GLYMA11G02350	GO:0005975, GO, carbohydrate metabolic process	-0.39592	0.826706	1.63626088	1.01272143
4277	GLYMA12G01510	GO:0005975, GO, carbohydrate metabolic process	-0.84175	0.059336	1.50359108	0.5400167
4278	GLYMA13G30440	GO:0008150, GO, biological_process	0.559495	0.472633	2.56494949	7.19565229
4279	GLYMA15G07700	PF00264, PFAM, Common central domain of tyrosinase	0.458456	0.694846	1.61895712	3.10280730
4280	GLYMA15G12600	GO:0006869, GO, lipid transport	0.833553	0.064382	3.16577852	12.2782517
4281	GLYMA17G08400	GO:0006032, GO, chitin catabolic process	0.945666	0.000294	6.19125740	16.2675754
4282	GLYMA17G14860	GO:0006869, GO, lipid transport	0.776484	0.105214	5.71132096	15.7799914
4283	GLYMA17G14890	GO:0006869, GO, lipid transport	0.617561	0.305278	10.7636469	25.8419523
4284	GLYMA18G47390	GO:0009611, GO, response to wounding	1.018065	0.000747	1.61895712	3.90067204
4285	GLYMA18G53440	GO:0008150, GO, biological_process	-2.04965	6.81E-35	91.1216585	16.8431564

Table S02: This table describes gene ontology terms which are significantly enriched or depleted in the set of genes differently expressed between soybean seedlings treated with an Acremonium zeae sp. with neutral effects on soybean growth and soybean seedlings treated with a Acremonium zeae sp. with beneficial effects on soybean growth.

“Genome count” represents the number of genes associated with the GO term that were found in the soybean genome. “Observed DEG count” represents the number of genes associated with the GO term that were differentially expressed in the Neutral v Beneficial contrast. “Expected DEG count” represents the number of genes associated with the GO term that are expected to be found by chance in a random set selection of that number of genes. “Status” represents whether genes with the GO term are over or under-represented in the set of DEGs. “Adj. p-value” represents the false discovery rate (Benjamini & Hochberg, 1995) adjusted p-values.

GO ID	GO Description	Gene ID	SEQ ID
GO:0000014	single-stranded DNA specific endodeoxyribonuclease activity	GLYMA15G07430, GLYMA15G07430	4286; 4286
GO:0003700	sequence-specific DNA binding transcription factor activity	GLYMA03G34730, GLYMA03G41750, GLYMA05G32040, GLYMA06G11700, GLYMA08G16190, GLYMA09G41670, GLYMA13G21350, GLYMA19G37410, GLYMA19G40650, GLYMA0041S00350, GLYMA01G41520, GLYMA01G44230, GLYMA02G00290, GLYMA03G33070, GLYMA03G34730, GLYMA04G35380, GLYMA05G32040, GLYMA06G20400, GLYMA08G14320, GLYMA08G16190, GLYMA08G18470, GLYMA13G18400, GLYMA13G21350, GLYMA15G00570, GLYMA17G06610, GLYMA18G43580, GLYMA19G34740, GLYMA19G37410, GLYMA01G43420, GLYMA03G05220, GLYMA03G33070, GLYMA04G04760, GLYMA05G34760, GLYMA05G36970, GLYMA06G04840, GLYMA06G13090, GLYMA07G06320, GLYMA08G02580, GLYMA08G14320, GLYMA08G17140, GLYMA09G08330, GLYMA09G41670, GLYMA10G04190, GLYMA10G04210, GLYMA10G44160, GLYMA13G17250, GLYMA13G18400, GLYMA13G19560, GLYMA15G00570, GLYMA15G19910, GLYMA17G05240, GLYMA17G35430, GLYMA18G44030, GLYMA19G35740, GLYMA19G35770, GLYMA20G35180	4288; 4295; 4292; 4296; 4297; 4201; 4298; 4299; 4300; 4301; 4302; 4303; 4304; 4305; 4288; 4306; 4292; 4307; 4308; 4297; 4309; 4310; 4298; 4311; 4312; 4313; 4314; 4299; 4131; 4148; 4305; 4158; 4174; 4315; 4316; 4179; 4183; 4188; 4308; 4193; 4317; 4201; 4318; 4202; 4206; 4319; 4310; 4228; 4311; 4320; 4245; 4248; 4253; 4259; 4321; 4269
GO:0003950	NAD+ ADP-ribosyltransferase activity	GLYMA04G35560	4289

GO:0004222	metalloendopeptidase activity	GLYMA01G41750, GLYMA01G04350	4290; 4287
GO:0006308	DNA catabolic process	GLYMA15G07430, GLYMA01G20900, GLYMA15G07430, GLYMA01G20900	4286; 4322; 4286; 4322
GO:0006879	cellular iron ion homeostasis	GLYMA13G27300, GLYMA13G27300	4291; 4291
GO:0006970	response to osmotic stress	GLYMA05G32040, GLYMA09G41670, GLYMA05G32040, GLYMA03G05220, GLYMA09G41670, GLYMA18G44030	4292; 4201; 4292; 4148; 4201; 4253
GO:0008237	metallopeptidase activity	GLYMA01G41750, GLYMA01G04350	4290; 4287
GO:0008270	zinc ion binding	GLYMA01G41750, GLYMA01G04350, GLYMA03G33070, GLYMA09G26100, GLYMA03G33070, GLYMA03G42390, GLYMA04G04760, GLYMA04G09110, GLYMA06G04840, GLYMA10G44160, GLYMA13G19560, GLYMA17G35430, GLYMA19G35740, GLYMA19G35770	4290; 4287; 4305; 4335; 4305; 4154; 4158; 4159; 4316; 4206; 4228; 4248; 4259; 4321
GO:0009611	response to wounding	GLYMA06G45240, GLYMA06G45280, GLYMA06G45370, GLYMA06G45410, GLYMA12G32750, GLYMA13G37720, GLYMA13G37770, GLYMA18G47390, GLYMA01G41290, GLYMA06G45240, GLYMA06G45370, GLYMA06G45410, GLYMA12G32750, GLYMA13G23680, GLYMA13G35820, GLYMA13G35850, GLYMA13G37720, GLYMA13G37750, GLYMA13G37770, GLYMA15G00570, GLYMA18G06810, GLYMA18G47390, GLYMA04G04760, GLYMA06G04840, GLYMA09G38930, GLYMA12G09830, GLYMA15G00570, GLYMA17G35430, GLYMA18G47390	4293; 4323; 4324; 4325; 4326; 4327; 4328; 4284; 4329; 4293; 4324; 4325; 4326; 4330; 4331; 4332; 4327; 4333; 4328; 4311; 4334; 4284; 4158; 4316; 4200; 4221; 4311; 4248; 4284
GO:0010120	camalexin biosynthetic process	GLYMA03G05220, GLYMA09G41670, GLYMA18G44030	4148; 4201; 4253
GO:0016891	endoribonuclease activity, producing 5'-phosphomonoesters	GLYMA15G07430, GLYMA15G07430	4286; 4286
GO:0034605	cellular response to heat	GLYMA03G05220, GLYMA09G41670, GLYMA18G44030	4148; 4201; 4253
GO:0043765	T/G mismatch-specific endonuclease activity	GLYMA15G07430, GLYMA15G07430	4286; 4286
GO:0046592	polyamine oxidase activity	GLYMA10G11700, GLYMA10G11700	4294; 4294

GO:0050660	flavin adenine dinucleotide binding	GLYMA04G12600, GLYMA10G11700, GLYMA10G11700, GLYMA19G44870, GLYMA04G12600, GLYMA04G12610, GLYMA19G44870	4162; 4294; 4294; 4336; 4162; 4163; 4336
GO:0070370	cellular heat acclimation	GLYMA03G05220, GLYMA09G41670, GLYMA18G44030	4148; 4201; 4253
GO:0071369	cellular response to ethylene stimulus	GLYMA13G27300, GLYMA13G27300	4291; 4291
GO:0071732	cellular response to nitric oxide	GLYMA13G27300, GLYMA13G27300	4291; 4291
GO:0072593	reactive oxygen species metabolic process	GLYMA04G35560	4289

Attorney docket no: 30807-32831PCT

Genes that are modulated in soybean in response to treatment with a beneficial endophyte include those involved in a variety of plant processes, such as plant defense (including responses to chitin and wounding), stress responses (including salt stress, water deprivation, cold, ozone, heat, osmotic), defense against oxidative stress (oxidation-reduction process, monooxygenase activity, oxidation-reduction process, ion binding, nitric oxide). For example, expression of genes involved in the following processes were modulated: cell wall modification, defense response, oxidation-reduction process, biological process, regulation of transcription, metabolic process, glucosinolate biosynthetic process, response to karrikin, protein phosphorylation, protein folding, response to chitin, proteolysis, response to auxin stimulus, DNA-dependent regulation of transcription, N-terminal protein myristoylation, response to oxidative stress, cellular component, leaf senescence, resistance gene-dependent defense response signaling pathway, zinc ion binding, response to cold, malate metabolic process, transport, catalytic activity, response to ozone, VQ motif, regulation of systemic acquired resistance, potassium ion transport, anaerobic respiration, multicellular organismal development, response to heat, methyltransferase activity, response to wounding, oxidation-reduction process, monooxygenase activity, oxidation-reduction process, carbohydrate metabolic process, exocytosis, nuclear-transcribed mRNA poly(A) tail shortening, sodium ion transport, glycerol metabolic process, response to water deprivation, response to salt stress, and chlorophyll biosynthetic process.

Attorney docket no: 30807-32831PCT

Example 6: Functional Characterization of Endophytes (Microbe RNA-SEQ Experiments)

[0081] This Example describes the ability of synthetic compositions comprising plant seeds and a single endophyte strain or a plurality of endophyte strains described herein, to confer beneficial traits to a host plant. Among other things, this Example provides exemplary characterization of modulations in a beneficial endophyte's transcriptome in response to host plant interactions, as compared to transcriptome changes in the transcriptome of a neutral (e.g., non-beneficial and non-pathogenic)microbe of the same genus.

[0082] RNA sequencing was used to explore differences in mRNA expression of genes common to the two strains of *Acremonium zeae*.

[0083] Among other things, this Example describe the ability of host plants (e.g., host plants described herein, e.g., dicots, e.g., soy, peanuts, and monocots, e.g., corn, soy, wheat, cotton, sorghum) to differentially modulate the transcriptome of a beneficial endophyte as compared to the transcriptome of a neutral microbe of the same genus. This Example describes surprising and unexpected modulations in the transcriptome of a beneficial endophyte in response to whole plant homogenate, compared to a neutral fungal strain of the same genus.

[0084] In particular, this Example describes an exemplary transcriptomic comparison between the functional capacity of a beneficial fungal endophyte genome and the genome of a neutral fungal microbe of the same genus. Briefly, each set of microbial predicted genes was annotated with pathway and orthologous group information from the KEGG database. Pathways and ortholog groups appearing in one genome but not the other were extracted and manually explored for biological relevance to the phenotype differences.

Fungal biomass

[0085] Beneficial (SYM00577) and neutral (SYM00300) fungal strains of *Acremonium zeae* were initially streaked onto PD agar and incubated at room temperature until colony formation. Distinct plugs consisting of spores and mycelia were used to inoculate 125 mL PD broth and cultured for 5 days at room temperature with agitation (200 RPM). Each strain was grown in three biological replicates in duplicates totaling 12 flasks.

[0086] On day 5 of culture, 1 mL of total plant homogenate obtained from 6 day old soybean seedlings extracted with 50 mM Phosphate-buffered saline (PBS) at a ratio of 2 mL buffer/gram

Attorney docket no: 30807-32831PCT

plant mass was added to the fungi. The plant homogenate solution was prepared in three replicates, and each replicate was applied to the corresponding beneficial and neutral fungal cultures. One mL of PBS solution was applied to each fungal biological replicate as the negative control.

[0087] Fungal biomass was harvested 24 hours after the addition of either the plant homogenate or PBS only solutions by centrifuging at 4500 RPM for 20 minutes in 50 mL Falcon tubes to allow culture separation prior to the removal of supernatant. Fungal tissues were stored immediately in -80 °C until total RNA isolation using standard extraction method using TriReagent (Sigma-Aldrich, St. Louis, MO, USA) and purification with RNeasy Mini Kit (Qiagen, Hilden, Germany).

Fungal RNA-SEQ

[0088] Initial quality control was performed using Agilent Bioanalyzer and Tapestation.

rRNA depletion

[0089] 1µg of total RNA was subjected to rRNA depletion using the RiboZero Yeast kit (Epicentre Biotechnologies, Illumina.com, catalog # MRZY1306). Manufacturer's instructions were strictly followed to perform rRNA depletion.

Stranded cDNA preparation

[0090] After rRNA depletion, depletedRNA was used to generate 1-2ug of cDNA using: Illumina TruSeq Stranded Total RNA LT kit (Illumina.com, catalog # RS-122-2201). Manufacturer's instructions were strictly followed to perform cDNA construction; and library construction.

RNA sequencing

[0091] Sequencing was performed on an Illumina HiSeq 2500, using Rapid run v2.0 chemistry which generated paired-end reads of 106 nucleotides according to Illumina manufacturer's instructions. The initial data analysis was started directly on the HiSeq 2500 System during the run. The HiSeq Control Software 2.2.58 in combination with RTA 1.18.64 (real time analysis) performed the initial image analysis and base calling. In addition, bcl2fastq1.8.4 generated and reported run statistics. Data was analyzed using FASTQC (Babraham Institute, Cambridge, UK)

Attorney docket no: 30807-32831PCT

comprising the sequence information which was used for all subsequent bioinformatics analyses. Sequences were de-multiplexed according to the 6bp index code with 1 mismatch allowed.

Analysis

[0092] Expression levels for each gene were quantified as transcripts per million (TPM) using Cufflinks. The Blast Best Reciprocal Hits (BRH) method was used to define orthologous groups for similar gene pairs across species. Expression was mapped directly to BRH groups to create an expression matrix and the limma method was used to uncover genes (1) differentially expressed with vs without plant homogenate within each species, (2) differentially expressed across species within each plant homogenate condition, and (3) responding differently to plant homogenate in the different species. The false discovery rate method was used to adjust p-values for multiple testing. In each case, significance was defined as adjusted p-value less than 0.05 and absolute log₂ fold change greater than 2.

Functional and Comparative Genomics

[0093] Prior to applying differential expression analysis, the functional capabilities of a beneficial and neutral *Acremonium zeae*, i.e., SYM00577 (beneficial) and SYM00300 (neutral), were contrasted at the gene function (GO) and pathway level. A shared goal of both the genome comparison and the transcriptome analyses was the construction of orthologous groups. In the case of comparative genomics, annotations of these orthologs provided an overview of shared capabilities, while for RNA-seq they provided anchors for comparison of expression data, i.e. rows in the expression matrix.

Differential KEGG Orthology Groups

[0094] The unique and shared orthology group (OG) terms were counted for SYM00577 and SYM00300. Most KO terms were shared by both strains, with 62 terms found in SYM00300 only, and 207 terms found in SYM00577 only, with 2,676 KO terms overlapping between both strains. This process was repeated for KEGG Pathways, and the total and shared number of pathways was again similar, with 324 of the pathways shared between strains. Unique pathways in SYM00577 that were *not* present in SYM00300, include, but are not limited to, indole diterpene alkaloid biosynthesis, biosynthesis of 12-, 14- and 16-membered macrolides, peptidoglycan biosynthesis, glycosphingolipid biosynthesis – lacto and neolacto series, indole

Attorney docket no: 30807-32831PCT

alkaloid biosynthesis, type I polyketide structures, biosynthesis of siderophore group nonribosomal peptides, beta-Lactam resistance, sphingolipid signaling pathway, vibrio cholera pathogenic cycle, central carbon metabolism in cancer, choline metabolism in cancer, and nicotinate and nicotinamide metabolism. Exemplary KEGG Pathway differences for SYM00577 are illustrated below in **Table 600**.

Table 600: Exemplary KEGG Pathways present in SYM0577, but absent in SYM0300

KEGG Term	KEGG Term Description	Number of Genes
ko00403	Indole diterpene alkaloid biosynthesis	1
ko00522	Biosynthesis of 12-, 14- and 16-membered macrolides	1
ko00550	Peptidoglycan biosynthesis	2
ko00601	Glycosphingolipid biosynthesis – lacto and neolacto series	1
ko00901	Indole alkaloid biosynthesis	1
ko01052	Type I polyketide structures	1
ko01053	Biosynthesis of siderophore group nonribosomal peptides	2
ko01501	Beta-Lactam resistance	7
ko04071	Sphingolipid signaling pathway	46
ko05111	Vibrio cholera pathogenic cycle	1
ko05230	Central carbon metabolism in cancer	29
ko05231	Choline metabolism in cancer	30

In the above example, the Sphingolipid signaling pathway included 46 genes. To determine whether all of the genes (i.e., orthologous groups) in the pathway were unique to only SYM00577, a query was performed to determine which of the Sphingolipid pathway genes in SYM00577 *do not* share any KEGG OG terms with SYM00300 genes.

[0095] Interestingly, even though the Sphingolipid Signaling Pathway annotation is attached to 46 genes in SYM00577 but no genes in SYM00300, only one orthologous group from that pathway (sphingomyelin phosphodiesterase, annotating 4 genes) is not present in SYM300.

[0096] Unique pathways in SYM00300 that were *not* present in SYM00577, include, but are not limited to, beta-Lactam resistance, DDT degradation, Flavone and flavonol biosynthesis, and ECM-receptor interaction. Exemplary KEGG Pathway differences for SYM00300 are illustrated below in **Table 700**.

Table 601: Exemplary KEGG Pathways present in SYM0300, but absent in SYM0577

KEGG Term	KEGG Term Description	Number of Genes
ko00312	Beta-Lactam resistance	4

Attorney docket no: 30807-32831PCT

ko00351	DDT degradation	3
ko00944	Flavone and flavonol biosynthesis	1
ko04512	ECM-receptor interaction	2

Blast Best Reciprocal Hits (BBRH)

[0097] The NCBI Blast+ software was installed and used to build blast databases from each set of amino acid sequences, then each transcriptome was blasted against the database created from the other. Best Reciprocal Hits (BRH) were calculated by filtering for high percent identity, gathering the best hits, and joining the targets from one output with the queries from the other. The result was a query-target-reciprocal trio, which was filtered for trios where the query was the same as its reciprocal. The e-value and bitscores from the two blast outputs were averaged (since they are asymmetric) for the BRH pairs, and an ortholog group identifier was created.

Calculation of in-paralogs

[0098] In-paralogs are paralogs that are the result of speciation first, then duplication of the genes later. In-paralogs are more likely to retain the same function as the ortholog than out-paralogs, which represent duplication, followed by speciation. Considering the high proportion of SYM00300 genes that have BRH orthologs, along with the realization that SYM00577 has nearly twice as many transcripts, we considered the possibility of a major genome duplication event somewhere in the phylogenetic history of SYM00577, and extended the orthologous groups to include in-paralogs.

[0099] An important step after BRH is, for each orthologous pair, to include same-species genes more similar to each member of the pair than the cross-species ortholog similarity. This was accomplished using all-versus-all Blast within the same species, to expand our orthologous groups.

[0100] Another approach to building ortholog groups was to apply a threshold to the same-species hits for each member of the ortholog pairs. To find the best threshold, we explored the distribution of scores in these BRH/same-species tables described above, normalizing by the ortholog score.

RNA-SEQ cross-species comparison

Attorney docket no: 30807-32831PCT

[0101] RNA-seq cufflinks FPKM values were generated for two species of fungus (*Acremonium zeae*), with three biological replicates each. An expression matrix was built using orthologous groups, to explore the structure of the data, characterize data quality, and to elucidate pathway-level expression differences between SYM00577 and SYM00300.

Table 602:

This table describes orthologous genes of *Acremonium zeae* sp. with beneficial and neutral effects on soybean growth, these genes show significant changes in expression between the two genotypes when grown in culture with soybean homogenate. "Median Exp. SYM00577" represents the median expression value in log₂ tpm across biological replicates of the beneficial *Acremonium* grown in media inoculated with soybean seedling homogenate extracted with 50 mM PBS. "Median Exp. SYM00300" represents the median expression value in log₂ tpm across biological replicates of the neutral *Acremonium* grown in media inoculated with soybean seedling homogenate extracted with 50 mM PBS. "Log FC" represents the estimate of the log₂-fold-change of the contrast. "B-statistic" represents the log-odds that the gene is differentially expressed. "t-statistic" represents the moderated t-statistic. "Adj. p-value" represents the false discovery rate (Benjamini & Hochberg, 1995) adjusted p-values.

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
694	g3058.t1	2499	g1604.t1		0	5.625962	5.651891	7.35527	14.190 07	8.51E-06
695	g3790.t1	2501	g2628.t1	K12486: SMAP	0	6.121031	5.983809	6.039604	11.335 24	1.91E-05
681	g4581.t1	3296	g4123.t1	K00574: E2.1.1.79, cfa	0.511902	7.31261	7.115847	5.836125	10.979 39	2.24E-05
682	g9772.t1	3297	g936.t1	K06874: K06874	1.832874	7.06298	5.150347	5.583339	10.561 06	2.71E-05
1454	g3066.t1	2510	g11773.t1		0	4.229364	4.33707	5.111231	9.8409 67	4.33E-05
1455	g2768.t1	3298	g9143.t1	K03937: NDUF54	0	3.159447	3.192054	5.100931	9.8260 62	4.35E-05
1456	g21086.t1	2530	g6575.t1		6.213302	0	-6.32587	4.86651	- 9.4952 9	5.53E-05
1457	g13116.t1	2518	g7771.t1		0	4.229765	4.831879	4.862002	9.4890 83	5.54E-05
1458	g900.t1	3299	g9375.t1		0	2.925165	2.991998	4.824313	9.4374 02	5.73E-05
693	g2076.t1	2498	g2520.t1		3.957232	13.01167	9.729519	4.68583	9.2507	6.67E-05

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statisti c	Adj. p- value
1459	g5141.t1	3300	g3839.t1	K06662: HRAD17, RAD24	1.158624	7.175348	6.392146	4.57545	87 9.1055 99	7.49E-05
1460	g10898.t1	2515	g5903.t1		0	2.733166	2.603795	4.241238	8.6839 22	0.00010 7
1461	g19933.t1	3301	g3124.t1	K10885: XRCC5, KU80, G2P2	0	2.454643	2.568635	4.162803	8.5886 28	0.00011 6
685	g6380.t1	2492	g764.t1	K05857: PLCD	3.201415	9.359327	5.628694	3.892588	8.2701 89	0.00015 2
689	g849.t1	2496	g9453.t1	K06997: K06997	2.698993	7.96329	5.067599	3.750578	8.1086 28	0.00017 1
1462	g156.t1	3302	g5221.t1		0	2.981748	2.98057	3.513183	7.8468 43	0.00021 5
1463	g10541.t1	3303	g6687.t1	K17862: PPOC	0	2.880335	2.956642	3.496903	7.8292 54	0.00021 9
1464	g15671.t1	3304	g6482.t1	K11771: SWI1, ADR6	0	2.123699	2.319853	3.367017	7.6905 34	0.00024 6
1465	g5602.t1	2531	g7524.t1	K14774: UTP25, DEF	0	4.214818	5.146089	3.215759	7.5324 72	0.00028 2
1466	g4223.t1	3305	g1757.t1		2.289499	7.236816	5.448174	3.206971	7.5234 01	0.00028 4
684	g2536.t1	3306	g3569.t1		9.671862	2.518007	7.85736	3.098463	- 7.4123 8	0.00031 6
1467	g8228.t1	3307	g10052.t1	K01674: cah	5.638975	1.15932	-4.58017	2.941341	- 7.2547 5	0.00036 6
1468	g10616.t1	3308	g4156.t1	K15562: BUR1, SGV1	0	4.260933	4.233331	2.939239	7.2526 62	0.00036 6
1469	g10359.t1	3309	g7715.t1		2.199706	9.30437	7.40778	2.907247	7.2210 16	0.00037 8
1470	g12048.t1	3310	g810.t1		0.205106	6.22836	5.696498	2.79987	7.1158 6	0.00041 2
1471	g7057.t1	3311	g6310.t1	K05610: UCHL5, UCH37	2.367427	6.390825	4.178102	2.772937	7.0897 35	0.00042 2
680	g1340.t1	2553	g523.t1		0	5.30819	5.122003	2.739527	7.0574 66	0.00043 4

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statisti c	Adj. p- value
1472	g5411.t1	3312	g8610.t1		0	5.724304	5.482331	2.691237	7.0110 91	0.00045 4
1474	g2755.t1	3314	g9155.t1	K13106: BUD13, CWC26	0	2.648734	2.611976	2.63723	6.9595 94	0.00047 5
1473	g9212.t1	3313	g11325.t1	K03380: E1.14.13.7	0.695829	8.890455	7.737352	2.638623	6.9609 17	0.00047 5
1475	g7541.t1	3315	g7266.t1	K01230: MAN1	0.593738	3.991249	3.523245	2.589692	6.9145 82	0.00049 4
1476	g10543.t1	3316	g6689.t1	K11866: STAMBP, AMSH	0	2.512821	2.348519	2.557397	6.8841 7	0.00050 6
1477	g1098.t1	3317	g4042.t1		0	8.363912	7.407417	2.550651	6.8778 34	0.00050 9
1478	g5757.t1	3318	g5200.t1	K16261: YAT	2.629263	6.731656	4.004055	2.491406	6.8224 41	0.00053 3
1479	g6616.t1	3319	g11275.t1	K00128: E1.2.1.3	14.15644	4.764987	-7.9496	2.391867	6.7303 6	0.00057 9
676	g7741.t1	2557	g7091.t1		7.176506	3.981694	-3.40286	2.312767	- 6	0.00061 8
1480	g3094.t1	3320	g11797.t1	K02155: ATPeVOC, ATP6L	0.181741	4.905207	4.139345	2.177837	6.5364 19	0.00069 9
1481	g4793.t1	3321	g3693.t1		0.802943	6.094219	5.125954	2.035034	6.4099 58	0.00079 7
1482	g4553.t1	3322	g4081.t1		1.09266	4.629	3.630404	1.987031	6.3679 56	0.00082 6
1483	g2790.t1	3323	g5023.t1		2.621767	6.913986	4.339207	1.945501	6.3318 19	0.00085 6
1484	g12353.t1	3324	g12077.t1		7.044527	1.163008	-6.15638	1.883313	- 5	0.0009 5
1485	g9391.t1	2535	g3643.t1	K12821: PRPF40, PRP40	3.337644	7.951706	4.079618	1.87347	6.2695 79	0.00090 8
1486	g501.t1	2522	g5516.t1	K11713: PGTB1	0.17786	7.158208	5.970183	1.860221	6.2581 9	0.00091 8
1487	g4315.t1	3325	g1973.t1	K00507: SCD, desC	2.439884	8.285639	5.723788	1.809797	6.2150 14	0.00095 6

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1488	g9843.t1	3326	g9771.t1	K00799: GST, gst	8.277156	1.535981	-6.40337	1.808206	-6.21366	0.000956
1489	g11092.t1	3327	g7982.t1		2.025136	6.798845	4.871183	1.802892	6.209122	0.000958
1490	g11703.t1	3328	g6616.t1	K01785: galM, GALM	5.853172	0.587191	-5.06599	1.752712	-6.16645	0.001006
1491	g11062.t1	3329	g1580.t1		0	8.467134	6.867295	1.691984	6.115148	0.001064
1492	g13143.t1	3330	g4290.t1	K10878: SPO11	0	2.383986	2.169112	1.68932	6.112906	0.001065
1493	g10366.t1	2548	g5460.t1		0	4.099839	3.972778	1.675269	6.101093	0.001078
1494	g9622.t1	3331	g7240.t1	K01648: ACLY	0	2.029549	2.402941	1.580259	6.02172	0.00118
677	g13489.t1	2556	g8733.t1		4.049293	1.53096	-2.39019	1.568038	-6.01157	0.001191
1495	g11681.t1	3332	g10864.t1	K01081: E3.1.3.5	2.030435	5.800198	3.546964	1.557877	6.003149	0.001197
1496	g13112.t1	3333	g7720.t1		0	2.5721	2.197403	1.547012	5.99415	0.001208
1497	g6237.t1	2500	g7135.t1		4.217621	11.98228	7.390343	1.524373	5.975438	0.00123
1498	g5325.t1	2546	g2235.t1	K17794: TIM23	5.393638	9.737867	4.665515	1.490748	5.947736	0.001262
1499	g7356.t1	3334	g10411.t1		5.363476	2.004245	-4.00808	1.46351	-5.92537	0.001296
1500	g502.t1	2516	g5517.t1		6.13678	0.881592	-5.04567	1.401059	-5.87435	0.001355
1501	g8003.t1	3335	g3392.t1		1.075006	6.028587	4.451645	1.395621	5.869934	0.001362
691	g5563.t1	2493	g7478.t1		4.683265	9.926473	4.734657	1.388209	5.863907	0.00137

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1502	g973.t1	3336	g8044.t1	K12733: PPI1	0	4.446627	4.44962	1.37841	5.8559 46	0.00137 9
1503	g9616.t1	3337	g7246.t1		0	3.761644	3.227741	1.346391	5.8299 96	0.00141 6
1504	g2349.t1	3338	g9226.t1	K10865: MRE11	5.092776	8.748668	3.95033	1.335801	5.8214 33	0.00142 7
1505	g2683.t1	2507	g4140.t1		5.881648	1.482684	-3.92467	1.322012	-	0.00144 5
1506	g3045.t1	2533	g1615.t1		3.526626	10.01023	6.461973	1.267461	5.8103 18	0.00152
1507	g2056.t1	3339	g2541.t1		0	2.16783	2.561107	1.216459	5.7256 28	0.00158 3
521	g11059.t1	2317	g2900.t1	K01074: PPT	0	3.417929	3.812645	1.160246	5.6809 31	0.00166 8
1508	g7593.t1	3340	g7644.t1	K10577: UBE2I, UBC9	5.000466	0	-4.49434	1.150461	-	0.00168 3
1509	g1121.t1	3341	g220.t1		0.238182	9.960466	8.035072	1.140622	5.6653 91	0.00169
1510	g13554.t1	3342	g4591.t1		0	7.155818	7.18618	1.13793	5.6632 62	0.00169 4
1511	g10068.t1	3343	g4260.t1		3.254602	6.373357	2.860288	1.096613	5.6306 59	0.00175 7
1512	g3061.t1	3344	g11768.t1		0	2.736145	2.449758	1.082316	5.6194 11	0.00177 6
1513	g7120.t1	3345	g5585.t1	K01537: E3.6.3.8	6.177509	2.088352	-4.42526	1.079268	-	0.00177 6
1514	g1980.t1	3346	g6240.t1		4.780929	1.696677	-3.47296	1.055478	-	0.00181 6
1515	g15450.t1	3347	g6505.t1		0	3.663174	4.662175	1.041385	5.5983 4	0.00183 7
1516	g10937.t1	3348	g9861.t1		3.34381	8.292693	5.149782	1.007277	5.5606 52	0.00190 1
1517	g2104.t1	3349	g2481.t1		0	8.858449	6.876201	0.947423	5.5141 13	0.00201

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1518	g1101.t1	3350	g4046.t1		0	4.4026	5.770884	0.936128	5.5053 63	0.00202 5
678	g2539.t1	2558	g3572.t1		2.326788	6.873537	4.818842	0.882431	5.4639 04	0.00212 1
1519	g3140.t1	3351	g5042.t1		0	2.321166	2.269216	0.871446	5.4554 5	0.00214 5
1520	g5369.t1	3352	g9557.t1		3.908588	6.910264	3.013639	0.855938	5.4435 33	0.00217 8
1521	g12261.t1	3353	g7374.t1	K00480: E1.14.13.1	0	8.154209	8.090694	0.846077	5.4359 64	0.00219 5
1522	g9519.t1	3354	g6593.t1	K03126: TAF12	0	9.766076	7.663496	0.828036	5.4221 37	0.00223 1
686	g857.t1	2491	g9451.t1	K01950: E6.3.5.1, NADSYN1, QNS1, nade	3.88692	0.53345	-3.15682	0.77121	5.3787 5	0.00233 9
1523	g8434.t1	2550	g10211.t1		0	5.304746	5.464585	0.750938	5.3633 28	0.00237 8
1524	g6597.t1	3355	g10126.t1		0	4.518563	5.208532	0.74287	5.3572	0.00239 7
1525	g5093.t1	3356	g2950.t1	K14688: SLC30A1, ZNT1	0	2.409393	2.458919	0.737239	5.3529 27	0.0024
1526	g823.t1	3357	g8190.t1		3.431051	7.673807	3.935357	0.734868	5.3511 28	0.00240 4
1527	g839.t1	3358	g9466.t1		0	4.219241	4.683516	0.682084	5.3111 88	0.00252 2
1528	g13121.t1	3359	g11183.t1		0	6.54144	6.317655	0.656359	5.2917 98	0.00258 1
1529	g847.t1	3360	g9458.t1		8.023071	3.66916	-3.61918	0.631424	5.2730 5	0.00263 6
1530	g4627.t1	3361	g6024.t1		0.792826	6.42714	5.759738	0.630803	5.2725 83	0.00263 6
1531	g10595.t1	3362	g10624.t1	K17987: NBR1	0	2.09236	2.123128	0.620131	5.2645 74	0.00266
1532	g12318.t1	3363	g7423.t1	K00166: BCKDHA, bkdA1	0	2.598413	2.602354	0.593035	5.2442 75	0.00272 3
1533	g12695.t1	3364	g8902.t1	K10842: MNAT1	0	3.108472	2.951239	0.560072	5.2196	0.00280

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1534	g14294.t1	3365	g4038.t1	K02980: RP-529e, RPS29	5.882987	3.465017	-2.42606	0.543504	51	0.00284
1535	g7862.t1	3366	g10519.t1	K13690: CMT1	4.585103	6.930322	2.588027	0.531605	5.2073	0.00287
1536	g2863.t1	3367	g11267.t1		0.167864	4.829719	5.552288	0.513015	5.1984	0.00291
1537	g1455.t1	2542	g6968.t1		4.374836	10.80524	6.455862	0.511076	5.1846	0.00292
1538	g2438.t1	3368	g6704.t1		9.091153	1.287615	-7.87656	0.465153	5.1831	0.00303
1539	g667.t1	3369	g2708.t1	K10256: FAD2	0.327373	4.952806	4.589933	0.444695	5.1491	0.00307
1540	g4890.t1	3370	g4524.t1	K01530: E3.6.3.1	5.691668	0.913041	-4.25594	0.443497	5.1340	0.00307
1542	g2756.t1	3372	g9154.t1		0	2.205609	2.199562	0.441939	5.1331	0.00307
1541	g20204.t1	3371	g9206.t1	K00274: MAO, aofH	0	6.517404	6.487337	0.442311	5.1320	0.00307
1543	g2398.t1	3373	g9298.t1		0	5.749657	5.429453	0.437917	5.1323	0.00307
1544	g9984.t1	3374	g9679.t1		0	7.061175	7.03614	0.33213	5.1290	0.00308
1545	g15304.t1	3375	g10452.t1		1.631174	5.484335	3.961905	0.302009	5.0514	0.00339
1547	g1470.t1	3377	g6945.t1		6.211143	0.601353	-6.20846	0.295485	5.0294	0.00348
1546	g11003.t1	3376	g1982.t1		0	6.436399	5.197988	0.296732	5.0247	0.00349
1548	g142.t1	3378	g5823.t1	K09051: SKO1, ATF1, PCR1	2.033429	6.991069	5.119512	0.271682	5.0256	0.00349
1549	g39.t1	3379	g2832.t1	K04450: ATF2, CREBP1	2.082302	6.377889	3.852174	0.21306	5.0074	0.00356
1550	g8675.t1	3380	g10949.t1		4.582792	1.158136	-3.14557	0.202072	4.9649	0.00376
									87	0.00380

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1551	g1012.t1	3381	g8081.t1	K01027: OXCT	5.414227	8.052451	2.663064	0.177006	4.9570 5	7
1552	g2399.t1	3382	g9299.t1		1.458025	7.000976	4.992111	0.176335	4.9389 84	0.00387 8
1553	g6515.t1	3383	g2075.t1	K02950: RP-S12, MRPS12, rpsl	1.845883	4.922544	2.936732	0.153955	4.9385 01	0.00387 8
1554	g6586.t1	2539	g10115.t1		5.631067	0.472025	-4.60323	0.143733	4.9224 03	0.00395 2
1555	g8523.t1	3384	g6295.t1		0	7.66857	6.377663	0.128487	4.9150 6	0.00398 3
1556	g6667.t1	3385	g2221.t1		2.68424	6.205712	2.966025	0.118613	4.9041 22	0.00403 8
1557	g12827.t1	3386	g7851.t1		0	4.848962	3.8249	0.081084	4.8970 45	0.00407
1558	g5681.t1	3387	g2305.t1		0	5.574437	5.607999	0.076246	4.8702 03	0.00421 3
1559	g8598.t1	3388	g11593.t1		3.906492	6.364882	2.414039	0.063154	4.8667 49	0.00422 3
1560	g14604.t1	3389	g6507.t1		0.987454	5.421424	4.548644	0.028742	4.8574 09	0.00426 7
1561	g3926.t1	2519	g3966.t1		5.357872	3.212704	-2.19688	-0.01172	4.8329 1	0.00439 5
1562	g3438.t1	3390	g4707.t1		1.724857	6.502863	4.96045	-0.02749	4.8042	0.00456
1563	g1922.t1	3391	g6158.t1	K08334: BECN1, VPS30, ATG6	0.398499	5.785388	4.960056	-0.03595	4.7930 29	0.00461 3
1564	g3435.t1	3392	g4711.t1		0	8.300404	6.565756	-0.04588	4.7870 47	0.00463 7
1565	g11568.t1	3393	g4160.t1	K11322: EPC	2.908649	5.395163	2.502674	-0.05175	4.7800 26	0.00467 6
1566	g4022.t1	3394	g3195.t1		6.571337	1.444687	-5.93348	-0.05319	4.7758 78	0.00469 8
1567	g1119.t1	3395	g218.t1	K15161: CCNC, SSN8	0	4.698233	4.08668	-0.05414	4.7748 6	0.00470 2
									4.7741	0.00470

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1568	g5372.t1	3396	g9560.t1		5.009004	0.930924	-4.29137	-0.05628	92	3
1569	g8513.t1	3397	g6303.t1	K01417: E3.4.24.-	2.66779	6.304272	3.371495	-0.06746	4.76478	0.004752
1570	g10723.t1	3398	g4265.t1	K15078: SLX1	6.249677	1.09824	-5.32732	-0.07338	4.76062	0.004767
1571	g7955.t1	3399	g10265.t1		7.449289	0.568709	-6.91497	-0.08661	4.75138	0.004818
1572	g8436.t1	3400	g7726.t1	K08257: E3.2.1.101	0	5.100303	5.10056	-0.1098	4.73499	0.004903
1573	g1465.t1	3401	g6950.t1		4.476144	0.61942	-4.17994	-0.11145	4.73383	0.004908
1574	g2407.t1	3402	g9484.t1	K13127: RNF113A, CWC24	7.768564	2.987939	-3.79401	-0.11976	4.728	0.00494
1575	g2487.t1	3403	g3514.t1	K15192: BTAF1, MOT1	3.532261	7.801782	4.747107	-0.1259	4.723684	0.00496
1576	g6309.t1	3404	g3004.t1		2.982283	6.81987	3.754204	-0.13074	4.720289	0.004976
1577	g1705.t1	3405	g4639.t1		1.748524	7.933591	6.241738	-0.13773	4.715388	0.005007
1578	g6321.t1	3406	g3017.t1		9.8442	5.01489	-4.79374	-0.14476	4.71045	0.005035
1579	g4284.t1	3407	g1936.t1	K18174: COA2	1.986154	6.571374	4.216021	-0.15159	4.705676	0.005055
1580	g20937.t1	3408	g7417.t1	K01266: dmpA	1.071718	4.362008	3.114427	-0.16727	4.694696	0.005126
1581	g6962.t1	3409	g6429.t1		5.332152	0.25936	-5.40138	-0.16906	4.69345	0.005132
1582	g18713.t1	3410	g4630.t1	K03083: GSK3B	1.333651	4.783178	4.745248	-0.17254	4.69101	0.005148
1583	g8296.t1	3411	g5088.t1		5.102827	0.74787	-5.06033	-0.17731	4.69101	0.00517

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
									4.6876 8	1
1584	g1028.t1	3412	g8097.t1	K10352: MYH	0	5.91366	5.909517	-0.18093	4.6851 46	0.00518 7
1585	g7984.t1	3413	g10232.t1		4.17451	0	-3.96717	-0.18723	4.6807 5	0.00521 5
1586	g2260.t1	3414	g10672.t1		0	11.59719	8.078404	-0.20485	4.6684 52	0.00529 6
1587	g2057.t1	3415	g2540.t1		0	3.495725	2.912854	-0.21761	4.6595 59	0.00535 8
1265	g16176.t1	2509	g5232.t1		4.464184	8.046322	3.412183	-0.22053	4.6575 25	0.00536 8
1588	g710.t1	3416	g9945.t1		3.004512	5.305027	3.457727	-0.26143	4.6290 86	0.00557 3
1589	g11909.t1	3417	g11960.t1	K00967: PCYT2	4.581714	0.355634	-4.34247	-0.2642	4.6271 6	0.00558 2
1590	g133.t1	3418	g5828.t1		0	6.458979	5.351051	-0.2661	4.6258 46	0.00558 4
1591	g16811.t1	3419	g6747.t1		5.812564	0.429992	-4.86386	-0.27492	4.6197 2	0.00562 9
1592	g1007.t1	3420	g8077.t1		8.250805	2.385735	-4.65062	-0.27955	4.6165 1	0.00564 9
1593	g2691.t1	3421	g3101.t1		6.59247	0.374474	-6.18721	-0.28128	4.6153 1	0.00565 6
1594	g941.t1	3422	g9318.t1	K01067: E3.1.2.1, ACH1	1.499245	7.499861	6.073538	-0.318	4.5899 4	0.00582 4
1595	g4067.t1	3423	g3251.t1		3.814933	6.244839	2.600899	-0.32454	4.5853 83	0.00586 2
1596	g7999.t1	3424	g3379.t1		3.95884	1.293984	-3.01927	-0.36383	4.5582 8	0.00608 6
1597	g6280.t1	3425	g12254.t1	K13719: OTU1, YOD1	10.87548	3.850161	-7.09783	-0.38264	-	0.00617

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1598	g2441.t1	3426	g6710.t1		7.528783	1.563904	-5.0227	-0.39468	4.5453 3	5 0.00622 4
1599	g6940.t1	3427	g6448.t1		0	6.016039	5.937675	-0.41441	4.5235 08	0.00634 1
1601	g5186.t1	3429	g3777.t1	K02934: RP-16e, RPL6	4.28578	0	-4.72311	-0.41768	4.5212 7	0.00634 9
1600	g3254.t1	3428	g8225.t1		0	5.869262	5.544325	-0.41746	4.5214 17	0.00634 9
1602	g2757.t1	3430	g9153.t1	K15053: CHMP7	0	2.528581	2.167777	-0.42072	4.5191 82	0.00636 5
1603	g8191.t1	3431	g9716.t1		2.640244	5.393849	2.932616	-0.42423	4.5167 7	0.00638 5
1604	g41.t1	2544	g2830.t1	K10740: RPA3	5.456896	1.684193	-3.50612	-0.43149	4.5118 6	0.00642 6
1605	g7930.t1	3432	g2853.t1	K01077: E3.1.3.1, phoA, phoB	5.436852	2.710109	-4.15755	-0.43376	4.5102 4	0.00643 2
1606	g9899.t1	3433	g3476.t1		0	5.790708	5.501572	-0.43434	4.5098 42	0.00643 2
1607	g6747.t1	3434	g4361.t1	K08793: STK32, YANK	1.640577	7.804707	6.025167	-0.43912	4.5065 69	0.00644 9
1609	g3450.t1	3436	g4695.t1	K11319: ING3	7.793056	1.832762	-5.3581	-0.44607	4.5018 2	0.00647 6
1608	g13903.t1	3435	g687.t1	K01426: E3.5.1.4, amiE	2.308161	5.757553	3.146851	-0.44596	4.5018 89	0.00647 6
1610	g4174.t1	3437	g1802.t1	K03164: TOP2	0	4.461914	4.257824	-0.44926	4.4996 26	0.00648 5
1611	g1817.t1	3438	g1704.t1	K13941: folKP	1.569971	6.747653	4.234672	-0.45137	4.4981 83	0.00649 8
1612	g16037.t1	3439	g4108.t1	K01744: aspA	4.664569	6.76341	2.175875	-0.45455	4.4960 07	0.00650 8
1613	g10914.t1	3440	g5925.t1		1.756741	4.535424	3.244364	-0.46789	4.4868	0.00658

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1614	g138.t1	3441	g3729.t1		4.847226	0.925828	-5.03041	-0.47101	92	0.00659
1615	g2936.t1	3442	g5964.t1		8.044894	0.248534	-6.73944	-0.47284	4.48476	0.00660
1616	g8866.t1	3443	g2108.t1	K13339: PEX6, PXAAA1	11.8966	2.107495	-8.86497	-0.48781	4.48351	0.00667
1617	g4740.t1	3444	g2014.t1	K02606: ORC4	4.269663	1.432791	-2.74295	-0.48799	4.47329	0.00667
1618	g17490.t1	3445	g10534.t1	K10777: LIG4, DNL4	1.37437	7.556488	5.810689	-0.48948	4.47317	0.00667
1619	g6095.t1	3446	g7353.t1		10.01399	0.524763	-9.03171	-0.51858	4.47214	0.00683
1620	g1092.t1	3447	g4035.t1		1.619955	5.721483	3.640435	-0.53362	4.45231	0.00690
1621	g12252.t1	3448	g235.t1		0.132439	3.243255	3.821541	-0.53381	4.44197	0.00690
1622	g6796.t1	3449	g4421.t1	K03680: EIF2B4	5.126406	0.843849	-4.22061	-0.54287	4.44197	0.00696
1623	g797.t1	3450	g8161.t1		0	3.053206	2.866046	-0.55063	4.43579	0.00700
1624	g5647.t1	3451	g1105.t1		5.271321	0.695521	-5.99485	-0.556	4.43052	0.00702
1625	g15866.t1	3452	g9844.t1		2.040941	8.117785	5.437517	-0.57127	4.42687	0.00711
1626	g6617.t1	3453	g11274.t1	K13953: adhP	9.164416	5.669006	-3.74273	-0.57468	4.41651	0.00713
1628	g6780.t1	3455	g4396.t1		4.325036	1.1994	-3.75976	-0.57681	4.41419	0.00714

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1627	g5153.t1	3454	g3822.t1		1.244336	5.595008	3.814632	-0.57638	4.4130 43	0.00714 2
1629	g5834.t1	3456	g1171.t1	K04393: CDC42	5.842709	0.801203	-4.48638	-0.5775	- 4.4122 9	0.00714 2
1630	g5375.t1	3457	g9563.t1		6.246832	2.775505	-3.21809	-0.59214	- 4.4023 7	0.00723 1
1631	g10368.t1	3458	g5462.t1	K00826: E2.6.1.42, ilvE	0.323199	4.887494	4.532182	-0.59353	4.4014 21	0.00723 2
1632	g2826.t1	3459	g9093.t1		5.715948	1.969325	-4.3438	-0.60813	- 4.3915 4	0.00731 2
1633	g8263.t1	3460	g10014.t1	K09540: SEC63	1.178199	4.647047	3.105882	-0.60945	4.3906 52	0.00731 7
1634	g1996.t1	3461	g6244.t1		0	2.161944	2.537016	-0.61338	4.3879 95	0.00734 3
1636	g565.t1	3463	g3893.t1		7.212095	4.016141	-3.8261	-0.62616	- 4.3793 5	0.00741 6
1635	g10532.t1	3462	g6657.t1		0	6.423209	4.950366	-0.62535	4.3799 02	0.00741 6
1637	g9223.t1	3464	g6550.t1	K14402: CPSF2, CFT2	4.757601	1.422654	-3.02304	-0.63182	- 4.3755 3	0.00745 6
1638	g4375.t1	3465	g2132.t1	K17777: TIM9	6.581887	2.288969	-5.04428	-0.64088	- 4.3694 2	0.00751 4
1639	g3924.t1	3466	g3968.t1	K03854: KTR	4.507947	8.80016	3.527047	-0.64187	4.3687 44	0.00751 7
1640	g5877.t1	3467	g10964.t1		1.237514	5.716716	4.577402	-0.65497	4.3599 12	0.00760 9
1641	g7244.t1	3468	g10768.t1		1.270272	6.454926	4.671181	-0.66639	4.3522 1	0.00769 4
1642	g3215.t1	3469	g6111.t1		6.28213	1.918338	-4.18097	-0.67385	- 4.3471 9	0.00774 6

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1643	g2744.t1	3470	g8873.t1		12.4437	4.004642	-6.34323	-0.67665	-4.3453	0.00776
1644	g10172.t1	3471	g8453.t1		1.719814	6.975262	4.867858	-0.67848	4.3440	0.00776
1646	g11998.t1	3473	g2455.t1	K01792: E5.1.3.15	4.113876	1.68217	-2.91764	-0.68435	-4.3401	0.00780
1645	g9935.t1	3472	g6028.t1		0	5.001669	5.050202	-0.68376	4.3405	0.00780
1647	g9810.t1	3474	g10828.t1		6.142355	2.944412	-3.12615	-0.68611	-4.3389	0.00781
1648	g2585.t1	3475	g1533.t1		1.186682	5.314928	4.416457	-0.70324	4.3274	0.00795
1649	g5812.t1	3476	g7683.t1		0.086084	5.755875	5.49766	-0.70639	4.3253	0.00797
1650	g7613.t1	3477	g7623.t1	K12177: COP53, CSN3	6.832706	1.20583	-6.6405	-0.71007	-4.3228	0.00799
1651	g21752.t1	3478	g11785.t1		9.138517	2.10622	-5.18056	-0.71052	-4.3225	0.00799
1652	g8125.t1	3479	g7937.t1	K14829: IP13	5.635984	8.165687	3.420929	-0.71501	4.3195	0.00802
1653	g1265.t1	3480	g446.t1		0	2.255216	2.515104	-0.72389	4.3135	0.00808
1654	g1851.t1	3481	g1893.t1	K14806: DDX31, DBP7	4.180789	6.833176	3.613285	-0.72476	4.3129	0.00808
1655	g5970.t1	3482	g7911.t1		0.787727	4.745143	3.037594	-0.72641	4.3118	0.00809
1656	g9210.t1	3483	g432.t1		0	5.395553	4.999741	-0.72979	4.3095	0.00810
1657	g4885.t1	3484	g5284.t1	K00451: HGD, hmgA	2.711021	9.250394	4.936597	-0.75813	4.2906	0.00832
1658	g9727.t1	3485	g1208.t1		0	2.707059	2.656284	-0.77155	4.2816	0.00840
1659	g1852.t1	3486	g1892.t1		9.129284	5.622142	-2.9499	-0.77281	-4.2807	0.00840

SEQ. ID SYM00577	SYM577 gene	SEQ. ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1661	g4708.t1	3488	g2052.t1		5.134526	2.604627	-2.75857	-0.77636	8	0.00841 9
1662	g1264.t1	3489	g447.t1	K07975: K07975	0	3.433264	3.424199	-0.77691	1	0.00841 9
1660	g9176.t1	3487	g6513.t1		1.38307	7.023037	5.604965	-0.77564	4	0.00841 9
1663	g10978.t1	3490	g5642.t1		0	9.109111	6.49256	-0.77811	9	0.00842
1664	g7775.t1	3491	g849.t1		5.558934	1.67851	-5.74356	-0.78625	39	0.00848 8
1665	g10472.t1	3492	g2156.t1		1.835908	10.77995	8.679924	-0.80576	4	0.00864 2
1666	g11361.t1	3493	g11673.t1	K01613: psd, PSD	5.614261	0.835332	-3.65067	-0.81024	66	0.00866 6
1667	g5499.t1	3494	g4955.t1		4.580901	7.497146	2.894342	-0.81895	8	0.00872 6
1668	g8184.t1	3495	g5029.t1	K05607: AUH	3.031275	0	-3.53658	-0.84752	73	0.00893 5
1669	g9878.t1	3496	g11628.t1	K05755: ARPC4	0	8.072633	7.232249	-0.84945	4	0.00894 8
1670	g10675.t1	3497	g8521.t1	K00688: E2.4.1.1, glgP, PYG	0.169628	5.781937	5.478988	-0.85152	52	0.00895 6
1671	g9232.t1	3498	g3432.t1	K00545: COMT	7.296935	0.411124	-6.22613	-0.8545	78	0.00898 4
1672	g9988.t1	3499	g9675.t1	K00130: betB, gbsA	0	2.553591	3.110324	-0.86233	4	0.00904 4
1673	g1414.t1	3500	g6284.t1		2.311758	6.717528	4.69322	-0.86385	89	0.00905 3
1674	g6733.t1	3501	g4345.t1	K09043: AP1F	0	5.001212	4.248888	-0.86816	79	0.00909 09
1675	g7043.t1	3502	g6332.t1		5.859345	10.2543	4.890605	-0.88033	09	0.00918 7
1676	g2705.t1	3503	g8367.t1	K00528: E1.18.1.2, fpr	7.551805	3.162022	-5.08662	-0.88328	24	0.00920 -

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1677	g10342.t1	3504	g51.t1		0	5.678545	5.567869	-0.88506	4.20717	0.00921
1678	g5928.t1	3505	g11021.t1	K09885: AQPF	5.755454	0.419682	-5.37723	-0.89503	4.19937	0.00927
1679	g8175.t1	3506	g7987.t1		1.51165	7.320745	5.975986	-0.89646	4.198423	0.00927
1680	g8032.t1	3507	g4282.t1		0	4.127275	3.299567	-0.91209	4.188055	0.00939
1681	g9814.t1	3508	g10824.t1	K03062: PSMC1, RPT2	1.362902	5.056672	3.336585	-0.91516	4.186022	0.00941
1682	g11969.t1	3509	g7462.t1		0.489568	5.568038	4.427228	-0.91543	4.185844	0.00941
1683	g10790.t1	3510	g10663.t1		0.828146	4.846815	3.562604	-0.92472	4.179692	0.00949
1684	g4805.t1	3511	g1632.t1		8.950015	5.163246	-3.59682	-0.93185	4.17497	0.00955
1685	g6554.t1	3512	g10090.t1	K15565: CTK3	5.222663	0.144855	-4.83662	-0.93476	4.17304	0.00957
1686	g1116.t1	3513	g4063.t1		1.005429	5.625694	3.855418	-0.94482	4.16639	0.00966
1687	g8449.t1	3514	g2682.t1	K05954: FNTB	0	5.399599	4.115948	-0.95049	4.162638	0.00969
1689	g6525.t1	3516	g2064.t1	K09493: CCT1, TCP1	9.538137	1.667123	-6.73424	-0.95515	4.15956	0.00972
1690	g5857.t1	3517	g1146.t1	K02320: POLA1	3.021693	6.891883	4.04023	-0.95542	4.159376	0.00972
1688	g1274.t1	3515	g460.t1		0	6.05494	9.515249	-0.95514	4.159568	0.00972
1691	g12431.t1	3518	g10686.t1	K07127: uraH, pucM, hluH	0	5.825339	4.833292	-0.95677	4.158489	0.00973
1692	g5322.t1	3519	g2238.t1	K03426: E3.6.1.22,	5.48509	2.765673	-3.98262	-0.95893	-	0.00974

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
				NUDT12, nudC					4.1570 6	3
1693	g10361.t1	3520	g7713.t1		2.118062	5.477606	3.633039	-0.96411	4.1536 38	0.00976 5
1694	g2712.t1	3521	g8360.t1		6.902933	0.496994	-4.89563	-0.97385	-	0.00983 3
1695	g6927.t1	3522	g6460.t1	K00485: FMO	9.696666	1.489752	-6.7401	-0.98605	-	0.00994 5
1696	g6520.t1	3523	g2069.t1		7.419005	0.788997	-5.06498	-0.98929	-	0.00997 4
1697	g15004.t1	3524	g3115.t1		4.410253	0.439607	-3.37848	-0.99169	-	0.00999 1
1698	g13717.t1	3525	g9904.t1	K01426: E3.5.1.4, amfE	2.122753	4.721599	2.459777	-0.99262	4.1348 23	0.00999 1
1699	g11731.t1	3526	g5851.t1	K00804: GGP51	0.641201	8.014106	6.275604	-0.99873	4.1307 92	0.01003 2
1700	g12319.t1	3527	g7427.t1	K06127: COQ5	0	3.18054	4.279183	-1.0114	4.1224 45	0.01015 8
1037	g11120.t1	2520	g739.t1	K11309: RTT109, KAT11	4.245031	0.362852	-4.44703	-1.02232	-	0.01026 2
1701	g10208.t1	3528	g11172.t1	K08737: MSH6	5.231935	0.620193	-4.43745	-1.02255	-	0.01026 2
1702	g4510.t1	3529	g10815.t1		0.110413	4.81464	3.815621	-1.03144	4.1151 1	0.01034 2
1703	g10697.t1	3530	g8542.t1	K01702: LEU1	0.263634	7.912518	6.023521	-1.04447	4.1006 86	0.01046 3
1704	g15805.t1	3531	g2331.t1	K02154: ATPeVOA, ATP6N	0	2.888609	4.034147	-1.04529	4.1001 49	0.01046 5
1705	g5031.t1	3532	g9002.t1	K02830: HRAD1, RAD17	3.089916	5.598348	2.991585	-1.04815	4.0982 68	0.01048 5
1706	g5436.t1	3533	g3139.t1	K16261: YAT	5.060429	1.262422	-4.0977	-1.04901	-	0.01048 5

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1707	g4238.t1	3534	g1742.t1		1.066099	4.155929	2.917914	-1.053	4.09508	0.010521
1708	g10868.t1	3535	g125.t1		0	3.653087	3.440687	-1.05442	4.094146	0.010537
1709	g6783.t1	3536	g4399.t1		6.220556	1.013936	-4.77542	-1.0556	4.09337	0.010537
1710	g3062.t1	3537	g11769.t1		0	2.560725	2.204735	-1.06092	4.089879	0.010585
1711	g10221.t1	3538	g11208.t1		6.889613	0.40438	-7.11534	-1.06965	4.08415	0.010672
1712	g1829.t1	3539	g1715.t1		5.791735	1.495617	-4.17043	-1.08999	4.07081	0.010861
1713	g8326.t1	3540	g5128.t1	K00505: TVR	3.610494	6.260581	3.534926	-1.09636	4.066632	0.010911
1714	g3155.t1	3541	g4991.t1		3.59858	7.647083	3.797219	-1.11173	4.056562	0.011074
1715	g2222.t1	3542	g11603.t1		0.225549	4.813511	4.351037	-1.12206	4.049805	0.011164
1716	g11759.t1	3543	g10216.t1		3.685926	0	-4.53515	-1.12292	4.04924	0.011168
1717	g8206.t1	3544	g8502.t1		3.420719	10.03021	6.493771	-1.1248	4.048012	0.011183
679	g4287.t1	2759	g1939.t1	K00275: pdxH, PNPO	0.807563	3.090838	2.176492	-1.13595	4.040719	0.011299
690	g7926.t1	2497	g8597.t1		6.166677	8.61834	2.778981	-1.13847	4.039073	0.011322
1718	g4064.t1	3545	g3254.t1	K00002: AKR1A1, adh	6.100438	1.079083	-4.91125	-1.15384	4.02903	0.011473
1720	g5795.t1	3547	g4862.t1	K00451: HGD, hmgA	3.591089	6.8767	2.956306	-1.15712	4.026889	0.011485
1719	g5609.t1	3546	g7533.t1		0.882686	5.320606	3.796705	-1.15678	4.027112	0.011485

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1721	g19766.t1	3548	g11689.t1	K08272: CAB39, MO25	4.724331	1.509326	-3.78959	-1.16405	-4.02236	0.011549
1722	g7985.t1	3549	g10231.t1		0	4.06043	3.846952	-1.16466	4.021964	0.01155
1723	g4377.t1	3550	g2134.t1		14.14762	6.168036	-7.54239	-1.1682	-4.01966	0.01158
1724	g10842.t1	3551	g9831.t1	K15283: SLC35E1	3.417746	7.907833	4.552081	-1.17777	4.013415	0.011665
1725	g3810.t1	3552	g5153.t1	K01539: ATP1A	5.831954	9.975934	4.809042	-1.1815	4.010981	0.011698
1726	g4351.t1	3553	g2123.t1		2.978188	5.643247	2.777696	-1.19302	4.003473	0.011817
1727	g12887.t1	3554	g7811.t1	K03868: RBX1, ROC1	0	6.027624	4.370298	-1.19414	4.002739	0.011824
1728	g13707.t1	3555	g7796.t1	K04706: PIAS1	6.517298	4.766243	-2.04941	-1.20773	-3.99389	0.011956
1729	g16831.t1	3556	g10344.t1		6.338633	1.444662	-4.08292	-1.20964	-3.99265	0.011974
1731	g3916.t1	3558	g3976.t1		4.817018	0.75673	-4.65895	-1.22292	-3.98401	0.012097
1730	g5660.t1	3557	g1082.t1		0	4.671882	3.638252	-1.22213	3.984518	0.012097
1732	g9151.t1	3559	g6484.t1		6.278283	0.8931	-5.76977	-1.23184	-3.97829	0.012199
1733	g12202.t1	3560	g9295.t1		0.672484	4.169208	2.907439	-1.23665	3.975077	0.012241
1734	g5282.t1	3561	g2288.t1		4.202468	0.654126	-3.30483	-1.23744	-3.97457	0.012244
1735	g7572.t1	3562	g7669.t1		3.978653	7.606234	3.70123	-1.2385	3.973875	0.012244
1736	g3235.t1	3563	g8210.t1		4.470468	8.184527	5.15127	-1.24494	3.9696	0.01230

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
697	g852.t1	2502	g9454.t1	K11824: AP2A	4.880882	7.286171	2.290375	-1.24576	3.969158	0.012307
1737	g6716.t1	3564	g4321.t1		9.948221	2.821953	-6.95531	-1.25354	3.96416	0.012386
1738	g2067.t1	3565	g2530.t1		7.69826	4.922109	-3.56419	-1.26788	3.95479	0.012535
1739	g7743.t1	3566	g7093.t1		2.175372	4.617996	2.642137	-1.27196	3.95215	0.012576
1740	g5491.t1	3567	g9819.t1		9.301085	2.365816	-5.52656	-1.27566	3.94974	0.012619
1741	g10936.t1	3568	g2319.t1		8.259645	1.32013	-5.22157	-1.27719	3.94876	0.012632
939	g4598.t1	2528	g6014.t1		4.80428	1.524453	-3.6354	-1.2848	3.94382	0.012715
1742	g10549.t1	3569	g6695.t1		0	1.785939	2.000492	-1.29585	3.93668	0.012829
527	g4985.t1	2324	g8953.t1		0.777528	7.11879	6.4966	-1.30752	3.929102	0.012948
578	g8174.t1	2376	g7986.t1		1.469754	6.185503	4.308101	-1.31185	3.926293	0.012985
1743	g2143.t1	3570	g11929.t1	K00772: E2.4.2.28, mtaP	4.8374	0.969878	-3.56778	-1.3345	3.91164	0.013284
1744	g9848.t1	3571	g9777.t1	K06970: rlmF	9.547112	5.371618	-3.97134	-1.34065	3.90767	0.013349
1745	g12220.t1	3572	g11110.t1	K07870: RHO1, ARH1	3.884302	6.478847	3.518086	-1.34423	3.905351	0.013393
1746	g2291.t1	3573	g10709.t1		5.385805	9.526471	4.775916	-1.34937	3.902029	0.013444
1747	g2147.t1	3574	g11880.t1	K14789: NOP6	6.507448	1.977499	-4.68012	-1.35307	3.89967	0.013467

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1748	g6355.t1	3575	g794.t1	K00236: SDHC, SDH3	0.536878	6.254053	4.787495	-1.36034	4	0.01355
1749	g2869.t1	3576	g11261.t1		0.327373	6.340001	4.80532	-1.36591	3.8949 46	0.01363
1750	g2360.t1	3577	g9254.t1	K12200: PDCD6IP, ALX, RIM20	3.801939	1.686361	-2.17748	-1.36819	-	0.01365
1751	g3560.t1	3578	g3325.t1		6.818439	0.789095	-4.92675	-1.37135	3.8898 8	0.01368
1752	g10589.t1	3579	g7032.t1		0	2.526539	3.338928	-1.37427	3.8878 4	0.01371
1753	g16530.t1	3580	g8785.t1		4.610888	0.254363	-4.08665	-1.38154	52	0.01381
1754	g5177.t1	3581	g3786.t1	K03321: TC.SULP	4.026352	0.667334	-3.40117	-1.38727	3.8812 6	0.01387
1755	g9386.t1	3582	g3647.t1	K01082: E3.1.3.7, cysQ, MET22, BPNT1	7.430096	4.382531	-3.00795	-1.38737	-	0.01387
1756	g6130.t1	3583	g7316.t1	K08657: TASP1	0.095949	5.575509	5.53383	-1.38749	3.8775 8	0.01387
1757	g8530.t1	3584	g6289.t1	K05532: MNNT1	0	5.816826	4.892278	-1.38966	3.8774 3	0.01389
1758	g21699.t1	3585	g5541.t1	K03448: FEN2, LIZ1	0.735044	3.625342	2.870907	-1.39176	3.8760 25	0.01390
1759	g9934.t1	3586	g6029.t1	K16575: ACTR1, ARP1	0	5.832405	5.597162	-1.39893	3.8746 73	0.01397
1760	g4777.t1	3587	g3680.t1		3.32587	5.729749	2.411959	-1.4021	3.8700 56	0.01401
1761	g11542.t1	3588	g4184.t1		7.517977	2.707186	-4.47011	-1.41398	3.8680 09	0.01417
1762	g2157.t1	3589	g11896.t1		3.702226	7.226007	3.353898	-1.41467	-	0.01417
1763	g16189.t1	3590	g1458.t1	K14454: GOT1	10.63207	6.499538	-6.07526	-1.41542	3.8603 6	0.01417

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
									3.8594 3	8
1764	g8348.t1	3591	g5159.t1		4.264457	6.507615	2.242904	-1.41809	3.8577 14	0.01420 2
1765	g1259.t1	3592	g452.t1		2.440869	6.057593	3.423879	-1.42343	3.8542 74	0.01426
1766	g2764.t1	3593	g9147.t1	K10745: RNASEH2C	0	2.695204	3.586065	-1.42688	3.8520 56	0.01429 7
1767	g7927.t1	3594	g8596.t1		4.918651	7.912131	3.059833	-1.4292	3.8505 62	0.01431 2
1768	g2676.t1	3595	g4133.t1	K00294: E1.2.1.88	0.612742	5.41036	4.447987	-1.4294	3.8504 34	0.01431 2
1769	g7548.t1	3596	g7259.t1		0.649867	5.412471	4.266032	-1.43441	3.8472 11	0.01436 6
1771	g5182.t1	3598	g3781.t1		9.026587	2.801517	-6.79697	-1.43708	- 3.8454 9	0.01439 1
1770	g7942.t1	3597	g9703.t1		2.085423	7.573442	5.338061	-1.43698	3.8455 59	0.01439 1
1772	g4091.t1	3599	g3293.t1	K01687: ilvD	6.303323	0.815929	-5.63696	-1.43932	- 3.8440 5	0.01441 8
1773	g12310.t1	3600	g7399.t1		0	7.275303	5.468252	-1.44443	3.8407 65	0.01448 9
1774	g3831.t1	3601	g2596.t1	K07005: K07005	0	4.871672	3.653881	-1.4486	3.8380 85	0.01454 6
1776	g3521.t1	3603	g2212.t1	K10666: RNf5	4.087847	5.915388	2.294451	-1.45392	3.8346 64	0.01460 6
1775	g22438.t1	3602	g4987.t1		5.797361	8.454162	3.989287	-1.45372	3.8347 97	0.01460 6
1777	g4129.t1	3604	g1851.t1		3.118092	5.15901	2.22408	-1.45469	3.8341 69	0.01461 6
1778	g12080.t1	3605	g7812.t1		5.157342	0.417205	-5.18316	-1.4566	- 3.8329 4	0.01463 2
1779	g18095.t1	3606	g931.t1		5.760364	1.160199	-6.11966	-1.45925	- 3.8312 6	0.01466 6

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1780	g2261.t1	3607	g10673.t1		4.246251	8.170102	5.158696	-1.46304	3.828806	0.014718
1781	g2951.t1	3608	g5953.t1	K11129: NHP2, NOLA2	4.43109	0.997175	-3.38379	-1.46821	3.82548	0.014759
1782	g2355.t1	3609	g9249.t1	K07192: FLOT	6.819585	1.646734	-5.57734	-1.47687	3.81992	0.014873
1783	g3075.t1	3610	g11781.t1		0	4.238844	3.140408	-1.48663	3.813664	0.014988
1784	g9642.t1	3611	g6905.t1		0	4.384934	5.279139	-1.48909	3.812083	0.015012
1786	g7748.t1	3613	g7098.t1	K12815: DHX38, PRP16	1.598146	5.454032	3.568819	-1.49259	3.809836	0.015052
1785	g10300.t1	3612	g22.t1		0	4.950892	4.957814	-1.49227	3.810047	0.015052
1787	g1381.t1	3614	g8684.t1		6.537476	0	-5.14045	-1.49524	3.80814	0.015084
1788	g3923.t1	3615	g3970.t1		5.651846	0.874231	-4.49336	-1.49537	3.80806	0.015086
1789	g2286.t1	3616	g10703.t1	K11362: HFI1, ADA1	1.780691	5.389549	3.610777	-1.50303	3.803144	0.015181
692	g5169.t1	2506	g3798.t1		4.28203	6.198144	2.254081	-1.50534	3.801665	0.015216
1790	g5917.t1	3617	g11006.t1		0.479676	3.343978	2.923854	-1.5088	3.799443	0.015254
1791	g6287.t1	3618	g8349.t1	K11366: USP22_27_51, UBP8	7.027226	0	-6.44608	-1.51412	3.79604	0.015334
1792	g6643.t1	3619	g10197.t1		5.091815	1.733439	-3.47331	-1.51828	3.79337	0.015397
1793	g12218.t1	3620	g11102.t1		2.315098	5.094179	2.505163	-1.52401	3.789702	0.015468

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1794	g7936.t1	3621	g11228.t1	K00232: E1.3.3.6, ACOX1, ACOX3	4.459893	9.555022	5.227644	-1.52659	3.7880 48	0.01550 3
1795	g5748.t1	3622	g5250.t1		1.632799	4.080474	2.918063	-1.52796	3.7871 72	0.01551 8
1796	g9069.t1	3623	g8579.t1		0	6.161139	6.446955	-1.53152	3.7848 89	0.01556
1797	g6312.t1	3624	g3007.t1	K05236: COPA	5.253098	7.43545	2.144029	-1.54263	3.7777 8	0.0157
1799	g8177.t1	3626	g7989.t1		9.520565	3.609284	-4.61836	-1.54631	- 3.7754 3	0.01574 2
1798	g14196.t1	3625	g5807.t1	K01754: E4.3.1.19, ilvA, tdc8	5.027436	7.101036	2.225321	-1.54586	3.7757 16	0.01574 2
1800	g6471.t1	3627	g5309.t1	K11237: BEM1	8.657428	1.580264	-5.3132	-1.54781	- 3.7744 7	0.01575 9
1801	g8179.t1	3628	g7991.t1	K15450: TYW3	1.394748	4.160609	2.833287	-1.55061	3.7726 78	0.01579 8
1802	g6447.t1	3629	g5339.t1		0.745984	4.49131	3.550615	-1.55175	3.7719 49	0.01580 8
1803	g4305.t1	3630	g1960.t1	K07179: R1OK2	2.332881	9.808031	7.49955	-1.56836	3.7613 23	0.01605 1
1804	g10921.t1	3631	g2051.t1		3.554471	15.34968	12.40633	-1.5698	3.7604 06	0.01606 7
1805	g7453.t1	3632	g6882.t1	K11230: SSK2	6.592207	0.47792	-6.24926	-1.57242	- 3.7587 3	0.01609 5
1806	g4994.t1	3633	g8965.t1		4.95489	0.379021	-5.0321	-1.57389	- 3.7577 9	0.01610 3
1807	g13512.t1	3634	g8777.t1	K07047: K07047	0	1.953187	2.809714	-1.57688	3.7558 8	0.01614 6
1808	g13145.t1	3635	g4288.t1	K12795: SUGT1, SGT1	0	3.863111	4.262765	-1.57792	3.7552 18	0.01615 6
1809	g2403.t1	3636	g9304.t1		3.466706	5.880267	2.766617	-1.58819	3.7486 58	0.0163
1810	g11546.t1	3637	g4179.t1		2.95634	4.859952	2.334894	-1.59077	3.7470	0.01633

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1811	g6245.t1	2545	g7144.t1		3.519044	0.986255	-2.56971	-1.59307	12	0.01635
1812	g20527.t1	3638	g9499.t1		0	2.423781	3.298103	-1.5938	3.7455	0.01635
1814	g485.t1	3640	g5481.t1		3.211934	0.513195	-3.05545	-1.59982	3.7412	0.01642
1813	g9589.t1	3639	g6640.t1	K14564: NOP56	0	4.752235	3.463157	-1.59979	3.7412	0.01642
1815	g17338.t1	3641	g4825.t1		3.253347	11.98725	6.42899	-1.60143	3.7402	0.01644
1816	g5556.t1	3642	g7468.t1		0.321853	8.712554	6.936626	-1.60594	3.7373	0.0165
683	g9852.t1	3089	g9791.t1		0.93993	4.257415	3.235897	-1.61117	3.7339	0.01656
1817	g9592.t1	3643	g6324.t1		0	3.24119	4.466041	-1.61236	3.7332	0.01657
1818	g9909.t1	3644	g3464.t1		4.899061	0.389899	-4.4519	-1.61774	3.7298	0.01664
1819	g347.t1	3645	g8852.t1	K01619: deoC, DERA	5.001834	2.638493	-2.09583	-1.61831	3.7294	0.01665
1820	g3024.t1	3646	g8280.t1	K15183: ELL	4.940617	6.802739	2.356057	-1.62092	3.7277	0.01667
1821	g3400.t1	3647	g10340.t1		4.574834	8.898182	4.895081	-1.62268	3.7266	0.01668
1822	g5059.t1	3648	g8329.t1	K15544: SSU72	3.885616	1.04666	-3.67463	-1.62812	3.7231	0.01676
1823	g13701.t1	3649	g7800.t1	K00227: SC5DL, ERG3	3.52458	8.32101	6.721913	-1.62826	3.7230	0.01676
1824	g7883.t1	3650	g8666.t1	K17871: ndh1	8.978821	4.745077	-4.2343	-1.62992	3.7220	0.01678
1825	g9357.t1	3651	g4026.t1		1.461054	4.608619	3.269834	-1.64365	3.7132	0.01702

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577 0	Median Exp. SYM00300 0	Log FC	B-statistic	t- statisti c	Adj. p- value
1826	g6504.t1	3652	g10649.t1	K01487: E3.5.4.3, guaD	3.115047	5.480797	3.226369	-1.64905	91 53	1 2
1827	g996.t1	3653	g8065.t1	K03859: PIGC, GP12	0	5.164011	5.152798	-1.65445	3.7064 1	0.01717 5
1828	g12072.t1	3654	g7819.t1		7.465114	4.358481	-4.43566	-1.66028	- 3.7027	0.01725 6
1829	g8430.t1	3655	g6112.t1		0	3.595832	4.134153	-1.664	3.7003 33	0.01729 3
1830	g1011.t1	3656	g8080.t1		1.836426	5.321783	3.474028	-1.66832	3.6975 83	0.01736
1831	g7418.t1	2549	g7203.t1	K17497: PMM	4.250746	0.725203	-3.91923	-1.6743	- 3.6937	0.01742 7
1832	g9496.t1	3657	g5757.t1		0.783088	6.487481	4.380159	-1.67836	3.6912 01	0.01748 4
1833	g9186.t1	3658	g6518.t1		4.151632	10.48721	6.043581	-1.68184	3.6889 85	0.01753 2
1834	g7004.t1	3659	g6378.t1	K11229: BCK1	0	2.324218	2.253785	-1.68839	3.6848 23	0.01763 8
1836	g8143.t1	3661	g7948.t1		4.054206	0.695466	-3.66885	-1.6899	- 3.6838	0.01763 9
1835	g11752.t1	3660	g9854.t1	K11086: SNRPB, SMB	5.274986	2.280814	-3.12018	-1.6896	- 3.6840	0.01763 9
1837	g17537.t1	3662	g9665.t1		4.57235	8.898002	4.283534	-1.69297	3.6819 12	0.01768 8
1838	g5667.t1	3663	g1075.t1		4.489128	2.536094	-2.39358	-1.70341	- 3.6752	0.01786 8
1839	g6664.t1	3664	g2224.t1	K13525: VCP, CDC48	2.105221	5.652047	4.78303	-1.70384	3.6750 05	0.01786 8
1840	g2801.t1	3665	g9129.t1		7.466543	0.556432	-6.6491	-1.70804	- 3.6723	0.01792 8
1841	g4812.t1	3666	g9598.t1		4.049791	6.42879	2.167629	-1.70915	3.6716	0.01792

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1843	g2466.t1	3668	g6718.t1		5.98403	0	-5.16123	-1.7182	28	0.01806
1842	g249.t1	3667	g11056.t1	K00276: AOC3, AOC2, tynA	5.423135	1.39377	-3.95337	-1.71813	3	0.01806
1844	g13312.t1	3669	g4520.t1	K01800: malA, GSTZ1	0	2.734484	3.220496	-1.71843	36	0.01806
1845	g9893.t1	3670	g3483.t1		0	6.706192	4.976759	-1.71907	31	0.01807
1846	g17202.t1	3671	g3078.t1		5.68592	2.231786	-3.83595	-1.72034	2	0.01807
1847	g5069.t1	3672	g8336.t1	K14521: NAT10, KRE33	0	3.583017	3.343135	-1.72847	64	0.01818
1848	g7275.t1	3673	g11843.t1		0.251195	5.321335	4.264195	-1.7299	59	0.01820
1849	g4877.t1	3674	g4496.t1		0.134441	10.17863	6.723251	-1.73151	31	0.01822
1850	g12737.t1	3675	g5715.t1		0	3.366893	5.496972	-1.7331	28	0.01825
1851	g3173.t1	3676	g11661.t1		3.672536	1.077381	-2.65537	-1.73393	3	0.01825
1852	g4631.t1	3677	g2422.t1		2.311883	4.745023	2.541357	-1.73959	07	0.01835
1853	g601.t1	3678	g3857.t1		0	4.551928	4.659305	-1.74334	28	0.01840
1854	g4634.t1	3679	g2419.t1		5.63215	7.748538	2.895179	-1.74706	72	0.01844
1855	g13170.t1	3680	g1290.t1	K01620: ltaE	0	1.960601	3.162229	-1.74722	67	0.01844
1856	g3136.t1	3681	g5050.t1		0	2.474936	2.012582	-1.75162	77	0.01851
1857	g14953.t1	3682	g1391.t1		3.334724	6.021478	2.572465	-1.75216	34	0.01851
1858	g11237.t1	3683	g1362.t1		2.76252	5.104646	2.123089	-1.76267	36376	0.01865

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1859	g1833.t1	3684	g1913.t1	K03248: EIF3G	0	3.706133	3.037564	-1.76489	76	0.01869 4
1860	g6040.t1	3685	g11728.t1	K16368: DGK1	9.681271	2.587529	-5.33304	-1.7661	3.6355	0.01870 7
1861	g11936.t1	3686	g10365.t1		4.454058	0.327662	-3.42743	-1.76646	3.6352	0.01870 7
1862	g4010.t1	3687	g8176.t1	K15427: SIT4, PPH1	5.918167	1.131513	-3.97297	-1.77022	3.6328	0.01874 5
1864	g3458.t1	3689	g4687.t1		2.234014	5.975139	2.819321	-1.77233	3.6315	0.01875 6
1865	g4936.t1	3690	g4576.t1		0.924146	3.716899	3.064721	-1.77306	3.6310	0.01875 6
1866	g1815.t1	3691	g1702.t1		2.685797	6.479459	3.431879	-1.77314	3.6310	0.01875 6
1863	g7697.t1	3688	g11510.t1		1.950115	6.128154	4.639048	-1.77179	3.6318	0.01875 6
1867	g1592.t1	3692	g12245.t1		0	4.518156	4.414945	-1.7816	3.6256	0.01888 8
1868	g9431.t1	3693	g10302.t1		5.228093	0.705484	-5.82699	-1.78382	3.6242	0.01891 5
1869	g10761.t1	3694	g12006.t1	K15082: RAD7	3.567408	6.390408	2.846424	-1.7985	3.6149	0.01914 81
1870	g6898.t1	3695	g1355.t1		2.604143	5.101685	2.991821	-1.80118	3.6132	0.01918 5
1871	g13109.t1	3696	g9757.t1	K01620: Itae	0	2.071355	2.163561	-1.80694	3.6096	0.01925 6
1872	g1060.t1	3697	g8133.t1		4.616756	0.514584	-3.57327	-1.81051	3.6073	0.01930 1
1873	g7618.t1	3698	g7618.t1		2.193329	5.285081	3.154401	-1.81683	3.6033	0.01939 4
1874	g1395.t1	3699	g6218.t1		3.913913	7.425386	3.628307	-1.82293	3.5995	0.01950 3

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statisti c	Adj. p- value
1875	g1934.t1	3700	g10921.t1		6.270225	2.041068	-5.92102	-1.82531	-3.59803	0.01953
1876	g10864.t1	3701	g114.t1		1.463031	4.938665	3.973683	-1.82564	3.59782	0.01953
1877	g10895.t1	3702	g5900.t1		0	4.186104	3.125415	-1.8289	3.595755	0.019562
1878	g5532.t1	3703	g11340.t1		1.931855	7.130479	5.020293	-1.83514	3.591812	0.019672
1879	g7251.t1	3704	g10776.t1		4.989318	0.254069	-3.57371	-1.85053	-3.58209	0.019932
1880	g3894.t1	3705	g3998.t1	K00846: KHK	2.877684	5.230358	3.413778	-1.86007	3.576066	0.020088
1881	g819.t1	3706	g8183.t1		3.722054	7.412978	4.05158	-1.86516	3.572854	0.020168
1882	g5100.t1	3707	g2942.t1	K06688: UBE2C, UBC11	0	1.914572	2.214387	-1.86814	3.570972	0.020216
1883	g5175.t1	3708	g3792.t1	K11498: CENPE	3.281173	0.222331	-4.74201	-1.88553	-3.56	0.020535
1884	g6483.t1	3709	g5291.t1	K13728: MAD2L2	1.918177	10.9648	7.40681	-1.89484	3.554125	0.020681
1885	g8029.t1	3710	g4279.t1	K01464: DPVS, dht, hyda	3.138026	5.812027	3.152124	-1.89915	3.551408	0.020756
1888	g1840.t1	3713	g1902.t1		4.350369	6.555403	3.614501	-1.90291	3.549042	0.020781
1886	g5081.t1	3711	g8569.t1	K00505: TYR	0	4.711171	4.573953	-1.9019	3.549673	0.020781
1887	g1692.t1	3712	g4651.t1		1.082713	6.142533	4.604924	-1.90263	3.549214	0.020781
1889	g11007.t1	3714	g8699.t1		0	1.587767	2.088946	-1.90951	3.544881	0.020897
1890	g1760.t1	3715	g1200.t1		0	3.246854	2.445799	-1.91563	3.541022	0.021005
1891	g10371.t1	3716	g10538.t1		0	4.965362	5.078563	-1.91874	3.539065	0.021065
1892	g7221.t1	3717	g5890.t1		5.661483	1.072226	-3.76681	-1.93127	-	0.02128

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
									3.5311 7	1
1893	g6375.t1	3718	g771.t1		8.208151	3.648937	-4.25444	-1.93282	-	0.02129 4
1896	g2909.t1	3721	g6002.t1		1.238494	4.449583	3.244239	-1.93586	3.5301 9	0.02132 2
1894	g5154.t1	3719	g3823.t1	K17095: ANXA7_11	3.505958	9.283634	4.528734	-1.93535	3.5286 04	0.02132 2
1895	g20345.t1	3720	g7516.t1		0	4.951177	4.852188	-1.93559	3.5284 53	0.02132 2
1897	g12606.t1	3722	g1144.t1		0	2.337207	2.424768	-1.94189	3.5244 87	0.02143
1898	g7465.t1	3723	g6869.t1		3.054874	8.104242	4.242867	-1.94419	3.5230 4	0.02145 2
1899	g5267.t1	3724	g9694.t1		1.826832	5.783242	3.837809	-1.9491	3.5199 47	0.02153 5
1900	g4664.t1	3725	g2382.t1		5.504862	1.603502	-4.21381	-1.95339	-	0.02159 3
1901	g17749.t1	2523	g12099.t1		7.598291	9.839638	2.512479	-1.95532	3.5160 31	0.02162 8
1902	g6418.t1	3726	g5371.t1	K03778: IdhA	2.853999	4.669676	2.946243	-1.95976	3.5132 37	0.02172 1
1903	g10763.t1	3727	g12010.t1	K01209: E3.2.1.55, abfA	2.945033	0	-3.29535	-1.96318	-	0.02177
1904	g666.t1	3728	g9881.t1		4.362664	0.664419	-3.76077	-1.96699	-	0.02183 8
1906	g1908.t1	3730	g8731.t1		2.211455	0	-3.68585	-1.97784	-	0.02204 4
1907	g3413.t1	3731	g4733.t1	K06902: UMF1	2.141863	7.189473	4.094946	-1.97792	3.5018 7	0.02204 4
1905	g9155.t1	3729	g6487.t1	K02324: POLE1	4.234902	8.900666	4.422793	-1.97738	3.5021 59	0.02204 4

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1908	g10394.t1	3732	g10563.t1		0	5.322562	4.509387	-1.9801	3.5004 5	0.02207 5
1909	g7696.t1	3733	g11509.t1		0.601935	3.107555	2.748423	-1.98765	3.4957 05	0.02220 2
1910	g2535.t1	3734	g3567.t1	K05758: ARPC2	11.15766	3.882187	-7.40548	-1.99331	- 3.4921 5	0.02230 6
1911	g8186.t1	3735	g7993.t1	K01079: serB, PSPH	4.063757	0.499721	-4.16492	-1.99443	- 3.4914 4	0.02232 2
1912	g4471.t1	3736	g6834.t1		0.878562	4.743026	3.759323	-1.99869	3.4887 64	0.02241 4
1913	g8237.t1	3737	g10043.t1		3.086194	5.293821	2.302039	-1.99973	3.4881 13	0.02241 8
1914	g9619.t1	3738	g7243.t1	K11339: MORF4L1, MRG15, EAF3	0	2.363574	3.497394	-2.00042	3.4876 75	0.02242 4
1915	g1911.t1	3739	g6147.t1	K08334: BECN1, VPS30, ATG6	4.443069	1.325402	-4.48934	-2.0025	- 3.4863 7	0.02245 8
1916	g7540.t1	3740	g7267.t1	K01179: E3.2.1.4	3.106323	7.044516	4.718377	-2.0027	3.4862 47	0.02245 8
1917	g2857.t1	3741	g9061.t1		4.958463	1.63825	-3.2435	-2.00585	- 3.4842 7	0.02250 2
1918	g5306.t1	3742	g2255.t1		5.053243	1.769587	-3.06328	-2.00736	- 3.4833 2	0.02250 7
1919	g4916.t1	3743	g4552.t1	K13950: pabAB	0	4.100904	3.309752	-2.00896	3.4823 11	0.02252 4
1920	g7255.t1	3744	g10781.t1		1.044041	5.343757	3.456906	-2.0128	3.4799 02	0.02260 7
1921	g5468.t1	3745	g8430.t1		4.014859	1.728033	-2.2011	-2.02184	- 3.4742 3	0.02280 7
1922	g10379.t1	3746	g10546.t1	K03507: DPB11	0	2.887983	2.379258	-2.02243	3.4738 57	0.02281 57
1923	g2332.t1	3747	g9197.t1	K09484: QUIB, qa-3	0.359609	4.730422	6.455702	-2.04055	3.4624	0.02321

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
640	g12554.t1	2440	g3576.t1	K02953: RP-S13e, RPS13	6.593986	3.286592	-3.5936	-2.0451	84 3.4596 3	6 0.02331 9
1924	g134.t1	3748	g5827.t1		6.48267	2.73113	-3.87561	-2.04641	3.4588 3	0.02333 9
1925	g6562.t1	3749	g10098.t1	K04627: STE3	6.840025	3.508287	-3.0943	-2.04677	3.4585 8	0.02333 9
1926	g835.t1	3750	g8204.t1		5.9061	3.739419	-2.89332	-2.05738	3.4519 3	0.02357 4
1927	g3961.t1	3751	g3929.t1	K15631: ABA3	4.682251	0.610791	-4.20667	-2.05917	3.4508 6	0.02360 6
1928	g9090.t1	3752	g8544.t1		9.042656	3.394564	-4.42541	-2.06054	3.4499 4	0.02362 2
1929	g8220.t1	3753	g10063.t1	K11380: NTO1	0.981794	5.762532	4.770402	-2.06314	3.4483 16	0.02365 9
1930	g1688.t1	3754	g4655.t1		3.67154	6.41277	3.431308	-2.06707	3.4458 53	0.02371 53
1931	g10593.t1	3755	g7036.t1		0	1.637191	2.310481	-2.06843	3.4449 99	0.02373 4
1932	g7454.t1	3756	g6881.t1	K13237: DECR2	7.244054	3.351771	-4.66071	-2.07246	3.4424 7	0.02382 6
1933	g1006.t1	3757	g8076.t1		5.641821	1.01679	-5.33245	-2.07757	3.4392 7	0.02392 4
1934	g558.t1	3758	g6454.t1		5.468701	2.998081	-3.81423	-2.07899	3.4383 8	0.02395 8
1935	g8492.t1	3759	g3364.t1		2.17787	5.143839	3.198935	-2.08565	3.4342 06	0.02407 7
1936	g3284.t1	3760	g8263.t1	K04567: KARS, lys	0	3.096837	2.750146	-2.09247	3.4299 33	0.02417 6
1937	g10375.t1	3761	g10542.t1	K18163: NDUFAF6	0	3.09048	3.372823	-2.09383	3.4290	0.02418

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statisti c	Adj. p- value
1938	g9651.t1	3762	g6914.t1		8.216351	3.957187	-3.97535	-2.09941	81	0.02429
1939	g6236.t1	3763	g7134.t1		1.92867	9.554801	7.372855	-2.10264	3.4235	0.02436
1940	g5143.t1	3764	g3836.t1		2.580565	8.674743	4.091749	-2.1038	59	0.02438
1941	g11455.t1	3765	g7021.t1		0.596448	5.043975	4.462447	-2.10687	38	0.02445
1942	g5389.t1	3766	g2429.t1		4.873893	0	-5.94573	-2.11075	16	0.02454
1943	g6232.t1	3767	g7130.t1		6.918168	0.488136	-5.39134	-2.11243	3.4184	0.02456
1944	g13866.t1	3768	g4613.t1	K15115: SLC25A32, MFT	0.791928	5.833256	4.134026	-2.11257	3.4174	0.02456
1945	g7546.t1	3769	g7261.t1	K06113: abnA_8	1.693461	6.005734	3.98049	-2.11746	41	0.02467
1946	g10144.t1	3770	g8474.t1	K17086: TM9SF2_4	6.358648	-2.274685	-5.01733	-2.12573	82	0.02486
1947	g8973.t1	3771	g11361.t1	K08496: GOSR2, BOS1	0	3.168015	2.664668	-2.12811	3.4091	0.02491
1948	g5708.t1	3772	g2670.t1		3.903218	6.617966	3.389449	-2.13389	16	0.02504
1950	g6963.t1	3774	g6427.t1	K14408: CSTF3, RNA14	6.941008	0	-5.14398	-2.13547	97	0.02506
1949	g15819.t1	3773	g6469.t1		6.143278	2.028742	-3.66691	-2.13542	3.4030	0.02506
1951	g9667.t1	3775	g4881.t1	K18757: LARP1	1.474494	5.026138	3.073674	-2.13624	4	0.02507
1952	g12694.t1	3776	g8901.t1		0	4.059599	3.514485	-2.13747	3.4025	0.02508

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1953	g3429.t1	3777	g4716.t1	K10755: RFC2_4	6.366861	3.029398	-4.00095	-2.13997	3.4002	0.02512
1954	g4582.t1	3778	g4118.t1		1.381451	5.626283	4.430383	-2.14063	3.3997 81	0.02512 6
1955	g3157.t1	3779	g4989.t1		3.100887	8.957858	6.174002	-2.15214	3.3925 85	0.02538 1
1956	g82.t1	3780	g2764.t1	K17422: MRPL41	0	6.458967	4.487087	-2.15351	3.3917 28	0.02539 6
1957	g624.t1	3781	g11304.t1		0.779024	4.503237	2.584446	-2.15576	3.3903 22	0.02542 7
1958	g1143.t1	3782	g253.t1		0	4.407125	4.086029	-2.16257	3.3860 6	0.02558 7
1959	g6371.t1	3783	g780.t1	K08287: E2.7.12.1	2.726445	7.392615	5.376711	-2.17655	3.3773 22	0.02590 5
1960	g1751.t1	3784	g9723.t1		2.795334	5.572355	3.187095	-2.17894	3.3758 31	0.02595 9
1961	g4236.t1	3785	g1745.t1		4.004311	6.248441	2.562026	-2.18036	3.3749 42	0.02598 7
1962	g8695.t1	3786	g11550.t1		4.911201	1.458168	-3.1977	-2.18135	3.3743 2	0.02600 4
859	g490.t1	2536	g5492.t1	K01230: MAN1	3.341994	5.830489	2.819683	-2.18329	3.3731 1	0.02604 6
1963	g5421.t1	3787	g5085.t1		8.070442	0.46074	-5.99862	-2.18759	3.3704 2	0.02613 5
1964	g2502.t1	3788	g3530.t1	K13288: orn, REX2, REX02	0	4.539539	4.217905	-2.18823	3.3700 25	0.02613 8
1965	g2567.t1	3789	g5735.t1		4.150469	7.075168	2.267847	-2.19188	3.3677 44	0.02620 5
1966	g4811.t1	3790	g9600.t1		3.984392	2.169587	-2.35064	-2.19298	3.3670 6	0.02622 4
1967	g6775.t1	3791	g4391.t1	K18748: SSD1	7.196236	1.868572	-5.15477	-2.20272	3.3609 8	0.02642 9
1969	g10391.t1	3793	g10558.t1		0	5.449561	5.122671	-2.21155	3.3554	0.02658

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1968	g1041.t1	3792	g8112.t1	K11227: PBS2	0	5.802497	5.568864	-2.2107	6	0.02658
1971	g11559.t1	3795	g4170.t1		5.952815	2.501869	-3.41726	-2.21296	3	0.02660
1970	g13704.t1	3794	g11109.t1		1.780391	5.388679	3.682525	-2.21285	3	0.02660
1972	g3779.t1	3796	g2656.t1		0	2.29459	3.055708	-2.21449	3	0.02662
1973	g2737.t1	3797	g9165.t1		8.111867	3.708757	-3.11076	-2.21608	7	0.02665
1974	g6644.t1	3798	g10196.t1		0.529024	4.052835	2.69518	-2.21902	3	0.02670
1975	g9251.t1	3799	g10432.t1		6.615159	0.815708	-4.57198	-2.2196	3	0.02671
1977	g5146.t1	3801	g3831.t1		1.613274	5.642097	3.424626	-2.22255	3	0.02675
1976	g7543.t1	3800	g7264.t1		1.778839	6.311218	3.7799	-2.22228	3	0.02675
1978	g7853.t1	3802	g10510.t1	K15306: RANBP1	0	1.987939	2.649547	-2.22545	3	0.02681
1979	g7747.t1	3803	g7097.t1	K14791: PWP1	1.814601	4.202941	2.631876	-2.22599	3	0.02682
1980	g3283.t1	3804	g8262.t1	K11400: ARP4	0	2.989351	3.88489	-2.22752	3	0.02685
1981	g3579.t1	3805	g3304.t1	K00472: E1.14.11.2	3.489594	9.820105	6.138885	-2.22818	3	0.02686
1982	g4997.t1	3806	g8967.t1		1.989279	5.409008	3.503902	-2.2339	3	0.02699
1983	g466.t1	3807	g8012.t1		4.101739	6.505153	2.812413	-2.23476	3	0.02700
1984	g3042.t1	3808	g1617.t1	K01638: E2.3.3.9, aceB, glcB	4.286461	1.427891	-2.69449	-2.23709	3	0.02706

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
1985	g2105.t1	3809	g2480.t1	K12189: VPS25, EAP20	5.392127	1.688441	-3.98468	-2.24246	-3.3361 7	0.02717 1
1986	g10030.t1	3810	g3456.t1	K03952: NDUF A8	4.085114	0.317024	-3.2909	-2.24726	-3.3331 7	0.02726 3
1987	g10020.t1	3811	g10918.t1	K01238: E3.2.1.-	0	2.377597	3.865002	-2.24806	3.3326 71	0.02727 4
1988	g6440.t1	3812	g9393.t1		1.856577	5.779447	3.68737	-2.25497	3.3283 62	0.02745 4
1989	g10867.t1	3813	g124.t1		0	4.39728	4.400864	-2.25581	3.3278 4	0.02746 7
1990	g3799.t1	3814	g863.t1		5.870835	2.857198	-2.27046	-2.25914	-3.3257 6	0.02753 4
1991	g10346.t1	3815	g44.t1	K18328: DBR1	0	2.241769	3.604053	-2.25968	3.3254 24	0.02753 4
1992	g9896.t1	3816	g3480.t1		0	5.417973	5.231502	-2.25972	3.3253 96	0.02753 4
1993	g7695.t1	3817	g11508.t1	K01640: E4.1.3.4, HMGCL, hmgL	0.184849	4.606471	4.094707	-2.26451	3.3224 14	0.02764
1994	g851.t1	3818	g9450.t1		7.233882	2.603782	-3.98752	-2.26621	-3.3213 5	0.02767 8
1995	g13873.t1	3819	g4607.t1	K14845: RAI1, DOM3Z	1.75337	5.060998	3.620071	-2.27209	3.3176 86	0.02781 8
1996	g5244.t1	3820	g2347.t1	K02877: RP-L15e, RPL15	4.414688	11.84847	5.818625	-2.27366	3.3167 08	0.02785 3
1997	g13106.t1	3821	g9753.t1	K01892: HARS, hisS	0	2.209128	2.453035	-2.27519	3.3157 51	0.02788 6
1998	g11726.t1	3822	g5854.t1		5.938268	0.538037	-5.1103	-2.27837	-3.3137 7	0.02796
1999	g2723.t1	3823	g9178.t1		4.416635	0.748978	-3.32728	-2.28414	-3.3101 7	0.02810 7
2000	g5988.t1	3824	g11687.t1		6.638403	4.410083	-2.22473	-2.28525	-	0.02812

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									3.3094 8	9
2001	g6939.t1	3825	g6449.t1	K01560: E3.8.1.2	1.458794	5.793547	4.011947	-2.29299	3.3046 59	0.02831 5
2003	g13415.t1	3827	g8381.t1	K00618: E2.3.1.1	5.219776	7.979734	3.470781	-2.29519	3.3032 85	0.02835 7
2002	g37.t1	3826	g2834.t1	K02926: RP-L4, MRPL4, rplD	1.828605	4.71647	4.723031	-2.29519	3.3032 85	0.02835 7
2004	g3662.t1	3828	g651.t1		0.872427	6.371311	4.041603	-2.29616	3.3026 81	0.02836 2
2005	g9235.t1	3829	g3428.t1		0	3.972927	4.57957	-2.29616	3.3026 79	0.02836 2
2006	g7674.t1	3830	g7572.t1		5.466518	2.783883	-4.32184	-2.29711	- 3.3020 9	0.02836 8
2007	g4036.t1	3831	g3210.t1		4.501248	0.83444	-3.4584	-2.29717	- 3.3020 5	0.02836 8
2008	g5276.t1	3832	g2295.t1		4.938586	0.923903	-3.91412	-2.30002	- 3.3002 8	0.02840 6
2009	g11802.t1	3833	g12042.t1		3.076257	6.471818	3.398775	-2.30107	3.2996 22	0.02842 6
2010	g9414.t1	3834	g3612.t1		6.623875	3.522539	-4.17633	-2.30173	- 3.2992 1	0.02843 4
656	g16181.t1	2457	g12075.t1	K08257: E3.2.1.101	5.57367	2.794291	-3.13674	-2.30477	- 3.2973 1	0.02847 7
2012	g10897.t1	3836	g5902.t1		0	2.586402	2.018878	-2.30447	3.2975 01	0.02847 7
2011	g7210.t1	3835	g5874.t1	K09780: K09780	1.114388	3.993513	3.261747	-2.30435	3.2975 79	0.02847 7
2013	g4453.t1	3837	g6809.t1		5.118903	0.695521	-6.34745	-2.31256	- 3.2924 7	0.02864 3
2014	g606.t1	3838	g3853.t1	K16261: YAT	3.858126	5.880152	2.075602	-2.32021	3.2876	0.02884

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
									98	3
2015	g4470.t1	3839	g6833.t1		1.147637	5.898161	3.859584	-2.3248	3.2848 38	0.02896 1
2016	g6738.t1	3840	g7868.t1		5.417721	3.126867	-3.45553	-2.32976	- 3.2817 5	0.02906 9
2017	g9769.t1	3841	g939.t1	K15326: TSEN54	2.152088	5.841014	4.075185	-2.33059	3.2812 31	0.02907 9
2018	g8609.t1	3842	g3035.t1	K11684: BDF1	5.659852	2.072019	-3.03129	-2.33159	- 3.2806 1	0.02909 8
2019	g7209.t1	3843	g5873.t1		1.535387	3.753918	2.595474	-2.33355	3.2793 88	0.02914 5
2020	g9079.t1	3844	g7839.t1		3.237265	5.083271	2.50233	-2.33749	3.2769 37	0.02923 8
2021	g488.t1	3845	g5490.t1		5.069028	0.661124	-3.94585	-2.33858	- 3.2762 6	0.02924 6
2022	g11121.t1	3846	g740.t1		1.095174	5.476241	3.763338	-2.33866	3.2762 12	0.02924 12
2023	g7270.t1	3847	g11833.t1	K01649: leuA	0.794723	4.590596	3.756172	-2.34295	3.2735 4	0.02929 2
2024	g8493.t1	3848	g3365.t1		3.869494	6.395043	2.369665	-2.35653	3.2650 84	0.02971 2
2025	g9798.t1	3849	g10841.t1	K04564: SOD2	6.169922	3.581629	-3.17615	-2.35997	- 3.2629 4	0.02980 9
2026	g4827.t1	3850	g711.t1		3.138123	5.609277	2.266361	-2.36209	3.2616 22	0.02986 5
2027	g7690.t1	3851	g7594.t1	K09705: K09705	6.512504	2.963367	-3.48703	-2.3645	- 3.2601 2	0.02991 7
2028	g6785.t1	3852	g4403.t1	K06111: EXOC4, SEC8L1	7.141887	3.434524	-3.10329	-2.36545	- 3.2595 4	0.02993 5
2029	g11719.t1	3853	g2321.t1		4.122011	2.09891	-3.55772	-2.36866	- 3.2575 6	0.03002 6

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
2030	g4828.t1	3854	g712.t1		5.692735	2.652303	-3.51649	-2.37281	4	0.03012
2031	g942.t1	3855	g9313.t1	K09241: GAL4	1.854413	3.96608	2.304511	-2.37691	3.252404	0.03022
2032	g11848.t1	3856	g8790.t1		2.601552	0.409353	-2.22171	-2.37796	3.25175	0.03025
2033	g21824.t1	3857	g7394.t1		0	5.23534	3.655249	-2.38527	3.247202	0.03046
2034	g2821.t1	3858	g11279.t1		5.756117	3.458502	-2.0711	-2.3872	3.24601	0.03051
2035	g6696.t1	3859	g11145.t1	K09704: K09704	7.789281	2.074215	-5.24082	-2.38775	3.24566	0.03052
2036	g4155.t1	3860	g1823.t1	K18551: SDT1	5.022148	1.693257	-2.97251	-2.38832	3.2453	0.03052
2037	g9766.t1	3861	g942.t1		3.212965	8.164358	4.327837	-2.39337	3.242162	0.03067
2039	g13908.t1	3863	g8736.t1		3.218518	0.78025	-2.44992	-2.39434	3.24156	0.03068
2038	g9809.t1	3862	g10829.t1		3.118004	5.544287	2.518375	-2.39418	3.24166	0.03068
2040	g6787.t1	3864	g4405.t1		1.161527	5.099231	3.21425	-2.39714	3.239817	0.03075
2041	g9405.t1	3865	g3622.t1		3.567627	5.477382	2.497615	-2.40468	3.23513	0.03097
2042	g2509.t1	3866	g3539.t1	K11874: UBP16	1.872531	5.493777	3.650258	-2.4068	3.233811	0.03103
2043	g5355.t1	3867	g9.t1		2.290026	0.356189	-2.03022	-2.40761	3.23331	0.03104
2044	g4497.t1	3868	g10803.t1		4.996184	7.333602	3.047979	-2.4116	3.230832	0.03114

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2045	g8224.t1	3869	g10058.t1		3.041354	5.822561	3.713464	-2.41714	3.2273 86	0.03126 4
2046	g4940.t1	3870	g4580.t1		2.195152	8.603997	5.13217	-2.41716	3.2273 71	0.03126 4
2047	g3634.t1	3871	g611.t1	K08331: ATG13	3.988422	0.822981	-3.37249	-2.42114	-	0.03138 5
2048	g228.t1	3872	g11036.t1	K14833: NOC2	5.004033	8.298645	2.944132	-2.43094	3.2188 05	0.03169 2
2049	g48.t1	3873	g2823.t1	K01433: purU	2.612144	5.741983	3.012018	-2.43232	3.2179 47	0.03171 3
2050	g281.t1	3874	g11374.t1		9.37879	4.604117	-4.12735	-2.43274	-	0.03171 3
2051	g12734.t1	3875	g5711.t1	K11662: ACTR6, ARP6	0	2.30116	2.840219	-2.43365	3.2171 25	0.03171 8
2052	g10764.t1	3876	g12011.t1	K01581: E4.1.1.17, ODC1, speC, speF	5.248823	0.219074	-4.66848	-2.4346	-	0.03173 7
2053	g3828.t1	3877	g2599.t1	K00505: TVR	0.869044	5.111409	3.294953	-2.43787	3.2144 99	0.03183 6
2054	g1137.t1	3878	g246.t1		5.271354	1.818388	-3.65818	-2.43939	-	0.03187 5
2055	g4066.t1	3879	g3252.t1		3.515498	1.112324	-2.46994	-2.44069	-	0.03190 6
2056	g10836.t1	3880	g9834.t1		0.621439	3.119334	2.691703	-2.44409	3.2127 5	0.03201 36
2057	g5068.t1	3881	g8335.t1	K14685: SLC40A1, FPN1	0	7.218235	6.29332	-2.44716	3.2087 23	0.03206 2
2058	g9620.t1	3882	g7242.t1	K01648: ACLY	0	3.90929	3.533252	-2.45537	3.2036 26	0.03225 3
2059	g5229.t1	3883	g2363.t1		5.943001	0.548669	-5.4291	-2.46004	-	0.03237 5
2060	g8605.t1	3884	g3038.t1		4.532655	1.818868	-2.9624	-2.46055	3.2007 2	0.03237 9

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
2061	g10730.t1	3885	g2912.t1	K01469: OPLAH; OXP1, opIAH	0	2.379516	2.107655	-2.46555	3.1973 1	0.03254 1
2062	g4774.t1	3886	g3677.t1	K15631: ABA3	9.027659	4.836111	-4.01499	-2.46683	3.1965 2	0.03257 2
2063	g4508.t1	3887	g10813.t1		0.165642	5.824528	5.711017	-2.46786	3.1958 65	0.03259 5
2064	g2571.t1	3888	g5739.t1		0.293052	8.085137	4.840508	-2.46935	3.1949 39	0.03262 39
2065	g5434.t1	3889	g3137.t1		5.143051	1.033474	-3.99467	-2.47101	3.1939 1	0.03266 5
2066	g1199.t1	3890	g353.t1	K02895: RP-L24, MRPL24, rplX	6.44631	2.830134	-5.33548	-2.4716	3.1935 4	0.03267 2
2067	g7868.t1	3891	g10526.t1	K02915: RP-L34e, RPL34	5.849423	1.765368	-4.55948	-2.47674	3.1903 5	0.03282 6
2068	g1161.t1	3892	g269.t1		5.46016	3.009009	-2.38008	-2.48667	3.1841 8	0.03305 6
2070	g4445.t1	3894	g6797.t1		4.844189	2.596249	-3.82423	-2.48854	3.1830 2	0.03308 2
2069	g10124.t1	3893	g92.t1		4.215995	9.33502	4.637226	-2.48825	3.1832 2	0.03308 2
2071	g3873.t1	3895	g4021.t1		2.22259	5.09223	2.889394	-2.49175	3.1810 28	0.03317 9
2072	g2508.t1	3896	g3536.t1		0	6.070724	4.543999	-2.49201	3.1808 7	0.03317 9
2073	g8450.t1	3897	g2681.t1		0	2.871722	2.959236	-2.4972	3.1776 46	0.03335 1
2074	g7865.t1	3898	g10523.t1		7.879406	5.602482	-4.36688	-2.51011	3.1696 3	0.03373 5
2075	g6937.t1	3899	g6455.t1	K13108: SNIP1	0.333353	7.112752	4.778096	-2.51256	3.1681 11	0.03381 1

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2076	g4596.t1	3900	g6012.t1	K12855: PRPF6, PRP6	1.297068	7.636161	5.013494	-2.51413	3.1671 37	0.03385 4
2077	g16131.t1	3901	g11950.t1	K00616: E2.2.1.2, talA, talB	4.139806	0.380959	-2.80605	-2.51525	3.1664 4	0.03386 1
2078	g465.t1	3902	g8013.t1	K14325: RNPS1	0.1118	6.347517	6.203301	-2.51547	3.1663 03	0.03386 1
2079	g1164.t1	3903	g270.t1		0.318216	3.991449	5.225959	-2.51682	3.1654 62	0.03388 3
2080	g2408.t1	3904	g9480.t1	K18550: ISN1	5.538089	8.86782	4.347478	-2.51899	3.1641 17	0.03393 5
2082	g16130.t1	3906	g7073.t1		4.225688	6.146706	2.4124	-2.52079	3.1630 02	0.03394 5
937	g8077.t1	2540	g7846.t1		6.655406	8.379386	2.917067	-2.52044	3.1632 18	0.03394 5
2081	g5524.t1	3905	g1651.t1		1.597727	5.655543	3.534574	-2.5205	3.1631 77	0.03394 5
2083	g13129.t1	3907	g7779.t1		3.365795	1.169273	-2.39087	-2.52343	3.1613 6	0.03402 8
2084	g10991.t1	3908	g5657.t1	K12627: LSM8	0	2.170848	3.541712	-2.52601	3.1597 61	0.03410 9
2085	g1929.t1	3909	g6163.t1	K01930: FPGS	2.613598	6.785311	3.342673	-2.52742	3.1588 84	0.03414 7
523	g10740.t1	2319	g11987.t1		0	2.813231	2.132602	-2.52798	3.1585 4	0.03415 3
2086	g11974.t1	3910	g12283.t1	K01537: E3.6.3.8	4.46077	8.720128	4.497107	-2.52922	3.1577 7	0.03418 5
2087	g2386.t1	3911	g9282.t1		2.552078	5.80107	2.857308	-2.52973	3.1574 52	0.03419 7
2088	g11089.t1	3912	g1541.t1		2.958185	5.916026	3.473746	-2.53269	3.1556 12	0.03427 1
549	g6123.t1	2346	g7324.t1		9.721609	0	-6.70978	-2.53776	3.1524 7	0.03441 7
2089	g2879.t1	3913	g9507.t1		1.588916	5.963453	4.232111	-2.53843	3.1520 52	0.03442 8

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statisti c	Adj. p- value
2090	g13476.t1	3914	g8719.t1		4.855623	0.713258	-4.14789	-2.54165	- 3.1500 5	0.03449 2
2091	g10480.t1	3915	g1680.t1		5.35355	2.766663	-3.30455	-2.54237	- 3.1496 4	0.03450 4
2092	g8013.t1	3916	g3404.t1		5.049113	0.484288	-4.63964	-2.54362	- 3.1488 3	0.03453 7
2093	g4367.t1	3917	g3791.t1	K03448: FEN2, LIZ1	5.072018	0.779082	-3.52579	-2.54647	- 3.1470 7	0.03458 7
2094	g6987.t1	3918	g10858.t1		0.511756	5.093495	4.425198	-2.54912	3.1454 16	0.03464 4
2095	g10431.t1	3919	g8407.t1	K14861: URB1	9.412961	2.402632	-4.79559	-2.55	- 3.1448 7	0.03466 3
2096	g8248.t1	3920	g10031.t1	K17424: MRPL43	1.653332	7.208956	3.793246	-2.55139	3.1440 09	0.03470 1
2097	g9278.t1	3921	g112.t1		5.376359	0.900471	-5.07129	-2.5543	- 3.1422 1	0.03479 5
561	g1198.t1	2358	g352.t1	K04513: RHOA	2.185924	5.599431	3.115826	-2.56335	3.1365 92	0.03508
2098	g7656.t1	3922	g7539.t1		9.484291	3.272208	-4.44358	-2.56665	- 3.1345 5	0.03516 3
2099	g9071.t1	3923	g8570.t1		0	4.308308	2.935063	-2.5715	3.1315 34	0.03529 5
2100	g2276.t1	3924	g10693.t1	K12761: SNF1	5.01028	6.964651	2.286462	-2.57593	3.1287 88	0.03543 1
2101	g14507.t1	3925	g11494.t1	K01187: malZ	7.827356	5.131373	-2.97808	-2.5835	- 3.1240 9	0.03565
2102	g4366.t1	3926	g2127.t1		3.108334	0.378977	-3.23784	-2.58635	- 3.1223 2	0.03574 6
2103	g5569.t1	3927	g7488.t1		2.55743	5.105776	2.804623	-2.58922	3.1205	0.03584

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
2104	g12588.t1	3928	g2936.t1		5.341725	1.287142	-4.50731	-2.59295	44	0.03593
2106	g192.t1	3930	g5819.t1		0	4.078839	3.742625	-2.5932	3.1182	0.03593
2105	g935.t1	3929	g9324.t1		1.589025	6.970304	5.205593	-2.59295	72	0.03593
2107	g7460.t1	3931	g6874.t1	K18176: COA3	0.679443	8.132716	6.326235	-2.59401	3.1180	0.03594
2108	g2807.t1	3932	g3734.t1	K01053: E3.1.1.17, gnl, RGN	6.975277	3.879255	-3.8776	-2.59679	3.1175	0.03603
2109	g4435.t1	3933	g6774.t1		3.295348	5.340307	2.156098	-2.59927	3.1158	0.03611
2110	g9401.t1	3934	g3633.t1	K12668: OST2, DAD1	5.100436	7.099716	3.045005	-2.60147	3.1129	0.03617
2111	g1263.t1	3935	g448.t1	K17421: MRPL40	0	5.570752	4.940149	-2.60151	3.1129	0.03617
2112	g3490.t1	3936	g2182.t1	K03350: APC3, CDC27	5.226216	7.504737	2.341709	-2.60332	3.1117	0.03622
2113	g10916.t1	3937	g267.t1		3.408478	5.633464	3.418244	-2.60479	3.1108	0.03622
2114	g921.t1	3938	g9342.t1	K18045: SIW14, OCA3	0	3.596272	3.808042	-2.60499	3.1107	0.03622
2116	g7478.t1	3940	g6858.t1		4.55802	0.837774	-3.42667	-2.61758	3.1029	0.03660
2115	g1744.t1	3939	g9730.t1	K16261: YAT	2.444031	4.709166	2.258978	-2.61755	3.1029	0.03660
2117	g10207.t1	3941	g11173.t1	K17866: DPH2	6.980775	0.764559	-4.05418	-2.62021	3.1013	0.03668
2118	g11843.t1	3942	g8773.t1	K00993: EPT1	3.000341	0.893639	-2.21354	-2.62048	3.1011	0.03668
2119	g3656.t1	3943	g636.t1		8.879204	5.164409	-2.89019	-2.62535	3.1011	0.03685

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
2120	g4331.t1	3944	g1983.t1		4.236756	1.896176	-3.14722	-2.62618	3.09814	0.036854
2121	g10256.t1	3945	g7194.t1		4.209344	0.708524	-3.33023	-2.62967	3.09762	0.036938
2122	g9189.t1	3946	g6521.t1	K05663: ABC.ATM	0.18774	5.583284	5.054504	-2.63044	3.09498	0.036954
2123	g9587.t1	3947	g6638.t1	K02976: RP-S26e, RPS26	0	3.89404	2.743634	-2.63219	3.093898	0.037009
2124	g3483.t1	3948	g2152.t1	K00472: E1.14.11.2	0	4.019165	3.218586	-2.63269	3.093584	0.037015
2125	g4515.t1	3949	g10820.t1		10.17358	3.683757	-4.93347	-2.6337	3.09296	0.03704
2126	g5855.t1	3950	g1148.t1	K12874: AQR	0	3.592743	3.462488	-2.63616	3.091433	0.037124
2127	g11080.t1	3951	g1560.t1	K13303: SGK2	3.663667	5.639852	2.488524	-2.63746	3.090627	0.03716
2128	g17161.t1	3952	g9655.t1		3.946776	6.251222	2.716762	-2.63779	3.090423	0.03716
2129	g913.t1	3953	g9352.t1		3.761447	1.842695	-2.6974	-2.64185	3.08791	0.037284
2131	g4992.t1	3955	g8962.t1		5.568434	1.070393	-4.64888	-2.64356	3.08685	0.037304
2130	g5921.t1	3954	g11009.t1		0.726064	3.654951	2.376852	-2.64348	3.086896	0.037304
2132	g10214.t1	3956	g11973.t1		4.391352	5.888419	2.232265	-2.64574	3.085498	0.037377
2134	g1192.t1	3958	g2652.t1		7.331953	0	-4.76693	-2.64809	3.08404	0.037428
2133	g5409.t1	3957	g8611.t1		0.487121	6.397764	4.771873	-2.64784	3.0841	0.03742

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
2135	g6619.t1	3959	g11272.t1	K11159: K11159	10.02313	7.677217	-2.84367	-2.64911	92	0.03745
2136	g5978.t1	3960	g11675.t1	K01187: malZ	4.632559	1.508608	-2.55697	-2.65074	3.0834 1	0.03750
2137	g9539.t1	3961	g6568.t1	K05906: PCYOX1, FCLY	0	3.166553	5.702237	-2.6513	3.0824 52	0.03751
2138	g13602.t1	3962	g10129.t1	K09579: PIN4	3.22586	7.700999	4.342095	-2.65456	3.0800 31	0.03760
2139	g10588.t1	3963	g7031.t1		0	5.84847	4.399222	-2.65698	3.0785 27	0.03767
2140	g8167.t1	3964	g7975.t1		4.268879	6.362638	3.264487	-2.66061	3.0762 81	0.03777
2141	g6658.t1	3965	g10210.t1		1.079636	5.470349	3.827162	-2.66129	3.0758 6	0.03778
2142	g1881.t1	3966	g4234.t1	K01725: cynS	4.230103	2.82032	-2.77283	-2.66619	3.0728 2	0.03794
2143	g11727.t1	3967	g5855.t1		3.728683	0.656698	-2.85634	-2.66698	3.0723 3	0.03796
2144	g3432.t1	3968	g4712.t1	K00505: TYR	0	3.109455	4.733726	-2.67446	3.0676 91	0.03822
2145	g20186.t1	3969	g6363.t1		5.012816	7.163425	2.999714	-2.68527	3.0609 93	0.03859
2146	g447.t1	3970	g8029.t1	K13431: SRPR	4.802134	1.949645	-2.92415	-2.69849	3.0528 7	0.03910
2147	g4444.t1	3971	g6795.t1		4.899102	2.093375	-3.84401	-2.69952	3.0521 6	0.03913
2148	g18374.t1	3972	g7684.t1	K12856: PRPF8, PRP8	4.95726	1.392127	-3.87785	-2.70169	3.0508 2	0.03918
2149	g8150.t1	3973	g7956.t1	K02959: RP-S16, MRPS16, rpsP	5.17122	2.06327	-3.42667	-2.70179	3.0507 6	0.03918

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statisti c	Adj. p- value
2150	g1210.t1	3974	g364.t1		5.549737	1.972661	-3.45578	-2.70577	-3.0482 9	0.03932 4
2151	g8164.t1	3975	g7965.t1		0.264932	6.326912	4.484822	-2.71181	3.0445 44	0.03956 5
2153	g8665.t1	3977	g2654.t1		4.448871	0	-4.40278	-2.71535	-3.0423 5	0.03964 4
2154	g6421.t1	3978	g5368.t1		3.418022	7.778884	4.446548	-2.71542	3.0423 1	0.03964 4
2152	g7000.t1	3976	g6384.t1	K15109: SLC25A20_29, CACT, CACL, CRC1	0	5.827294	5.75825	-2.71486	3.0426 55	0.03964 4
2155	g3832.t1	3979	g2595.t1		1.491655	5.211867	3.871807	-2.71908	3.0400 44	0.03975 5
2156	g10272.t1	3980	g2373.t1		6.233817	2.342297	-5.51583	-2.72027	-3.0393 1	0.03977 8
2158	g4169.t1	3982	g1810.t1		2.732171	7.333986	3.584184	-2.72283	3.0377 19	0.03979 3
2157	g10739.t1	3981	g11986.t1		0	3.441589	3.584342	-2.72269	3.0378 04	0.03979 3
2159	g5894.t1	3983	g10982.t1	K03030: PSMD14, RPN11, POH1	5.235811	0	-4.2666	-2.72651	-3.0354 4	0.03990 6
2160	g3017.t1	3984	g8289.t1		4.253797	2.232303	-2.01665	-2.72969	-3.0334 7	0.04002 8
2161	g2235.t1	3985	g10642.t1		0	8.944426	6.651699	-2.73008	3.0332 26	0.04002 9
2162	g444.t1	3986	g8037.t1		5.926244	1.755078	-4.43879	-2.73748	-3.0286 4	0.04028 9
2163	g8162.t1	3987	g7962.t1		2.242593	6.181948	2.975066	-2.7414	3.0262 15	0.04044 15
2164	g3781.t1	3988	g2653.t1		0	5.388341	4.391813	-2.74166	3.0260 51	0.04044 51
2165	g446.t1	3989	g8030.t1		1.248806	3.196143	2.232547	-2.74479	3.0241	0.04054

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
2166	g8813.t1	3990	g11548.t1		4.479092	1.564747	-2.31147	-2.75228	12	0.04084
2168	g484.t1	3992	g5480.t1	K01083: E3.1.3.8	6.104152	1.195312	-3.75188	-2.76953	3.0194	0.04152
2167	g6382.t1	3991	g762.t1	K11578: ZW10	4.043617	7.246112	3.318946	-2.76929	3.0087	0.04152
2169	g13874.t1	3993	g4606.t1		2.192003	4.933315	3.081033	-2.77099	3.0078	0.04156
2170	g9768.t1	3994	g940.t1		1.599958	5.142409	3.111563	-2.77117	3.0077	0.04156
2171	g7100.t1	3995	g5567.t1		3.101236	4.623123	2.647789	-2.77245	3.0069	0.04160
2172	g7685.t1	3996	g7577.t1		4.579641	1.059627	-4.79509	-2.77348	3.0063	0.04163
2174	g6166.t1	3998	g9581.t1	K10844: ERCC2, XPD	3.612569	6.046916	2.409001	-2.77444	3.0057	0.04164
2173	g20840.t1	3997	g5601.t1	K09958: K09958	0	3.295785	3.355548	-2.77424	3.0058	0.04164
2175	g4928.t1	3999	g4568.t1	K10752: RBBP4, HAT2, CAF1, MIS16	0.721987	4.891137	3.366959	-2.7761	3.0047	0.04168
2177	g4731.t1	4001	g2023.t1		3.62063	8.542099	3.637606	-2.78256	3.0007	0.04194
2176	g13702.t1	4000	g7799.t1		1.507271	5.575516	5.445863	-2.78244	3.0007	0.04194
2178	g6999.t1	4002	g6385.t1		0	5.909998	6.710453	-2.78479	2.9993	0.04198
2179	g1200.t1	4003	g354.t1	K03189: ureG	3.906083	6.287127	3.500283	-2.78517	2.9990	0.04198
2180	g894.t1	4004	g9381.t1		1.98344	3.689145	2.509227	-2.78645	2.9983	0.04201
2181	g4606.t1	4005	g11246.t1		6.888917	0.934867	-4.17521	-2.7892	2.9966	0.04212
2182	g5836.t1	4006	g1169.t1	K01078: E3.1.3.2	4.897435	0.540874	-3.08894	-2.78981	-	0.04213

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
									2.9962 2	2
2183	g6795.t1	4007	g4420.t1	K0620: argJ	1.412783	6.285553	3.554814	-2.7905	2.9957 89	0.04214 8
2184	g13700.t1	4008	g7801.t1	K06666: TUP1	4.676696	9.110953	5.842219	-2.79358	2.9938 81	0.04223 7
2185	g4127.t1	4009	g1853.t1		6.883091	3.151116	-3.23591	-2.79424	- 2.9934 7	0.04223 8
2186	g3498.t1	4010	g2189.t1	K0888: PI4K	4.387206	8.035595	3.806841	-2.79735	2.9915 49	0.04236 5
2187	g922.t1	4011	g9339.t1		0.335414	5.594	3.51525	-2.80783	2.9850 57	0.04283 2
2188	g2095.t1	4012	g2498.t1		2.312071	5.547566	3.491828	-2.8095	2.9840 22	0.04289 3
2189	g3886.t1	4013	g4006.t1		0.369905	5.31491	3.411646	-2.81293	2.9818 92	0.04302 7
2191	g2907.t1	4015	g4478.t1	K01361: E3.4.21.96	2.736066	5.91864	3.746675	-2.81508	2.9805 64	0.04308 7
2190	g4132.t1	4014	g1848.t1		3.459488	8.742363	3.852241	-2.8149	2.9806 73	0.04308 7
2192	g102.t1	4016	g2922.t1	K15628: PXA	4.533487	1.423633	-3.06092	-2.81692	- 2.9794 2	0.04312 4
2193	g22195.t1	4017	g11335.t1		5.038549	3.116899	-3.18678	-2.82113	- 2.9768 2	0.04325 6
2194	g6067.t1	4018	g11760.t1		2.556856	5.057211	2.182582	-2.82589	2.9738 66	0.04341 4
2195	g7479.t1	4019	g6857.t1		6.476209	0.753273	-5.14745	-2.82832	- 2.9723 6	0.04349 2
2196	g6849.t1	4020	g1428.t1	K14312: NUP155	5.863337	2.74764	-3.23983	-2.8286	- 2.9721 8	0.04349 2
2197	g6740.t1	4021	g4353.t1		3.814661	6.39705	3.411605	-2.83035	2.9710 99	0.04355 9

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
2198	g1017.t1	4022	g8086.t1		1.006221	4.462038	2.793294	-2.83106	2.9706 64	0.04357 5
2199	g20453.t1	4023	g7824.t1		0	2.0793	2.784209	-2.83156	2.9703 53	0.04358 3
2200	g1014.t1	4024	g8083.t1	K13577: SLC25A10, DIC	2.388955	4.532509	2.338145	-2.83672	2.9671 53	0.04381
2201	g3487.t1	4025	g2179.t1		0	3.411165	3.277123	-2.83823	2.9662 19	0.04385
2202	g3156.t1	4026	g4990.t1		3.806958	6.990748	5.291192	-2.84227	2.9637 14	0.04397 5
2203	g21845.t1	4027	g8491.t1		0	2.721806	3.270562	-2.84342	2.9630 02	0.04401 4
2204	g2266.t1	4028	g10682.t1		4.867023	3.323245	-2.83067	-2.84548	- 2.9617 3	0.04406 9
2205	g11688.t1	4029	g10852.t1		3.032144	0.893416	-2.19305	-2.85456	- 2.9561	0.04444 8
2206	g6381.t1	4030	g763.t1		5.116653	0.131962	-3.22317	-2.85525	- 2.9556 7	0.04446 4
2208	g10499.t1	4032	g1661.t1		4.339082	6.042177	2.559442	-2.85649	2.9549 04	0.04449 1
2207	g17551.t1	4031	g8157.t1	K00558: DNMT1, dcm	2.888377	6.949835	3.089797	-2.85616	2.9551 08	0.04449 1
2209	g5340.t1	4033	g9534.t1		0.545456	7.258622	4.798642	-2.85837	2.9537 43	0.04454 8
2210	g5285.t1	4034	g2285.t1		2.96395	7.10547	3.24264	-2.85885	2.9534 44	0.04455 5
2211	g7357.t1	4035	g10412.t1		5.528929	0.619143	-3.97539	-2.86359	- 2.9505 1	0.04473 4
2213	g726.t1	4037	g10236.t1		0.483715	2.68877	2.384127	-2.86588	2.9490 88	0.04481 1
2212	g3514.t1	4036	g2206.t1	K11397: EAF1, VID21	1.206815	6.642767	4.853325	-2.86574	2.9491 77	0.04481 1
2214	g7257.t1	4038	g10783.t1		1.642966	6.188124	2.989166	-2.87117	2.9458 13	0.04503 5

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statisti c	Adj. p- value
2215	g10215.t1	4039	g11972.t1		2.58645	7.403204	4.385523	-2.87151	2.9456 02	0.04503 5
2216	g12395.t1	4040	g9538.t1		5.861009	2.002652	-3.8787	-2.87539	- 2.9432	0.04517 4
2217	g341.t1	4041	g8842.t1		5.788696	9.05636	2.247676	-2.87854	2.9412 43	0.04531 2
2218	g2488.t1	4042	g3515.t1	K06669: SMC3, CSPG6	1.945941	7.641363	3.740235	-2.88255	2.9387 61	0.04547 3
2219	g713.t1	4043	g9934.t1		5.331222	0.664695	-4.38202	-2.88525	- 2.9370	0.04556 5
2220	g3763.t1	4044	g2673.t1		5.825851	3.254634	-2.56829	-2.88539	-2.937 8	0.04556 5
2221	g7424.t1	4045	g7209.t1		5.373092	9.386519	3.006451	-2.88618	2.9365 1	0.04557
2222	g5043.t1	4046	g10906.t1	K01426: E3.5.1.4, amiE	2.242898	6.456313	3.847076	-2.89168	2.9331 01	0.04580 8
2223	g7402.t1	4047	g7184.t1		5.091428	2.484421	-2.06938	-2.89544	- 2.9307	0.04591 1
2224	g6538.t1	4048	g10076.t1	K12830: SF3B3, SAP130, RSE1	0	3.092763	3.060265	-2.90278	2.9262 25	0.04624 3
2225	g10909.t1	4049	g5917.t1		2.072461	4.929452	2.681301	-2.90454	2.9251 3	0.04631 4
2226	g10722.t1	4050	g4266.t1	K12827: SF3A3, SAP61, PRP9	3.415338	6.31204	3.035059	-2.90712	2.9235 32	0.04642 7
2227	g4840.t1	4051	g4450.t1		3.23602	0.449458	-3.90188	-2.91106	- 2.9210	0.04653 7
2228	g1066.t1	4052	g8139.t1	K01922: PPCS, coaB	1.857534	4.106673	3.234378	-2.91469	2.9188 41	0.04668 9
2229	g6576.t1	4053	g10109.t1		3.964575	0	-4.86543	-2.91615	- 2.9179	0.04674 5
2230	g107.t1	4054	g2928.t1	K03539: RPP1, RPP30	3.197967	0.803547	-2.46999	-2.92305	- 2.9136	0.04703 8

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
2231	g3425.t1	4055	g4720.t1	K02605: ORC3	6.578091	4.722727	-2.20212	-2.92326	-2.91353	0.047038
2232	g1018.t1	4056	g8087.t1	K04565: SOD1	2.947764	8.680712	5.056988	-2.92384	2.913169	0.04705
2234	g5391.t1	4058	g2427.t1		3.793826	0.942173	-4.97661	-2.92597	-2.91185	0.047091
2233	g7764.t1	4057	g879.t1		3.456716	1.497029	-2.42385	-2.92569	-2.91203	0.047091
506	g8644.t1	2302	g2276.t1	K01166: E3.1.27.1	0	10.03085	6.401697	-2.92547	2.91216	0.047091
2236	g1094.t1	4060	g4037.t1	K02358: tuf, TUFM	7.685682	5.149397	-2.8793	-2.93139	-2.90849	0.047263
2235	g712.t1	4059	g9943.t1		2.563775	7.171783	3.80414	-2.93127	2.908563	0.047263
2237	g2419.t1	4061	g11542.t1		0.666287	3.962309	2.387936	-2.93259	2.907749	0.047307
2238	g2608.t1	4062	g9643.t1	K00135: gabb	1.638785	4.294982	3.144001	-2.93448	2.906575	0.047387
2239	g8147.t1	4063	g7952.t1	K11246: SHO1	6.066325	2.713104	-3.95602	-2.93607	-2.90559	0.047433
2240	g5705.t1	4064	g10360.t1		0.642825	4.418076	3.166773	-2.93679	2.905146	0.047433
2241	g1222.t1	4065	g374.t1		2.642618	5.883278	3.175464	-2.93706	2.90498	0.047433
2242	g8664.t1	4066	g3812.t1		7.432168	1.550855	-4.57283	-2.93851	-2.90408	0.04749
2243	g4764.t1	4067	g1994.t1		6.940047	1.130412	-4.17201	-2.93963	-2.90338	0.047531
2244	g6851.t1	4068	g1427.t1		2.284011	3.932777	2.957195	-2.94037	2.902925	0.047551

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statistic	Adj. p- value
2245	g10946.t1	4069	g5078.t1	K11236: CDC24	4.982918	0.83865	-3.5024	-2.94195	-2.90195	0.047598
2246	g1752.t1	4070	g9722.t1		2.831268	5.535026	2.675068	-2.94838	2.897963	0.047896
2247	g566.t1	4071	g3892.t1	K14708: SIC26A11	0.609198	5.65481	3.423398	-2.95146	2.896054	0.048021
2248	g3553.t1	4072	g3337.t1		5.206188	1.970138	-6.17884	-2.95714	-2.89253	0.048268
2249	g383.t1	4073	g7452.t1	K03978: eng8	3.305487	5.192025	2.780869	-2.95719	2.892499	0.048268
2250	g7722.t1	4074	g3091.t1	K03014: RPB6, POLR2F	0	4.540834	4.042193	-2.96294	2.888936	0.048493
2251	g5453.t1	4075	g3167.t1		4.7696	0.934559	-3.55662	-2.96747	-2.88612	0.048686
2252	g9542.t1	4076	g6565.t1	K01381: E3.4.23.25	0	3.886173	3.681133	-2.969	2.885177	0.048749
2254	g1347.t1	4078	g3449.t1	K01273: E3.4.13.19, DPEP1	4.946987	0.532441	-3.43411	-2.972	-2.88332	0.048837
2253	g4317.t1	4077	g1977.t1		2.161002	7.174394	3.592405	-2.97197	2.883339	0.048837
2255	g5426.t1	4079	g3123.t1	K09539: DNAJC19	7.936931	3.022359	-5.07555	-2.97281	-2.88282	0.048862
2256	g22408.t1	4080	g9317.t1	K05351: E1.1.1.9	0	5.279355	4.074546	-2.97436	2.881852	0.048927
2257	g6391.t1	4081	g5410.t1	K00480: E1.14.13.1	10.39213	2.102041	-5.87521	-2.97645	-2.88056	0.048977
2258	g4848.t1	4082	g4461.t1		5.837897	1.338468	-3.27267	-2.97698	-2.88023	0.048977
2259	g5255.t1	4083	g2333.t1		5.719887	4.103219	-2.31021	-2.97885	-2.87901	0.049041

SEQ ID SYM00577	SYM577 gene	SEQ ID SYM00300	SYM300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t- statisti c	Adj. p- value
2261	g10716.t1	4085	g11754.t1		4.124991	1.869399	-2.24701	-2.98266	7	0.04917 3
2260	g5384.t1	4084	g9571.t1	K13099: CD2BP2, PP1R59	0	5.725959	3.979521	-2.98264	2.8767 1	0.04917 3
2262	g2819.t1	4086	g9111.t1	K16066: ydfG	5.823181	2.29085	-5.24434	-2.98895	2.8728 1	0.04942 1
2265	g10820.t1	4089	g5705.t1		1.446801	4.641792	2.923813	-2.99351	2.8699 78	0.04957 7
2263	g10158.t1	4087	g8462.t1		0	2.396169	3.866683	-2.9926	2.8705 43	0.04957 7
2264	g844.t1	4088	g9461.t1		0	4.027461	4.070888	-2.99313	2.8702 18	0.04957 7
2267	g2834.t1	4091	g9028.t1		4.114412	0.517908	-3.11219	-2.99494	2.8691	0.0496
2266	g10485.t1	4090	g1675.t1		0	4.900393	4.371976	-2.99484	2.8691 53	0.0496
2268	g11904.t1	4092	g11956.t1	K00681: ggt	3.288998	0.166182	-3.64625	-2.99768	2.8673 9	0.04971 3
2269	g21731.t1	4093	g6097.t1		2.691539	0.619933	-4.08621	-3.00053	2.8656 3	0.04984 9
2270	g1202.t1	4094	g356.t1	K14768: UTP7, WDR46	1.026847	3.791611	2.583054	-3.00301	2.8640 88	0.04995 7
2271	g9859.t1	4095	g11476.t1		0	4.020067	4.04691	-3.00328	2.8639 21	0.04995 7

Table 603:

This table describes orthologous genes of *Acremonium zeae* sp. with beneficial and neutral effects on soybean growth, these genes show significant changes in expression between the two genotypes when grown in culture without soybean homogenate. "Median

Exp. SYM00577" represents the median expression value in log2 tpm across biological replicates of the beneficial Acremonium grown in media inoculated with 50 mM PBS buffer. "Median Exp. SYM00300" represents the median expression value in log2 tpm across biological replicates of the neutral Acremonium grown in media inoculated with 50 mM PBS buffer. "Log FC" represents the estimate of the log2-fold-change of the contrast. "B-statistic" represents the log-odds that the gene is differentially expressed. "t-statistic" represents the moderated t-statistic. "Adj. p-value" represents the false discovery rate (Benjamini & Hochberg, 1995) adjusted p-values.

SEQ ID	sym577 gene	SEQ ID SYM00300	sym300 gene	Description	Median Exp. SYM00577	Median Exp. SYM00300	Log FC	B-statistic	t-statistic	Adj. p- value
687	g13072.t 1	2494	g9142.t1		0	8.254570732	8.20516 2	7.709718	15.19085	5.97E-06
700	g10575.t 1	2526	g10634.t 1		0	5.044729998	5.21006 9	5.708895	10.76568	2.93E-05
674	g5345.t1	2555	g9530.t1	K03510: POLI	5.845894518	0.825824927	-4.70074	5.191774	-9.95863	4.34E-05
688	g68.t1	2495	g909.t1	K00106: XDH	7.003820996	1.8413995	-4.97725	5.089442	-9.80948	4.75E-05
701	g12045.t 1	2524	g804.t1	K12393: AP1M	6.653853259	0.902872062	-5.9827	4.978805	-9.65176	5.17E-05
702	g1230.t1	2527	g388.t1		0	5.088279289	4.70762 4	4.928839	9.581698	5.38E-05
703	g2767.t1	2559	g9144.t1	K02139: ATPeFF, ATP17	0	2.891582245	2.88367 6	4.49609	9.003087	8.38E-05
704	g7900.t1	2560	g8630.t1		6.140021427	2.188447902	-4.35168	4.123845	-8.54179	0.000127
686	g857.t1	2491	g9451.t1	K01950: E6.3.5.1, NADSYN1, QNS1, nadE	3.802514601	8.452816333	4.96761 4	4.058607	8.464065	0.000136
675	g5348.t1	2554	g1.t1		0	4.361478247	4.20718 7	3.745443	8.102858	0.000183
705	g10859.t 1	2552	g120.t1	K17842: carT, CAO-2	0	4.099415046	4.00102 5	3.630507	7.974961	0.000207
706	g8300.t1	2561	g5097.t1	K15136: SRB5, MED18	7.025134642	2.609740762	-4.37343	3.601634	-7.94321	0.000212
707	g2262.t1	2562	g10678.t 1	K11205: GCLM	0	6.497290601	5.70704 1	3.4962	7.828495	0.000234
708	g8448.t1	2563	g2683.t1	K00966: GMPP	0	11.29461044	9.89167 7	3.448641	7.777378	0.000245
709	g10027.t 1	2564	g3454.t1		0	2.522819857	2.63081 3	3.252018	7.570029	0.00029

517	g13099.t1 1	2313	g8761.t1		0	7.516860158	7.229	2.98496	7.298142	0.000373
710	g1584.t1	2517	g2859.t1		7.332050712	1.763743187	-5.35718	2.961709	-7.27498	0.00038
690	g7926.t1	2497	g8597.t1		6.853860482	1.736488111	-4.94929	2.879288	-7.19348	0.000407
711	g9140.t1	2565	g6474.t1	K02434: gaB, PET112	7.89701243	1.054868326	-8.62274	2.615828	-6.93929	0.000517
558	g9065.t1	2355	g8585.t1	K03234: EEF2	0	1.996511676	2.07504 6	2.565361	6.891657	0.000539
712	g3334.t1	2566	g4792.t1		0	2.790411134	2.62037 5	2.511141	6.840843	0.000565
713	g3376.t1	2567	g10478.t1 1		0	2.519717879	2.38744 8	2.41189	6.748785	0.000619
714	g9.t1	2568	g3899.t1		0	4.899566565	4.13960 4	2.330919	6.674579	0.000663
692	g5169.t1	2506	g3798.t1		4.865818268	0.928859379	-3.94891	2.315037	-6.66012	0.00067
685	g6380.t1	2492	g764.t1	K05857: PLCD	5.073855922	0.2955559632	-4.51752	2.290181	-6.63754	0.000686
696	g3920.t1	2508	g3972.t1		5.062011561	0.848055404	-4.26687	2.268441	-6.61786	0.0007
715	g10569.t1 1	2569	g8038.t1		0	2.348179343	2.48172 5	2.246454	6.598008	0.000711
716	g4884.t1	2570	g5157.t1		3.493672904	7.387448493	4.16446 2	2.159094	6.519689	0.000767
717	g12587.t1 1	2571	g2937.t1		5.143110791	1.384010569	-3.67942	1.930876	-6.31914	0.000935
718	g9196.t1	2572	g6530.t1	K01937: pyrG, CTPS	2.877811039	6.539766193	3.91018 7	1.874559	6.270516	0.000984
719	g5920.t1	2573	g11008.t1 1	K02894: RP-L23e, RPL23	2.351855506	0	-2.24072	1.759813	-6.17247	0.001088
720	g5591.t1	2547	g7515.t1		5.584485038	0.894846762	-4.42228	1.658568	-6.08708	0.001189
721	g7216.t1	2574	g5885.t1		4.657263756	1.441622985	-3.3104	1.633153	-6.0658	0.001218
722	g4371.t1	2575	g2128.t1		5.510282495	0	-4.44208	1.572778	-6.01551	0.001275
698	g657.t1	2503	g9863.t1		4.4628192	1.558896118	-3.19078	1.546359	-5.99361	0.001305
723	g5419.t1	2576	g5084.t1		8.315874976	0.383504801	-6.22029	1.532513	-5.98216	0.001318
724	g5712.t1	2577	g1012.t1		5.583909958	0.874379809	-5.05512	1.414511	-5.88532	0.001468
725	g5938.t1	2578	g8896.t1		0	3.178052882	3.1153	1.380226	5.857421	0.001515
726	g2504.t1	2579	g3532.t1		0	2.743866247	2.53041 7	1.349556	5.832557	0.001563
727	g7969.t1	2580	g10252.t1 1	K03639: MOCS1, mosa	4.758242645	8.67938655	4.03496	1.313775	5.803657	0.001613

728	g1770.t1	2581	g1188.t1		6.058400928	1.675692023	-4.12482	1.299312	-5.79201	0.001627
729	g815.t1	2582	g8179.t1		7.400064361	4.320735935	-3.01739	1.245211	-5.74859	0.001712
730	g3624.t1	2583	g600.t1	K14297: NUP98, ADAR2	5.106519345	1.117898542	-4.15716	1.207594	-5.71856	0.001762
731	g3218.t1	2584	g6107.t1		4.600691335	0.295759975	-4.21399	1.185637	-5.70109	0.001799
732	g6563.t1	2585	g10099.t1		7.052996504	3.472329984	-3.5087	1.155325	-5.67703	0.001844
733	g5058.t1	2586	g8328.t1		6.170884433	0	-5.05686	1.131697	-5.65833	0.001884
734	g2063.t1	2587	g2535.t1	K01426: E3.5.1.4, amIE	6.62697264	2.303932777	-4.90902	1.127765	-5.65523	0.001886
735	g7620.t1	2588	g9046.t1		1.469790922	4.894808598	3.48707	1.017153	5.568359	0.002056
737	g8108.t1	2590	g7917.t1		5.22299962	2.496100539	-2.7244	0.995641	-5.55158	0.002086
736	g13149.t1	2589	g4276.t1		0	3.748353789	3.25162	0.996266	5.552068	0.002086
738	g15293.t1	2591	g6106.t1		2.346160706	0.097742219	-2.19296	0.994155	-5.55042	0.002087
739	g10986.t1	2592	g5652.t1	K02141: ATPeFH, ATP14	0	4.494039562	5.03806	0.963629	5.526686	0.002143
740	g2758.t1	2593	g9152.t1	K10627: RAD18	0	4.883694275	4.29983	0.927171	5.498432	0.002209
741	g4882.t1	2594	g4502.t1		6.687936705	3.543460499	-3.27253	0.888456	-5.46854	0.002228
742	g1999.t1	2595	g6250.t1		0	3.201001736	3.22737	0.878381	5.460786	0.002292
743	g3555.t1	2596	g3333.t1	K01624: FBA, fbaA	4.536933474	1.134755003	-3.43033	0.868413	-5.45312	0.002307
744	g4741.t1	2597	g2013.t1	K03237: EIF2S1	6.043892772	1.31228389	-4.40225	0.830737	-5.42421	0.002375
745	g5254.t1	2598	g2334.t1	K02137: ATPeFOO, ATP5O, ATP5	5.144250658	2.18981705	-3.00766	0.818268	-5.41466	0.002395
746	g5568.t1	2529	g7485.t1		2.950253937	7.105767696	4.12637	0.80081	5.401317	0.002438
747	g19199.t1	2599	g12080.t1	K01102: PDP	4.719048671	1.219706529	-3.83331	0.756008	-5.36718	0.002518
748	g4710.t1	2600	g6681.t1	K03457: TC.NCS1	5.545619928	1.014147489	-4.86358	0.686637	-5.31463	0.002646
749	g1003.t1	2601	g8072.t1	K03626: EGD2, NACA	9.544725129	5.108026741	-4.51544	0.681969	-5.3111	0.002652
750	g12699.t1	2602	g8909.t1		0	6.189343256	5.96832	0.664673	5.298059	0.00269
751	g3631.t1	2603	g607.t1		5.634764008	1.594206545	-4.0374	0.625713	-5.26876	0.00276
752	g10888.t1	2604	g176.t1	K00463: INDO	0	4.02637883	3.25062	0.610465	5.257326	0.002793

697	g852.t1	2502	g9454.t1	K11824: AP2A	5.513795279	2.276512626	-3.03289	0.608594	-5.25592	0.002796
753	g10211.t 1	2605	g11976.t 1		6.236601553	2.916440322	-3.19554	0.597045	-5.24728	0.002823
754	g158.t1	2606	g5219.t1		0	5.582396377	5.11116	0.592518	5.243887	0.002833
755	g6128.t1	2607	g7318.t1	K13953: adhP	0.559800663	7.127819277	5.64683 8	0.588484	5.24087	0.002836
691	g5563.t1	2493	g7478.t1		4.371792513	0	-4.207	0.547655	-5.2104	0.002938
756	g5223.t1	2608	g3707.t1	K03515: REV1	7.079279048	1.723275185	-5.46022	0.54628	-5.20937	0.00294
680	g1340.t1	2553	g523.t1		5.657989905	2.558100341	-3.77627	0.53802	-5.20322	0.002955
757	g6031.t1	2609	g11529.t 1	K01885: EARS, glx	8.997952533	1.491025779	-7.37296	0.51175	-5.18369	0.003013
758	g5074.t1	2610	g2984.t1		0	6.655679639	7.34395 2	0.499918	5.174915	0.003026
759	g6741.t1	2611	g4354.t1		2.11282087	5.448500076	4.10119 9	0.496168	5.172135	0.003035
760	g829.t1	2612	g8197.t1	K13577: SLC25A10, DIC	0	6.849405724	6.55510 4	0.494322	5.170766	0.003039
761	g7264.t1	2613	g11828.t 1		5.499599524	1.415264641	-4.13804	0.465403	-5.14936	0.003123
762	g2074.t1	2614	g2522.t1		4.591860791	7.078833392	3.29949 3	0.45963	5.145095	0.003137
763	g9395.t1	2615	g3638.t1	K06116: GPP1	2.323291749	7.447835109	4.19799 4	0.459465	5.144973	0.003137
764	g9849.t1	2616	g9778.t1		9.223686565	4.691855389	-4.09505	0.428461	-5.1221	0.003216
765	g11803.t 1	2617	g12043.t 1		2.387616958	6.765913108	4.65626 1	0.394211	5.096913	0.003318
766	g11916.t 1	2618	g661.t1		7.715759124	1.189911629	-6.35022	0.3901	-5.09389	0.003321
767	g1153.t1	2619	g5028.t1		4.692839925	0.711873688	-4.12247	0.378768	-5.08558	0.003347
768	g5373.t1	2620	g9561.t1		5.888238765	0.935705267	-4.23339	0.376965	-5.08426	0.00335
769	g7390.t1	2621	g7172.t1		7.350351967	1.129748696	-5.65043	0.372725	-5.08115	0.00336
770	g10732.t 1	2622	g4256.t1		0	2.447676888	2.51643	0.360788	5.072408	0.003395
771	g10093.t 1	2623	g9511.t1		4.296964996	7.412793324	2.89405	0.344563	5.060539	0.003447
772	g10839.t 1	2624	g9837.t1		6.8729034	0	-6.33439	0.32456	-5.04593	0.003498
773	g10191.t	2625	g11148.t		6.023102414	1.409452743	-5.2232	0.315504	-5.03933	0.00352

774	1	g3013.t1	2626	1	g8294.t1	5.470261921	0	-5.44413	0.305958	-5.03237	0.003541
775		g7841.t1	2627	1	g10495.t1	4.614472875	0.757799789	-3.27057	0.251911	-4.9931	0.003718
776	1	g21528.t1	2512	1	g10587.t1	3.911232108	0.261005346	-4.64558	0.221495	-4.97108	0.003811
777		g9138.t1	2628		g6473.t1	4.198675014	0.770128672	-3.1553	0.143776	-4.91509	0.004074
778		g4873.t1	2629		g4492.t1	5.713341579	2.816941964	-3.86408	0.10615	-4.88812	0.004228
779		g7446.t1	2630		g6892.t1	7.48417852	1.943606982	-5.03828	0.095087	-4.88021	0.004261
780		g8021.t1	2631		g8248.t1	4.309793696	6.49982563	2.31487	0.091858	4.8779	0.004272
781		g100.t1	2632		g2920.t1	0	2.543445727	2.52742	0.077045	4.867319	0.00432
782		g1180.t1	2633		g337.t1	6.10473465	0.378277281	-5.07738	0.074749	-4.86568	0.004327
783	1	g14694.t1	2634		g6409.t1	9.825681474	1.554052399	-6.86013	0.073057	-4.86447	0.004331
784		g6706.t1	2521		g4310.t1	7.446014886	3.740313179	-3.30861	0.057195	-4.85316	0.004389
785	1	g14790.t1	2635		g5147.t1	1.686007548	6.647954724	6.11427	0.049884	4.847953	0.004415
786		g8676.t1	2636	1	g10948.t1	3.991647742	0.809756341	-3.46435	0.037282	-4.83898	0.004447
787		g4402.t1	2637		g2161.t1	0	4.419507408	4.45762	0.01987	4.826605	0.004499
788		g1963.t1	2638		g6215.t1	6.923009485	1.722062181	-5.09666	0.004896	-4.81597	0.004554
789		g132.t1	2639		g5829.t1	0	8.147623562	6.45960	-0.00779	4.806976	0.004594
790	1	g11512.t1	2640		g4219.t1	6.309781587	3.849786723	-2.31991	-0.01622	-4.80101	0.004625
791	1	g10280.t1	2641	1	g10638.t1	0	6.450195037	4.96722	-0.02376	4.795666	0.00466
792		g796.t1	2642		g8160.t1	0.721237136	8.130353179	6.31502	-0.03164	4.790094	0.004696
793	1	g15000.t1	2643		g3110.t1	5.469156461	0.297925928	-5.04598	-0.03768	-4.78582	0.004716
794		g7638.t1	2644		g7605.t1	0	5.862148582	5.70793	-0.06956	4.763314	0.004863
795	1	g11518.t1	2645		g4213.t1	5.935642711	3.230236428	-2.8374	-0.10943	-4.73525	0.005047

796	g85.t1	2646	g2767.t1		5.850559685	1.199045091	-4.36726	-0.11833	-4.729	0.00509
797	g489.t1	2647	g5491.t1	K05857: PLCD	5.789975493	0.871860339	-7.01828	-0.12739	-4.72264	0.005126
798	g8243.t1	2648	g10036.t1		4.646855045	0.330447252	-5.92622	-0.1483	-4.70798	0.005219
800	g4842.t1	2650	g4453.t1	K13120: FAM32A	5.230120767	1.098104153	-4.19885	-0.16955	-4.6931	0.005312
799	g10374.t1	2649	g10541.t1	K15505: RAD5	0	2.933131491	3.29013	-0.16944	4.69318	0.005312
801	g10174.t1	2651	g8450.t1	K11557: SPC24	1.118361424	6.021652199	4.83424	-0.17145	4.691775	0.005318
803	g3427.t1	2653	g4718.t1	K12854: SNRNP200, BRR2	7.533706795	2.002833589	-5.05292	-0.19244	-4.67711	0.005407
802	g1849.t1	2652	g1896.t1	K00938: E2.7.4.2, mvak2	8.103944385	3.578287021	-4.08273	-0.18889	-4.67959	0.005407
804	g19694.t1	2654	g7947.t1	K02142: ATPeJ, ATP18	4.724478914	0.648456799	-3.72185	-0.21394	-4.66212	0.005504
805	g6500.t1	2655	g2087.t1	K11548: NUF2, CDCA1	4.167333488	2.020784202	-2.43559	-0.21784	-4.6594	0.005514
808	g11718.t1	2657	g2320.t1		6.955332876	0.580666117	-6.38818	-0.22369	-4.65532	0.005525
807	g2706.t1	2513	g8366.t1	K11649: SMARCC	5.407509356	2.809100574	-2.35658	-0.22257	-4.65611	0.005525
806	g3663.t1	2656	g656.t1	K00632: E2.3.1.16, fadA	6.107648999	4.097390482	-2.23548	-0.2214	-4.65692	0.005525
809	g4795.t1	2658	g3691.t1		2.814605061	5.263030629	2.68504	-0.23653	4.646388	0.005581
810	g9159.t1	2659	g6490.t1		12.37001214	1.906016093	-7.95994	-0.23905	-4.64464	0.005585
812	g7897.t1	2661	g8633.t1	K12191: CHMP2A	6.149239272	3.374272912	-2.55359	-0.24971	-4.63722	0.005633
811	g4381.t1	2660	g2138.t1	K14846: RPF1	4.661983349	2.229412642	-2.2735	-0.24919	-4.63759	0.005633
813	g15305.t1	2662	g10450.t1	K01915: glnA, GLUL	1.326818728	5.191947	3.21825	-0.25601	4.632846	0.005659
814	g12732.t1	2663	g5706.t1		0	5.175711473	5.28434	-0.27649	4.618638	0.005755
815	g9791.t1	2664	g893.t1		4.682251788	0.457571639	-3.67907	-0.28594	-4.61209	0.0058
816	g14760.t1	2665	g9241.t1		2.816496891	5.901553526	3.15538	-0.2866	4.611627	0.0058
817	g5187.t1	2666	g3776.t1	K01277: E3.4.14.4, DPP3	5.729836476	1.938854906	-4.27181	-0.29258	-4.60749	0.005825
818	g7634.t1	2667	g7610.t1	K10773: NTH	6.081778745	3.751441415	-2.52835	-0.29951	-4.60269	0.005855
819	g13477.t1	2668	g8720.t1	K10295: FBXO9	5.178686522	0.847940328	-3.32137	-0.32592	-4.58442	0.006017
820	g12592.t1	2669	g2931.t1		6.934534554	2.5557465	-4.96282	-0.34887	-4.56858	0.006156

821	g10987.t 1	2670	g5653.t1		0	5.505094032	4.42075 8	-0.36167	4.559767	0.006238
822	g12590.t 1	2671	g2934.t1		6.223414116	2.080339763	-3.66131	-0.36679	-4.55624	0.006268
823	g10222.t 1	2672	g11207.t 1		4.643453596	0.715469044	-4.2781	-0.38183	-4.54589	0.006357
825	g3983.t1	2674	g7058.t1	K01613: psd, PISO	5.451665752	1.425755818	-3.75003	-0.3861	-4.54296	0.006362
824	g11510.t 1	2673	g4221.t1		4.286646074	0.732571213	-3.30399	-0.38598	-4.54303	0.006362
826	g9393.t1	2675	g3641.t1		8.751164208	1.858084528	-5.0271	-0.39476	-4.537	0.006412
827	g9881.t1	2676	g11623.t 1		0	5.108233831	5.23122	-0.39838	4.534514	0.006433
828	g13221.t 1	2677	g672.t1		0	2.220629054	2.40642	-0.40728	4.528399	0.00648
829	g3561.t1	2678	g3326.t1		4.733400818	0.999936795	-4.02216	-0.42399	-4.51694	0.006569
830	g8670.t1	2679	g10955.t 1		4.749528223	0.956968472	-3.3446	-0.42698	-4.51489	0.006581
831	g708.t1	2680	g9946.t1		0.954625619	7.666771535	4.88968	-0.44251	4.504248	0.006673
832	g11009.t 1	2681	g5663.t1	K11121: SIR2	0	4.462106061	3.36231	-0.44719	4.501046	0.006692
833	g7419.t1	2682	g7204.t1	K13754: SLC24A6, NCKX6	6.27610662	0.798417819	-5.95745	-0.45635	-4.49478	0.006748
835	g3224.t1	2684	g6091.t1		3.344134063	0.745638707	-2.59361	-0.48058	-4.47822	0.006877
834	g12947.t 1	2683	g9800.t1		0	2.039008683	2.44925	-0.48038	4.478357	0.006877
836	g6094.t1	2685	g7354.t1		6.09853587	1.272304701	-4.60015	-0.49143	-4.47081	0.006946
837	g7427.t1	2686	g7212.t1	K01549: TIM11, ATP21	5.301910749	3.138905614	-2.18675	-0.49273	-4.46993	0.006946
838	g6135.t1	2687	g7308.t1	K03844: ALG11	4.695297001	0	-3.96218	-0.49789	-4.46641	0.006961
839	g5057.t1	2688	g8325.t1	K00326: E1.6.2.2	5.161405198	0.441358118	-4.38384	-0.50196	-4.46364	0.006974
840	g3875.t1	2689	g4019.t1		1.368553327	4.07697119	2.53701	-0.50227	4.463427	0.006974
841	g21658.t 1	2690	g4834.t1		6.709472946	3.744824974	-2.67465	-0.52217	-4.44987	0.007097
842	g7438.t1	2691	g7223.t1		4.971359373	0.658532988	-3.53015	-0.52453	-4.44827	0.007102
843	g7605.t1	2692	g7631.t1	K06942: K06942	4.937065903	0	-4.46853	-0.54372	-4.43522	0.007224
844	g6721.t1	2693	g4326.t1		1.642040135	5.483246572	3.82060	-0.54429	4.434824	0.007224

845	g7857.t1	2694	g10514.t1		0	4.218558155	3.36866	-0.54552	4.433987	0.007229
846	g3614.t1	2695	g588.t1	K12604: CNOT1, NOT1	6.72026689	0.531333536	-5.80897	-0.5699	-4.41744	0.007352
847	g11968.t1	2696	g7463.t1		0	5.125810617	4.20058	-0.57194	4.416052	0.007359
848	g6429.t1	2697	g5353.t1		5.059361503	1.508836141	-4.45308	-0.57862	-4.41153	0.007396
849	g20508.t1	2698	g3950.t1		0	4.196864651	4.10862	-0.58006	4.410547	0.007402
850	g7165.t1	2699	g555.t1		3.895318144	0	-4.14265	-0.58148	-4.40958	0.007408
851	g4535.t1	2700	g4065.t1		8.36766264	2.386025864	-6.90475	-0.60002	-4.39703	0.007531
852	g20378.t1	2701	g3507.t1		0	7.391829386	7.34137	-0.61198	4.388939	0.007608
853	g8160.t1	2702	g11151.t1		7.072684453	0.280401415	-6.23052	-0.6128	-4.38838	0.007609
854	g6555.t1	2703	g10091.t1	K00286: E1.5.1.2, proC	5.981191238	0	-5.84296	-0.61807	-4.38482	0.007637
855	g5572.t1	2704	g7489.t1		6.099888984	10.89359383	4.48380	-0.62462	4.380391	0.00768
856	g2329.t1	2543	g9194.t1		7.114801788	3.574070188	-2.75777	-0.63106	-4.37604	0.007723
857	g1250.t1	2705	g434.t1		5.533904052	3.185653977	-2.63104	-0.63216	-4.3753	0.007727
858	g11133.t1	2706	g753.t1	K06972: K06972	4.000597283	0	-3.93177	-0.63567	-4.37293	0.007745
859	g490.t1	2536	g5492.t1	K01230: MAN1	4.455711732	0.821736911	-3.64067	-0.66191	-4.35523	0.007924
860	g7575.t1	2707	g7666.t1	K11272: MRC1	7.443866007	1.513388401	-5.92967	-0.67062	-4.34936	0.007991
861	g6402.t1	2708	g5392.t1		0	5.288562871	5.16440	-0.67364	4.347332	0.008003
519	g31.t1	2315	g2840.t1	K02437: govH, GCSH	7.667805418	2.153109228	-5.17926	-0.68969	-4.33653	0.008113
862	g11374.t1	2709	g5061.t1	K16803: CKAP5, XMAP215	0	2.924286464	3.49428	-0.6901	4.33625	0.008113
863	g6116.t1	2710	g7333.t1	K02258: COX11	0	4.831002225	5.17011	-0.7042	4.326775	0.008209
864	g7600.t1	2711	g7636.t1	K17768: TOM70	5.478745927	0.350736603	-4.55951	-0.71336	-4.32062	0.008262
865	g7609.t1	2712	g7627.t1		6.110778129	0.897423937	-5.14471	-0.71421	-4.32005	0.008264
866	g670.t1	2713	g9895.t1		5.389860972	3.02046933	-2.23527	-0.72773	-4.31098	0.008362
867	g3288.t1	2714	g8948.t1		0	4.148359441	4.70077	-0.72891	4.310188	0.008367
868	g1739.t1	2715	g9739.t1	K01918: panC	1.723333708	7.241823447	4.71758	-0.73179	4.308255	0.008388

869	g2853.t1	2716	g9055.t1		3.661150117	0.362821722	-3.21259	-0.73646	-4.30512	0.008418
870	g11104.t1	2717	g718.t1		5.331556226	1.94750928	-2.81205	-0.74858	-4.297	0.008489
871	g2178.t1	2718	g11917.t1		4.412098474	0	-3.47396	-0.75224	-4.29455	0.00851
872	g4449.t1	2719	g6805.t1		7.334855344	0.627760328	-5.29907	-0.7639	-4.28674	0.008589
873	g5221.t1	2720	g3709.t1	K01240: URH1	4.395333747	0.951987955	-3.0524	-0.76717	-4.28455	0.008614
874	g2815.t1	2721	g9114.t1	K01193: E3.2.1.26, sacA	6.290191463	0.734008502	-6.22448	-0.77307	-4.28061	0.008657
875	g2269.t1	2722	g10685.t1		2.551428828	0.296780765	-2.07634	-0.77841	-4.27704	0.008695
876	g2163.t1	2723	g11902.t1		5.298538589	2.694353324	-2.70682	-0.79002	-4.26927	0.008782
877	g3515.t1	2724	g2207.t1		3.347586286	6.450463175	3.82448	-0.79922	4.263133	0.008844
878	g6074.t1	2725	g3347.t1		6.324042809	2.140747407	-6.13606	-0.81393	-4.25332	0.008927
879	g11929.t1	2726	g2071.t1		6.098181798	2.173954682	-4.47826	-0.81655	-4.25157	0.00894
880	g6915.t1	2727	g1291.t1	K00505: TYR	6.540932521	1.6914174	-4.77307	-0.81897	-4.24996	0.008951
881	g1756.t1	2728	g1207.t1	K15201: GTP3C3, TFC4	6.731005978	2.35645327	-4.64979	-0.83531	-4.23907	0.009074
882	g6770.t1	2729	g4386.t1		5.731686881	3.30963121	-2.17414	-0.83911	-4.23654	0.009106
883	g10376.t1	2730	g10544.t1	K02990: RP-56, MRPS6, rpsF	0	2.158000596	2.42587	-0.84519	4.232488	0.00916
884	g9812.t1	2731	g10826.t1	K01899: LSC1	5.913334166	2.531678954	-3.1414	-0.84671	-4.23148	0.009169
885	g9618.t1	2732	g7244.t1		0	2.194869885	2.40267	-0.84832	4.230406	0.009172
886	g2442.t1	2733	g6711.t1	K10998: CSM3, SWI3	6.56163386	2.193043465	-3.49995	-0.85623	-4.22514	0.009214
887	g17691.t1	2734	g559.t1		5.586773168	0.314001411	-5.55798	-0.86027	-4.22245	0.009226
889	g10183.t1	2736	g11138.t1	K17878: NNT1	4.422235435	0.712887218	-4.88085	-0.86671	-4.21817	0.009265
888	g7714.t1	2735	g3081.t1	K01070: frmB, ESD, fghA	4.789610997	0.611123391	-3.75978	-0.86634	-4.21842	0.009265
890	g2359.t1	2737	g9253.t1		8.893941672	1.141019105	-7.87059	-0.88299	-4.20736	0.009375
891	g4991.t1	2738	g8961.t1	K15901: CG1121, TPRKB	5.458778357	1.709043647	-3.91338	-0.8871	-4.20463	0.009395
892	g106.t1	2739	g2927.t1		4.560793659	1.101158731	-3.40776	-0.88917	-4.20326	0.009404
893	g7472.t1	2740	g6864.t1	K10839: RAD23, HR23	6.506527453	2.213804236	-4.55459	-0.90647	-4.19178	0.00955
894	g4849.t1	2741	g4462.t1		6.018049911	1.275657111	-4.20948	-0.91395	-4.18682	0.009596

895	g4668.t1	2742	g10566.t1	K01312: PRSS	9.271875621	0.352165126	-7.40328	-0.918	-4.18414	0.009626
896	g9585.t1	2743	g6636.t1	K06675: SMC4	0	2.683347982	2.35442	-0.92977	4.176344	0.00973
897	g2963.t1	2744	g5934.t1		4.375328682	0.740211298	-2.9098	-0.93127	-4.17535	0.00974
898	g7232.t1	2745	g10757.t1	K09313: CUTL	8.116353121	2.395376228	-4.44254	-0.9342	-4.17341	0.009764
899	g19769.t1	2746	g11692.t1		4.972241584	0.686771667	-4.62795	-0.94048	-4.16926	0.009812
900	g7022.t1	2747	g6357.t1		0	4.469180465	6.91987	-0.94401	4.166923	0.009837
901	g9259.t1	2748	g10437.t1		6.69953931	2.882217215	-4.44428	-0.94674	-4.16512	0.009859
902	g12328.t1	2749	g7434.t1	K01710: E4.2.1.46, rfb8, rffg	3.685729613	0	-2.81719	-0.9494	-4.16336	0.009881
903	g2849.t1	2750	g9051.t1		7.214498977	3.486426657	-4.11858	-0.95426	-4.16014	0.009921
904	g17779.t1	2751	g662.t1		4.282054458	1.24041635	-3.15204	-0.95549	-4.15933	0.009928
905	g8550.t1	2752	g5428.t1	K08838: STK24_25_MST4	5.000505255	0.925832893	-3.77285	-0.9583	-4.15747	0.009945
906	g10940.t1	2753	g1025.t1	K00100: E1.1.1.-	4.956194307	1.938081563	-3.28418	-0.95965	-4.15658	0.009953
907	g11117.t1	2754	g735.t1		5.648961974	0	-5.52502	-0.96997	-4.14977	0.010045
562	g1904.t1	2359	g5010.t1	K16261: YAT	2.226821689	8.926092537	4.67377	-0.97066	4.149315	0.010046
908	g3804.t1	2755	g8748.t1		5.793251762	1.081386438	-4.42774	-0.97346	-4.14747	0.01007
909	g3244.t1	2756	g8218.t1	K02838: ffr, MRRF, RRF	0	4.33702816	4.27001	-0.97624	4.14563	0.010094
910	g11369.t1	2757	g10756.t1		5.176727673	2.524623108	-3.0042	-0.98484	-4.13995	0.010182
611	g7102.t1	2410	g5569.t1		4.138124976	2.196818636	-2.56782	-0.98876	-4.13737	0.010206
911	g677.t1	2758	g9875.t1	K07140: K07140	5.281680888	0.559439018	-3.98216	-0.99896	-4.13064	0.010292
679	g4287.t1	2759	g1939.t1	K00275: pdxH, PNPO	4.95193285	2.335225171	-2.22283	-1.00489	-4.12674	0.010332
912	g7511.t1	2760	g10316.t1	K08286: E2.7.11.-	6.009945831	1.511594622	-3.89684	-1.00716	-4.12524	0.010351
913	g1830.t1	2761	g1716.t1		7.072977042	1.544496353	-5.26083	-1.01212	-4.12197	0.01038
914	g6552.t1	2762	g10088.t1	K14572: MDN1, REA1	4.349948417	6.391579804	2.42347	-1.01251	4.121713	0.01038

915	g74.t1	2763	g917.t1	K00480: E1.14.13.1	5.955742918	1.714884516	-3.78652	-1.01346	-4.12109	0.010382
916	g5429.t1	2764	g3125.t1		4.987582363	1.729090589	-4.13011	-1.0233	-4.11461	0.010466
917	g8498.t1	2765	g3370.t1		5.820660636	0.413151614	-5.47293	-1.02797	-4.11154	0.010506
918	g7844.t1	2766	g10497.t1		5.848243945	1.578952778	-4.16193	-1.03098	-4.10956	0.010524
919	g5407.t1	2767	g8613.t1		0	5.534733082	4.71133	-1.03102	4.109529	0.010524
921	g4889.t1	2769	g4523.t1	K14209: SLC36A, PAT	5.82364098	0.611123391	-5.50761	-1.03508	-4.10686	0.010547
920	g2118.t1	2768	g2464.t1	K01560: E3.8.1.2	3.940755827	0.663970885	-2.81812	-1.03464	-4.10715	0.010547
922	g4577.t1	2770	g4105.t1		2.560658097	5.985251291	3.58926	-1.03779	4.105077	0.010566
923	g6091.t1	2771	g7357.t1	K12193: VPS24, CHMP3	2.859023838	6.502695672	3.09191	-1.04093	4.103011	0.010586
924	g4043.t1	2772	g3220.t1		5.096464748	1.443935828	-4.5113	-1.05361	-4.09468	0.010703
925	g10590.t1	2773	g7033.t1	K01190: lacZ	0	2.243268623	3.09529	-1.06313	4.088427	0.010784
926	g11987.t1	2774	g2441.t1	K15172: SUT5H, SPT5	6.055881291	2.362058349	-3.85574	-1.06897	-4.0846	0.010834
927	g7118.t1	2775	g5583.t1	K06670: SCC1, MCD1, RAD21	7.656991383	0.390883076	-7.66832	-1.07595	-4.08002	0.010905
928	g9841.t1	2776	g9760.t1		8.545788709	2.867657374	-4.92548	-1.082	-4.07604	0.010958
929	g10869.t1	2777	g134.t1		0	4.541052906	5.75511	-1.09914	4.06481	0.011149
930	g8799.t1	2778	g9975.t1		4.851135285	2.848977141	-2.03413	-1.10105	-4.06356	0.011158
931	g3513.t1	2779	g2205.t1	K12041: SLC9A6_7, NHE6_7	4.628300692	7.602958834	4.62685	-1.10473	4.061149	0.011189
932	g4464.t1	2780	g6823.t1	K00111: glpA, glpD	4.913318358	1.479604123	-3.34305	-1.1065	-4.05999	0.011196
933	g912.t1	2781	g9350.t1		6.681560463	1.806751763	-4.31686	-1.11196	-4.05142	0.011342
934	g6047.t1	2482	g264.t1		5.833182512	0.677369437	-5.13698	-1.12643	-4.04694	0.011405
935	g8273.t1	2782	g9995.t1		5.609052156	1.060347821	-4.34904	-1.14015	-4.03798	0.011561
936	g8132.t1	2783	g7944.t1	K14526: POP7, RPP2	5.431104442	0.674479047	-4.05357	-1.14688	-4.03357	0.011602
937	g8077.t1	2540	g7846.t1		6.924579829	3.179764724	-3.71311	-1.15782	-4.02643	0.011726
938	g10164.t1	2784	g6116.t1		6.523454108	2.07702255	-4.71124	-1.17646	-4.01427	0.011932
940	g8187.t1	2785	g7995.t1	K03325: TC.ACR3	8.04995065	0.87529095	-5.79877	-1.18683	-4.0075	0.012033
939	g4598.t1	2528	g6014.t1		3.985835911	8.056156653	3.69429	-1.18652	4.007708	0.012033

941	g10685.t 1	2786	g8531.t1		4.755054229	0.597731661	-5.22216	-1.18923	-4.00594	0.012049
942	g4368.t1	2787	g3790.t1		5.47962036	0.600445772	-5.6468	-1.19165	-4.00436	0.012073
944	g5574.t1	2789	g7491.t1	K11370: AHC1	7.953609684	0	-8.04647	-1.19703	-4.00086	0.012107
943	g10154.t 1	2788	g8466.t1	K03661: AIPeV08, ATP6F	2.459230154	8.648411182	5.52473 8	-1.19676	4.001038	0.012107
945	g6618.t1	2790	g11273.t 1	K14333: DH8D	8.223627165	4.489647578	-3.74758	-1.20103	-3.99825	0.012152
946	g4717.t1	2791	g2039.t1		6.556761484	0.832520653	-5.79326	-1.2067	-3.99456	0.012204
947	g3409.t1	2792	g6220.t1		6.131735085	2.932298929	-4.4842	-1.21334	-3.99024	0.012261
948	g11995.t 1	2793	g2451.t1		4.464464914	0.151188629	-4.14283	-1.21373	-3.98998	0.012261
949	g2327.t1	2794	g9192.t1		4.697725891	3.031852784	-2.51819	-1.22384	-3.98341	0.01238
950	g4993.t1	2795	g8964.t1		5.277688941	1.187953513	-4.53745	-1.225	-3.98265	0.012388
951	g9979.t1	2796	g9685.t1	K15148: MED7	0	5.949359522	6.52054 8	-1.22659	3.981618	0.012402
952	g6193.t1	2797	g11718.t 1		6.836216759	0.250673031	-7.32329	-1.23434	-3.97658	0.012461
953	g4069.t1	2798	g3263.t1		4.437917777	1.954717425	-2.12779	-1.24126	-3.97208	0.012532
954	g10250.t 1	2799	g3606.t1		12.0823581	5.349202675	-5.14517	-1.24396	-3.97033	0.012561
955	g5983.t1	2800	g11682.t 1		5.452835216	1.46241328	-3.94481	-1.24535	-3.96942	0.012564
957	g11115.t 1	2802	g733.t1		6.202864972	1.546483629	-4.74294	-1.24702	-3.96834	0.012572
956	g3228.t1	2801	g6074.t1		4.204057944	1.75745979	-2.38792	-1.24691	-3.96841	0.012572
958	g9407.t1	2803	g3620.t1		4.931825845	2.242713995	-2.80653	-1.2614	-3.959	0.012715
959	g1828.t1	2804	g1714.t1	K13535: CLD1	4.463119082	0.759418996	-4.44127	-1.27477	-3.95032	0.012862
960	g3944.t1	2805	g3947.t1		5.535649157	0	-5.19232	-1.288	-3.94174	0.012985
961	g7851.t1	2806	g10505.t 1		5.044625434	2.009449375	-2.88495	-1.28967	-3.94066	0.013001
962	g18788.t 1	2807	g387.t1		6.532520126	0	-5.41093	-1.29136	-3.93956	0.013009
963	g9384.t1	2808	g3650.t1	K02210: MCM7, CDC47	6.91078027	1.571021615	-4.64794	-1.29234	-3.93894	0.013015
964	g1127.t1	2809	g226.t1	K13210: FUBP	7.124489061	2.229618353	-5.13781	-1.29958	-3.93424	0.013094
965	g96.t1	2810	g2917.t1		0	5.492331766	4.17189 5	-1.30404	3.931351	0.013134

966	g6648.t1	2811	g10192.t1	K12868: SYF2	0	3.516802163	3.25613 ₆	-1.30608	3.930031	0.013156
967	g1350.t1	2812	g7381.t1		0	3.889064314	4.85063 ₄	-1.30889	3.928212	0.013188
968	g13893.t1	2813	g6198.t1	K07034: K07034	6.848687422	0	-6.40524	-1.31197	-3.92621	0.013224
969	g4507.t1	2814	g10812.t1		3.840346233	0.671708995	-3.61124	-1.31998	-3.92103	0.013315
970	g3241.t1	2815	g8215.t1		0	5.467296488	6.06006 ₈	-1.32773	3.916022	0.013403
971	g11754.t1	2816	g9856.t1	K01779: E5.1.1.13	5.221579117	2.774475816	-2.73909	-1.33008	-3.9145	0.013416
972	g1351.t1	2817	g6327.t1		0	1.545461152	2.30928 ₈	-1.34311	3.906078	0.013561
973	g2037.t1	2818	g2568.t1	K12659: ARG56	0	2.389962015	2.94391 ₄	-1.34345	3.905856	0.013561
974	g1683.t1	2819	g4660.t1	K10625: UBR1	3.398274676	0	-4.674	-1.35076	-3.90114	0.013653
975	g12749.t1	2820	g12137.t1		0	4.230324352	4.82623 ₇	-1.35244	3.900048	0.013662
976	g9482.t1	2821	g5768.t1		6.71765746	1.451437878	-4.59504	-1.36048	-3.89485	0.013771
977	g11380.t1	2822	g5068.t1		0	7.45098535	7.48302 ₆	-1.3621	3.893807	0.013774
978	g6127.t1	2823	g7319.t1	K07213: ATOX1, ATX1, copZ	11.50816411	4.935645484	-6.72817	-1.37221	-3.88728	0.013876
979	g270.t1	2824	g7700.t1		6.248619031	2.885761626	-3.92892	-1.37418	-3.88601	0.013881
980	g6423.t1	2825	g5361.t1		3.403273853	6.221604639	2.69508 ₉	-1.38022	3.882118	0.013943
981	g10729.t1	2826	g2908.t1	K03448: FEN2, LIZ1	0	3.964745867	3.30321 ₃	-1.38528	3.878855	0.014
982	g3774.t1	2827	g6851.t1		0	3.457188398	2.66416 ₈	-1.38842	3.876826	0.01404
983	g8680.t1	2828	g10944.t1	K13621: BTA1	0	5.217325652	5.06517 ₉	-1.39706	3.871256	0.014155
985	g11533.t1	2830	g4194.t1	K00928: lvsC	8.670529213	3.613657545	-5.20151	-1.40566	-3.86571	0.014246
984	g2060.t1	2829	g2537.t1		4.647437267	0	-3.66136	-1.40528	-3.86596	0.014246
987	g6588.t1	2832	g10117.t1		5.93851127	1.623174665	-4.60564	-1.40762	-3.86446	0.014246
986	g9187.t1	2831	g6519.t1		0.369867578	6.089917916	7.04998 ₈	-1.40678	3.864993	0.014246

988	g2854.t1	2833	g4992.t1		3.667696129	8.241283975	5.52305 ₈	-1.40977	3.863072	0.014268
989	g173.t1	2834	g5800.t1	K07119: K07119	9.370340141	4.321377749	-3.96851	-1.41225	-3.86147	0.014299
990	g10561.t1	2342	g1546.t1		0	4.450650367	6.04405 ₆	-1.42629	3.852432	0.014477
991	g5941.t1	2835	g2881.t1		0	2.254791406	2.03821 ₁	-1.4329	3.848179	0.01457
992	g2978.t1	2836	g8309.t1		0	10.62344924	7.90147 ₂	-1.43469	3.847032	0.014582
993	g1958.t1	2837	g6209.t1		9.099456694	1.119311238	-6.95438	-1.43536	-3.8466	0.014585
994	g12003.t1	2838	g10167.t1		4.021343839	0.753679573	-3.29178	-1.44029	-3.84343	0.014654
995	g18673.t1	2839	g8118.t1		1.798228538	5.146898574	3.43054 ₁	-1.44724	3.838958	0.014756
996	g11700.t1	2841	g6614.t1	K03860: PIGQ, GP1	4.969629765	0.352559564	-4.46723	-1.45227	-3.83573	0.014818
997	g5957.t1	2842	g6229.t1	K01056: PTH1, pth, spoVC	0	1.976704664	2.01366	-1.45267	3.835472	0.014818
998	g21700.t1	2840	g5543.t1		3.167921414	5.319048056	2.74517	-1.45215	3.835802	0.014818
999	g8304.t1	2843	g5092.t1	K10253: K10253	4.621044993	0.255280379	-3.70757	-1.4678	-3.82575	0.015036
1000	g697.t1	2845	g9928.t1	K03941: NDUF58	5.799554424	1.181054579	-4.15809	-1.4692	-3.82485	0.015042
1001	g10287.t1	2844	g36.t1	K15444: TRM9	0	5.874305957	5.78380 ₃	-1.46917	3.824872	0.015042
1002	g2303.t1	2846	g10723.t1	K07441: ALG14	5.074009843	1.567191477	-3.7165	-1.47258	-3.82268	0.015079
1003	g6384.t1	2847	g759.t1		6.12726441	3.083653978	-2.87756	-1.48007	-3.81787	0.015176
1004	g7586.t1	2848	g7651.t1		5.043611275	1.963825039	-3.6841	-1.49291	-3.80963	0.015336
1005	g8534.t1	2849	g6285.t1		0	6.247010754	5.02051 ₉	-1.52096	3.791656	0.015745
1006	g5408.t1	2850	g8612.t1	K00276: AOC3, AOC2, tynA	0	8.151281431	5.76651	-1.52222	3.790847	0.015749
1007	g8194.t1	2851	g8514.t1		6.303747883	2.955946512	-2.77841	-1.52803	-3.78712	0.015822
1008	g13118.t1	2852	g7773.t1		0	2.046350551	2.42984 ₄	-1.5376	3.781003	0.01595
1009	g9153.t1	2853	g6485.t1	K18716: NUP42, RIP1	6.170706947	3.061140417	-4.53758	-1.53902	-3.78009	0.015957
1010	g6545.t1	2854	g10082.t1	K03885: ndh	0	3.860530568	3.48447	-1.54576	3.775781	0.016064

1010	g7749.t1	2855	g7099.t1	K01512: acyP	1.405819898	5.724724114	3.99267 5	-1.56158	3.765662	0.01626
1011	g19631.t 1	2856	g6634.t1		2.571565788	0.506732919	-2.42296	-1.56584	-3.76294	0.016307
1012	g522.t1	2857	g889.t1		10.81615793	0	-8.03958	-1.5726	-3.75861	0.016414
1013	g3484.t1	2858	g2151.t1		0	3.773241919	4.60370 7	-1.57385	3.757817	0.016422
1014	g12598.t 1	2859	g12.t1		5.489807798	2.727386827	-2.67853	-1.57834	-3.75495	0.016483
1016	g2711.t1	2861	g8361.t1	K07195: EXOC7, EXO70	4.061048103	0.82017382	-4.30659	-1.58513	-3.75061	0.016586
1015	g579.t1	2860	g3880.t1	K14826: FPR3_4	4.281193383	0.923209684	-3.22546	-1.58489	-3.75076	0.016586
1017	g5304.t1	2862	g2266.t1		1.064282379	6.276337463	4.13242 1	-1.58843	3.748508	0.01663
1018	g15818.t 1	2863	g5620.t1		5.095758915	1.04393275	-3.79971	-1.60492	-3.73798	0.016879
1019	g11541.t 1	2864	g4185.t1	K15710: SHPRH	9.337717858	3.868672254	-4.98764	-1.60709	-3.73659	0.016905
1020	g5073.t1	2865	g8342.t1	K08008: NOX, GP91	0	3.029525217	4.77062 2	-1.60735	3.73643	0.016905
1022	g6955.t1	2867	g6434.t1	K14860: TMA16	5.89989351	1.267905318	-6.51374	-1.61151	-3.73378	0.016916
1021	g6610.t1	2866	g10146.t 1		9.37786699	5.898480598	-4.99071	-1.61123	-3.73396	0.016916
1023	g11689.t 1	2868	g10851.t 1	K10405: KIFC1	3.582191481	0.519463263	-3.48082	-1.62299	-3.72646	0.017089
1024	g4428.t1	2869	g6761.t1		7.515504705	2.722287062	-5.41187	-1.62797	-3.72328	0.017144
1025	g3928.t1	2870	g3964.t1		7.606070252	2.558264062	-4.77608	-1.64316	-3.7136	0.017342
1028	g4373.t1	2873	g2130.t1	K13501: TRP1	5.255678294	0.925732567	-4.57859	-1.64785	-3.71061	0.017346
1027	g10552.t 1	2872	g6698.t1		0	2.63960419	2.31192	-1.64604	3.711768	0.017346
1026	g4264.t1	2871	g1718.t1		0	6.178156431	4.99837 4	-1.64578	3.711931	0.017346
1029	g7551.t1	2874	g7255.t1	K14640: SLC20A, PIT	2.536552173	0	-2.40333	-1.65666	-3.705	0.017474
1030	g73.t1	2875	g914.t1		4.346084349	0.493988199	-4.09124	-1.66098	-3.70226	0.017537
1031	g10225.t 1	2876	g11203.t 1		9.413047495	0.613538354	-6.24471	-1.66287	-3.70106	0.017554
1032	g5522.t1	2877	g1649.t1	K11699: RDR, RDRP	5.864561275	1.938062923	-3.04363	-1.66588	-3.69914	0.017592
1033	g7042.t1	2878	g6333.t1		4.730082423	1.654400295	-2.98841	-1.67296	-3.69463	0.017699

1034	g4256.t1	2879	g1726.t1	K11254: H4	5.392555643	3.344095815	-2.53578	-1.68387	-3.68769	0.017848
1036	g1108.t1	2881	g4055.t1	K11131: DKC1, NOLA4, CBF5	4.027072029	1.511031928	-2.40023	-1.68571	-3.68653	0.017848
1035	g8681.t1	2880	g10943.t1	K00237: SDHD, SDH4	0	8.70058704	7.01727	-1.68454	3.687266	0.017848
1037	g11120.t1	2520	g739.t1	K11309: RTT109, KAT11	5.304552729	8.043114244	3.98187	-1.68842	3.684801	0.017891
1038	g10725.t1	2882	g4263.t1	K01495: GCH1, foIE	7.095909192	1.607176292	-5.94728	-1.69053	-3.68346	0.017922
1039	g9660.t1	2883	g4874.t1		0.457027413	5.574517372	4.43676	-1.69563	3.680219	0.018002
1040	g8820.t1	2884	g3030.t1		5.372767428	0.370292524	-4.05667	-1.6974	-3.67909	0.018007
1041	g4065.t1	2885	g3253.t1	K03362: FBXW1_11, BTRC, beta-TRCP	3.768457818	1.950585648	-2.47011	-1.69787	-3.67879	0.018007
1042	g5448.t1	2886	g3163.t1		5.226224828	3.242059589	-2.42483	-1.70473	-3.67444	0.018122
1043	g7588.t1	2887	g7649.t1		6.811316171	1.76280266	-3.78597	-1.7088	-3.67185	0.018192
1044	g3582.t1	2888	g5074.t1	K00293: LV59	3.263233452	1.316734534	-2.09676	-1.71032	-3.67089	0.018202
1045	g6422.t1	2889	g5364.t1		2.147147382	5.164303702	2.86171	-1.71391	3.668603	0.018254
483	g10693.t1	2485	g8538.t1		5.662368091	3.168076577	-4.05295	-1.71839	-3.66576	0.018333
1046	g6032.t1	2890	g11214.t1		8.820793561	3.54374382	-7.9404	-1.72085	-3.6642	0.018372
1047	g6561.t1	2891	g10097.t1		5.654687421	2.820296417	-2.65197	-1.7243	-3.66201	0.018411
1048	g2191.t1	2892	g11582.t1	K03352: APC5	4.67408688	1.782772866	-3.29686	-1.72886	-3.65912	0.018482
1049	g8669.t1	2893	g10956.t1		4.818547725	2.715853793	-3.19505	-1.73268	-3.65669	0.018539
1050	g5585.t1	2894	g7506.t1	K14300: NUP133	5.450216932	2.124950228	-3.36335	-1.73378	-3.656	0.018551
1051	g6577.t1	2895	g2327.t1		8.791267353	3.370950467	-4.38699	-1.73587	-3.65467	0.018573
1052	g4912.t1	2896	g4547.t1		0	4.635965828	4.67610	-1.73742	3.653682	0.018585
1053	g5600.t1	2897	g7522.t1	K17787: AIMS	0	3.93663278	3.90738	-1.74421	3.649379	0.018705
1054	g59.t1	2898	g2750.t1	K09529: DNAJC9	0	5.496293536	5.67719	-1.75422	3.643028	0.018876
1055	g2459.t1	2899	g6731.t1		2.631378842	1.157983737	-2.10785	-1.75717	-3.64116	0.018906

1056	g3841.t1	2900	g2574.t1		5.178143897	2.175433875	-2.89829	-1.7677	-3.63449	0.019072
1058	g10928.t1	2902	g11230.t1	K09291: TPR	2.438636081	5.135322312	2.16702	-1.76965	3.633253	0.019092
1057	g4517.t1	2901	g10822.t1		0	5.512328424	5.55466	-1.7695	3.633348	0.019092
1059	g5642.t1	2903	g9240.t1		10.22312916	5.571257573	-3.6137	-1.77777	-3.62811	0.01922
1060	g5649.t1	2904	g1103.t1		4.544636216	0.801147961	-4.17727	-1.77847	-3.62766	0.019225
1061	g11163.t1	2905	g4845.t1	K00838: ARO8	0.832183706	5.305901271	4.23491	-1.78279	3.624925	0.019305
1062	g5464.t1	2906	g8437.t1	K01487: E3.5.4.3, guaD	4.270772945	0.22548607	-4.11742	-1.79064	-3.61996	0.019439
1063	g6448.t1	2907	g5337.t1		0.704996832	4.000286115	4.30490	-1.79379	3.617966	0.019484
1064	g546.t1	2908	g5611.t1		5.264731099	1.369172577	-3.2191	-1.79682	-3.61605	0.019538
1065	g970.t1	2909	g8041.t1		5.740601251	1.557405801	-3.67053	-1.80007	-3.61399	0.019576
1066	g196.t1	2910	g5304.t1		4.777372465	1.654308781	-2.76658	-1.80086	-3.61349	0.019583
1067	g1283.t1	2911	g473.t1		0	3.842656586	6.80229	-1.80742	3.609337	0.019702
1068	g12044.t1	2912	g803.t1		5.498118982	3.142019176	-2.65907	-1.80959	-3.60797	0.019728
1069	g9074.t1	2913	g8565.t1		0	5.223284374	5.13370	-1.81049	3.607396	0.019737
1070	g10056.t1	2914	g2782.t1	K05351: E1.1.1.1.9	7.25059785	2.52330656	-4.70108	-1.82053	-3.60105	0.019899
1071	g12237.t1	2915	g11133.t1	K17878: NNT1	4.149357354	1.472587157	-3.10449	-1.82085	-3.60084	0.019899
1072	g4465.t1	2916	g6824.t1		5.086524971	0.645587044	-4.07666	-1.82154	-3.60041	0.019901
1073	g1040.t1	2917	g8111.t1		0	5.890637103	5.87077	-1.8259	3.597655	0.019975
1074	g8432.t1	2918	g2491.t1		0	5.00001954	4.19031	-1.82818	3.596214	0.020014
1075	g9956.t1	2919	g11404.t1		0	6.541463318	5.35561	-1.83034	3.594846	0.02005
1077	g4593.t1	2921	g6010.t1		6.800127858	3.549959281	-2.93876	-1.83506	-3.59186	0.020132
1076	g449.t1	2920	g8027.t1		2.548177204	6.213381276	3.47853	-1.83504	3.591878	0.020132
1078	g15695.t1	2922	g10590.t1		0	7.173454513	6.18512	-1.83708	3.590587	0.020145
1079	g7238.t1	2923	g10763.t1		6.636516842	0	-4.81827	-1.84088	-3.58819	0.020217

1080	g2270.t1	2924	1	K01551: arsA, ASNA1	1.338776738	5.795884869	4.02434 2	-1.84369	3.586412	0.020268
1081	g7667.t1	2925	1	K01469: OPLAH, OXP1, opIAH	4.982517875	0.932891826	-3.4849	-1.845	-3.58558	0.020287
1082	g5077.t1	2926		K01193: E3.2.1.26, sacA	0	2.960911198	3.37498 4	-1.84621	3.584819	0.020303
1083	g6226.t1	2927		K12609: CAF120	5.821481969	0.802806449	-5.22139	-1.85419	-3.57978	0.020457
1084	g5075.t1	2928			0	4.80563983	3.71365 3	-1.85653	3.578302	0.020488
1085	g13910.t1	2929			3.759982388	0.360268275	-3.12849	-1.87274	-3.56807	0.020807
1086	g8085.t1	2930			7.812628972	1.145353766	-4.97699	-1.87917	-3.56401	0.02092
1087	g10423.t1	2931		K14327: UPE2, RENT2	5.380749971	0.19444946	-4.70673	-1.88023	-3.56334	0.020927
1088	g11332.t1	2932			4.160151798	2.045122287	-2.26209	-1.8804	-3.56323	0.020927
1089	g7007.t1	2933		K12600: SK13, TTC37	0	2.790129292	3.61827 9	-1.88398	3.560979	0.020986
1090	g2160.t1	2934			2.646205187	0.257249951	-3.58225	-1.88632	-3.5595	0.021018
1091	g3470.t1	2935		K00140: mmsA, iolA, ALDH6A1	6.130826774	0.21865482	-4.84924	-1.88786	-3.55853	0.021042
1092	g10929.t1	2936		K14805: DDX24, MAK5	4.672508797	1.17072715	-3.01023	-1.8894	-3.55756	0.021066
1093	g5608.t1	2937			0.756308574	5.212354025	3.85322 7	-1.88984	3.557283	0.021066
1094	g7845.t1	2938		K03434: PIGL	8.181737455	1.583646888	-6.91124	-1.89564	-3.55362	0.021156
1095	g15860.t1	2939		K09831: ERG5	5.065082896	0.529768939	-3.57805	-1.89631	-3.5532	0.02116
1096	g584.t1	2940		K01520: dut, DUT	4.447661542	0.440246825	-4.18025	-1.89957	-3.55115	0.021224
1097	g5992.t1	2941		K06276: PDPK1	4.323838023	1.006472653	-3.77529	-1.90915	-3.54511	0.021424
1098	g9408.t1	2942			6.248005823	2.598887614	-2.71989	-1.90919	-3.54508	0.021424
1099	g12324.t1	2943		K03936: NDUF53	4.250138533	1.633961537	-2.27784	-1.91946	-3.53861	0.021607
1100	g8165.t1	2944			0.505090398	5.931877819	3.97394 7	-1.92982	3.532082	0.021785

1101	g6804.t1	2945	g4428.t1	K15128: MED6	3.937924735	1.226226038	-3.06025	-1.93078	-3.53148	0.021797
1102	g4151.t1	2946	g1828.t1	K03327: TC.MATE, SLC47A, norM, mdtK, dinf	5.671937128	3.119497464	-2.69006	-1.93393	-3.5295	0.021849
1103	g7170.t1	2947	g560.t1		5.705181185	2.50956836	-3.52997	-1.93676	-3.52772	0.021905
1104	g8819.t1	2948	g3028.t1	K09252: E3.1.1.73	6.425640233	2.167666125	-4.21806	-1.94078	-3.52518	0.021957
1105	g10490.t1	2949	g1671.t1		0.267350656	5.289400866	4.58514	-1.94331	3.523591	0.021995
1106	g10438.t1	2950	g8414.t1	K11090: LA, SS8	4.175176818	0.564083606	-3.119	-1.94491	-3.52258	0.022022
1107	g7152.t1	2951	g11953.t1		4.892910278	0	-4.28485	-1.94745	-3.52098	0.022069
1108	g7945.t1	2952	g9700.t1	K15272: SLC35A1_2_3	3.910911941	6.892708872	2.84479	-1.94782	3.520755	0.022069
1110	g5482.t1	2954	g9825.t1	K03544: clpX, CLPX	5.959845259	3.962799023	-2.6218	-1.95044	-3.5191	0.02211
1109	g9746.t1	2953	g1027.t1		0	3.49762073	3.17180	-1.95002	3.519371	0.02211
1111	g7512.t1	2955	g10315.t1	K10268: FBX12_20	5.036102597	1.924325269	-2.88696	-1.95351	-3.51717	0.022172
1112	g9423.t1	2956	g10310.t1	K17678: MRH4	5.698279892	0.794188824	-4.53867	-1.95601	-3.5156	0.02221
1113	g4358.t1	2957	g427.t1	K15394: ACE1	8.430767836	2.590016536	-4.22487	-1.96125	-3.5123	0.022313
1114	g2440.t1	2958	g6709.t1		8.194390826	0.959769507	-5.65514	-1.96222	-3.51169	0.022326
1115	g7412.t1	2959	g7196.t1	K17786: MOS2	4.719997185	0.149385666	-4.56381	-1.96848	-3.50776	0.022424
1116	g7292.t1	2960	g11859.t1	K17267: COPG	5.289893047	1.985649581	-3.35694	-1.96926	-3.50726	0.022424
479	g10141.t1	2484	g8477.t1		5.541093332	2.791373031	-2.40723	-1.9695	-3.50711	0.022424
1117	g5887.t1	2961	g10973.t1		7.17403047	0.786931333	-5.65287	-1.97046	-3.50651	0.022436
1119	g1144.t1	2963	g256.t1		4.804829552	0.756889395	-4.9479	-1.97225	-3.50539	0.022447
1118	g6530.t1	2962	g10068.t1	K12345: SRDSA3	6.05975643	0.765101758	-4.56855	-1.97188	-3.50562	0.022447
1120	g1388.t1	2964	g3922.t1	K11108: RCL1	0	3.606104684	4.17277	-1.97523	3.50351	0.022506
660	g8547.t1	2461	g10270.t1	K02865: RP-L10Ae, RPL10A	4.653519091	0.569101736	-4.25142	-1.97772	-3.50195	0.022536
1121	g1443.t1	2965	g6990.t1		6.353729544	3.715374057	-2.42559	-1.97777	-3.50191	0.022536

557	g5845.t1	2354	g1158.t1	K02985: RP-S3e, RPS3	6.78958802	3.97973657	-3.61504	-1.98019	-3.50039	0.022571
1122	g1775.t1	2966	g1180.t1		2.44192219	5.786705282 9	3.07524	-1.98055	3.500163	0.022571
1123	g5301.t1	2967	g2268.t1		4.832199777	1.450036735	-4.59182	-1.9812	-3.49976	0.022576
1124	g5630.t1	2968	g1133.t1	K10808: RRM2	3.538433491	8.044277291 1	4.33217	-1.98319	3.498506	0.022613
1125	g10024.t1	2969	g8702.t1		0	4.379295342 5	4.69893	-1.98525	3.497209	0.022641
1126	g2219.t1	2970	g2626.t1		5.454955353	0.251432019	-3.8457	-1.99306	-3.4923	0.02281
1127	g3982.t1	2971	g7057.t1	K07824: E1.14.13.12	4.476939292	1.319684937	-2.77154	-1.99439	-3.49147	0.02281
1129	g8840.t1	2973	g1272.t1		3.816201878	6.770081287 8	3.04505	-1.99951	3.488248	0.022869
1128	g9861.t1	2972	g11455.t1	K06101: ASH1L	0	4.633512356 3	4.52771	-1.99917	3.488465	0.022869
1130	g4800.t1	2974	g676.t1		5.81071258	0.839736228	-3.94597	-2.00606	-3.48413	0.022998
1131	g11654.t1	2975	g8005.t1		2.909017487	6.248705968 5	3.37810	-2.00904	3.482265	0.023049
1132	g1136.t1	2976	g245.t1		10.59339274	4.772886191	-4.68428	-2.01923	-3.47586	0.02327
1133	g7223.t1	2977	g5892.t1		5.576672157	1.870596878	-3.72025	-2.02093	-3.4748	0.02329
1134	g3646.t1	2978	g623.t1		6.238451943	1.598186508	-3.95284	-2.02649	-3.4713	0.023385
1135	g11372.t1	2979	g5059.t1		0	3.180254596 8	2.74805	-2.0306	3.468725	0.023466
1138	g6590.t1	2982	g10119.t1		4.776549031	0	-3.51612	-2.03519	-3.46585	0.023548
1136	g1968.t1	2980	g6227.t1		5.415945903	1.846262242	-2.98674	-2.0347	-3.46615	0.023548
1137	g991.t1	2981	g8058.t1		4.169458418	6.394078234 5	3.70113	-2.03493	3.46601	0.023548
1139	g14.t1	2983	g11312.t1		5.71723547	2.200469261	-2.90045	-2.03611	-3.46527	0.02356
1140	g8611.t1	2984	g3033.t1		3.208304365	6.684869911 3	4.60084	-2.03808	3.46403	0.023599
1141	g6942.t1	2985	g6445.t1	K00988: APA1_2	0.122356187	4.223472162 9	3.71909	-2.04026	3.462663	0.023643
1142	g4972.t1	2986	g8937.t1	K13953: adhP	1.662757196	5.891631852	4.01311	-2.04335	3.460725	0.023699
1143	g11708.t1	2987	g6617.t1		6.393154936	0.574680488	-5.63531	-2.05038	-3.45631	0.023866
1144	g6627.t1	2988	g10177.t1		4.492307379	0	-4.73854	-2.05245	-3.45502	0.023898

1145	g3793.t1	2989	g2622.t1	K0632: E2.3.1.16, fadA	2.683933449	0.762155863	-2.33328	-2.05833	-3.45133	0.024039
1146	g5362.t1	2990	g9549.t1		5.333486397	1.869084159	-3.81693	-2.06267	-3.44861	0.02414
1147	g14458.t1	2991	g213.t1	K03417: prpB	5.793822468	0.460510026	-4.53188	-2.06694	-3.44593	0.024224
1148	g3972.t1	2992	g7050.t1	K09274: K09274	4.82960772	2.115464547	-2.69328	-2.07351	-3.44181	0.024331
1149	g9183.t1	2993	g6515.t1		1.762573342	7.079679643	4.15509	-2.07513	3.440795	0.02435
1150	g3346.t1	2994	g4782.t1		0	3.996837394	3.37163	-2.07771	3.439177	0.024406
1151	g15347.t1	2995	g9963.t1		5.425175011	3.445024571	-3.15188	-2.0797	-3.43793	0.024436
1152	g610.t1	2996	g3850.t1		0	2.724738444	4.72184	-2.07971	3.437925	0.024436
1153	g5842.t1	2997	g1161.t1		4.563717732	6.156540077	2.03726	-2.0869	3.433418	0.024569
1154	g13891.t1	2998	g7379.t1		0	5.395995421	4.86386	-2.08715	3.433268	0.024569
1155	g13895.t1	2999	g3474.t1	K07407: E3.2.1.22B, galA, rafA	6.607561086	4.158554252	-2.60137	-2.08937	-3.43187	0.024609
1156	g5991.t1	3000	g11690.t1	K11650: SMARCD	6.177996747	0.576104948	-4.263	-2.08984	-3.43158	0.02461
1157	g6045.t1	3001	g11733.t1		2.901234647	8.987765157	5.80763	-2.09548	3.428044	0.024702
1158	g5636.t1	3002	g1113.t1	K08818: CDC2L	7.197842208	1.025911245	-5.25317	-2.10189	-3.42403	0.024838
1159	g7137.t1	2541	g530.t1	K09702: K09702	5.111190124	0.46928073	-4.29408	-2.10378	-3.42285	0.024853
1160	g2933.t1	3003	g5977.t1		6.559889482	1.898194519	-3.99948	-2.11649	-3.41489	0.025137
1161	g505.t1	3004	g5519.t1		3.863129552	6.615728181	2.44593	-2.12415	3.410093	0.025321
1162	g7769.t1	3005	g7721.t1		5.577160458	1.98974677	-3.2893	-2.13007	-3.40639	0.025436
1163	g7156.t1	3006	g544.t1		6.758034692	0.550773544	-5.82435	-2.13342	-3.40429	0.025476
1165	g930.t1	3008	g9329.t1		5.15713035	2.062962464	-2.56378	-2.13372	-3.4041	0.025476
1164	g13110.t1	3007	g9758.t1		0	2.27010416	3.87195	-2.13369	3.404124	0.025476
1166	g586.t1	3009	g3871.t1		3.781116872	0.130099531	-3.60762	-2.14382	-3.39779	0.025688
577	g1391.t1	2375	g3917.t1		3.770913064	1.227337296	-2.68731	-2.14399	-3.39768	0.025688
1168	g10165.t1	3011	g7723.t1	K01455: E3.5.1.49	5.879458438	2.187241836	-3.86391	-2.15334	-3.39184	0.025911
1167	g2887.t1	3010	g10878.t1	K00102: E1.1.2.4, dld	4.602956869	2.179867653	-2.46981	-2.15315	-3.39195	0.025911

689	g849.t1	2496		1				3.120625144	0.692301308	-2.11851	-2.15658	-3.38981	0.025968
1169	g7214.t1	3012		g5878.t1	K06997: K06997			4.495077603	0	-3.33078	-2.16097	-3.38706	0.026065
1170	g18895.t1	3013		g5859.t1	K10845: TTDA, GTF2H5, TFBS			5.98025722	0.117852324	-4.59309	-2.16486	-3.38463	0.026138
1171	g8250.t1	3014		g10029.t1				4.39864019	7.809600987	3.39498	-2.17214	3.380082	0.026274
1172	g2364.t1	3015		g9259.t1				9.213191896	3.489449551	-5.38194	-2.1741	-3.37886	0.026289
1173	g560.t1	3016		g7760.t1	K07819: B3GALT1			0	2.547125215	2.00548	-2.17957	3.375436	0.026433
1174	g5544.t1	3017		g11318.t1	K01874: MARS, metG			5.478905924	1.205809707	-3.53649	-2.18062	-3.37478	0.026451
1175	g2772.t1	3018		g9139.t1	K14840: NOP53, GLTSCR2			0	4.504187056	3.48522	-2.18408	3.372617	0.026537
1176	g5248.t1	3019		g2343.t1				8.877204443	2.997703245	-4.70877	-2.1848	-3.37217	0.026545
532	g27.t1	2329		g1583.t1				6.169854164	4.284198791	-2.89306	-2.18645	-3.37113	0.026568
1177	g10546.t1	3020		g6691.t1	K12196: VPS4			0	2.055350266	2.10281	-2.18629	3.371236	0.026568
1178	g12603.t1	3021		g1139.t1	K13201: T1A1, T1A1L1			3.823455116	1.065757314	-2.74675	-2.18876	-3.3697	0.026622
1179	g2082.t1	3022		g2515.t1				4.08648863	0.419218481	-3.44889	-2.19514	-3.36571	0.026769
1180	g4868.t1	3023		g4487.t1	K18106: GAAA			5.341364148	1.56593075	-3.25482	-2.19916	-3.3632	0.026846
666	g9261.t1	2467		g10439.t1	K01336: E3.4.21.48			4.328483282	2.215262412	-2.51243	-2.19953	-3.36297	0.026846
1181	g4732.t1	3024		g2022.t1				3.266778123	7.967784506	3.78969	-2.20442	3.359911	0.026965
1183	g8014.t1	3026		g3407.t1	K05994: E3.4.11.10			5.396879706	0.439592246	-4.17848	-2.20633	-3.35872	0.026993
1182	g2889.t1	3025		g10880.t1				5.096458376	2.729262266	-2.29259	-2.20614	-3.35884	0.026993
1184	g6241.t1	3027		g7141.t1				2.980899445	5.57372668	2.99467	-2.20671	3.35848	0.026993
1185	g10185.t1	3028		g11141.t1	K12842: SR140			4.806643797	1.972250473	-3.66739	-2.20879	-3.35718	0.027029
1186	g3181.t1	3029		g4963.t1				5.389590661	3.444021927	-2.6427	-2.20945	-3.35677	0.027036
1187	g11146.t1	3030		g259.t1				0	6.234452055	4.52641	-2.21441	3.353674	0.027156
1188	g3478.t1	3031		g4668.t1	K15118: SLC25A38			7.188127807	0.666767656	-5.89063	-2.21606	-3.35264	0.027187
1189	g10812.t	3032		g11469.t				4.970990313	1.431805036	-2.73708	-2.21814	-3.35135	0.027228

1190	g5729.t1	3033	1	g5268.t1	4.667119257	1.758398652	-2.50173	-2.2199	-3.35025	0.027267
1191	g5773.t1	3034		g5183.t1	K18468: VPS35	0	-2.90432	-2.22779	-3.34532	0.027463
1192	g8342.t1	3035		g5156.t1	7.147347587	4.289313069	-2.89998	-2.2316	-3.34294	0.027563
1193	g2809.t1	3036		g9099.t1	8.970300194	3.622997906	4.26489	-2.23498	-3.34083	0.027638
1194	g3231.t1	3037		g6067.t1	5.450346027	0	-4.96789	-2.23666	-3.33979	0.027676
1195	g15441.t1	3038		g27.t1	K02135: ATPeF1E, ATP5E, ATP15	0	3.72480	-2.238	3.338948	0.027703
1196	g4098.t1	3039		g3297.t1	6.95311286	0.150996268	-5.81014	-2.24117	-3.33697	0.027773
1197	g4149.t1	3040		g1830.t1	5.595722786	9.860906704	3.91561	-2.24474	3.334743	0.027867
1198	g10768.t1	3041		g811.t1	K13281: uvsE, UVE1	2.018280024	-3.29096	-2.24832	-3.33251	0.02795
1199	g6034.t1	3042		g11722.t1	3.569534287	0.521226153	-2.51415	-2.25484	-3.32844	0.028085
1200	g7215.t1	3043		g5884.t1	4.164169033	1.616753056	-2.47644	-2.26216	-3.32387	0.028255
1201	g8488.t1	3044		g3354.t1	3.054782379	8.26554451	3.67873	-2.2697	3.319177	0.028434
1202	g8852.t1	3045		g1260.t1	0.276187354	4.110227051	3.12143	-2.2707	3.318549	0.028452
1203	g17481.t1	3046		g6577.t1	K03457: TC.NCS1	0	-3.46084	-2.27203	-3.31772	0.028471
1204	g6412.t1	3047		g5378.t1	0	6.454245699	4.80025	-2.27216	3.31764	0.028471
1205	g5249.t1	3048		g2342.t1	4.593408785	2.333125085	-2.29042	-2.27289	-3.31719	0.028481
1206	g4308.t1	3049		g1957.t1	K01934: E6.3.3.2	0.977864811	-3.10874	-2.27469	-3.31607	0.028523
1207	g9497.t1	3050		g5756.t1	K12816: CDC40, PRP17	6.369846039	3.96967	-2.28074	3.312295	0.028645
480	g3149.t1	2377		g4998.t1	K01213: E3.2.1.67	0	5.05218	-2.29031	3.306327	0.028891
1208	g16357.t1	3051		g3292.t1	2.274644449	6.642495757	3.65486	-2.29659	3.302412	0.029061
1209	g7653.t1	3052		g7536.t1	K02218: CSNK1, CK1	1.609655567	-3.10003	-2.29822	-3.3014	0.029099
1210	g2461.t1	3053		g6733.t1	K17498: SPN1, IWS1	0.537444052	-3.16588	-2.3086	-3.29493	0.0294
1211	g2212.t1	3054		g11601.t1	K15116: SLC25A33_36, RIM2	2.751924072	-2.41127	-2.31001	-3.29405	0.029419
1212	g10883.t1	3055		g172.t1	0	3.218252001	2.29218	-2.31043	3.293789	0.029419

1213	g7108.t1	3056	g5573.t1		4.49020983	1.428868948	-5.17599	-2.31348	-3.29189	0.029502
1214	g4692.t1	3057	g10596.t1	K00559: E2.1.1.41, SMT1, ERG6	5.217966775	0	-4.43958	-2.3144	-3.29132	0.029519
1215	g7001.t1	3058	g6383.t1		0	3.269277905	3.25060 ₉	-2.31504	3.29092	0.029526
1217	g11520.t1	3060	g4211.t1	K01273: E3.4.13.19, DPEP1	5.534704503	1.679588747	-3.69176	-2.31962	-3.28807	0.029632
1216	g470.t1	3059	g8009.t1	K03235: EF3, TEF3	2.63960049	0.413728279	-3.66277	-2.31946	-3.28817	0.029632
1218	g2297.t1	3061	g10716.t1		6.357052968	0.740815837	-4.61457	-2.32036	-3.2876	0.029643
1219	g7855.t1	3062	g10512.t1		5.263495212	2.246381404	-2.56985	-2.32321	-3.28583	0.029721
1221	g1216.t1	3064	g370.t1		7.767118225	5.274857999	-2.76524	-2.326	-3.28409	0.029784
1220	g15283.t1	3063	g10473.t1		0.148112638	3.597680572	3.86456 ₈	-2.32577	3.284235	0.029784
1222	g5238.t1	3065	g2356.t1		8.469488529	1.8423323775	-6.58325	-2.3311	-3.28092	0.029895
1223	g16230.t1	3066	g10013.t1		6.19115729	1.549847227	-4.95006	-2.3385	-3.27631	0.030121
1226	g14146.t1	3069	g3433.t1		5.134598916	0	-3.69373	-2.33977	-3.27552	0.030123
1225	g882.t1	3068	g9407.t1	K12468: PAD1	5.834927879	7.524019066	3.11195	-2.33963	3.275605	0.030123
1224	g10984.t1	3067	g5650.t1		0	3.058662563	3.40710 ₁	-2.33921	3.275869	0.030123
1227	g6996.t1	3070	g6388.t1	K01104: E3.1.3.48	0	6.684739153	5.25392 ₅	-2.34351	3.273191	0.030231
1228	g4042.t1	3071	g3218.t1	K10426: DCTN4	3.476006591	0.824375553	-2.8745	-2.34446	-3.2726	0.030248
1229	g10440.t1	3072	g8416.t1		4.661283453	2.396963708	-3.00648	-2.34837	-3.27017	0.030363
1230	g3798.t1	3073	g9469.t1		6.108299926	1.801505479	-3.74373	-2.35226	-3.26774	0.030434
1233	g5250.t1	3076	g2341.t1		4.192956387	2.110417944	-2.71795	-2.35314	-3.26719	0.030434
1231	g17491.t1	3074	g10533.t1		2.340628751	5.104359936	3.34349 ₈	-2.35272	3.267457	0.030434
1232	g5149.t1	3075	g3828.t1	K11369: RTG2	2.742167769	5.745670985	4.04487 ₂	-2.35272	3.267456	0.030434
1234	g10738.t1	3077	g11985.t1	K10798: PARP	0	6.207294428	5.05972 ₅	-2.3571	3.264731	0.030488
1235	g188.t1	3078	g5816.t1	K18342: OTUD6	4.706797138	1.42083914	-4.18554	-2.35888	-3.26362	0.030533

678	g2539.t1	2558	g3572.t1		8.765149435	6.260432332	-2.87811	-2.35928	-3.26338	0.030533
1236	g9576.t1	3079	g6624.t1	K05355: hexPS, COQ1	0	2.554894937	3.22116	-2.36306	3.26102	0.030604
1237	g7963.t1	3080	g10258.t1		6.877809835	1.401061786	-5.00254	-2.36399	-3.26044	0.030621
1238	g2081.t1	3081	g2516.t1		3.748359597	0.609941541	-2.61083	-2.37166	-3.25567	0.030835
1239	g4635.t1	3082	g2418.t1		4.337082348	1.030670213	-3.00281	-2.37336	-3.25461	0.030878
1240	g1191.t1	3083	g351.t1	K14997: SLC38A11	0.860169772	4.900013294	2.97858	-2.37713	3.252265	0.030977
1241	g3500.t1	3084	g2191.t1		1.215931569	6.936301079	6.11925	-2.37828	3.251549	0.031002
1242	g1860.t1	3085	g1884.t1		5.590523487	2.5557465	-2.92429	-2.37869	-3.25129	0.031002
1243	g7767.t1	3086	g891.t1		4.764291974	0.394275237	-5.55384	-2.38214	-3.24915	0.031067
1244	g2268.t1	3087	g10684.t1		5.863717773	0.278611595	-4.4083	-2.38343	-3.24835	0.03108
1245	g4613.t1	3088	g7741.t1	K00463: INDO	1.444624706	3.80329617	2.17660	-2.38439	3.247751	0.031098
683	g9852.t1	3089	g9791.t1		7.876491011	4.26909549	-2.81084	-2.39122	-3.2435	0.031274
1246	g4349.t1	3090	g2121.t1		1.532279358	7.011463446	4.87274	-2.39865	3.238883	0.03147
1247	g8581.t1	3091	g6606.t1	K00558: DNMT1, dcm	4.21948707	0.630336439	-5.33079	-2.40589	-3.23438	0.031676
1249	g9842.t1	3093	g9770.t1	K18576: XEG	6.122795741	1.361365172	-6.17274	-2.40937	-3.23221	0.031754
1248	g2125.t1	3092	g2952.t1	K01480: E3.5.3.11, speB	4.351289056	1.416547398	-2.95902	-2.40906	-3.23241	0.031754
1250	g10362.t1	3094	g5453.t1		4.153669397	1.595880592	-2.66682	-2.41506	-3.22868	0.031908
1257	g12070.t1	3101	g7821.t1	K15356: VRG4, GONST1	4.864054909	0.460510026	-4.71756	-2.4197	-3.22579	0.031957
1256	g4657.t1	3100	g2389.t1		5.666968159	0.321502083	-4.36415	-2.41953	-3.2259	0.031957
1252	g6958.t1	3096	g6431.t1	K11968: ARIH1	3.357418226	0.095701333	-3.62143	-2.41882	-3.22634	0.031957
1253	g19310.t1	3097	g9485.t1		5.087660505	2.997819493	-2.41441	-2.41917	-3.22612	0.031957
1255	g10767.t1	3099	g12013.t1	K16833: PPP1R2, IPP2	3.101333549	1.02165507	-2.06684	-2.41943	-3.22596	0.031957
1251	g11977.t1	3095	g12286.t1		5.145090044	8.173976979	2.42015	-2.41811	3.226784	0.031957
1254	g8978.t1	3098	g11390.t1		0	4.740307825	4.14482	-2.41933	3.226023	0.031957

1258	g21710.t 1	3102	g9500.t1		1.238938387	3.734242323	3.20989 3	-2.42554	3.222163	0.032104
1259	g7491.t1	3103	g10328.t 1		3.324272702	0.292287423	-2.5088	-2.42722	-3.22112	0.032149
1260	g7956.t1	3104	g10264.t 1		6.737632146	0	-4.52249	-2.43476	-3.21643	0.032321
1261	g7964.t1	3105	g10257.t 1		6.468663015	2.565678496	-3.82371	-2.43516	-3.21619	0.032321
1262	g7455.t1	3106	g6879.t1		7.133634176	2.350511691	-4.46812	-2.43579	-3.21579	0.032322
1264	g7919.t1	3108	g8603.t1		7.707220525	5.344305103	-2.48556	-2.43812	-3.21434	0.032362
1263	g6189.t1	3107	g9611.t1		3.290429112	6.571773343	2.85916 7	-2.43769	3.214609	0.032362
1265	g16176.t 1	2509	g5232.t1		3.961883001	1.690859985	-2.35469	-2.43856	-3.21407	0.032363
1266	g8674.t1	3109	g10950.t 1		4.335667589	1.644834875	-2.29957	-2.43968	-3.21337	0.032377
1267	g9656.t1	3110	g4870.t1	K12844: PRPF31	1.499922726	5.995240597	4.14452 2	-2.44487	3.210148	0.032511
1268	g7488.t1	3111	g10325.t 1	K11240: MSG5	4.501108392	0.613661381	-3.60908	-2.4515	-3.20603	0.032688
1269	g7672.t1	3112	g7571.t1		3.989155638	1.357471583	-3.34293	-2.45175	-3.20587	0.032688
1270	g55.t1	3113	g2746.t1	K14567: UTP14	5.127910319	6.999646309	2.57135 4	-2.45654	3.2029	0.032843
1272	g9412.t1	3115	g3614.t1		7.062307238	0.410055385	-4.46156	-2.45932	-3.20117	0.0329
1271	g1753.t1	3114	g9720.t1		4.044374876	5.846317087	2.75140 2	-2.45908	3.201321	0.0329
1273	g10977.t 1	3116	g5641.t1	K10735: GINS4, SLD5	4.051828119	8.612393187	4.98755 5	-2.47134	3.193707	0.03327
1274	g17737.t 1	3117	g6552.t1	K01893: NARS, asns	6.388427463	4.460451965	-2.16214	-2.47597	-3.19083	0.033354
1275	g10487.t 1	3118	g1673.t1	K17774: MDM10	2.164706382	4.843319565	3.62583 3	-2.47943	3.188681	0.033451
1276	g6558.t1	3119	g10094.t 1	K00643: E2.3.1.37, ALAS	6.31176497	2.48933491	-3.18947	-2.48208	-3.18703	0.033532
1277	g2287.t1	3120	g9659.t1		4.38553855	6.941829687	3.21668 8	-2.4855	3.184907	0.033614
1278	g842.t1	3121	g9463.t1		0	4.044547142	3.95281 1	-2.48774	3.18352	0.033652
1279	g2517.t1	3122	g3549.t1		5.937036867	2.027078484	-3.14005	-2.49094	-3.18153	0.033741

1280	g3451.t1	3123	g4694.t1	K18803: HPM1	7.686438949	4.233781072	-2.70319	-2.49375	-3.17979	0.033786
1281	g6141.t1	3124	g7301.t1		4.843357772	0.856838746	-3.43	-2.49677	-3.17791	0.033868
1282	g12211.t1	3125	g8489.t1		4.086552127	0.933666875	-3.29049	-2.4978	-3.17727	0.033888
1283	g9200.t1	3126	g6534.t1		6.260040742	2.764634545	-2.90907	-2.50672	-3.17173	0.034162
1284	g5321.t1	3127	g2239.t1		7.891730863	3.602558714	-3.87368	-2.50755	-3.17122	0.034169
1285	g3577.t1	3128	g3306.t1		7.444698622	1.243570464	-4.43732	-2.51028	-3.16953	0.03425
1286	g16033.t1	3129	g8312.t1	K14961: RBP5, SWD1, CPS50	6.814335139	0	-4.98563	-2.51933	-3.1639	0.034515
1287	g370.t1	3130	g8886.t1	K05351: E1.1.1.9	2.495983173	0	-2.61273	-2.52005	-3.16346	0.034527
1288	g11747.t1	3131	g5055.t1		5.579800871	0	-5.65729	-2.52153	-3.16254	0.034567
1289	g307.t1	3132	g9470.t1	K00450: E1.1.3.11.4	0	4.296941509	3.37964	-2.52502	3.160374	0.034684
1290	g4252.t1	3133	g1730.t1	K14554: UTP21, WDR36	5.046177386	0	-4.35342	-2.52588	-3.15984	0.034692
1291	g13249.t1	3134	g7068.t1	K00101: E1.1.2.3, lld	0	2.243022049	2.36154	-2.53745	3.152658	0.035035
1292	g97.t1	3135	g2918.t1	K17550: PPP1R7, SDS22	6.872034629	1.343604487	-4.47691	-2.53859	-3.15195	0.035064
1293	g11152.t1	3136	g4836.t1	K01736: aroC	4.537533205	12.27861396	6.43595	-2.54243	3.149569	0.035195
1294	g277.t1	3137	g11370.t1		0	3.079036559	2.87571	-2.54813	3.146033	0.035339
1296	g1874.t1	3139	g4227.t1		3.147814191	5.126168567	2.97991	-2.55508	3.141723	0.035531
1295	g10285.t1	3138	g38.t1		0	3.651708721	6.25453	-2.55454	3.142055	0.035531
1297	g7205.t1	3140	g5869.t1	K04712: DEGS	3.678254356	0.752860849	-2.40347	-2.55623	-3.14101	0.035546
1298	g3975.t1	3141	g7052.t1	K03127: TAF13	5.226674743	2.844506041	-3.29814	-2.56215	-3.13733	0.035745
1299	g6129.t1	3142	g7317.t1	K18584: ACTR3, ARP3	0.131743499	5.532439821	3.97691	-2.56833	3.133498	0.035969
1300	g1071.t1	3143	g8144.t1	K15163: SR88, MED12	9.338879184	2.598174135	-4.65483	-2.57512	-3.12929	0.036158
1301	g9776.t1	3144	g933.t1	K18696: GDE1	4.318349985	2.568252231	-2.16956	-2.57518	-3.12925	0.036158
1302	g9449.t1	3145	g10284.t1	K08286: E2.7.11.-	0.930122123	5.973997216	3.69996	-2.57627	3.128576	0.036169
1303	g8139.t1	3146	g11353.t1		5.695078874	3.389930558	-2.65431	-2.58118	-3.12553	0.036322
1304	g3952.t1	3147	g3939.t1		3.467152816	8.346322304	4.39571	-2.58284	3.124498	0.036357

1306	g4583.t1	3149	g3309.t1		1.533947618	4.292967522	5	-2.58921	3.120549	0.036563
1305	g20261.t1	3148	g5213.t1	K15918: GLYK	0	1.938193397	5	-2.58912	3.120602	0.036563
1307	g7529.t1	3150	g7276.t1		6.576826873	2.083647571	4.58843	-2.5904	-3.11981	0.036595
1308	g6754.t1	3151	g4367.t1	K02209: MCMS, CDC46	2.459200585	5.055158724	7	-2.5914	3.11919	0.036619
1311	g491.t1	3154	g5498.t1		6.698116368	3.721035259	-3.28029	-2.59415	-3.11749	0.036659
1309	g7837.t1	3152	g8557.t1		6.106640364	3.365204838	-2.32578	-2.59377	-3.11772	0.036659
1310	g987.t1	3153	g8056.t1		0	3.027945316	8	-2.59389	3.117647	0.036659
1313	g17939.t1	3156	g10899.t1		6.818707989	5.005569394	-2.67236	-2.60024	-3.11371	0.036861
1312	g2164.t1	3155	g11903.t1		5.515137675	2.685444972	-2.26759	-2.5999	-3.11392	0.036861
1314	g3906.t1	3157	g3985.t1	K03190: ureD, ureH	2.671010414	5.33593488	2	-2.60354	3.111663	0.036951
1315	g1097.t1	3158	g4041.t1		0.505695041	3.969049246	4.48503	-2.60467	3.110959	0.036981
1317	g3623.t1	3160	g595.t1	K16466: CETN3	4.801115612	1.915084147	-3.20944	-2.60598	-3.11015	0.036988
1316	g8411.t1	3159	g4430.t1		0	2.810557222	1	-2.60547	3.110465	0.036988
1318	g20530.t1	3161	g9496.t1		0	3.999056646	6	-2.60652	3.109816	0.036994
1319	g1348.t1	3162	g3450.t1	K10438: E1.14.13.63, phacB	3.588175282	1.235710845	-2.25653	-2.60816	-3.1088	0.037045
1320	g3797.t1	3163	g2615.t1		6.056986997	2.555508643	-2.7468	-2.61051	-3.10734	0.037124
1321	g7399.t1	3164	g7182.t1		5.018202134	2.232656771	-2.93727	-2.61149	-3.10673	0.037149
1322	g5488.t1	3165	g9822.t1		3.362985644	6.104316624	4	-2.61209	3.106356	0.037158
1323	g9157.t1	3166	g6488.t1	K02324: POLE1	1.973709427	4.469428234	5	-2.61992	3.101503	0.037412
1324	g14847.t1	3167	g1437.t1	K00641: metX	6.994074013	3.436994314	-2.90018	-2.63256	-3.09366	0.037835
1325	g6957.t1	3168	g6432.t1	K10746: EXO1	6.131134701	0.388290481	-4.29624	-2.63704	-3.09089	0.037954
1326	g3447.t1	3169	g4698.t1		4.987346272	1.724391306	-4.26254	-2.63726	-3.09075	0.037954
1327	g9400.t1	3170	g3632.t1		4.819542549	7.125673734	3.13700	-2.63773	3.09046	0.037954

1328	g10198.t 1	3171	g11163.t 1		5.978274196	2.788975408	2	-2.6404	-3.08881	0.038033
1331	g7497.t1	3174	g10332.t 1		5.769438155	2.358653046	-3.9471	-2.64303	-3.08718	0.03808
1330	g7426.t1	3173	g7211.t1	K07151: STT3	6.089321429	2.57287541	-2.74784	-2.64279	-3.08733	0.03808
1329	g8972.t1	3172	g11360.t 1	K00949: thiN, TPK1, THI80	0	4.277976912	2.87682 6	-2.64269	3.087385	0.03808
1332	g11012.t 1	3175	g5666.t1		0	5.38381861	3.85658 9	-2.6484	3.083847	0.038255
1335	g2680.t1	3178	g4137.t1	K03305: TC.POT	4.251138075	0.905078368	-3.52825	-2.65137	-3.08201	0.038301
1334	g12334.t 1	3177	g7439.t1		4.832463772	1.425823624	-3.26532	-2.65114	-3.08215	0.038301
1333	g4070.t1	3176	g3266.t1	K08502: VAM7	5.539846457	2.546984577	-2.7732	-2.65099	-3.08224	0.038301
1336	g6026.t1	3179	g11719.t 1		6.095844652	0.68430684	-4.28462	-2.66367	-3.07438	0.038767
1337	g3846.t1	3180	g3215.t1		5.151000423	1.006964699	-3.90954	-2.66555	-3.07322	0.03883
1338	g5774.t1	3181	g5182.t1		4.645161281	0	-3.4513	-2.66704	-3.07229	0.038877
1339	g3929.t1	3182	g3963.t1	K08866: TTK, MPS1	6.449588576	3.278968193	-3.36947	-2.66843	-3.07143	0.03892
1340	g2818.t1	3183	g9112.t1		5.23098229	2.042748595	-4.97039	-2.67161	-3.06946	0.038992
1341	g4639.t1	3184	g3141.t1		4.295463374	0	-3.88825	-2.67162	-3.06945	0.038992
1342	g7766.t1	3185	g886.t1	K00276: AOC3, AOC2, tyrA	3.696502907	1.950100615	-2.2513	-2.67226	-3.06906	0.039003
1343	g5178.t1	3186	g3785.t1	K10732: GINS1, PSF1	3.205102409	0.465489204	-2.9998	-2.67294	-3.06864	0.039016
1344	g6934.t1	3187	g8796.t1		5.750734244	3.373972395	-2.72485	-2.67465	-3.06758	0.039072
1345	g1969.t1	3188	g6228.t1		3.400168294	1.126194748	-2.65712	-2.67603	-3.06672	0.039115
1346	g172.t1	3189	g12085.t 1	K01531: E3.6.3.2, mgA, mgT8	6.497766777	1.752973654	-3.4052	-2.67672	-3.0663	0.039129
1347	g11564.t 1	3190	g4163.t1	K00274: MAO, aofH	2.200547724	5.983180821	3.28493 4	-2.67943	3.064613	0.039212
1348	g6920.t1	3191	g6466.t1	K05607: AUH	3.935782227	1.559896558	-2.81933	-2.68386	-3.06187	0.039338
1349	g155.t1	3192	g5222.t1	K00129: E1.2.1.5	0	2.038635734	2.66213 9	-2.68959	3.058314	0.039519
1351	g4054.t1	3194	g3233.t1	K00222: TM7SF2, ERG24	4.246709844	0.753125695	-3.82499	-2.6984	-3.05285	0.039787
1350	g259.t1	3193	g11071.t 1		2.005826005 *	6.702898665	4.84418 8	-2.69807	3.053061	0.039787

1352	g2113.t1	3195	g6610.t1		5.320518398	1.691648425	-3.58956	-2.70003	-3.05185	0.039841
1353	g18993.t1	3196	g1481.t1		6.460112374	2.188072612	-3.62105	-2.70385	-3.04948	0.039958
1354	g9213.t1	3197	g9107.t1	K01535: E3.6.3.6	0.221964669	4.444533441	4.86188	-2.70441	3.049135	0.039966
1355	g8608.t1	3198	g3036.t1		6.171130211	2.686136331	-2.9841	-2.70848	-3.04661	0.040111
1359	g559.t1	3202	g3897.t1		6.201870178	1.933937599	-3.99892	-2.71429	-3.04301	0.040268
1357	g1111.t1	3200	g4058.t1	K17792: TIM54	5.442528526	1.477478055	-3.04273	-2.71355	-3.04347	0.040268
1358	g2917.t1	3201	g5991.t1		5.742797006	3.575636867	-2.07424	-2.71393	-3.04323	0.040268
1356	g13698.t1	3199	g7803.t1	K15015: SLC32A, VGAT	3.095824509	6.420340227	3.45395	-2.71294	3.043849	0.040268
1360	g3970.t1	3203	g9872.t1	K14455: GOT2	6.495895484	1.144303422	-3.38447	-2.71544	-3.0423	0.040287
1361	g6219.t1	3204	g7117.t1	K15030: EIF3M	9.064552828	7.245420142	-3.3623	-2.71784	-3.04081	0.040375
1362	g9425.t1	3205	g10308.t1	K08850: AURKX	4.730673883	0.868742846	-4.27344	-2.72342	-3.03735	0.040551
1363	g7501.t1	3206	g10336.t1	K18160: NDUF2	5.345072335	0.733430789	-4.13019	-2.72367	-3.03719	0.040551
1364	g859.t1	3207	g9445.t1		6.22964011	1.992693147	-3.27148	-2.72413	-3.03692	0.040555
1365	g1915.t1	3208	g6151.t1		7.270928698	4.976410906	-2.43324	-2.73052	-3.03295	0.040756
1366	g12217.t1	3209	g1989.t1	K00826: E2.6.1.42, IlvE	3.918920739	1.387924318	-2.78762	-2.73448	-3.0305	0.040915
1367	g4170.t1	3210	g1809.t1		0.622664993	6.671635624	3.83957	-2.74399	3.024609	0.041257
1368	g9398.t1	2532	g3634.t1		4.794435739	1.682112273	-3.12889	-2.74644	-3.02309	0.041334
1369	g11911.t1	3211	g11961.t1		4.426580032	0.838075179	-3.7127	-2.75198	-3.01966	0.04155
1370	g1975.t1	3212	g6235.t1	K03676: gpxC, GLRX, GLRX2	5.422460166	3.194829169	-2.95272	-2.75339	-3.01878	0.041581
1371	g8163.t1	3213	g7963.t1	K16261: VAT	4.292364721	2.128178192	-2.1584	-2.75419	-3.01829	0.041601
1372	g7701.t1	3214	g5632.t1	K16261: VAT	3.918348151	2.429142725	-2.02558	-2.76273	-3.013	0.041938
1373	g9062.t1	3215	g8589.t1		0	4.231781639	4.01005	-2.76633	3.010768	0.042068
1374	g21743.t1	3216	g11779.t1	K01969: E6.4.1.4B	3.581364482	0.847557335	-4.15212	-2.76857	-3.00938	0.042138
1375	g5576.t1	3217	g7494.t1		8.893181528	1.120853281	-5.86159	-2.77127	-3.00771	0.042212
1376	g3089.t1	3218	g11792.t1	K00914: PIK3C3, VPS34	6.7596142	1.576374675	-4.25202	-2.77342	-3.00637	0.042277

1377	g5685.t1	3219	g1056.t1	K13524: ABAT	0	2.06537591	2.44012	-2.78145	3.001401	0.042547
1378	g4641.t1	3220	g2414.t1	K03685: rnc, DROSHA, RNT1	0.412316469	4.991257678	3.33254 ₉	-2.78404	2.999796	0.042649
1379	g2363.t1	3221	g9258.t1		6.486658248	1.454471294	-6.28212	-2.79029	-2.99592	0.042862
1380	g21382.t1	3222	g5714.t1	K07734: palB	6.462845057	2.264599961	-3.14521	-2.79042	-2.99584	0.042862
1381	g6400.t1	3223	g5394.t1		0	4.971894272	4.30701 ₄	-2.7932	2.994118	0.042975
1382	g10337.t1	3224	g56.t1		4.374119128	0.945262194	-2.67548	-2.79768	-2.99134	0.043133
1383	g5528.t1	3225	g1657.t1	K02896: RP-L24e, RPL24	5.059362323	2.912712707	-2.81694	-2.80156	-2.98894	0.043281
1384	g11343.t1	3226	g11653.t1	K10981: POL4	6.259801244	1.648126626	-4.35678	-2.80503	-2.98679	0.043411
1385	g5150.t1	3227	g3827.t1		2.931671142	5.392109666	3.10278 ₄	-2.81072	2.983263	0.043629
1386	g6763.t1	3228	g4378.t1	K02321: POLA2	8.302494784	5.13409511	-2.44481	-2.81189	-2.98254	0.043667
1387	g5671.t1	3229	g1071.t1	K11853: USP34	0	4.496504481	3.60119 ₂	-2.81539	2.98037	0.043799
1388	g11809.t1	3230	g12052.t1	K11364: SGF29	3.463947854	6.116692885	2.83362 ₃	-2.81691	2.979429	0.043837
1389	g11797.t1	3231	g11951.t1		3.516751262	1.679255644	-2.65677	-2.82277	-2.9758	0.044083
1390	g10681.t1	3232	g8527.t1		5.58963777	3.099515857	-2.57245	-2.82433	-2.97483	0.04413
1391	g4325.t1	3233	g11437.t1		13.11970013	2.933682888	-7.21408	-2.82725	-2.97302	0.044229
1392	g9381.t1	3234	g3653.t1		5.511774101	1.012685905	-3.81034	-2.82909	-2.97188	0.044293
1393	g7852.t1	3235	g10509.t1		6.882721316	5.021376437	-3.07319	-2.8293	-2.97175	0.044293
616	g5090.t1	2415	g2954.t1	K08486: STX18_2_3	0	3.867535804	3.83647 ₆	-2.8345	2.968529	0.044458
1394	g3829.t1	3236	g2598.t1		0.266144622	4.669261532	3.50036	-2.8361	2.967538	0.044518
1395	g11535.t1	3237	g4192.t1	K17279: REEP5_6	0.360331706	9.163288499	7.51040 ₂	-2.83657	2.967251	0.044524
1396	g6481.t1	3238	g5293.t1	K01886: QARS, glnS	5.748896345	1.179880874	-5.49899	-2.83881	-2.96586	0.044606
1397	g3005.t1	3239	g8297.t1		4.660135675	0.923693205	-4.96111	-2.83903	-2.96573	0.044606
1398	g4078.t1	3240	g3277.t1		3.936715366	2.213435275	-2.83788	-2.83933	-2.96554	0.044606
1399	g2855.t1	3241	g9059.t1	K00627: DIAT, aceF,	5.436104451	0.350451845	-3.90005	-2.84415	-2.96255	0.044805

1400	g3918.t1	3242	g3974.t1	pdhC	K00297: metF, MTHFR	5.369411331	6.805636855	2.48466	-2.84783	2.960272	0.044957
1401	g7179.t1	3243	g566.t1		K09523: DNAIC3	0.627178139	4.16165657	3.40931	-2.84799	2.960173	0.044957
1402	g12408.t1	3244	g8249.t1			6.349198309	4.267606287	-4.36478	-2.85278	-2.9572	0.045157
1403	g9652.t1	3245	g6915.t1			4.964995182	3.229940066	-3.59518	-2.85436	-2.95623	0.045182
1404	g7523.t1	3246	g7288.t1		K13704: ABHD12	1.294755574	5.275553403	5.59140	-2.85471	2.95601	0.045182
1405	g14653.t1	3247	g2855.t1			5.738900905	1.835542251	-3.20682	-2.86057	-2.95238	0.045453
1406	g4096.t1	3248	g3295.t1		K17362: ACOT13	4.848799761	1.091069648	-3.86237	-2.86465	-2.94985	0.045602
1407	g18248.t1	3249	g2041.t1			4.35781588	7.901252086	3.78435	-2.86851	2.947457	0.045759
1408	g1237.t1	3250	g7426.t1			5.683015328	2.488598283	-2.99706	-2.87184	-2.94539	0.045853
1410	g3632.t1	3252	g608.t1			3.639980584	1.944176831	-2.64596	-2.87251	-2.94498	0.045853
1409	g5562.t1	3251	g7477.t1			4.810359052	9.131036427	4.16886	-2.87246	2.945014	0.045853
1411	g5477.t1	3253	g8419.t1		K01876: DARS, aspS	5.822436425	3.686550344	-3.1569	-2.87291	-2.94473	0.045855
1412	g9515.t1	3254	g6599.t1		K10729: SID2	5.470455054	2.40515865	-2.98726	-2.87443	-2.94379	0.045909
1413	g10318.t1	3255	g72.t1			3.677226697	5.754668913	3.28968	-2.88275	2.938638	0.046244
1414	g24.t1	3256	g12134.t1			2.224553826	7.898332502	4.24237	-2.8828	2.938606	0.046244
1415	g8240.t1	3257	g10040.t1		K17784: MINOS1, MOS1	4.505441621	2.059214773	-3.2426	-2.88456	-2.93751	0.046298
1416	g7496.t1	3258	g10330.t1			4.295198041	0.62681007	-4.62511	-2.88616	-2.93652	0.046343
1418	g5019.t1	3260	g8992.t1		K00763: pncB, NAPRT1	5.789644312	0	-4.02631	-2.88687	-2.93608	0.046344
1417	g9422.t1	3259	g10311.t1		K17678: MRH4	4.99116655	2.76827123	-2.74095	-2.8868	-2.93613	0.046344
1419	g6947.t1	3261	g6439.t1			4.318049534	0.859611004	-3.26378	-2.89495	-2.93107	0.046698
1420	g1449.t1	3262	g6978.t1			7.510804913	5.552335444	-3.23923	-2.89616	-2.93033	0.046742
1421	g11952.t1	3263	g5425.t1		K11886: ECM29	3.293996124	0.612527291	-2.70149	-2.90035	-2.92773	0.046902
1422	g4463.t1	3264	g6821.t1		K03441: GLP-F	5.769121905	0.957880078	-3.49533	-2.90325	-2.92593	0.047032

1423	g4565.t1	3265	g4096.t1		0.919084112	5.08912066	3.48622	-2.90372	2.925643	0.047038
1424	g5152.t1	3266	g3825.t1		3.965633731	9.790435178	4.13410	-2.9047	2.925032	0.047071
1425	g5796.t1	3267	g4861.t1		4.412444745	6.978987815	2.71429	-2.9071	2.923548	0.047159
1426	g2106.t1	3268	g2479.t1	K17877: NIT-6	4.442382018	1.795290638	-2.90776	-2.90858	-2.92263	0.047216
1427	g2132.t1	3269	g9887.t1		6.595948877	2.130028726	-3.56948	-2.91683	-2.91752	0.047586
1428	g2743.t1	3270	g8874.t1		10.26584456	3.775688511	-5.63147	-2.91883	-2.91628	0.047669
1429	g3255.t1	3271	g8226.t1		0	4.623799698	4.75327	-2.91912	2.916098	0.047669
1430	g2515.t1	3272	g3546.t1	K03935: NDUF52	2.995934045	5.779005536	2.98391	-2.91952	2.915847	0.047672
1431	g11846.t1	3273	g8779.t1		5.108325438	0.456052036	-4.50763	-2.91997	-2.91557	0.047677
1432	g4309.t1	3274	g1956.t1	K15436: TRPO3, MTR10	3.512784384	0.746291622	-3.75578	-2.92157	-2.91458	0.047742
1433	g342.t1	3275	g8843.t1	K14617: LMBRD1	5.048487126	6.613903693	2.61442	-2.92704	2.91119	0.047918
1434	g10330.t1	3276	g65.t1	K10592: HUWE1, MULE, ARF-BP1	0	6.217591133	4.49467	-2.92903	2.909954	0.048004
1435	g12736.t1	3277	g5713.t1		0	2.67764343	3.58779	-2.93123	2.908589	0.048101
1436	g3120.t1	3278	g11825.t1		0	2.782475712	2.38281	-2.93213	2.908034	0.048112
1437	g6122.t1	3279	g7325.t1		3.73309277	0	-3.82204	-2.93383	-2.90698	0.048183
1438	g7506.t1	3280	g1313.t1	K02510: hpal, hpcH	5.681359113	2.954196465	-4.30541	-2.93555	-2.90591	0.048255
1439	g4219.t1	3281	g1764.t1		5.026702428	3.19824011	-2.28706	-2.93664	-2.90523	0.048294
1440	g5995.t1	3282	g11694.t1	K08501: STX8	5.459232545	0.507403584	-3.61957	-2.94175	-2.90207	0.048544
1441	g10838.t1	3283	g9836.t1		4.87039805	2.795973757	-2.14792	-2.94515	-2.89996	0.048705
626	g2308.t1	2425	g10725.t1		5.237036425	3.494277968	-2.61152	-2.94809	-2.89814	0.048825
1442	g6039.t1	3284	g11727.t1	K14809: DDX55, SPB4	5.042634955	2.144742508	-3.54449	-2.95453	-2.89415	0.049112
1443	g4021.t1	3285	g3194.t1		4.255555246	1.771901086	-3.07477	-2.95556	-2.89351	0.049148
1444	g7825.t1	3286	g8668.t1		7.009481452	4.830504535	-2.37807	-2.95614	-2.89315	0.049161
1445	g7886.t1	3287	g8663.t1		5.301291022	3.603605432	-2.98612	-2.95905	-2.89135	0.049265

1446	g13691.t 1	3288	g9725.t1		2.720405954	4.969707656	2.36102 3	-2.95911	2.891306	0.049265
1447	g3039.t1	3289	g8267.t1	K14779: DDx52, ROK1	4.859751136	2.56647477	-2.80026	-2.95956	-2.89103	0.049269
1448	g5768.t1	3290	g5189.t1	K02948: RP-S11, MRP511, rpsK	3.223518382	6.638489334	3.70018 9	-2.95986	2.890843	0.049269
1449	g8149.t1	3291	g7955.t1		7.075631425	1.400206991	-4.60509	-2.96226	-2.88936	0.049369
1450	g13905.t 1	3292	g4807.t1		5.937192138	4.105355745	-2.28795	-2.96241	-2.88926	0.049369
1451	g9050.t1	3293	g5712.t1		0	1.428557276	2.85004 1	-2.96403	2.888256	0.049437
1452	g11913.t 1	3294	g658.t1	K14264: BNA3	3.176589195	0.818863118	-2.7115	-2.96755	-2.88608	0.049608
1453	g11806.t 1	3295	g12049.t 1	K17260: ACTR2, ARP2	3.412479141	8.573811497	4.00477 2	-2.96831	2.885605	0.049628

Table 604:

This table describes orthologous genes of *Acremonium zeae* sp. with beneficial and neutral effects on soybean growth, these genes show significant genotype specific changes in expression when grown in culture with and without plant homogenate. "Median Exp. SYM00577 Plant" represents the median expression value in log2 tpm across biological replicates of the beneficial *Acremonium* grown in media inoculated with soybean seedling homogenate extracted with 50 mM PBS. "Median Exp. SYM00577 Mock" represents the median expression value in log2 tpm across biological replicates of the beneficial *Acremonium* grown in media inoculated with 50 mM PBS buffer. "Median Exp. SYM00300 Plant" seedling homogenate extracted with 50 mM PBS. "Median Exp. SYM00300" represents the median expression value in log2 tpm across biological replicates of the neutral *Acremonium* grown in media inoculated with soybean seedling homogenate extracted with 50 mM PBS. "Median Exp. SYM00300 Mock" represents the median expression value in log2 tpm across biological replicates of the neutral *Acremonium* grown in media inoculated with 50 mM PBS buffer. "Log FC" represents the estimate of the log2-fold-change of the contrast. "B-statistic" represents the log-odds that the gene is differentially expressed. "t-statistic" represents the moderated t-statistic. "Adj. p-value" represents the false discovery rate (Benjamini & Hochberg, 1995) adjusted p-values.

SEQ ID SYM0057	sym57 7 gene	SEQ ID SYM0030	sym30 O gene	Description	Median Exp. SYM00577 Plant	Median Exp. SYM00577 Mock	Median Exp. SYM00300 Plant	Median Exp. SYM00300 Mock	Log FC	B- statistic	t- statistic	Adj. p- value
685	g6380. t1	2492	g764.t 1	K05857: PLCD	3.2014147 5	5.073855922	9.359327016	0.295559632	10.1462 1	4.34253 8	10.541 36	0.00573 8
686	g857.t 1	2491	g9451. t1	K01950: E6.3.5.1, NADSYN1, QNS1, nadE	3.8869203 69	3.802514601	0.533450094	8.452816333	-8.12443	3.97738 8	- 9.7883 5	0.00583 8
687	g1307 2.t1	2494	g9142. t1		0	0	2.137400252	8.254570732	-6.46147	3.20127 2	- 8.4588 4	0.00931 5
675	g5348. t1	2554	g1.t1		5.7032830 97	0	4.093445794	4.361478247	-5.78572	2.80058 5	- 7.8793 2	0.00931 5
674	g5345. t1	2555	g9530. t1	K03510: POLI	0	5.845894518	0.472127747	0.825824927	5.24145 8	2.78051 8	7.8518 32	0.00931 5
688	g68.t1	2495	g909.t 1	K00106: XDH	6.7881073 71	7.003820996	7.792433369	1.8413995	5.85013 1	2.99489 4	8.1528 02	0.00931 5
689	g849.t 1	2496	g9453. t1	K06997: K06997	2.6989926 01	3.120625144	7.963289978	0.692301308	7.18610 4	2.97948 9	8.1306 2	0.00931 5
690	g7926. t1	2497	g8597. t1		6.1666773 32	6.853860482	8.618339677	1.736488111	7.72827 2	2.84641 1	7.9426 14	0.00931 5
680	g1340. t1	2553	g523.t 1		0	5.657989905	5.308190284	2.558100341	8.89827 6	3.33693 7	8.6696 16	0.00931 5
691	g5563. t1	2493	g7478. t1		4.6832647 3	4.371792513	9.926472681	0	8.94165 3	2.76503 5	7.8307 14	0.00931 5
692	g5169. t1	2506	g3798. t1		4.2820301 1	4.865818268	6.198143572	0.928859379	6.20299 2	2.4341	7.3975 97	0.01412 6
677	g1348 9.t1	2556	g8733. t1		4.0492933 59	0	1.530959943	1.496465963	-3.96529	2.15092 7	- 7.0520 7	0.01853 1
694	g3058. t1	2499	g1604. t1		0	0	5.62596164	1.924786245	3.93230 4	2.09054 6	6.9810 83	0.01853 1
693	g2076. t1	2498	g2520. t1		3.9572315 52	3.655783096	13.01166964	2.835668263	10.4478 6	2.12735 1	7.0242 42	0.01853 1
695	g3790. t1	2501	g2628. t1	K12486: SMAP	0	0	6.121031288	1.019511648	5.08087 8	1.93808	6.8057 6	0.02159 5
676	g7741. t1	2557	g7091. t1		7.1765057 71	2.550284622	3.981693891	3.632045248	-4.74363	1.71889 5	- 6.5629	0.02595 5

697	g852.t 1	2502	g9454. t1	K11824: AP2A	4.8808824 59	5.513795279	7.286171288	2.276512626	5.32327	1.68203	5	0.02595
696	g3920. t1	2508	g3972. t1		4.1277639 96	5.062011561	6.356788736	0.848055404	5.96206 7	*1.69646 6	6.5231 18	0.02595
678	g2539. t1	2558	g3572. t1		2.3267884 17	8.765149435	6.873536849	6.260432332	7.69694 7	1.34474 4	6.1711 18	0.03934 8
699	g2257. t1	2504	g1066 8.t1		0	0	3.910887164	10.12999017	-6.28123	1.22348	- 6.0496 8	0.04203 2
698	g657.t 1	2503	g9863. t1		4.6882008 62	4.4628192	5.925534706	1.558896118	4.56331 4	1.23507 6	6.0611 79	0.04203 2

Table 605:

This table describes genes of a *Acremonium zeae* sp. with beneficial effects on soybean growth, these genes show significant changes in expression when grown in culture with and without plant homogenate. "Median Exp. Plant" represents the median expression value in log₂ tpm across biological replicates grown in media inoculated with soybean seedling homogenate extracted with 50 mM PBS. "Median Exp. Mock" represents the median expression value in log₂ tpm across biological replicates grown in media inoculated with 50 mM PBS buffer. "Log FC" represents the estimate of the log₂-fold-change of the contrast. "B-statistic" represents the log-odds that the gene is differentially expressed. "t-statistic" represents the moderated t-statistic. "Adj. p-value" represents the false discovery rate (Benjamini & Hochberg, 1995) adjusted p-values.

SEQ ID	Description	sym577 gene	Median Exp. Plant	Median Exp. Mock	Log FC	B-statistic	t-statistic	Adj. p-value
674	K03510: POLI	g5345.t1	0	5.845894518	- 5.4820 2	5.27457 6	- 11.613 8	0.002239
675		g5348.t1	5.703283097	0	5.5890 81	4.88653 3	10.764 33	0.002344
677		g13489.t1	4.049293359	0	3.9400 48	4.43805 5	9.9096 33	0.002595
676		g7741.t1	7.176505771	2.550284622	5.0880 09	4.46360 2	9.9552 17	0.002595
678		g2539.t1	2.326788417	8.765149435	- 7.0312 5	3.15066 7	- 7.9724 7	0.014249
680		g1340.t1	0	5.657989905	- 5.6404 2	2.99161 3	- 7.7717 8	0.014249
679	K00275: pdxH, PNPO	g4287.t1	0.807562533	4.95193285	- 4.1951 8	3.00505 1	- 7.7884 8	0.014249
681	K00574: E2.1.1.79, cfa	g4581.t1	0.51190239	5.56764375	- 4.8498 4	2.75309	- 7.4830 6	0.017529
682	K06874: K06874	g9772.t1	1.832873801	5.323512963	- 3.5948 6	2.65771 5	- 7.3714 5	0.017819
683		g9852.t1	0.939929541	7.876491011	- 5.9383 4	2.18983 6	- 6.8524 2	0.030523
684		g2536.t1	9.671862421	2.653812149	6.9934 91	1.94463 1	6.5974 3	0.03853

Example 7: Functional Characterization of Endophytes (Secreted Proteomics Experiments)

5 [0102] This Example describes the ability of synthetic compositions comprising plant seeds and a single endophyte strain or a plurality of endophyte strains described herein, to confer beneficial traits to a host plant. Among other things, this Example provides exemplary characterization of modulations in a beneficial endophyte's secretome, as compared to the secretome of a neutral microbe of the same genus.

10 [0103] Mass spectrometry was used to explore differences in secreted proteins between beneficial endophytes and neutral microbes. Four genera were selected for the secreted proteomic analysis (two fungal and two bacterial): *Acremonium*, *Phoma*, *Stenotrophomonas*, and *Agrobacterium*. For each genus, a beneficial endophyte and neutral microbe were selected: SYM00577 (SEQ ID NO: 344) and SYM00300 (SEQ ID NO: 449); SYM15774 (SEQ ID NO: 447) and SYM01331 (SEQ ID NO: 450); SYM00906 (SEQ ID NO: 439) and SYM00865 (SEQ ID NO: 451); and SYM01004 (SEQ ID NO: 441) and SYM00091 (SEQ ID NO: 427).

20 [0104] Microbes were cultivated in three biological replicates for each strain. Briefly, each bacterium was initially streaked on Reasoner's 2A (R2A) agar, distinct CFUs selected and cultured in 10 mL R2A broth for 4 days. Fungal strains were streaked on potato dextrose (PD) agar and individual plugs containing spores and mycelial tissues were used to initiate growth in 10 mL PD broth for 6 days. All strains were grown with agitation at room temperature. Microbial culture filtrate was harvested by centrifuging at 4500 RPM for 20 minutes in 15 mL Falcon tubes to allow culture separation and removal of the supernatant. Five mL of culture supernatant were used for secreted proteomics analysis. All steps were performed in sterile conditions. Culture filtrates were kept in dry ice after harvest at all times to preserve protein stability. Media only samples consisting of PDB and R2A were tested independently to ensure the absence of intact proteins that could potentially interfere with the secreted microbial peptides.

30 [0105] Prior to mass spectrometry, samples were concentrated on a Pall 3kD MWCO MicroSep Spin Column (VWR Cat# 89132-006) and quantified at 1:10 dilution by Qubit fluorometry (Life Technologies). 12µg of each sample was separated ~1.5cm on a 10% Bis-Tris Novex mini-gel (Invitrogen) using the MES buffer system. The gel was stained with coomassie and each lane was excised into ten equally sized segments.

[0106] Gel pieces were processed using a robot (ProGest, DigiLab) with the following protocol:

- Washed with 25mM ammonium bicarbonate followed by acetonitrile.
- Reduced with 10mM dithiothreitol at 60°C followed by alkylation with 50mM iodoacetamide at RT.
- Digested with trypsin (Promega) at 37°C for 4h.
- Quenched with formic acid and the supernatant was analyzed directly without further processing.

10 Mass Spectrometry

[0107] The digests were analyzed by nano LC/MS/MS with a Waters NanoAcquity HPLC system interfaced to a ThermoFisher Q Exactive. Peptides were loaded on a trapping column and eluted over a 75µm analytical column at 350nL/min; both columns were packed with Proteo Jupiter resin (Phenomenex). A 30min gradient was employed (5h total). The mass spectrometer was operated in data-dependent mode, with MS and MS/MS performed in the Orbitrap at 70,000 FWHM and 17,500 FWHM resolution, respectively. The fifteen most abundant ions were selected for MS/MS.

[0108] Data were searched using a local copy of Mascot with the following parameters: Fixed modification: Carbamidomethyl (C); Variable modifications: Oxidation (M), Acetyl (Protein N-term), Pyro-Glu (N-term Q), Deamidation (NQ); Mass values: Monoisotopic; Peptide Mass Tolerance: 10 ppm; Fragment Mass Tolerance: 0.02 Da; Max Missed Cleavages: 2.

[0109] Mascot DAT files were parsed into the Scaffold software for validation, filtering and to create a non-redundant list per sample. Data were filtered 1% protein and peptide level false discovery rate (FDR) and requiring at least two unique peptides per protein.

Differential Secreted Protein Expression and Functional Enrichment Analysis

Data Acquisition and Processing

[0110] Protein sequence data, KEGG annotations and corresponding protein mass spectrometry spectral count data were provided to a vendor. Data were provided for beneficial (A) and non-beneficial (B) species pairs from two fungal and two bacterial genera. All data were converted into file formats and a local database suitable for subsequent processing, analysis and parallelization.

Protein Ortholog Identification

[0111] Pairs/groups of orthologous proteins were identified using a modified version of the OrthoMCL pipeline. Orthologs were identified as reciprocal best BLASTP hits, and then clusters of orthologous proteins were defined using the modified OrthoMCL pipeline. This process was done independently for the within genera and the between genera analyses.

5 BLASTP was run in parallel on the Georgia Tech PACE HPC environment.

Protein Functional Annotation

[0112] KEGG annotations for individual proteins were provided to the vendor based on the whole genome sequence annotations. The program BLAST2GO was used to annotate proteins with gene ontology (GO) terms based on sequence similarity to previously annotated
10 proteins.

Protein Expression Quantification and Normalization

[0113] Individual protein expression levels were taken as the number of observed spectra (*i.e.* the spectra count) corresponding to each protein. Protein spectra counts were retrieved across three replicates for each species. Missing counts for any given ortholog or replicate
15 were assigned values of 0. Individual protein expression levels (spectra counts) were then normalized by the total number of observed spectra for each replicate. This process was done independently for the three replicates corresponding to each member of the A-B pair of every species. Fold-change (FC) values for orthologous pairs/groups were computed as $\log_2 A/B$ spectra counts for the purpose of functional enrichment analysis

Protein Differential Expression Analysis

[0114] Differential protein expression analysis was done for a) pairs of orthologous proteins from the within genera analysis and b) groups of orthologous proteins from the between genera analysis. Differential expression was quantified by comparing the within group normalized spectra count variation to the between group normalized spectra count
25 variation using the Students ttest. A Benjamini-Hochberg False Discover Rate threshold of 0.2 was used to identify differentially abundant orthologous proteins.

Pathway and Functional Enrichment Analysis

[0115] Enrichment analysis was done in parallel using both KEGG and GO annotations with the hypergeometric test and via Gene Set Enrichment Analysis (GSEA). For the
30 hypergeometric test, for any given functional annotation category (*i.e.* KEGG pathway or GO term), the number of proteins up-regulated in the beneficial member of the orthologous pair

(species A) was compared to the total number of proteins up-regulated in the complete set of orthologs. For GSEA analysis, orthologous protein pairs/groups were ranked by FC values and the distribution of FC values was evaluated for a shift using the clusterprofiler R package.

5

SYM00577 secreted proteomic analysis

Table 700: 25 most abundant proteins secreted by SYM00577; “Median Abundance” represents the median value across three biological replicates in units of spectra per hundred spectra

SEQ ID	Protein ID	Median Abundance	GO Terms	KEGG Terms
477	1AXg13 463.t1	1.171575	GO:0008152: metabolic process; GO:0016798: hydrolase activity, acting on glycosyl bonds	none
478	1AXg10 805.t1	1.042072	GO:0004348: glucosylceramidase activity; GO:0005576: extracellular region; GO:0005975: carbohydrate metabolic process; GO:0006665: sphingolipid metabolic process; GO:0030248: cellulose binding	none
479	1AXg10 141.t1	0.63105	GO:0005975: carbohydrate metabolic process; GO:0016787: hydrolase activity	none
480	1AXg31 49.t1	0.581995	GO:0005975: carbohydrate metabolic process; GO:0016798: hydrolase activity, acting on glycosyl bonds	KEGG Orthology: K01213: E3.2.1.67: galacturan 1,4-alpha-galacturonidase [EC:3.2.1.67]; KEGG PATHWAY: ko00040: Pentose and glucuronate interconversions; ; KEGG PATHWAY: ko00500: Starch and sucrose metabolism;
481	1AXg52 93.t1	0.516427	GO:0003723: RNA binding; GO:0033897: ribonuclease T2 activity; GO:0090502: RNA phosphodiester bond hydrolysis, endonucleolytic	KEGG Orthology: K01166: E3.1.27.1: ribonuclease T2 [EC:3.1.27.1]
482	1AXg10 578.t1	0.498434	GO:0004190: aspartic-type endopeptidase activity; GO:0006508: proteolysis	none
483	1AXg10 693.t1	0.404474	GO:0000328: fungal-type vacuole lumen; GO:0016020: membrane; GO:0032366: intracellular sterol transport	none
484	1AXg11 973.t1	0.336207	GO:0005886: plasma membrane; GO:0005975: carbohydrate metabolic process; GO:0016021: integral component of membrane; GO:0016740:	none

			transferase activity; GO:0016787: hydrolase activity; GO:0031225: anchored component of membrane	
485	1AXg12 40.t1	0.322054	GO:0003993: acid phosphatase activity; GO:0016311: dephosphorylation; GO:0046872: metal ion binding	KEGG Orthology: K01078: E3.1.3.2: acid phosphatase [EC:3.1.3.2]; KEGG PATHWAY: ko00627: Aminobenzoate degradation: ; KEGG PATHWAY: ko00740: Riboflavin metabolism: ; KEGG PATHWAY: ko05152: Tuberculosis: Tuberculosis, or TB, is an infectious disease caused by Mycobacterium tuberculosis. One third of the world's population is thought to be infected with TB. About 90% of those infected result in latent infections, and about 10% of latent infections develop active diseases when their immune system is impaired due to the age, other diseases such as AIDS or exposure to immunosuppressive drugs. TB is transmitted through the air and primarily attacks the lungs, then it can spread by the circulatory system to other parts of body. Once TB bacilli have entered the host by the respiratory route and infected macrophages in the lungs, they interfere with phagosomal maturation, antigen presentation, apoptosis and host immune system to establish persistent or latent infection.
486	1AXg45 16.t1	0.315618	GO:0005975: carbohydrate metabolic process; GO:0016740: transferase activity; GO:0031224: intrinsic component of membrane	none
487	1AXg53 58.t1	0.294999	GO:0005976: polysaccharide metabolic process; GO:0016798: hydrolase activity, acting on glycosyl bonds; GO:0030246: carbohydrate binding	KEGG Orthology: K01178: E3.2.1.3: glucoamylase [EC:3.2.1.3]; KEGG PATHWAY: ko00500: Starch and sucrose metabolism:
488	1AXg94 78.t1	0.283328	GO:0044464: cell part	none
489	1AXg32 73.t1	0.275195	GO:0008233: peptidase activity	KEGG Orthology: K01312: PRSS: trypsin [EC:3.4.21.4]; KEGG PATHWAY: ko04080: Neuroactive ligand-receptor interaction: ; KEGG PATHWAY: ko04972: Pancreatic secretion: The pancreas performs both exocrine and endocrine functions. The exocrine pancreas consists of two parts, the acinar and duct cells. The primary functions of pancreatic acinar cells are to synthesize and secrete digestive enzymes. Stimulation of the cell by secretagogues such as acetylcholine (ACh) and cholecystokinin (CCK) causes the generation of an intracellular Ca ²⁺ signal. This signal, in turn,

				triggers the fusion of the zymogen granules with the apical plasma membrane, leading to the polarised secretion of the enzymes. The major task of pancreatic duct cells is the secretion of fluid and bicarbonate ions (HCO₃⁻), which neutralize the acidity of gastric contents that enter the duodenum. An increase in intracellular cAMP by secretin is one of the major signals of pancreatic HCO₃⁻ secretion. Activation of the CFTR Cl⁻ channel and the CFTR-dependent Cl⁻/HCO₃⁻ exchange activities is responsible for cAMP-induced HCO₃⁻ secretion.; KEGG PATHWAY: ko04974: Protein digestion and absorption: Protein is a dietary component essential for nutritional homeostasis in humans. Normally, ingested protein undergoes a complex series of degradative processes following the action of gastric, pancreatic and small intestinal enzymes. The result of this proteolytic activity is a mixture of amino acids and small peptides. Amino acids (AAs) are transported into the enterocyte (intestinal epithelial cell) by a variety of AA transporters that are specific for cationic (basic) AA, neutral AA, and anionic (acidic) AA. Small peptides are absorbed into enterocytes by the PEPT1 transporter. Inside enterocytes peptides are hydrolyzed, and the resulting amino acids are released together with those absorbed by AA transporters into blood via multiple, basolateral, AA transporters. Hydrolysis-resistant peptides, however, are transported out of the cells by a basolateral peptide transporter that has not been identified molecularly.; KEGG PATHWAY: ko05164: Influenza A: Influenza is a contagious respiratory disease caused by influenza virus infection. Influenza A virus is responsible for both annual seasonal epidemics and periodic worldwide pandemics. Novel strains that cause pandemics arise from avian influenza virus by genetic reassortment among influenza viruses and two surface glycoproteins HA and NA form the basis of serologically distinct virus types. The innate immune system recognizes invaded virus through multiple mechanisms. Viral non-structural NS1 protein is a multifunctional virulence factor that interfere IFN-mediated antiviral response. It inhibits IFN production by blocking activation of transcription factors such as NF-kappa B, IRF3 and AP1. NS1 further inhibits the activation of IFN-induced antiviral genes. PB1-F2 protein is another virulence factor that induce apoptosis of infected cells, which results in life-threatening bronchiolitis.
490	1AXg81 15.t1	0.234864	GO:0008152: metabolic process; GO:0016787:	none

			hydrolase activity	
491	1AXg12 530.t1	0.232187	GO:0000103: sulfate assimilation; GO:0005634: nucleus; GO:0005829: cytosol; GO:0006457: protein folding; GO:0015035: protein disulfide oxidoreductase activity; GO:0016671: oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor; GO:0034599: cellular response to oxidative stress; GO:0044281: small molecule metabolic process; GO:0045454: cell redox homeostasis; GO:0055114: oxidation-reduction process; GO:0071704: organic substance metabolic process; GO:1900429: negative regulation of filamentous growth of a population of unicellular organisms	KEGG Orthology: K03671: trxA: thioredoxin 1
492	1AXg92 66.t1	0.218366	GO:0016491: oxidoreductase activity	none
493	1AXg12 742.t1	0.214329	GO:0004553: hydrolase activity, hydrolyzing O-glycosyl compounds; GO:0071704: organic substance metabolic process	none
494	1AXg69 59.t1	0.213513	GO:0004190: aspartic-type endopeptidase activity; GO:0006508: proteolysis	none
495	1AXg93 6.t1	0.208768	GO:0008152: metabolic process; GO:0019239: deaminase activity	none
496	1AXg13 882.t1	0.208427	GO:0008152: metabolic process; GO:0016788: hydrolase activity, acting on ester bonds	KEGG Orthology: K01078: E3.1.3.2: acid phosphatase [EC:3.1.3.2]; KEGG PATHWAY: ko00627: Aminobenzoate degradation: ; KEGG PATHWAY: ko00740: Riboflavin metabolism: ; KEGG PATHWAY: ko05152: Tuberculosis: Tuberculosis, or TB, is an infectious disease caused by Mycobacterium tuberculosis. One third of the world's population is thought to be infected with TB. About 90% of those infected result in latent infections, and about 10% of latent infections develop active diseases when their immune system is impaired due to the age, other diseases such as AIDS or exposure to immunosuppressive drugs. TB is transmitted

				through the air and primarily attacks the lungs, then it can spread by the circulatory system to other parts of body. Once TB bacilli have entered the host by the respiratory route and infected macrophages in the lungs, they interfere with phagosomal maturation, antigen presentation, apoptosis and host immune system to establish persistent or latent infection.
497	1AXg97 50.t1	0.191554	GO:0005576: extracellular region; GO:0030248: cellulose binding; GO:0045493: xylan catabolic process; GO:0046373: L-arabinose metabolic process; GO:0046556: alpha-L-arabinofuranosidase activity	none
498	1AXg65 73.t1	0.188047	GO:0004568: chitinase activity; GO:0005975: carbohydrate metabolic process; GO:0006032: chitin catabolic process	none
499	1AXg92. t1	0.186476	GO:0016998: cell wall macromolecule catabolic process; GO:0052861: glucan endo-1,3-beta-glucanase activity, C-3 substituted reducing group; GO:0052862: glucan endo-1,4-beta-glucanase activity, C-3 substituted reducing group	none
500	1AXg91 92.t1	0.167015	GO:0005975: carbohydrate metabolic process	none
501	1AXg11 043.t1	0.1663	GO:0003824: catalytic activity; GO:0044238: primary metabolic process; GO:0071704: organic substance metabolic process	none

SYM00577 versus SYM00300

Table 701: Differential secreted protein abundance between SYM00577 and SYM00300.

This table describes the differential protein expression between pairs of orthologous proteins from a genus, where one member of the pair has a beneficial effect on plant growth and the other has a neutral effect. "A.mean" represents the average normalized spectral counts between biological replicates of the beneficial member of the pair. "B.mean" represents the average normalized spectral counts between biological replicates of the neutral member of

the pair. "Fold change" represents the fold change difference between the two organisms.

"FDR q-value" represents the false discovery rate corrected q-value.

SEQ ID Beneficial	A.protein	SEQ ID Neutral	B.protein	KEGG	GO	A.mean	B.mean	Fold- change	absFC	FDR q-value
502	1AX g102 2.t1	2297	1BXg 8091 .t1	Biosynthesis of amino acids, Carbon metabolism, E2.2.1.2, talA, talB, Pentose phosphate pathway	carbohydrate metabolic process, cytosol, nucleus, pentose-phosphate shunt, non-oxidative branch, sedoheptulose-7- phosphate:D- glyceraldehyde-3- phosphate glyceronetransferase activity	0	0.37	-8.5	8.5	0.03
487	1AX g535 8.t1	2298	1BXg 9546 .t1	E3.2.1.3, Starch and sucrose metabolism	carbohydrate binding, hydrolase activity, acting on glycosyl bonds, polysaccharide metabolic process	0.3	0	8.2	8.2	0.02
503	1AX g884 1.t1	2299	1BXg 1271 .t1	Cysteine and methionine metabolism, E3.3.1.1, ahcY	adenosylhomocysteinase activity, cytosol, one-carbon metabolic process, phosphatidylcholine biosynthetic process, S- adenosylhomocysteine catabolic process, triglyceride metabolic process	0	0.24	-7.9	7.9	0.01
504	1AX g208 08.t 1	2300	1BXg 8757 .t1	None	carbohydrate metabolic process, hydrolase activity, acting on glycosyl bonds, hydrolase activity, hydrolyzing O-glycosyl compounds, metabolic process	0	0.24	-7.9	7.9	0.02
505	1AX g105 83.t 1	2301	1BXg 1063 1.t1	None	cell wall macromolecule catabolic process, lysozyme activity, peptidoglycan catabolic process	0.16	0	7.4	7.4	0.05
506	1AX g864 4.t1	2302	1BXg 2276 .t1	E3.1.27.1	cytoplasmic part, ribonuclease T2 activity, RNA binding, RNA phosphodiester bond hydrolysis, endonucleolytic, single-organism cellular process	0	0.13	-7.1	7.1	0.02
507	1AX g360 .t1	2303	1BXg 8875 .t1	None	None	0	0.12	-6.9	6.9	0.01

508	1AX g996 0.t1	2304	1BXg 1125 0.t1	Purine metabolism, ylbA, UGHY	None	0	0.12	-6.9	6.9	0.02
509	1AX g100 66.t 1	2305	1BXg 2721 .t1	None	nuclease activity	0	0.12	-6.9	6.9	0.03
510	1AX g995 4.t1	2306	1BXg 1140 2.t1	None	hydrolase activity, metabolic process	0	0.12	-6.9	6.9	0.04
511	1AX g110 78.t 1	2307	1BXg 1562 .t1	None	None	0	0.1	-6.7	6.7	0.02
512	1AX g716 0.t1	2308	1BXg 550. t1	Aminobenzoate degradation, Folate biosynthesis, phoD, Two- component system	None	0	0.1	-6.7	6.7	0.02
513	1AX g797 8.t1	2309	1BXg 1024 0.t1	None	hydrolase activity	0	0.09	-6.6	6.6	0.02
514	1AX g859 9.t1	2310	1BXg 3056 .t1	None	None	0.1	0	6.6	6.6	0.02
515	1AX g118 64.t 1	2311	1BXg 8819 .t1	None	glucose metabolic process, L-xylulose reductase (NADP+) activity, mannitol 2-dehydrogenase (NADP+) activity, mitochondrion, oxidation-reduction process, protein homotetramerization, xylulose metabolic process	0	0.1	-6.6	6.6	0.02
516	1AX g134 64.t 1	2312	1BXg 8758 .t1	None	hydrolase activity, metabolic process	0	0.09	-6.6	6.6	0.02
517	1AX g130 99.t 1	2313	1BXg 8761 .t1	None	carbohydrate metabolic process, hydrolase activity, hydrolyzing O-glycosyl compounds, intracellular part	0	0.09	-6.5	6.5	0.02

518	1AX g107 28.t 1	2314	1BXg 4259 .t1	None	hydrolase activity, metabolic process	0.09	0	6.5	6.5	0.05
519	1AX g31. t1	2315	1BXg 2840 .t1	gcvH, GCSH, Glycine, serine and threonine metabolism, Glyoxylate and dicarboxylate metabolism	glycine cleavage complex, glycine decarboxylation via glycine cleavage system, mitochondrion, one-carbon metabolic process, oxidation-reduction process, protein lipoylation	0	0.08	-6.4	6.4	0.02
520	1AX g447 6.t1	2316	1BXg 5721 .t1	None	endonuclease activity, exonuclease activity, nuclease activity, nucleic acid phosphodiester bond hydrolysis	0	0.09	-6.4	6.4	0.02
521	1AX g110 59.t 1	2317	1BXg 2900 .t1	Fatty acid elongation, Fatty acid metabolism, Lysosome, PPT	endoplasmic reticulum, palmitoyl-(protein) hydrolase activity, protein depalmitoylation, vacuolar acidification, vacuole	0.08	0	6.3	6.3	0.02
522	1AX g103 28.t 1	2318	1BXg 8689 .t1	None	None	0	0.06	-6	6	0.01
523	1AX g107 40.t 1	2319	1BXg 1198 7.t1	None	cell part	0	0.24	-6	6	0.02

524	1AX g183 92.t 1	2320	1BXg 1166 4.t1	Adrenergic signaling in cardiomyocytes, Alcoholism, Alzheimer's disease, Amphetamine addiction, Calcium signaling pathway, CALM, cAMP signaling pathway, cGMP-PKG signaling pathway, Circadian entrainment, Dopaminergic synapse, Estrogen signaling pathway, Gastric acid secretion, Glioma, GnRH signaling pathway, Inflammatory mediator regulation of TRP channels, Insulin signaling pathway, Long-term potentiation, Melanogenesis, Neurotrophin signaling pathway, Olfactory transduction, Oocyte meiosis, Oxytocin signaling pathway, Pertussis, Phosphatidylinositol signaling system, Phototransduction, Phototransduction - fly, Plant-pathogen interaction, Rap1 signaling pathway, Ras signaling pathway, Salivary secretion, Tuberculosis, Vascular smooth muscle contraction	ascospore-type prospore-specific spindle pole body remodeling, ATP hydrolysis coupled proton transport, barrier septum, calcium ion binding, calcium-dependent protein binding, cell budding, cell division site, cellular bud neck, cellular bud tip, central plaque of spindle pole body, cytosol, hydrogen ion transmembrane transporter activity, incipient cellular bud site, integral component of membrane, karyogamy involved in conjugation with cellular fusion, lysosomal microautophagy, maintenance of protein location in spindle pole body, mating projection tip, mitotic spindle assembly, mitotic spindle pole body, mycelium development, new growing cell tip, NLS-bearing protein import into nucleus, nucleus, old growing cell tip, phosphatidylinositol biosynthetic process, proton-transporting V-type ATPase, V0 domain, receptor-mediated endocytosis, regulation of cell cycle, spitzenkorper, spore germination, transcription factor import into nucleus, vacuole fusion, non-autophagic	0	0.06	-6	6	0.03
				358						

525	1AX g344 6.t1	2321	1BXg 4699 .t1	None	None	0	0.06	-6	6	0.03
526	1AX g395 9.t1	2322	1BXg 3931 .t1	Amino sugar and nucleotide sugar metabolism, E3.2.1.14	hydrolase activity, hydrolyzing O-glycosyl compounds, organic substance metabolic process	0	0.06	-6	6	0.04
494	1AX g695 9.t1	2323	1BXg 7026 .t1	None	aspartic-type endopeptidase activity, proteolysis	0.23	0	5.9	5.9	0.02
527	1AX g498 5.t1	2324	1BXg 8953 .t1	None	FMN binding, oxidation- reduction process, oxidoreductase activity	0	0.06	-5.9	5.9	0.04
528	1AX g429 1.t1	2325	1BXg 1944 .t1	E3.2.1.101	hydrolase activity	0.05	0	5.8	5.8	0.02
529	1AX g672 8.t1	2326	1BXg 4339 .t1	ndk, NME, Purine metabolism, Pyrimidine metabolism	ATP binding, CDP phosphorylation, cellular response to DNA damage stimulus, CTP biosynthetic process, cytosol, GTP biosynthetic process, identical protein binding, integral component of membrane, mitochondrial intermembrane space, nucleoside diphosphate kinase activity, nucleus, UTP biosynthetic process	0	0.06	-5.8	5.8	0.02
530	1AX g102 68.t 1	2327	1BXg 2378 .t1	None	hydrolase activity, acting on glycosyl bonds, metabolic process	0.05	0	5.8	5.8	0.02
531	1AX g327 7.t1	2328	1BXg 3155 .t1	None	hydrolase activity, membrane	0.06	0	5.8	5.8	0.03
532	1AX g27. t1	2329	1BXg 1583 .t1	None	acid phosphatase activity, dephosphorylation	0	0.05	-5.8	5.8	0.04

533	1AX g162 7.t1	2330	1BXg 7860 .t1	None	cell redox homeostasis, Golgi trans cisterna, integral component of plasma membrane, oligopeptide transport, oligopeptide transporter activity, peroxisome, positive regulation of monopolar cell growth, regulation of phospholipid translocation, regulation of vacuole organization, transmembrane transport, vacuole fusion, non- autophagic	0	0.05	-5.7	5.7	0.02
534	1AX g523 5.t1	2331	1BXg 2358 .t1	Antigen processing and presentation, Endocytosis, Epstein-Barr virus infection, Estrogen signaling pathway, HSPA1_8, Influenza A, Legionellosis, MAPK signaling pathway, Measles, Protein processing in endoplasmic reticulum, Spliceosome, Toxoplasmosis	ATP binding, integral component of membrane	0	0.05	-5.7	5.7	0.02
535	1AX g769 3.t1	2332	1BXg 9970 .t1	None	carbohydrate binding, carbohydrate catabolic process, hydrolase activity, hydrolyzing O-glycosyl compounds	0	0.05	-5.7	5.7	0.03
536	1AX g782 7.t1	2333	1BXg 8670 .t1	Ribosome, RP- S16e, RPS16	ribosome, structural constituent of ribosome, translation	0	0.05	-5.6	5.6	0.02
537	1AX g966 2.t1	2334	1BXg 4876 .t1	None	integral component of membrane, transmembrane transport, transmembrane transporter activity	0	0.05	-5.6	5.6	0.02

538	1AX g528 9.t1	2335	18Xg 2280 .t1	Alanine, aspartate and glutamate metabolism, beta-Alanine metabolism, Butanoate metabolism, E4.1.1.15, gadB, gadA, GAD, GABAergic synapse, Taurine and hypotaurine metabolism, Type I diabetes mellitus	calmodulin binding, cellular response to oxidative stress, cytoplasm, glutamate catabolic process, glutamate decarboxylase activity, pyridoxal phosphate binding	0	0.05	-5.6	5.6	0.02
539	1AX g104 86.t 1	2336	18Xg 1674 .t1	SLC39A1_2_3, ZIP1_2_3	integral component of membrane, low-affinity zinc II ion transport, low-affinity zinc ion transmembrane transporter activity, plasma membrane, zinc II ion transmembrane transport, zinc ion transmembrane transporter activity	0	0.05	-5.6	5.6	0.03
540	1AX g121 00.t 1	2337	18Xg 7176 .t1	Cell cycle, Epstein-Barr virus infection, Hippo signaling pathway, Hippo signaling pathway - fly, Neurotrophin signaling pathway, Oocyte meiosis, PI3K-Akt signaling pathway, Viral carcinogenesis, YWHAH	monooxygenase activity, oxidation-reduction process, protein domain specific binding	0	0.05	-5.6	5.6	0.03
541	1AX g538 3.t1	2338	18Xg 9570 .t1	Alzheimer's disease, Biosynthesis of amino acids, Carbon fixation in photosynthetic organisms, Carbon metabolism, GAPDH, gapA, Glycolysis / Gluconeogenesis , HIF-1 signaling pathway	glucose metabolic process, glyceraldehyde-3- phosphate dehydrogenase (NAD+) (phosphorylating) activity, glycolytic process, NAD binding, NADP binding, oxidation-reduction process	0	0.05	-5.5	5.5	0.02

542	1AX g101 97.t 1	2339	1BXg 1116 1.t1	E3.1.4.46, glpQ, ugpQ, Glycerophosphol ipid metabolism	glycerophosphodiester phosphodiesterase activity, lipid metabolic process	0	0.04	-5.4	5.4	0.01
543	1AX g443 3.t1	2340	1BXg 6768 .t1	E3.2.1.6	hydrolase activity, hydrolyzing O-glycosyl compounds, metabolic process	0	0.04	-5.4	5.4	0.04
544	1AX g393 2.t1	2341	1BXg 3960 .t1	FoxO signaling pathway, PRMT1	cytosol, identical protein binding, mRNA export from nucleus, negative regulation of DNA-templated transcription, termination, nucleus, peptidyl-arginine methylation, to asymmetrical-dimethyl arginine, positive regulation of transcription elongation from RNA polymerase II promoter, protein-arginine omega-N asymmetric methyltransferase activity, protein-arginine omega-N monomethyltransferase activity	0	0.04	-5.4	5.4	0.04
545	1AX g105 61.t 1	2342	1BXg 1546 .t1	None	oxidoreductase activity	0	0.04	-5.3	5.3	0.02
546	1AX g321 6.t1	2343	1BXg 6110 .t1	None	lipid metabolic process, organic substance metabolic process, phosphoric diester hydrolase activity, primary metabolic process	0	0.04	-5.3	5.3	0.05
547	1AX g727 7.t1	2344	1BXg 1184 5.t1	EEF1A, Legionellosis, RNA transport	cytoplasm, GTP binding, GTPase activity, translation elongation factor activity, translational elongation	0	0.04	-5.2	5.2	0.02
548	1AX g108 03.t 1	2345	1BXg 2053 .t1	None	carbohydrate metabolic process, cellulose binding, extracellular region, hydrolase activity, hydrolyzing O-glycosyl compounds	0	0.04	-5.2	5.2	0.02
549	1AX g612 3.t1	2346	1BXg 7324 .t1	None	None	0	0.04	-5.2	5.2	0.02

550	1AX g483 4.t1	2347	1BXg 4445 .t1	None	carbohydrate metabolic process, hydrolase activity, hydrolyzing O-glycosyl compounds, integral component of membrane	0.03	0	5.1	5.1	0.02
551	1AX g133 04.t1	2348	1BXg 9661 .t1	None	carbohydrate metabolic process, hydrolase activity, hydrolyzing O-glycosyl compounds	0.01	0.19	-5	5	0.01
552	1AX g317 1.t1	2349	1BXg 2692 .t1	E3.2.1.4, Starch and sucrose metabolism	hydrolase activity, hydrolyzing O-glycosyl compounds, polysaccharide catabolic process	0	0.03	-5	5	0.02
553	1AX g712 6.t1	2350	1BXg 5592 .t1	Amino sugar and nucleotide sugar metabolism, Butirosin and neomycin biosynthesis, Carbohydrate digestion and absorption, Carbon metabolism, Central carbon metabolism in cancer, Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, HIF-1 signaling pathway, HK, Insulin signaling pathway, Starch and sucrose metabolism, Streptomycin biosynthesis, Type II diabetes mellitus	ATP binding, canonical glycolysis, carbohydrate phosphorylation, cellular glucose homeostasis, cytosol, fructokinase activity, fructose 6-phosphate metabolic process, fructose import, fructose metabolic process, glucokinase activity, glucose 6-phosphate metabolic process, glucose binding, glucose import, mannokinase activity, mannose metabolic process, mitochondrion, nucleus, regulation of transcription by glucose, replicative cell aging	0	0.03	-5	5	0.04
554	1AX g174 9.t1	2351	1BXg 9726 .t1	None	None	0	0.03	-4.9	4.9	0.02

555	1AX g109 73.t 1	2352	1BXg 5639 .t1	K16330, Pyrimidine metabolism	cytoplasm, endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA), hydrolase activity, acting on glycosyl bonds, kinase activity, phosphorylation, pseudouridine synthesis, Pwp2p-containing subcomplex of 90S preribosome, small-subunit processome	0	0.03	-4.9	4.9	0.02
556	1AX g269 5.t1	2353	1BXg 6589 .t1	None	None	0	0.03	-4.9	4.9	0.03
557	1AX g584 5.t1	2354	1BXg 1158 .t1	Ribosome, RP- S3e, RPS3	cytoplasmic translation, cytosolic small ribosomal subunit, DNA catabolic process, endonucleolytic, DNA-(apurinic or apyrimidinic site) lyase activity, preribosome, small subunit precursor, ribosomal small subunit export from nucleus, RNA binding, rRNA export from nucleus, structural constituent of ribosome	0	0.03	-4.9	4.9	0.04
558	1AX g906 5.t1	2355	1BXg 8585 .t1	AMPK signaling pathway, EEF2, Oxytocin signaling pathway	GTP binding, GTPase activity, integral component of membrane, translation elongation factor activity, translational elongation	0	0.03	-4.9	4.9	0.04
559	1AX g105 39.t 1	2356	1BXg 6684 .t1	None	None	0	0.03	-4.8	4.8	0.02
560	1AX g468 3.t1	2357	1BXg 1058 0.t1	E3.2.1.8, xynA	D-xylose metabolic process, endo-1,4-beta-xylanase activity, xylan catabolic process	0	0.03	-4.8	4.8	0.02

561	1AX g119 8.t1	2358	1BXg 352. t1	Adherens junction, Axon guidance, Bacterial invasion of epithelial cells, cAMP signaling pathway, cGMP- PKG signaling pathway, Chemokine signaling pathway, Colorectal cancer, Endocytosis, Focal adhesion, Leukocyte transendothelial migration, MAPK signaling pathway - yeast, MicroRNAs in cancer, Neurotrophin signaling pathway, Oxytocin signaling pathway, Pancreatic secretion, Pathogenic Escherichia coli infection, Pathways in cancer, Pertussis, Platelet activation, Proteoglycans in cancer, Rap1 signaling pathway, Ras signaling pathway, Regulation of actin cytoskeleton, RHOA, Sphingolipid signaling pathway, T cell receptor signaling pathway, TGF- beta signaling pathway, Tight junction, Tuberculosis, Vascular smooth muscle contraction, Viral	1,3-beta-D-glucan synthase complex, actin cytoskeleton reorganization, budding cell bud growth, cellular bud neck, cellular bud tip, Golgi apparatus, GTP binding, GTPase activity, incipient cellular bud site, mating projection tip, peroxisome, positive regulation of endocytosis, positive regulation of protein kinase C signaling, protein transport, regulation of cell size, regulation of cell wall (1->3)-beta-D-glucan biosynthetic process, regulation of exocyst localization, regulation of fungal-type cell wall organization, regulation of vacuole fusion, non- autophagic, small GTPase mediated signal transduction	0	0.03	-4.8	4.8	0.04
					365					

562	1AX g190 4.t1	2359	1BXg 5010 .t1	YAT	amino acid transmembrane transport, amino acid transmembrane transporter activity, integral component of membrane	0	0.03	-4.7	4.7	0.02
563	1AX g317 6.t1	2360	1BXg 4958 .t1	HXT, Meiosis - yeast	integral component of membrane, substrate-specific transmembrane transporter activity, transmembrane transport	0	0.02	-4.6	4.6	0.02
564	1AX g100 60.t 1	2361	1BXg 2790 .t1	E3.2.1.8, xynA	endo-1,4-beta-xylanase activity, xylan catabolic process	0	0.02	-4.5	4.5	0.02
565	1AX g570 9.t1	2362	1BXg 9980 .t1	2-Oxocarboxylic acid metabolism, Biosynthesis of amino acids, C5- Branched dibasic acid metabolism, leuB, Valine, leucine and isoleucine biosynthesis	3-isopropylmalate dehydrogenase activity, ATP binding, ATP hydrolysis coupled proton transport, ATP metabolic process, cytosol, glyoxylate cycle, leucine biosynthetic process, magnesium ion binding, NAD binding, oxidation-reduction process, proton-transporting ATPase activity, rotational mechanism, proton-transporting V-type ATPase, V1 domain	0	0.02	-4.5	4.5	0.02
566	1AX g827 5.t1	2363	1BXg 5365 .t1	None	None	0.02	0	4.5	4.5	0.02
567	1AX g190 9.t1	2364	1BXg 6126 .t1	None	peptidase activity	0.02	0	4.5	4.5	0.03
568	1AX g475 2.t1	2365	1BXg 2001 .t1	AMPK signaling pathway, Pancreatic secretion, RAB8A, MEL	ascospore-type prospore assembly, autophagy, cytosol, exocytosis, Golgi to plasma membrane transport, GTP binding, GTPase activity, incipient cellular bud site, intracellular protein transport, membrane, membrane addition at site of cytokinesis, metabolic process, nucleocytoplasmic transport, nucleus, small GTPase mediated signal transduction, transport vesicle, vesicle fusion	0	0.02	-4.5	4.5	0.03

569	1AX g376 5.t1	2366	1BXg 2666 .t1	None	catalytic activity, integral component of membrane, metabolic process	0	0.02	-4.4	4.4	0.02
570	1AX g289 1.t1	2367	1BXg 1088 2.t1	None	carboxypeptidase activity, metalloproteinase activity, proteolysis, zinc ion binding	0	0.02	-4.4	4.4	0.03
478	1AX g108 05.t 1	2368	1BXg 9667 .t1	None	carbohydrate metabolic process, cellulose binding, extracellular region, glucosylceramidase activity, sphingolipid metabolic process	0.98	0.05	4.4	4.4	0.04
571	1AX g589 1.t1	2369	1BXg 1097 9.t1	E5.2.1.8	apoptotic process, cytosol, mitochondrion, nucleus, peptidyl-prolyl cis-trans isomerase activity, protein folding, protein peptidyl-prolyl isomerization	0	0.02	-4.4	4.4	0.05
572	1AX g100 65.t 1	2370	1BXg 2722 .t1	None	None	0.36	0.02	4.3	4.3	0.02
573	1AX g197 25.t 1	2371	1BXg 7679 .t1	Ribosome, RP-L7e, RPL7	ribosome	0	0.02	-4.3	4.3	0.02
574	1AX g207 23.t 1	2372	1BXg 2050 .t1	None	integral component of membrane, transmembrane transport, transmembrane transporter activity	0	0.02	-4.3	4.3	0.02
575	1AX g211 75.t 1	2373	1BXg 6238 .t1	Ribosome, RP-L13Ae, RPL13A	large ribosomal subunit, structural constituent of ribosome, translation	0	0.02	-4.3	4.3	0.04
576	1AX g229 2.t1	2374	1BXg 1071 0.t1	ARN	integral component of membrane, transmembrane transport	0	0.02	-4.2	4.2	0.01
577	1AX g139 1.t1	2375	1BXg 3917 .t1	None	cytosol, nucleus, proteolysis, serine-type peptidase activity	0	0.02	-4.2	4.2	0.05

578	1AX g817 4.t1	2376	18Xg 7986 .t1	None	catalytic activity, cell, cell redox homeostasis, glycerol ether metabolic process, integral component of membrane, membrane, oxidation-reduction process, protein disulfide oxidoreductase activity, single-organism cellular process, single-organism metabolic process, translation	0	0.02	-4.1	4.1	0.03
480	1AX g314 9.t1	2377	18Xg 4998 .t1	E3.2.1.67, Pentose and glucuronate interconversions, Starch and sucrose metabolism	carbohydrate metabolic process, cell wall organization, extracellular region, hydrolase activity, acting on glycosyl bonds, polygalacturonase activity	0.55	0.03	4	4	0.02
579	1AX g418 4.t1	2378	18Xg 1792 .t1	None	integral component of membrane	0.02	0	4	4	0.03
580	1AX g575 1.t1	2379	18Xg 7894 .t1	Carbohydrate digestion and absorption, E3.2.1.1, amyA, malS, Starch and sucrose metabolism	alpha-amylase activity, carbohydrate metabolic process, cation binding, oxidation-reduction process, oxidoreductase activity, starch binding	0.02	0	4	4	0.03
581	1AX g107 45.t 1	2380	18Xg 1199 3.t1	None	None	0.02	0	4	4	0.03
582	1AX g897 7.t1	2381	18Xg 1138 8.t1	TC.POT	integral component of membrane, oligopeptide transport, transporter activity	0	0.02	-4	4	0.04

583	1AX g250 3.t1	2382	1BXg 3531 .t1	Amino sugar and nucleotide sugar metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis , Pentose phosphate pathway, pgm, Purine metabolism, Starch and sucrose metabolism, Streptomycin biosynthesis	carbohydrate metabolic process, intramolecular transferase activity, phosphotransferases, magnesium ion binding, nucleus	0	0.02	-4	4	0.05
584	1AX g335 8.t1	2383	1BXg 4769 .t1	None	None	0	0.07	-3.9	3.9	0
585	1AX g831 7.t1	2384	1BXg 5117 .t1	None	None	0	0.07	-3.9	3.9	0
586	1AX g427 8.t1	2385	1BXg 1931 .t1	AFG1, LACE1, zapE	ATP binding, cellular response to oxidative stress, misfolded or incompletely synthesized protein catabolic process, mitochondrial inner membrane, protein import into peroxisome matrix	0	0.01	-3.9	3.9	0.02
587	1AX g110 50.t 1	2386	1BXg 2887 .t1	None	proteolysis, serine-type carboxypeptidase activity	0.06	0	3.9	3.9	0.03
588	1AX g824 7.t1	2387	1BXg 1003 2.t1	Biosynthesis of amino acids, Carbon fixation in photosynthetic organisms, Carbon metabolism, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis , Inositol phosphate metabolism, TPI, tpiA	canonical glycolysis, gluconeogenesis, mitochondrion, nucleus, pentose-phosphate shunt, triose-phosphate isomerase activity	0.01	0.09	-3.9	3.9	0.04

589	1AX g553 1.t1	2388	1BXg 1134 4.t1	E3.2.1.6	carbohydrate metabolic process, hydrolase activity, hydrolyzing O-glycosyl compounds	0	0.01	-3.8	3.8	0.02
590	1AX g952 1.t1	2389	1BXg 6591 .t1	None	cellular aromatic compound metabolic process, ferric iron binding, integral component of membrane, oxidation-reduction process, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	0	0.01	-3.8	3.8	0.02
591	1AX g113 77.t 1	2390	1BXg 307. t1	XEG	carbohydrate metabolic process, hydrolase activity, acting on glycosyl bonds, hydrolase activity, hydrolyzing O-glycosyl compounds	0	0.01	-3.8	3.8	0.03
592	1AX g765 8.t1	2391	1BXg 7553 .t1	Cysteine and methionine metabolism, E1.8.4.14	cellular response to oxidative stress, cytoplasm, methionine-R-sulfoxide reductase activity, oxidation-reduction process	0	0.01	-3.8	3.8	0.04
593	1AX g125 5.t1	2392	1BXg 439. t1	None	None	0.14	0.01	3.8	3.8	0.04
594	1AX g110 60.t 1	2393	1BXg 1582 .t1	None	integral component of membrane, transmembrane transport	0	0.01	-3.7	3.7	0.02
595	1AX g690 7.t1	2394	1BXg 8642 .t1	None	None	0.01	0	3.7	3.7	0.02
596	1AX g197 6.t1	2395	1BXg 6237 .t1	None	intracellular ribonucleoprotein complex	0.01	0	3.7	3.7	0.02
597	1AX g102 16.t 1	2396	1BXg 1197 1.t1	None	cell redox homeostasis, cellular response to oxidative stress, glutathione peroxidase activity, mitochondrion, oxidation-reduction process, response to cadmium ion, thioredoxin peroxidase activity	0	0.01	-3.7	3.7	0.02

598	1AX g825 1.t1	2397	18Xg 1002 8.t1	None	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, metabolic process	0	0.01	-3.7	3.7	0.03
599	1AX g645 7.t1	2398	18Xg 5328 .t1	None	integral component of membrane, membrane, transmembrane transport	0	0.01	-3.7	3.7	0.03
600	1AX g112 01.t 1	2399	18Xg 8976 .t1	None	None	0.2	0.01	3.7	3.7	0.05
601	1AX g214 45.t 1	2400	18Xg 1174 3.t1	Ribosome, RP-SAe, RPSA	cytosolic small ribosomal subunit, ribosomal small subunit assembly, structural constituent of ribosome, translation	0	0.01	-3.6	3.6	0.03
602	1AX g126 10.t 1	2401	18Xg 3489 .t1	None	acid phosphatase activity, dephosphorylation, integral component of membrane	0.05	0	3.6	3.6	0.04
603	1AX g81. t1	2402	18Xg 1097 5.t1	None	None	0	0.01	-3.6	3.6	0.04
604	1AX g318 8.t1	2403	18Xg 9954 .t1	None	None	0.01	0	3.5	3.5	0.02
605	1AX g734 1.t1	2404	18Xg 1038 9.t1	None	None	0	0.01	-3.5	3.5	0.03
606	1AX g834 0.t1	2405	18Xg 5140 .t1	Oxidative phosphorylation, ppa	aerobic respiration, cellular metabolic process, cytoplasm, inorganic diphosphatase activity, magnesium ion binding, mitochondrion, phosphate-containing compound metabolic process	0	0.01	-3.5	3.5	0.04
607	1AX g658 5.t1	2406	18Xg 1011 4.t1	FTR, efeU	high-affinity iron ion transmembrane transport, high-affinity iron permease complex, integral component of membrane, iron ion transmembrane transporter activity, metabolic process, transferase activity	0	0.01	-3.5	3.5	0.04

608	1AX g178 5.t1	2407	18Xg 1175 .t1	Amino sugar and nucleotide sugar metabolism, Glycosaminoglyc an degradation, Glycosphingolipi d biosynthesis - ganglio series, Glycosphingolipi d biosynthesis - globo series, HEXA_B, Lysosome, Other glycan degradation	beta-N- acetylhexosaminidase activity, carbohydrate metabolic process	0.02	0.17	-3.4	3.4	0.01
609	1AX g282 7.t1	2408	18Xg 9091 .t1	map	aminopeptidase activity, fumagillin biosynthetic process, metal ion binding, metalloexopeptidase activity, proteolysis	0.01	0	3.4	3.4	0.02
610	1AX g328 5.t1	2409	18Xg 8264 .t1	None	cell part	0	0.01	-3.4	3.4	0.02
611	1AX g710 2.t1	2410	18Xg 5569 .t1	None	None	0	0.01	-3.4	3.4	0.02
612	1AX g975 1.t1	2411	18Xg 1036 .t1	E3.6.3.6, Oxidative phosphorylation	ATP binding, ATP biosynthetic process, hydrogen ion transmembrane transport, hydrogen-exporting ATPase activity, phosphorylative mechanism, integral component of membrane, metal ion binding	0	0.01	-3.4	3.4	0.02
613	1AX g311 4.t1	2412	18Xg 1181 6.t1	None	hydrolase activity, positive regulation of translation, positive regulation of translational elongation, positive regulation of translational termination, ribosome binding, RNA binding, translation elongation factor activity, translational elongation, translational frameshifting	0	0.01	-3.4	3.4	0.03
614	1AX g204 7.t1	2413	18Xg 2549 .t1	None	carbohydrate metabolic process, cell wall, cell wall organization, hydrolase activity, hydrolyzing O- glycosyl compounds, transferase activity	0.05	0.46	-3.3	3.3	0.02

615	1AX g524 .t1	2414	1BXg 8254 .t1	None	integral component of membrane, transmembrane transport	0	0.01	-3.3	3.3	0.02
616	1AX g509 0.t1	2415	1BXg 2954 .t1	SNARE interactions in vesicular transport, STX1B_2_3, Synaptic vesicle cycle	integral component of membrane, vesicle- mediated transport	0	0.01	-3.3	3.3	0.02
617	1AX g652 4.t1	2416	1BXg 2065 .t1	Alzheimer's disease, Cardiac muscle contraction, Huntington's disease, Non- alcoholic fatty liver disease (NAFLD), Oxidative phosphorylation, Parkinson's disease, Two- component system, UQCRES1, RIP1, petA	2 iron, 2 sulfur cluster binding, aerobic respiration, hydrogen ion transmembrane transport, metal ion binding, mitochondrial electron transport, ubiquinol to cytochrome c, mitochondrial respiratory chain complex III, ubiquinol- cytochrome-c reductase activity	0	0.01	-3.3	3.3	0.03
618	1AX g948 5.t1	2417	1BXg 5765 .t1	None	ATP binding, ATPase activity, endoplasmic reticulum, integral component of membrane, metabolic process	0.01	0	3.3	3.3	0.04
619	1AX g346 0.t1	2418	1BXg 4685 .t1	Biosynthesis of amino acids, hisG, Histidine metabolism	ATP phosphoribosyltransferase activity, cytosol, histidine biosynthetic process, magnesium ion binding	0	0.05	-3.2	3.2	0.01
620	1AX g325 9.t1	2419	1BXg 8229 .t1	PMPCB, MAS1	metal ion binding, metalloendopeptidase activity, mitochondrial processing peptidase complex, protein processing involved in protein targeting to mitochondrion	0	0.01	-3.2	3.2	0.02
621	1AX g760 7.t1	2420	1BXg 7629 .t1	None	integral component of membrane	0	0.01	-3.2	3.2	0.02
622	1AX g316 0.t1	2421	1BXg 1334 .t1	PHO84	inorganic phosphate transmembrane transporter activity, integral component of membrane, phosphate ion transport, transmembrane transport	0.01	0.1	-3.1	3.1	0

623	1AX g459 .t1	2422	1BXg 8019 .t1	E3.2.1.101	catalytic activity, membrane	0.03	0	3.1	3.1	0.01
624	1AX g111 34.t 1	2423	1BXg 6417 .t1	None	cytoplasmic part, endomembrane system, integral component of membrane, intracellular membrane-bounded organelle, transmembrane transport	0	0.01	-3.1	3.1	0.02
625	1AX g148 33.t 1	2424	1BXg 6900 .t1	Calcium signaling pathway, cGMP- PKG signaling pathway, HTLV-I infection, Huntington's disease, Parkinson's disease, SLC25A4S, ANT	ADP transport, ATP:ADP antiporter activity, DNA repair, integral component of membrane, kinetochore assembly, mitochondrial ATP transmembrane transport, mitochondrial inner membrane	0	0.01	-3.1	3.1	0.02
626	1AX g230 8.t1	2425	1BXg 1072 5.t1	None	NAD(P)+ transhydrogenase activity, single-organism process	0	0.01	-3.1	3.1	0.02
627	1AX g736 9.t1	2426	1BXg 1042 0.t1	SLC25A23S	3'-phospho-5'-adenylyl sulfate transmembrane transport, 3'- phosphoadenosine 5'- phosphosulfate transmembrane transporter activity, 5'-adenylyl sulfate transmembrane transport, 5'-adenylyl sulfate transmembrane transporter activity, integral component of membrane, intracellular ribonucleoprotein complex, mitochondrion, ribosome, structural constituent of ribosome, translation	0	0.01	-3.1	3.1	0.04
628	1AX g185 8.t1	2427	1BXg 1886 .t1	None	intracellular part	0	0.01	-3.1	3.1	0.05
629	1AX g816 6.t1	2428	1BXg 7974 .t1	None	membrane	0	0.01	-3.1	3.1	0.05
630	1AX g296 0.t1	2429	1BXg 5945 .t1	None	None	0.13	0.02	3	3	0.01

631	1AX g421 3.t1	2430	1BXg 1766 .t1	None	membrane	0	0.01	-3	3	0.02
632	1AX g408 3.t1	2431	1BXg 3283 .t1	None	integral component of membrane, plasma membrane, transport	0	0.01	-3	3	0.02
633	1AX g317 5.t1	2432	1BXg 2690 .t1	E3.2.1.-	carbohydrate metabolic process, cellulose binding, extracellular region, hydrolase activity, hydrolyzing O-glycosyl compounds	0.01	0	3	3	0.03
634	1AX g115 76.t 1	2433	1BXg 1148 1.t1	None	flavin adenine dinucleotide binding, oxidation- reduction process, oxidoreductase activity, acting on CH-OH group of donors	0	0.01	-3	3	0.04
635	1AX g511 .t1	2434	1BXg 3351 .t1	None	oxidoreductase activity	0.1	0.01	2.9	2.9	0.01
636	1AX g873 4.t1	2435	1BXg 1156 2.t1	None	chitin binding, chitin catabolic process, chitinase activity, extracellular region, pathogenesis, polysaccharide catabolic process	0	0.01	-2.9	2.9	0.02
637	1AX g674 8.t1	2436	1BXg 4362 .t1	E3.2.1.58, Starch and sucrose metabolism	endoplasmic reticulum, fungal-type cell wall beta- glucan biosynthetic process, glucan endo-1,6-beta- glucosidase activity, integral component of membrane, regulation of cell shape	0	0.01	-2.9	2.9	0.05

638	1AX g100 79.t 1	2437	1BXg 2701 .t1	HSPA5, BIP, Prion diseases, Protein export, Protein processing in endoplasmic reticulum, Thyroid hormone synthesis	'de novo' posttranslational protein folding, ATP binding, ATPase activity, ER- associated ubiquitin- dependent protein catabolic process, Golgi apparatus, karyogamy involved in conjugation with cellular fusion, luminal surveillance complex, nuclear membrane, posttranslational protein targeting to membrane, translocation, response to unfolded protein, SRP- dependent cotranslational protein targeting to membrane, translocation, unfolded protein binding	0	0.01	-2.8	2.8	0.02
639	1AX g101 29.t 1	2438	1BXg 8487 .t1	None	None	0	0.01	-2.8	2.8	0.05
482	1AX g105 78.t 1	2439	1BXg 1208 9.t1	None	aspartic-type endopeptidase activity, proteolysis	0.53	0.08	2.7	2.7	0.02
640	1AX g125 54.t 1	2440	1BXg 3576 .t1	Ribosome, RP- S13e, RPS13	cytoplasmic translation, cytosolic small ribosomal subunit, maturation of SSU- rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), mycelium development, small ribosomal subunit rRNA binding, structural constituent of ribosome	0.01	0	2.7	2.7	0.02
641	1AX g154 17.t 1	2441	1BXg 6538 .t1	Protein processing in endoplasmic reticulum, UBE2D_E, UBC4, UBC5, Ubiquitin mediated proteolysis	acid-amino acid ligase activity, APC-Cdc20 complex activity, ATP binding, cytosol, nuclear SCF ubiquitin ligase complex, positive regulation of mitotic metaphase/anaphase transition, protein processing, protein ubiquitination involved in ubiquitin-dependent protein catabolic process, SCF-dependent proteasomal ubiquitin- dependent protein catabolic process, ubiquitin conjugating enzyme activity	0.01	0	2.7	2.7	0.02

642	1AX g447 3.t1	2442	1BXg 9969 .t1	SLC39A1_2_3, ZIP1_2_3	cellular response to zinc ion starvation, endoplasmic reticulum, high-affinity zinc II ion transport, high-affinity zinc uptake transmembrane transporter activity, integral component of plasma membrane, regulation of transcription from RNA polymerase II promoter in response to iron ion starvation	0.01	0.06	-2.6	2.6	0.01
643	1AX g131 71.t 1	2443	1BXg 1289 .t1	E3.2.1.28, treA, treF, Starch and sucrose metabolism	alpha,alpha-trehalase activity, trehalose metabolic process	0.03	0	2.6	2.6	0.02
644	1AX g454 4.t1	2444	1BXg 4073 .t1	Ribosome, RP- L9e, RPL9	ribosome, rRNA binding, structural constituent of ribosome, translation	0.01	0	2.6	2.6	0.02
645	1AX g138 85.t 1	2445	1BXg 1224 1.t1	Ether lipid metabolism, Glycerophosphol ipid metabolism, Inositol phosphate metabolism, plcC, Thyroid hormone signaling pathway	hydrolase activity, acting on ester bonds, metabolic process	0.06	0.36	-2.5	2.5	0
646	1AX g807 9.t1	2446	1BXg 7852 .t1	None	hydrolase activity, metabolic process	0.01	0.05	-2.5	2.5	0.02
647	1AX g100 2.t1	2447	1BXg 8071 .t1	Alzheimer's disease, ATPeF0D, ATP5H, ATP7, Huntington's disease, Oxidative phosphorylation, Parkinson's disease	ATP synthesis coupled proton transport, mitochondrial proton- transporting ATP synthase, stator stalk, protein complex assembly, proton- transporting ATP synthase activity, rotational mechanism, proton- transporting ATPase activity, rotational mechanism	0	0	2.4	2.4	0.02
648	1AX g149 38.t 1	2448	1BXg 3779 .t1	ARF1, Endocytosis, Legionellosis, Vibrio cholerae infection	Golgi apparatus, GTP binding, hydrolase activity, intracellular protein transport, metabolic process, small GTPase mediated signal transduction	0	0	2.4	2.4	0.02

649	1AX g214 8.t1	2449	1BXg 1188 1.t1	Adherens junction, Amyotrophic lateral sclerosis (ALS), Axon guidance, B cell receptor signaling pathway, Bacterial invasion of epithelial cells, cAMP signaling pathway, Chemokine signaling pathway, Choline metabolism in cancer, Colorectal cancer, Epithelial cell signaling in Helicobacter pylori infection, Fc epsilon RI signaling pathway, Fc gamma R- mediated phagocytosis, Focal adhesion, Leukocyte transendothelial migration, MAPK signaling pathway, Natural killer cell mediated cytotoxicity, Neurotrophin signaling pathway, Non- alcoholic fatty liver disease (NAFLD), Osteoclast differentiation, Pancreatic cancer, Pancreatic secretion, Pathways in cancer, Phagosome, PI3K-Akt signaling pathway, Proteoglycans in cancer, RAC1, Rap1 signaling pathway, Ras signaling	ascospore formation, cell division, conidium formation, developmental pigmentation, endomembrane system, fungal-type vacuole membrane, GTP binding, GTPase activity, intracellular protein transport, metabolic process, nucleocytoplasmic transport, pathogenesis, plasma membrane, small GTPase mediated signal transduction	0	0	2.4	2.4	0.02
378										

650	1AX g748 1.t1	2450	1BXg 6855 .t1	None	integral component of membrane, membrane, transmembrane transport	0	0	-2.4	2.4	0.02
651	1AX g962 4.t1	2451	1BXg 7238 .t1	None	anchored component of membrane, carbohydrate metabolic process, fungal- type cell wall, hydrolase activity, plasma membrane, transferase activity	0.01	0.06	-2.4	2.4	0.03
652	1AX g777 1.t1	2452	1BXg 7838 .t1	None	proteolysis, serine-type endopeptidase activity	0.11	0.02	2.4	2.4	0.03
653	1AX g104 2.t1	2453	1BXg 8113 .t1	None	membrane	0.02	0.1	-2.3	2.3	0.01
654	1AX g102 47.t 1	2454	1BXg 3602 .t1	None	None	0	0.02	-2.3	2.3	0.02
493	1AX g127 42.t 1	2455	1BXg 2905 .t1	None	hydrolase activity, hydrolyzing O-glycosyl compounds, mycelium development, organic substance metabolic process	0.21	1.08	-2.3	2.3	0.02
655	1AX g152 99.t 1	2456	1BXg 1045 7.t1	K07975	cellular bud, cytosol, establishment or maintenance of actin cytoskeleton polarity, establishment or maintenance of cell polarity regulating cell shape, GTP binding, GTPase activity, membrane, metabolic process, microtubule cytoskeleton organization, nucleus, positive regulation of exocytosis, positive regulation of formin- nucleated actin cable assembly, protein transport, regulation of cell separation after cytokinesis, small GTPase mediated signal transduction	0	0	2.3	2.3	0.02
656	1AX g161 81.t 1	2457	1BXg 1207 5.t1	E3.2.1.101	carbohydrate catabolic process, hydrolase activity, mannan endo-1,6-alpha- mannosidase activity	0	0	-2.3	2.3	0.02

657	1AX g482 0.t1	2458	1BXg 705. t1	None	None	0.19	0.95	-2.3	2.3	0.02
658	1AX g487 9.t1	2459	1BXg 4499 .t1	Amoebiasis, Endocytosis, Phagosome, RAB7A, Salmonella infection, Tuberculosis	cytosol, fungal-type vacuole membrane, GTP binding, GTPase activity, intracellular protein transport, mitochondrial outer membrane, nucleocytoplasmic transport, piecemeal microautophagy of nucleus, plasma membrane, positive regulation of vacuole fusion, non-autophagic, protein localization to vacuole, regulation of endocytosis, retrograde transport, endosome to Golgi, small GTPase mediated signal transduction, vacuolar acidification, vacuole inheritance, vesicle fusion with vacuole	0	0	2.3	2.3	0.02
659	1AX g586 4.t1	2460	1BXg 1089 8.t1	APRT, apt, Purine metabolism	adenine phosphoribosyltransferase activity, adenine salvage, AMP salvage, cytosol	0	0	2.3	2.3	0.02
660	1AX g854 7.t1	2461	1BXg 1027 0.t1	Ribosome, RP- L10Ae, RPL10A	large ribosomal subunit, RNA binding, structural constituent of ribosome, translation	0	0	2.3	2.3	0.02
661	1AX g212 8.t1	2462	1BXg 1191 9.t1	None	carboxypeptidase activity, membrane	0.02	0	2.2	2.2	0.01
662	1AX g745 2.t1	2463	1BXg 6885 .t1	cdd, CDA, Drug metabolism - other enzymes, Pyrimidine metabolism	cytidine deaminase activity, cytidine deamination, cytoplasm, zinc ion binding	0.09	0.02	2.2	2.2	0.03
663	1AX g456 3.t1	2464	1BXg 4094 .t1	ribH, RIB4, Riboflavin metabolism	6,7-dimethyl-8- ribityllumazine synthase activity, mitochondrial intermembrane space, riboflavin binding, riboflavin biosynthetic process, riboflavin synthase complex, transferase activity	0.02	0.08	-2.2	2.2	0.04

664	1AX g109 07.t 1	2465	1BXg 5915 .t1	None	cytosol, GU repeat RNA binding, intracellular part, microsatellite binding, nucleus, RNA binding, sequence-specific DNA binding, single-stranded telomeric DNA binding	0	0	2.1	2.1	0.02
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665	1AX g429 9.t1	2466	18Xg 1953 .t1	Acute myeloid leukemia, Alcoholism, Aldosterone-regulated sodium reabsorption, Axon guidance, B cell receptor signaling pathway, Bladder cancer, Central carbon metabolism in cancer, Chemokine signaling pathway, Choline metabolism in cancer, Cholinergic synapse, Chronic myeloid leukemia, Colorectal cancer, Dorsal-ventral axis formation, Endometrial cancer, ErbB signaling pathway, Estrogen signaling pathway, Fc epsilon RI signaling pathway, FoxO signaling pathway, Gap junction, Glioma, GnRH signaling pathway, Hepatitis B, Hepatitis C, HTLV-I infection, Insulin signaling pathway, KRAS, KRAS2, Long-term depression, Long-term potentiation, MAPK signaling pathway, MAPK signaling pathway - fly, Melanogenesis, Melanoma, MicroRNAs in cancer, Natural killer cell mediated	GTP binding, GTPase activity, intracellular, intracellular protein transport, metabolic process, nucleocytoplasmic transport, plasma membrane, small GTPase mediated signal transduction	0	0	2.1	2.1	0.02
382										

666	1AX g926 1.t1	2467	1BXg 1043 9.t1	E3.4.21.48	dibasic protein processing, serine-type endopeptidase activity	0.01	0.03	-2.1	2.1	0.02
667	1AX g919 3.t1	2468	1BXg 8760 .t1	None	chitosanase activity, extracellular region, polysaccharide catabolic process	0.17	0.04	2.1	2.1	0.02
668	1AX g466 9.t1	2469	1BXg 1056 7.t1	None	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, integral component of membrane, metabolic process	0	0	-2.1	2.1	0.03
669	1AX g199 89.t 1	2470	1BXg 9824 .t1	glgB, Starch and sucrose metabolism	1,4-alpha-glucan branching enzyme activity, ATP binding, ATP hydrolysis coupled proton transport, ATP synthesis coupled proton transport, cation binding, cytoplasm, glycogen biosynthetic process, hydrolase activity, hydrolyzing O-glycosyl compounds, proton- transporting ATP synthase activity, rotational mechanism, proton- transporting ATP synthase complex, catalytic core F(1)	0	0	-2.1	2.1	0.05
670	1AX g288 2.t1	2471	1BXg 1086 9.t1	Glycerophosphol ipid metabolism, PLB	lysophospholipase activity, phospholipid catabolic process	0.06	0.01	2	2	0
671	1AX g552 1.t1	2472	1BXg 1647 .t1	Ribosome, RP- S4e, RPS4	ribosome, rRNA binding, structural constituent of ribosome, translation	0	0	2	2	0.02
672	1AX g290 8.t1	2473	1BXg 6003 .t1	AXL2	None	0.02	0	2	2	0.02
673	1AX g696 0.t1	2474	1BXg 9737 .t1	None	aspartic-type endopeptidase activity, proteolysis	0.1	0.03	2	2	0.05

[0116] A total of 892 proteins were detected across all *Acremonium* samples with two or more unique peptides at the false discovery rates indicated above.

SYM15774 secreted proteomic analysis

Table 702: 25 most abundant proteins secreted by SYM15774; “Median Abundance” represents the median value across three biological replicates in units of spectra per hundred spectra

SEQ ID	Protein ID	Median Abundance	GO Terms	KEGG Terms
4510	3AXg6236.t1	1.09684	GO:0005576: extracellular region	none
4511	3AXg9048.t1	1.031017	GO:0000287: magnesium ion binding; GO:0006400: tRNA modification; GO:0008193: tRNA guanylyltransferase activity; GO:0016787: hydrolase activity	none
4512	3AXg678.t1	0.62687	GO:0016787: hydrolase activity	none
4513	3AXg934.t1	0.558301	GO:0003735: structural constituent of ribosome; GO:0005840: ribosome; GO:0006412: translation	KEGG Orthology: K02927: RP-L40e, RPL40: large subunit ribosomal protein L40e; KEGG PATHWAY: ko03010: Ribosome:
4514	3AXg7460.t1	0.527389	GO:0005886: plasma membrane; GO:0005975: carbohydrate metabolic process; GO:0016021: integral component of membrane; GO:0016740: transferase activity; GO:0016787: hydrolase activity; GO:0031225: anchored component of membrane	none
4515	3AXg10862.t1	0.523646	GO:0004650: polygalacturonase activity; GO:0005576: extracellular region; GO:0005975: carbohydrate metabolic process; GO:0071555: cell wall organization	KEGG Orthology: K01213: E3.2.1.67: galacturan 1,4-alpha-galacturonidase [EC:3.2.1.67]; KEGG PATHWAY: ko00040: Pentose and glucuronate interconversions: ; KEGG PATHWAY: ko00500: Starch and sucrose metabolism:
4516	3AXg8590.t1	0.400556	GO:0008061: chitin binding	KEGG Orthology: K00799: GST, gst: glutathione S-transferase [EC:2.5.1.18]; KEGG PATHWAY: ko00480: Glutathione metabolism: ; KEGG PATHWAY: ko00980: Metabolism of xenobiotics by cytochrome P450: ; KEGG PATHWAY: ko00982: Drug metabolism - cytochrome P450: ; KEGG PATHWAY: ko05204: Chemical carcinogenesis: It has been estimated that exposure to environmental chemical carcinogens may contribute significantly to the causation of a sizable fraction, perhaps a majority, of human cancers. Human carcinogens act through a variety of genotoxic and non-genotoxic mechanisms. Genotoxic carcinogens can attack biological macromolecules such as DNA and RNA either directly or indirectly through metabolism, resulting in

				the formation of adducts with these macromolecules. If DNA adducts escape cellular repair mechanisms and persist, they may lead to miscoding, resulting in permanent mutations. Non-genotoxic carcinogens act by the mechanisms such as induction of inflammation, immunosuppression, formation of reactive oxygen species, activation of receptors, and epigenetic silencing. Together, these genotoxic and non-genotoxic mechanisms can alter signal-transduction pathways that finally result in hypermutability, genomic instability, loss of proliferation control, and resistance to apoptosis - some of the characteristic features of cancer cells.
4517	3AXg5014.t1	0.375314	GO:0004553: hydrolase activity, hydrolyzing O-glycosyl compounds; GO:0005975: carbohydrate metabolic process	none
4518	3AXg2998.t1	0.374684	GO:0016614: oxidoreductase activity, acting on CH-OH group of donors; GO:0018130: heterocycle biosynthetic process; GO:0044550: secondary metabolite biosynthetic process; GO:0050660: flavin adenine dinucleotide binding; GO:0055114: oxidation-reduction process; GO:1901362: organic cyclic compound biosynthetic process	none
4519	3AXg4073.t1	0.311962	GO:0005975: carbohydrate metabolic process; GO:0016787: hydrolase activity	none
4520	3AXg3348.t1	0.291735	GO:0006629: lipid metabolic process; GO:0008081: phosphoric diester hydrolase activity	none
4521	3AXg1507.t1	0.287808	GO:0005886: plasma membrane; GO:0005975: carbohydrate metabolic process; GO:0016021: integral component of membrane; GO:0016740: transferase activity; GO:0031225: anchored component of membrane	none
4522	3AXg2571.t1	0.275402	GO:0008152: metabolic process; GO:0016787: hydrolase activity	none
4523	3AXg9962.t1	0.272744	GO:0016020: membrane	none
4524	3AXg965.t1	0.254561	GO:0003723: RNA binding; GO:0004521: endoribonuclease activity; GO:0016020: membrane; GO:0090502: RNA phosphodiester bond hydrolysis, endonucleolytic	none
4525	3AXg5987.t1	0.252385	GO:0004252: serine-type	KEGG Orthology: K01279: TPP1,

			endopeptidase activity; GO:0005576: extracellular region; GO:0006508: proteolysis; GO:0008240: tripeptidyl-peptidase activity	CLN2: tripeptidyl-peptidase I [EC:3.4.14.9]; KEGG PATHWAY: ko04142: Lysosome: Lysosomes are membrane-delimited organelles in animal cells serving as the cell's main digestive compartment to which all sorts of macromolecules are delivered for degradation. They contain more than 40 hydrolases in an acidic environment (pH of about 5). After synthesis in the ER, lysosomal enzymes are decorated with mannose-6-phosphate residues, which are recognized by mannose-6-phosphate receptors in the trans-Golgi network. They are packaged into clathrin-coated vesicles and are transported to late endosomes. Substances for digestion are acquired by the lysosomes via a series of processes including endocytosis, phagocytosis, and autophagy.
4526	3AXg8810.t1	0.232932	GO:0004252: serine-type endopeptidase activity; GO:0006508: proteolysis	KEGG Orthology: K01279: TPP1, CLN2: tripeptidyl-peptidase I [EC:3.4.14.9]; KEGG PATHWAY: ko04142: Lysosome: Lysosomes are membrane-delimited organelles in animal cells serving as the cell's main digestive compartment to which all sorts of macromolecules are delivered for degradation. They contain more than 40 hydrolases in an acidic environment (pH of about 5). After synthesis in the ER, lysosomal enzymes are decorated with mannose-6-phosphate residues, which are recognized by mannose-6-phosphate receptors in the trans-Golgi network. They are packaged into clathrin-coated vesicles and are transported to late endosomes. Substances for digestion are acquired by the lysosomes via a series of processes including endocytosis, phagocytosis, and autophagy.
4527	3AXg1658.t1	0.226403	GO:0016614: oxidoreductase activity, acting on CH-OH group of donors; GO:0050660: flavin adenine dinucleotide binding; GO:0055114: oxidation-reduction process	none
4528	3AXg2961.t1	0.220484	GO:0016491: oxidoreductase activity; GO:0046872: metal ion binding; GO:0055114: oxidation-reduction process	KEGG Orthology: K00505: TYR: tyrosinase [EC:1.14.18.1]; KEGG PATHWAY: ko00350: Tyrosine metabolism; ; KEGG PATHWAY:

				ko00740: Riboflavin metabolism: ; KEGG PATHWAY: ko00950: Isoquinoline alkaloid biosynthesis: Isoquinoline alkaloids are tyrosine-derived plant alkaloids with an isoquinoline skeleton. Among them benzyloquinoline alkaloids form an important group with potent pharmacological activity, including analgesic compounds of morphine and codeine, and anti-infective agents of berberine, palmatine, and magnoflorine. Biosynthesis of isoquinoline alkaloids proceeds via decarboxylation of tyrosine or DOPA to yield dopamine, which together with 4-hydroxyphenylacetaldehyde, an aldehyde derived from tyrosine, is converted to reticuline, an important precursor of various benzyloquinoline alkaloids.; KEGG PATHWAY: ko00965: Betalain biosynthesis: Betalains are water-soluble nitrogen-containing pigments that are present in plants belonging to the order Caryophyllales (such as cactus and amaranth families) and in higher fungi. They contain betalamic acid as the chromophore and are classified into two types: betacyanins and betaxanthins. Betacyanins contain a cyclo-DOPA residue and exhibit red/violet coloration, while betaxanthins contain different amino acids or amino side chains and exhibit a yellow/orange coloration. The condensation of betalamic acid with amino acids (including cyclo-DOPA or amines) in plants is a spontaneous reaction, not an enzyme-catalyzed reaction.; KEGG PATHWAY: ko04916: Melanogenesis: Cutaneous melanin pigment plays a critical role in camouflage, mimicry, social communication, and protection against harmful effects of solar radiation. Melanogenesis is under complex regulatory control by multiple agents. The most important positive regulator of melanogenesis is the MC1 receptor with its ligands melanocortic peptides. MC1R activates the cyclic
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				AMP (cAMP) response-element binding protein (CREB). Increased expression of MITF and its activation by phosphorylation (P) stimulate the transcription of tyrosinase (TYR), tyrosinase-related protein 1 (TYRP1), and dopachrome tautomerase (DCT), which produce melanin. Melanin synthesis takes place within specialized intracellular organelles named melanosomes. Melanin-containing melanosomes then move from the perinuclear region to the dendrite tips and are transferred to keratinocytes by a still not well-characterized mechanism.
4529	3AXg1976.t1	0.215291	GO:0004190: aspartic-type endopeptidase activity; GO:0006508: proteolysis	none
4530	3AXg11128.t1	0.213705	GO:0005619: ascospore wall; GO:0005783: endoplasmic reticulum; GO:0030476: ascospore wall assembly	none
4531	3AXg4486.t1	0.20608	GO:0008152: metabolic process; GO:0016491: oxidoreductase activity; GO:0016787: hydrolase activity; GO:0046872: metal ion binding	none
4532	3AXg6046.t1	0.205931	GO:0005975: carbohydrate metabolic process; GO:0008810: cellulase activity	none
4533	3AXg3384.t1	0.192121	GO:0003824: catalytic activity	none
4534	3AXg2856.t1	0.187827	GO:0006508: proteolysis; GO:0008236: serine-type peptidase activity	none

SYM15774 versus SYM01331

Table 703: Differential secreted protein abundance between SYM15774 and SYM01331.

This table describes the differential protein expression between pairs of orthologous proteins from a genus, where one member of the pair has a beneficial effect on plant growth and the other has a neutral effect. "A.mean" represents the average normalized spectral counts between biological replicates of the beneficial member of the pair. "B.mean" represents the average normalized spectral counts between biological replicates of the neutral member of the pair. "Fold change" represents the fold change difference between the two organisms. "FDR q-value" represents the false discovery rate corrected q-value.

SEQ ID Beneficial	A.protein	SEQ ID Neutral	B.protein	KEGG	GO	A.mean	B.mean	Fold- change	FDR q- value
4535	3AXg4278.t1	4337	3BXg6074.t1	E3.1.1.73	carboxylic ester hydrolase activity	0.136	0	7.1	1.20E-02
4536	3AXg230.t1	4338	3BXg7469.t1	Axon guidance, CFL, Fc gamma R-mediated phagocytosis, Pertussis, Regulation of actin cytoskeleton	actin cortical patch, actin filament binding, actin filament depolymerization, actin filament severing, ATP binding, cell division site, cell tip, endocytosis, Golgi to plasma membrane protein transport, integral component of membrane, protein refolding	0.041	0	5.4	1.20E-02
4537	3AXg6225. t1	4339	3BXg6585. t1	Arginine and proline metabolism, beta- Alanine metabolism, MPO, PAO1	oxidation-reduction process, oxidoreductase activity	0.028	0	4.9	1.20E-02
4538	3AXg8418.t1	4340	3BXg7838.t1	None	flavin adenine dinucleotide binding, oxidation-reduction process, oxidoreductase activity, acting on CH-OH group of donors, phosphatidylinositol binding	0.015	0	4	1.20E-02
4539	3AXg6767.t1	4341	3BXg3303.t1	None	cell wall, cell wall modification, hydrolase activity, acting on ester bonds, metabolic process, pectinesterase activity	0.045	0.00 3	3.4	1.20E-02
4519	3AXg4073. t1	4342	3BXg8531. t1	None	carbohydrate metabolic process, hydrolase activity	0.297	0.05 4	2.4	1.20E-02

4540	3AXg1023 7.t1	4343	3BXg1101. t1	XEG	cellulase activity, polysaccharide catabolic process	0.127	0.03	2	1.20E-02
4541	3AXg6263. t1	4344	3BXg1123 8.t1	None	None	0.204	0.04 9	2	1.20E-02
4542	3AXg5745. t1	4345	3BXg6273. t1	None	fungal-type cell wall, fungal-type vacuole, metallopeptidase activity, proteolysis	0.054	0.24 6	-2.2	1.20E-02
4543	3AXg10791.t1	4346	3BXg9786.t1	bglX, Cyanoamino acid metabolism, Phenylpropanoid biosynthesis, Starch and sucrose metabolism	beta-glucosidase activity, carbohydrate metabolic process	0.003	0.09 4	-4.4	1.20E-02
4544	3AXg7602. t1	4347	3BXg1169 5.t1	None	aspartic-type endopeptidase activity, proteolysis	0	0.06	-5.9	1.20E-02
4545	3AXg8955. t1	4348	3BXg2490. t1	None	None	0	0.13 2	-7.1	1.20E-02
4546	3AXg1865.t 1	4349	3BXg9015.t 1	None	carbohydrate metabolic process, hydrolase activity, hydrolyzing O- glycosyl compounds	0	0.14 5	-7.2	1.20E-02
4547	3AXg1097 7.t1	4350	3BXg7338. t1	None	None	0.062	0.00 9	2.6	1.30E-02
4548	3AXg8244.t1	4351	3BXg2216.t1	E3.4.11.10	aminopeptidase activity, extracellular region, metal ion binding, nuclear pore, nucleocytoplasmic transport, proteolysis, structural constituent of nuclear pore	0	0.00 3	-2	1.30E-02
4549	3AXg2047. t1	4352	3BXg7322. t1	E3.1.1.73	hydrolase activity, metabolic process	0	0.00 7	-3	1.30E-02

4550	3AXg2487. t1	4353	3BXg4014. t1	CTSA, Lysosome, Renin- angiotensin system	proteolysis, serine- type carboxypeptidase activity	0	0.01 8	-4.2	1.30E-02
4551	3AXg3683. t1	4354	3BXg679.t 1	None	metallocarboxypepti dase activity, proteolysis, zinc ion binding	0	0.05 4	-5.8	1.30E-02
4552	3AXg5735. t1	4355	3BXg6263. t1	E3.4.21.48	dibasic protein processing, serine- type endopeptidase activity	0	0.07	-6.2	1.30E-02
4553	3AXg8371. t1	4356	3BXg1100 1.t1	E4.2.2.10	extracellular region, pectin lyase activity, polysaccharide catabolic process	0	0.17 1	-7.4	1.30E-02
4554	3AXg8798.t1	4357	3BXg4519.t1	None	integral component of membrane, membrane, negative regulation of G2/M transition of mitotic cell cycle	0.041	0	5.4	1.40E-02
4555	3AXg3404.t1	4358	3BXg4400.t1	None	choline dehydrogenase activity, flavin adenine dinucleotide binding, oxidation- reduction process	0.169	0.00 4	5	1.40E-02
4556	3AXg3735. t1	4359	3BXg4453. t1	None	membrane	0.023	0	4.6	1.40E-02
4557	3AXg9146. t1	4360	3BXg2444. t1	None	integral component of membrane	0.017	0	4.2	1.40E-02
4558	3AXg10088.t1	4361	3BXg1846.t1	None	endonuclease activity, exonuclease activity, integral component of membrane, nucleic acid phosphodiester bond hydrolysis	0.075	0.00 9	3	1.40E-02

4559	3AXg10485.t1	4362	3BXg821.t1	Amino sugar and nucleotide sugar metabolism, Glycosaminoglycan degradation, Glycosphingolipid biosynthesis - ganglio series, Glycosphingolipid biosynthesis - globo series, HEXA_B, Lysosome, Other glycan degradation	beta-N-acetylglucosaminidase activity, carbohydrate metabolic process, extracellular region, N-acetylglucosamine catabolic process	0.027	0.156	-2.5	1.40E-02
4560	3AXg8514.t1	4363	3BXg7997.t1	None	choline dehydrogenase activity, flavin adenine dinucleotide binding, oxidation-reduction process	0.074	0.551	-2.9	1.40E-02
4561	3AXg8930.t1	4364	3BXg5868.t1	None	integral component of membrane	0	0.008	-3.2	1.40E-02
4562	3AXg6329.t1	4365	3BXg3212.t1	E1.1.99.1, betaA, CHDH, Glycine, serine and threonine metabolism	alcohol metabolic process, choline dehydrogenase activity, DNA binding, flavin adenine dinucleotide binding, metal ion binding, oxidation-reduction process, regulation of transcription, DNA-templated	0.039	0.388	-3.3	1.40E-02
4563	3AXg9850.t1	4366	3BXg11232.t1	None	catalytic activity, chromatin silencing by small RNA, cytosol, endoplasmic reticulum unfolded protein response, nucleus	0	0.023	-4.6	1.40E-02
4564	3AXg1923.t1	4367	3BXg9196.t1	None	hydrolase activity, metabolic process	0	0.033	-5.1	1.40E-02
4565	3AXg6350.t1	4368	3BXg12502.t1	None	proteolysis, serine-type peptidase activity	0.015	0.67	-5.4	1.40E-02

4566	3AXg9423.t1	4369	3BXg390.t1	Betalain biosynthesis, Isoquinoline alkaloid biosynthesis, Melanogenesis, Riboflavin metabolism, TYR, Tyrosine metabolism	ion binding, metabolic process, metal ion binding, oxidation-reduction process, oxidoreductase activity	0	0.048	-5.6	1.40E-02
4567	3AXg5033.t1	4370	3BXg7845.t1	None	cellular process, membrane, metabolic process, single-organism process	0	0.098	-6.6	1.40E-02
4568	3AXg4645.t1	4371	3BXg8440.t1	None	None	0	0.121	-6.9	1.40E-02
4527	3AXg1658.t1	4372	3BXg6710.t1	None	flavin adenine dinucleotide binding, oxidation-reduction process, oxidoreductase activity, acting on CH-OH group of donors	0.219	0	7.8	1.50E-02
4569	3AXg8951.t1	4373	3BXg5043.t1	None	hydrolase activity, acting on ester bonds, nucleic acid metabolic process	0.169	0	7.4	1.50E-02
4570	3AXg3962.t1	4374	3BXg2058.t1	None	flavin adenine dinucleotide binding, oxidation-reduction process, oxidoreductase activity, acting on CH-OH group of donors	0.098	0	6.6	1.50E-02
4571	3AXg9121.t1	4375	3BXg2385.t1	E3.1.1.11, Pentose and glucuronate interconversions, Starch and sucrose metabolism	aspartyl esterase activity, cell wall, cell wall modification, extracellular region, pectin catabolic process, pectinesterase activity	0.098	0	6.6	1.50E-02
4572	3AXg6312.t1	4376	3BXg3233.t1	None	flavin adenine dinucleotide binding, oxidation-reduction process, oxidoreductase activity, acting on CH-OH group of donors	0.059	0	5.9	1.50E-02

4573	3AXg4810.t 1	4377	3BXg1560.t 1	E3.2.1.4, Starch and sucrose metabolism	carbohydrate metabolic process, hydrolase activity, hydrolyzing O-glycosyl compounds	0.049	0	5.7	1.50E-02
4574	3AXg1577.t t1	4378	3BXg3030.t t1	None	hydrolase activity, metabolic process	0.026	0	4.8	1.50E-02
4575	3AXg5120.t1	4379	3BXg10267.t1	EEF1B	cytosol, eukaryotic translation elongation factor 1 complex, guanyl-nucleotide exchange factor activity, maintenance of translational fidelity, negative regulation of actin filament bundle assembly, positive regulation of GTPase activity, regulation of translational termination, translation elongation factor activity, translational elongation	0.015	0	4	1.50E-02
4576	3AXg2881.t1	4380	3BXg6431.t1	msrA	cellular response to hydrogen peroxide, cytosol, integral component of membrane, L-methionine biosynthetic process from methionine sulphoxide, L-methionine-(S)-S-oxide reductase activity, nucleus, oxidation-reduction process, peptide-methionine (S)-S-oxide reductase activity, protein repair	0.005	0	2.7	1.50E-02
4577	3AXg2995.t1	4381	3BXg8638.t1	Influenza A, Neuroactive ligand-receptor interaction, Pancreatic secretion, Protein digestion and absorption, PRSS	proteolysis, serine-type endopeptidase activity	0.071	0.01	2.7	1.50E-02

4578	3AXg6701.t1	4382	38Xg7716.t1	Epstein-Barr virus infection, HTLV-I infection, RAN, Ribosome biogenesis in eukaryotes, RNA transport	cytosol, GTP binding, GTPase activity, intracellular protein transport, membrane, metabolic process, negative regulation of G2/M transition of mitotic cell cycle, nuclear pore, nucleocytoplasmic transport, small GTPase mediated signal transduction, structural constituent of nuclear pore	0.005	0	2.7	1.50E-02
4579	3AXg1055.8.t1	4383	38Xg1009.5.t1	None	None	0.005	0	2.6	1.50E-02
4580	3AXg9106.t1	4384	38Xg2351.t1	None	cytoplasm	0.004	0	2.3	1.50E-02
4581	3AXg573.t1	4385	38Xg5286.t1	None	aspartic-type endopeptidase activity, membrane, proteolysis	0.044	0.009	2.2	1.50E-02
4525	3AXg5987.t1	4386	38Xg5319.t1	Lysosome, TPP1, CLN2	extracellular region, proteolysis, serine-type endopeptidase activity, tripeptidyl-peptidase activity	0.261	0.057	2.2	1.50E-02
4582	3AXg10624.t1	4387	38Xg1050.t1	None	choline dehydrogenase activity, flavin adenine dinucleotide binding, integral component of membrane, oxidation-reduction process, transmembrane transport, transporter activity	0.172	0.038	2.1	1.50E-02
4520	3AXg3348.t1	4388	38Xg5195.t1	None	lipid metabolic process, phosphoric diester hydrolase activity	0.286	0.065	2.1	1.50E-02

4583	3AXg1574.t1	4389	3BXg791.t1	None	ATP binding, calmodulin binding, calmodulin-dependent protein kinase activity, cytosol, glucose catabolic process, manganese ion binding, negative regulation of calcineurin-NFAT signaling cascade, negative regulation of G2/M transition of mitotic cell cycle, negative regulation of transcription by transcription factor localization, negative regulation of transcription from RNA polymerase II promoter, nucleus, phosphoglycerate mutase activity, protein phosphorylation, regulation of nuclear division	0.003	0	2	1.50E-02
4584	3AXg3704.t1	4390	3BXg4116.t1	None	None	0.04	0.176	-2.1	1.50E-02
4585	3AXg7050.t1	4391	3BXg10636.t1	E3.2.1.101	catalytic activity, hydrolase activity	0.014	0.064	-2.1	1.50E-02
4586	3AXg11147.t1	4392	3BXg3457.t1	None	defense response to bacterium, defense response to fungus, spore wall	0.01	0.065	-2.6	1.50E-02
4587	3AXg809.t1	4393	3BXg9916.t1	None	acetyltransferase activity, metabolic process, transferase activity	0	0.016	-4.1	1.50E-02
4588	3AXg1606.t1	4394	3BXg8171.t1	Betalain biosynthesis, Isoquinoline alkaloid biosynthesis, Melanogenesis, Riboflavin metabolism, TYR, Tyrosine metabolism	metabolic process, N-acetyltransferase activity, oxidation-reduction process, oxidoreductase activity, transferase activity, transferring acyl groups	0	0.038	-5.3	1.50E-02

4589	3AXg5600. t1	4395	3BXg3227. t1	None	None	0	0.08 6	-6.4	1.50E-02
4590	3AXg676.t 1	4396	3BXg6951. t1	None	None	0	0.31 9	-8.3	1.50E-02
4591	3AXg8215. t1	4397	3BXg2453. t1	None	None	0.002	0.05 4	-4.3	1.70E-02
4592	3AXg4581. t1	4398	3BXg7071. t1	None	hydrolase activity, metabolic process	0.076	0	6.3	1.80E-02
4593	3AXg3000.t1	4399	3BXg8643.t1	None	flavin adenine dinucleotide binding, oxidation-reduction process, oxidoreductase activity, oxidoreductase activity, acting on CH-OH group of donors	0	0.04 2	-5.4	1.80E-02
4594	3AXg3931.t1	4400	3BXg1983.t1	None	choline dehydrogenase activity, flavin adenine dinucleotide binding, oxidation- reduction process	0.081	0	6.4	1.90E-02
4595	3AXg3946.t 1	4401	3BXg1965.t 1	None	copper ion binding, oxidation-reduction process, oxidoreductase activity	0.025	0	4.7	1.90E-02
4596	3AXg1894. t1	4402	3BXg9149. t1	None	carbohydrate metabolic process, catalytic activity	0.016	0	4	2.00E-02
4597	3AXg3686.t 1	4403	3BXg689.t1	None	copper ion binding, oxidation-reduction process, oxidoreductase activity	0.022	0.16 6	-2.9	2.00E-02

4598	3AXg9632.t1	4404	3BXg8688.t1	None	beta-N-acetylhexosaminidase activity, carbohydrate metabolic process, integral component of membrane	0	0.026	-4.8	2.00E-02
4599	3AXg7875.t1	4405	3BXg925.t1	E3.1.3.25, IMPA, suhB, Inositol phosphate metabolism, Phosphatidylinositol signaling system, Streptomycin biosynthesis	DNA binding, integral component of membrane, phosphatidylinositol phosphorylation	0	0.031	-5	2.00E-02
4600	3AXg6708.t1	4406	3BXg7541.t1	None	membrane	0	0.036	-5.2	2.00E-02
4601	3AXg7523.t1	4407	3BXg2252.t1	None	hydrolase activity, metabolic process	0.029	0.007	2	2.10E-02
4602	3AXg9481.t1	4408	3BXg11985.t1	Amino sugar and nucleotide sugar metabolism, E3.2.1.14	carbohydrate metabolic process, chitin catabolic process, chitinase activity, hydrolase activity, hydrolyzing O-glycosyl compounds, organic substance metabolic process, transferase activity, transferring glycosyl groups	0.059	0.345	-2.5	2.10E-02
4603	3AXg11091.t1	4409	3BXg13016.t1	None	hydrolase activity, hydrolyzing O-glycosyl compounds, metabolic process	0	0.007	-3	2.10E-02

4604	3AXg505.t1	4410	3BXg6843.t1	Amino sugar and nucleotide sugar metabolism, Butirosin and neomycin biosynthesis, Carbohydrate digestion and absorption, Carbon metabolism, Central carbon metabolism in cancer, Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, HIF-1 signaling pathway, HK, Insulin signaling pathway, Starch and sucrose metabolism, Streptomycin biosynthesis, Type II diabetes mellitus	ATP binding, carbohydrate phosphorylation, cellular glucose homeostasis, cytosol, fructokinase activity, fructose 6-phosphate metabolic process, glucokinase activity, glucose 6-phosphate metabolic process, glucose binding, glycolytic fermentation, glycolytic process, integral component of membrane, mannokinase activity, mannose metabolic process, nuclear pore, nucleocytoplasmic transport, structural constituent of nuclear pore	0	0.01 1	-3.6	2.10E-02
4605	3AXg671.t1	4411	3BXg6947.t1	None	FMN binding, membrane, oxidation-reduction process, oxidoreductase activity	0	0.01 5	-4	2.10E-02
4606	3AXg907.t1	4412	3BXg1071.t1	None	None	0	0.04 8	-5.6	2.10E-02
4607	3AXg10465.t1	4413	3BXg14385.t1	E3.2.1.58, Starch and sucrose metabolism	carbohydrate metabolic process, hydrolase activity, hydrolyzing O-glycosyl compounds, integral component of membrane, transmembrane transport	0	0.23 5	-7.9	2.10E-02
4608	3AXg1008.t1	4414	3BXg9515.t1	None	choline dehydrogenase activity, flavin adenine dinucleotide binding, oxidation-reduction process	0.068	0	6.1	2.20E-02

4609	3AXg2591.t1	4415	3BXg1833.t1	Betalain biosynthesis, Isoquinoline alkaloid biosynthesis, Melanogenesis, Riboflavin metabolism, TYR, Tyrosine metabolism	metal ion binding, oxidation-reduction process, oxidoreductase activity	0.126	0.023	2.4	2.20E-02
4610	3AXg4824.t1	4416	3BXg1527.t1	None	None	0.04	0	5.4	2.30E-02
4518	3AXg2998.t1	4417	3BXg8641.t1	None	flavin adenine dinucleotide binding, heterocycle biosynthetic process, organic cyclic compound biosynthetic process, oxidation-reduction process, oxidoreductase activity, acting on CH-OH group of donors, secondary metabolite biosynthetic process	0.37	0.038	3.3	2.30E-02
4611	3AXg8768.t1	4418	3BXg429.t1	None	hydrolase activity, metabolic process	0.011	0.145	-3.6	2.30E-02
4612	3AXg1113.t1	4419	3BXg7381.t1	None	None	0	0.021	-4.5	2.30E-02
4613	3AXg3576.t1	4420	3BXg5515.t1	None	None	0	0.063	-6	2.30E-02
4614	3AXg1056.t1	4421	3BXg1010.t1	None	metalloprotease activity, proteolysis, zinc ion binding	0.016	0	4.1	2.50E-02
4615	3AXg4536.t1	4422	3BXg3121.t1	Galactose metabolism, malZ, Starch and sucrose metabolism	carbohydrate binding, carbohydrate metabolic process, cellular process, glucosidase activity, hydrolase activity, hydrolyzing O-glycosyl compounds, integral component of membrane	0.047	0.003	3.8	2.50E-02

4616	3AXg4165.t1	4423	3BXg6890.t1	bglX, Cyanoamino acid metabolism, Phenylpropanoid biosynthesis, Starch and sucrose metabolism	hydrolase activity, hydrolyzing O-glycosyl compounds, integral component of membrane, polysaccharide catabolic process	0	0.01	-3.4	2.50E-02
4617	3AXg8420.t1	4424	3BXg7817.t1	yteR, yesR	hydrolase activity, metabolic process	0.007	0.147	-4.3	2.50E-02
4618	3AXg6634.t1	4425	3BXg5671.t1	None	acid phosphatase activity, dephosphorylation	0.004	0.022	-2.1	2.60E-02
4619	3AXg5462.t1	4426	3BXg503.t1	None	carbohydrate metabolic process, hydrolase activity	0	0.03	-5	2.60E-02
4620	3AXg9660.t1	4427	3BXg10410.t1	None	copper ion binding, oxidation-reduction process, oxidoreductase activity	0	0.032	-5	2.60E-02
4621	3AXg736.t1	4428	3BXg7066.t1	None	biosynthetic process, carbohydrate metabolic process, cellulose binding, extracellular region, hydrolase activity, hydrolyzing O-glycosyl compounds, positive regulation of GTPase activity, pyridoxal phosphate binding, regulation of Rho protein signal transduction, Rho guanyl-nucleotide exchange factor activity	0	0.062	-6	2.60E-02
4622	3AXg3304.t1	4429	3BXg5239.t1	None	None	0.07	0	6.1	2.70E-02
4511	3AXg9048.t1	4430	3BXg11565.t1	None	hydrolase activity, magnesium ion binding, tRNA guanylyltransferase activity, tRNA modification	0.974	0.079	3.6	2.70E-02

4623	3AXg2688.t1	4431	3BXg10864.t1	AMPK signaling pathway, Fructose and mannose metabolism, HIF-1 signaling pathway, PFKFB	6-phosphofructo-2-kinase activity, ATP binding, carbohydrate phosphorylation, cytosol, dephosphorylation, fructose 2,6-bisphosphate metabolic process, fructose metabolic process, fructose-2,6-bisphosphate 2-phosphatase activity	0.01	0	3.5	2.70E-02
4624	3AXg9670.t1	4432	3BXg5175.t1	CTSA, Lysosome, Renin-angiotensin system	fungus-type vacuole, nuclear pore, nucleocytoplasmic transport, phytochelatin biosynthetic process, proteolysis, serine-type carboxypeptidase activity, structural constituent of nuclear pore	0.005	0.046	-3	2.70E-02
4625	3AXg2904.t1	4433	3BXg6481.t1	E3.2.1.58, Starch and sucrose metabolism	carbohydrate metabolic process, hydrolase activity, hydrolyzing O-glycosyl compounds, membrane part	0	0.021	-4.5	2.70E-02
4626	3AXg10815.t1	4434	3BXg9780.t1	None	heme binding, oxidation-reduction process, peroxidase activity, response to oxidative stress	0.125	0	7	2.90E-02
4627	3AXg2002.t1	4435	3BXg2128.t1	CNBP	nucleic acid binding, zinc ion binding	0.026	0	4.8	3.10E-02
4628	3AXg3713.t1	4436	3BXg4131.t1	None	hydrolase activity, metabolic process	0.026	0	4.7	3.10E-02

4629	3AXg3872.t1	4437	3BXg4226.t1	COPB1, SEC26	COPI vesicle coat, cytosol, ER to Golgi transport vesicle, ER to Golgi vesicle-mediated transport, intracellular protein transport, kinase activity, phosphorylation, structural molecule activity	0.022	0	4.5	3.10E-02
4630	3AXg6318.t1	4438	3BXg3226.t1	None	hydrolase activity, hydrolase activity, acting on glycosyl bonds, organic substance metabolic process, oxidoreductase activity, primary metabolic process, single-organism metabolic process	0.012	0	3.7	3.10E-02
4631	3AXg10010.t1	4439	3BXg11186.t1	None	dephosphorylation, phosphatase activity	0	0.088	-6.5	3.10E-02
4632	3AXg1263.t1	4440	3BXg1724.t1	None	chitin binding, copper ion binding, oxidation-reduction process, oxidoreductase activity	0.03	0	4.9	3.20E-02
4633	3AXg8122.t1	4441	3BXg9830.t1	None	None	0.024	0	4.6	3.20E-02
4515	3AXg10862.t1	4442	3BXg9632.t1	E3.2.1.67, Pentose and glucuronate interconversions, Starch and sucrose metabolism	carbohydrate metabolic process, cell wall organization, extracellular region, polygalacturonase activity	0.552	0.095	2.5	3.20E-02
4634	3AXg5813.t1	4443	3BXg1361.t1	Ascorbate and aldarate metabolism, Caprolactam degradation, Carbon metabolism, Degradation of aromatic compounds, E3.1.1.17, gnl, RGN, Pentose phosphate pathway	hydrolase activity, metabolic process	0	0.12	-6.9	3.40E-02

4635	3AXg2285.t1	4444	3BXg5413.t1	None	heme binding, integral component of membrane, oxidation-reduction process, peroxidase activity, response to oxidative stress	0.045	0	5.5	3.60E-02
4636	3AXg3048.t1	4445	3BXg8570.t1	None	copper ion binding, endoplasmic reticulum, ferrous iron import into cell, metal ion binding, oxidation-reduction process, oxidoreductase activity	0	0.01	-3.5	3.60E-02
4637	3AXg3573.t1	4446	3BXg5567.t1	None	None	0	0.019	-4.4	3.60E-02
4638	3AXg457.t1	4447	3BXg2952.t1	gcvH, GCSH, Glycine, serine and threonine metabolism, Glyoxylate and dicarboxylate metabolism	glycine cleavage complex, glycine decarboxylation via glycine cleavage system, mitochondrion, one-carbon metabolic process, oxidation-reduction process, protein lipoylation	0.039	0	5.3	3.90E-02
4639	3AXg2903.t1	4448	3BXg6482.t1	None	None	0	0.017	-4.1	3.90E-02
4640	3AXg10837.t1	4449	3BXg9608.t1	None	cellular process, membrane part, pectin catabolic process, pectin lyase activity	0	0.043	-5.5	3.90E-02
4641	3AXg10151.t1	4450	3BXg10552.t1	None	1,3-beta-glucanosyltransferase activity, anchored component of membrane, ascospore wall assembly, carbohydrate metabolic process, endoplasmic reticulum, hydrolase activity, integral component of membrane, plasma membrane	0.058	0	5.9	4.10E-02

4642	3AXg9889.t 1	4451	3BXg7932.t 1	None	extracellular region, mannan catabolic process, mannan endo-1,4-beta- mannosidase activity	0.009	0	3.4	4.10E-02
4643	3AXg6766. t1	4452	3BXg3304. t1	None	integral component of membrane, transmembrane transport	0.061	0	6	4.20E-02
4644	3AXg9025.t1	4453	3BXg3854.t1	None	carbon-nitrogen ligase activity, with glutamine as amido- N-donor, metabolic process, transferase activity	0.015	0	4	4.20E-02
4645	3AXg9960.t1	4454	3BXg7994.t1	ABC.MR	ATP binding, ATPase activity, coupled to transmembrane movement of substances, integral component of membrane, isomerase activity, metabolic process, mitochondrion, transmembrane transport	0	0.04 1	-5.4	4.20E-02
4646	3AXg8755.t1	4455	3BXg86.t1	None	acid phosphatase activity, dephosphorylation, heme binding, integral component of membrane, iron ion binding, membrane, oxidation-reduction process, oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	0.011	0	3.6	4.30E-02
4647	3AXg1998.t1	4456	3BXg2125.t1	None	aminopeptidase activity, integral component of membrane, metallopeptidase activity, proteolysis, zinc ion binding	0	0.01 9	-4.3	4.30E-02

4648	3AXg4651.t1	4457	3BXg12484.t1	Nicotinate and nicotinamide metabolism, Purine metabolism, Pyrimidine metabolism, surE	hydrolase activity, integral component of membrane, metabolic process, substrate-specific transmembrane transporter activity, transmembrane transport	0.031	0	5	4.40E-02
4649	3AXg1281.t1	4458	3BXg5746.t1	Antigen processing and presentation, Endocytosis, Epstein-Barr virus infection, Estrogen signaling pathway, HSPA1_8, Influenza A, Legionellosis, MAPK signaling pathway, Measles, Protein processing in endoplasmic reticulum, Spliceosome, Toxoplasmosis	ATP binding	0.027	0	4.8	4.50E-02
4650	3AXg2954.t1	4459	3BXg1020.2.t1	None	cutinase activity, extracellular region, metabolic process	0.02	0	4.4	4.50E-02
4651	3AXg8116.t1	4460	3BXg9765.t1	E3.2.1.8, xynA	endo-1,4-beta-xylanase activity, polysaccharide catabolic process	0	0.047	-5.6	4.50E-02
4652	3AXg9229.t1	4461	3BXg511.t1	None	cell cycle, cell division, cyclin-dependent protein serine/threonine kinase regulator activity, integral component of membrane, regulation of protein kinase activity	0.02	0	4.4	4.60E-02
4653	3AXg5237.t1	4462	3BXg5596.t1	Aminobenzoate degradation, Folate biosynthesis, phoD, Two-component system	metabolic process, oxidation-reduction process	0.067	0	6.1	4.70E-02
4654	3AXg9949.t1	4463	3BXg5805.t1	None	None	0.061	0	6	5.00E-02

4655	3AXg1124 7.t1	4464	3BXg648.t 1	None	integral component of membrane	0.009	0	3.3	5.00E-02
4656	3AXg9208. t1	4465	3BXg534.t 1	None	integral component of membrane, membrane	0.011	0.16 8	-3.8	5.00E-02
4657	3AXg7858.t1	4466	3BXg1035.t1	None	flavin adenine dinucleotide binding, membrane, oxidation-reduction process, oxidoreductase activity, acting on CH-OH group of donors	0	0.07 6	-6.3	5.00E-02

[0117] A total of 697 proteins were detected across all *Phoma* samples with two or more unique peptides at the false discovery rates indicated above.

SYM01004 secreted proteomic analysis

- 5 **Table 704: 25 most abundant proteins secreted by SYM01004; “Median Abundance” represents the median value across three biological replicates in units of spectra per hundred spectra**

SEQ ID	Protein ID	Median Abundance	GO Terms	KEGG Terms
4742	5AYg74 8.t1	0.999348	GO:0005198: structural molecule activity; GO:0005576: extracellular region; GO:0009420: bacterial-type flagellum filament; GO:0071973: bacterial-type flagellum-dependent cell motility	KEGG Orthology: K02406: fliC: flagellin; KEGG PATHWAY: ko02020: Two-component system: Two-component signal transduction systems enable bacteria to sense, respond, and adapt to changes in their environment or in their intracellular state. Each two-component system consists of a sensor protein-histidine kinase (HK) and a response regulator (RR). In the prototypical two-component pathway, the sensor HK phosphorylates its own conserved His residue in response to a signal(s) in the environment. Subsequently, the phosphoryl group of HK is transferred onto a specific Asp residue on the RR. The activated RR can then effect changes in cellular physiology, often by regulating gene expression. Two-component pathways thus often enable cells to sense and respond to stimuli by inducing changes in transcription.; KEGG PATHWAY: ko02040: Flagellar assembly; ; KEGG PATHWAY: ko04626: Plant-pathogen interaction: Plants lack animal-like adaptive immunity mechanisms, and therefore have evolved a specific system with multiple layers against invading pathogens. The

				primary response includes the perception of pathogens by cell-surface pattern-recognition receptors (PRRs) and is referred to as PAMP-triggered immunity (PTI). Activation of FLS2 and EFR triggers MAPK signaling pathway that activates defense genes for antimicrobial compounds. The increase in the cytosolic Ca²⁺ concentration is also a regulator for production of reactive oxygen species and localized programmed cell death/hypersensitive response. The secondary response is called effector-triggered immunity (ETI). Pathogens can acquire the ability to suppress PTI by directly injecting effector proteins into the plant cell through secretion systems. In addition, pathogens can manipulate plant hormone signaling pathways to evade host immune responses using coronatine toxin. Some plants possess specific intracellular surveillance proteins (R proteins) to monitor the presence of pathogen virulence proteins. This ETI occurs with localized programmed cell death to arrest pathogen growth, resulting in cultivar-specific disease resistance.; KEGG PATHWAY: ko05132: Salmonella infection: Salmonella infection usually presents as a self-limiting gastroenteritis or the more severe typhoid fever and bacteremia. The common disease-causing Salmonella species in human is a single species, Salmonella enterica, which has numerous serovars.; KEGG PATHWAY: ko05134: Legionellosis: Legionellosis is a potentially fatal infectious disease caused by the bacterium Legionella pneumophila and other legionella species. Two distinct clinical and epidemiological syndromes are associated with Legionella species: Legionnaires' disease is the more severe form of the infection, which may involve pneumonia, and Pontiac fever is a milder respiratory illness.
4743	5AYg74 7.t1	0.973878	GO:0005198: structural molecule activity; GO:0005576: extracellular region; GO:0009420: bacterial-type flagellum filament; GO:0071973: bacterial-type flagellum-dependent cell motility	KEGG Orthology: K02406: fliC: flagellin; KEGG PATHWAY: ko02020: Two-component system: Two-component signal transduction systems enable bacteria to sense, respond, and adapt to changes in their environment or in their intracellular state. Each two-component system consists of a sensor protein-histidine kinase (HK) and a response regulator (RR). In the prototypical two-component pathway, the sensor HK phosphorylates its own conserved His residue in response to a signal(s) in the environment. Subsequently, the phosphoryl group of HK is transferred onto a specific Asp residue on the RR. The activated RR can then effect changes in cellular physiology, often by regulating gene expression. Two-component pathways thus often enable cells to sense and

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4744	5AYg74 6.t1	0.393566	GO:0005198: structural molecule activity; GO:0005576: extracellular region; GO:0009420: bacterial-type flagellum filament; GO:0071973: bacterial-type flagellum-dependent cell motility	KEGG Orthology: K02406: fliC: flagellin; KEGG PATHWAY: ko02020: Two-component system: Two-component signal transduction systems enable bacteria to sense, respond, and adapt to changes in their environment or in their intracellular state. Each two-component system consists of a sensor protein-histidine kinase (HK) and a response regulator (RR). In the prototypical two-component pathway, the sensor HK phosphorylates its own conserved His

				residue in response to a signal(s) in the environment. Subsequently, the phosphoryl group of HK is transferred onto a specific Asp residue on the RR. The activated RR can then effect changes in cellular physiology, often by regulating gene expression. Two-component pathways thus often enable cells to sense and respond to stimuli by inducing changes in transcription.; KEGG PATHWAY: ko02040: Flagellar assembly; ; KEGG PATHWAY: ko04626: Plant-pathogen interaction: Plants lack animal-like adaptive immunity mechanisms, and therefore have evolved a specific system with multiple layers against invading pathogens. The primary response includes the perception of pathogens by cell-surface pattern-recognition receptors (PRRs) and is referred to as PAMP-triggered immunity (PTI). Activation of FLS2 and EFR triggers MAPK signaling pathway that activates defense genes for antimicrobial compounds. The increase in the cytosolic Ca²⁺ concentration is also a regulator for production of reactive oxygen species and localized programmed cell death/hypersensitive response. The secondary response is called effector-triggered immunity (ETI). Pathogens can acquire the ability to suppress PTI by directly injecting effector proteins into the plant cell through secretion systems. In addition, pathogens can manipulate plant hormone signaling pathways to evade host immune responses using coronatine toxin. Some plants possess specific intracellular surveillance proteins (R proteins) to monitor the presence of pathogen virulence proteins. This ETI occurs with localized programmed cell death to arrest pathogen growth, resulting in cultivar-specific disease resistance.; KEGG PATHWAY: ko05132: Salmonella infection: Salmonella infection usually presents as a self-limiting gastroenteritis or the more severe typhoid fever and bacteremia. The common disease-causing Salmonella species in human is a single species, Salmonella enterica, which has numerous serovars.; KEGG PATHWAY: ko05134: Legionellosis: Legionellosis is a potentially fatal infectious disease caused by the bacterium Legionella pneumophila and other legionella species. Two distinct clinical and epidemiological syndromes are associated with Legionella species: Legionnaires' disease is the more severe form of the infection, which may involve pneumonia, and Pontiac fever is a milder respiratory illness.
4745	5AYg32 9.t1	0.208236	GO:0004519: endonuclease activity; GO:0004550: nucleoside diphosphate	KEGG Orthology: K00940: ndk, NME: nucleoside-diphosphate kinase [EC:2.7.4.6]; KEGG PATHWAY: ko00230: Purine metabolism; ;

			kinase activity; GO:0005524: ATP binding; GO:0005737: cytoplasm; GO:0006165: nucleoside diphosphate phosphorylation; GO:0006183: GTP biosynthetic process; GO:0006228: UTP biosynthetic process; GO:0006241: CTP biosynthetic process; GO:0046872: metal ion binding; GO:0090305: nucleic acid phosphodiester bond hydrolysis	KEGG PATHWAY: ko00240: Pyrimidine metabolism:
4746	5AYg14 83.t1	0.204231	GO:0015288: porin activity; GO:0016020: membrane; GO:0055085: transmembrane transport	none
4747	5AYg19 01.t1	0.201732	GO:0004970: ionotropic glutamate receptor activity; GO:0006810: transport; GO:0016020: membrane; GO:0030288: outer membrane-bounded periplasmic space; GO:0035235: ionotropic glutamate receptor signaling pathway	KEGG Orthology: K02030: ABC.PA.S: polar amino acid transport system substrate-binding protein
4748	5AYg26 21.t1	0.184662	GO:0003735: structural constituent of ribosome; GO:0005840: ribosome; GO:0006412: translation	KEGG Orthology: K02884: RP-L19, MRPL19, rplS: large subunit ribosomal protein L19; KEGG PATHWAY: ko03010: Ribosome:
4749	5AYg18 82.t1	0.177	GO:0003735: structural constituent of ribosome; GO:0005840: ribosome; GO:0006412: translation	KEGG Orthology: K02879: RP-L17, MRPL17, rplQ: large subunit ribosomal protein L17; KEGG PATHWAY: ko03010: Ribosome:
4750	5AYg89. t1	0.175201	GO:0000049: tRNA binding; GO:0003735: structural constituent of ribosome; GO:0006412: translation; GO:0015935: small ribosomal subunit; GO:0019843: rRNA binding	KEGG Orthology: K02992: RP-S7, MRPS7, rpsG: small subunit ribosomal protein S7; KEGG PATHWAY: ko03010: Ribosome:
4751	5AYg12 81.t1	0.167696	GO:0006935: chemotaxis; GO:0042597: periplasmic space	KEGG Orthology: K10546: ABC.GGU.S, chvE: putative multiple sugar transport system substrate-binding protein; KEGG PATHWAY: ko02010: ABC transporters: The ATP-binding cassette (ABC) transporters form one of the largest known protein families, and are widespread in bacteria, archaea, and eukaryotes. They couple ATP hydrolysis to active transport of a wide variety of substrates such as ions, sugars, lipids, sterols, peptides, proteins, and drugs. The structure of a

				prokaryotic ABC transporter usually consists of three components; typically two integral membrane proteins each having six transmembrane segments, two peripheral proteins that bind and hydrolyze ATP, and a periplasmic (or lipoprotein) substrate-binding protein. Many of the genes for the three components form operons as in fact observed in many bacterial and archaeal genomes. On the other hand, in a typical eukaryotic ABC transporter, the membrane spanning protein and the ATP-binding protein are fused, forming a multi-domain protein with the membrane-spanning domain (MSD) and the nucleotide-binding domain (NBD).
4752	5AYg77 7.t1	0.156177	GO:0000413: protein peptidyl-prolyl isomerization; GO:0003755: peptidyl-prolyl cis-trans isomerase activity; GO:0006457: protein folding	KEGG Orthology: K03768: PPIB, ppiB: peptidyl-prolyl cis-trans isomerase B (cyclophilin B) [EC:5.2.1.8]
4753	5AYg16 92.t1	0.155178	GO:0003677: DNA binding; GO:0005737: cytoplasm; GO:0006355: regulation of transcription, DNA-templated	KEGG Orthology: K03704: cspA: cold shock protein (beta-ribbon, CspA family)
4754	5AYg12 47.t1	0.152662	GO:0006865: amino acid transport	KEGG Orthology: K01999: livK: branched-chain amino acid transport system substrate-binding protein; KEGG PATHWAY: ko02010: ABC transporters: The ATP-binding cassette (ABC) transporters form one of the largest known protein families, and are widespread in bacteria, archaea, and eukaryotes. They couple ATP hydrolysis to active transport of a wide variety of substrates such as ions, sugars, lipids, sterols, peptides, proteins, and drugs. The structure of a prokaryotic ABC transporter usually consists of three components; typically two integral membrane proteins each having six transmembrane segments, two peripheral proteins that bind and hydrolyze ATP, and a periplasmic (or lipoprotein) substrate-binding protein. Many of the genes for the three components form operons as in fact observed in many bacterial and archaeal genomes. On the other hand, in a typical eukaryotic ABC transporter, the membrane spanning protein and the ATP-binding protein are fused, forming a multi-domain protein with the membrane-spanning domain (MSD) and the nucleotide-binding domain (NBD).
4755	5AYg22 56.t1	0.149078	GO:0016021: integral component of membrane	KEGG Orthology: K16079: omp31: outer membrane immunogenic protein
4756	5AYg20 8.t1	0.14751	GO:0003735: structural constituent of ribosome;	KEGG Orthology: K02986: RP-S4, rpsD: small subunit ribosomal protein S4; KEGG PATHWAY:

			GO:0006412: translation; GO:0015935: small ribosomal subunit; GO:0019843: rRNA binding	ko03010: Ribosome:
4757	5AYg18 76.t1	0.146416	GO:0000049: tRNA binding; GO:0003735: structural constituent of ribosome; GO:0005840: ribosome; GO:0006412: translation; GO:0019843: rRNA binding	KEGG Orthology: K02931: RP-L5, MRPL5, rplE: large subunit ribosomal protein L5; KEGG PATHWAY: ko03010: Ribosome:
4758	5AYg99 8.t1	0.145775	GO:0004801: sedoheptulose-7- phosphate:D- glyceraldehyde-3- phosphate glyceronetransferase activity; GO:0005737: cytoplasm; GO:0005975: carbohydrate metabolic process; GO:0006098: pentose-phosphate shunt	KEGG Orthology: K00616: E2.2.1.2, talA, talB: transaldolase [EC:2.2.1.2]; KEGG PATHWAY: ko00030: Pentose phosphate pathway: The pentose phosphate pathway is a process of glucose turnover that produces NADPH as reducing equivalents and pentoses as essential parts of nucleotides. There are two different phases in the pathway. One is irreversible oxidative phase in which glucose-6P is converted to ribulose-5P by oxidative decarboxylation, and NADPH is generated [MD:M00006]. The other is reversible non- oxidative phase in which phosphorylated sugars are interconverted to generate xylulose-5P, ribulose-5P, and ribose-5P [MD:M00007]. Phosphoribosyl pyrophosphate (PRPP) formed from ribose-5P [MD:M00005] is an activated compound used in the biosynthesis of histidine and purine/pyrimidine nucleotides. This pathway map also shows the Entner-Doudoroff pathway where 6-P-gluconate is dehydrated and then cleaved into pyruvate and glyceraldehyde-3P [MD:M00008].; KEGG PATHWAY: ko01200: Carbon metabolism: Carbon metabolism is the most basic aspect of life. This map presents an overall view of central carbon metabolism, where the number of carbons is shown for each compound denoted by a circle, excluding a cofactor (CoA, CoM, THF, or THMPT) that is replaced by an asterisk. The map contains carbon utilization pathways of glycolysis (map00010), pentose phosphate pathway (map00030), and citrate cycle (map00020), and six known carbon fixation pathways (map00710 and map00720) as well as some pathways of methane metabolism (map00680). The six carbon fixation pathways are: (1) reductive pentose phosphate cycle (Calvin cycle) in plants and cyanobacteria that perform oxygenic photosynthesis, (2) reductive citrate cycle in photosynthetic green sulfur bacteria and some chemolithoautotrophs, (3) 3- hydroxypropionate bi-cycle in photosynthetic green nonsulfur bacteria, two variants of 4- hydroxybutyrate pathways in Crenarchaeota called (4) hydroxypropionate-hydroxybutyrate cycle and (5) dicarboxylate-hydroxybutyrate

				cycle, and (6) reductive acetyl-CoA pathway in methanogenic bacteria.; KEGG PATHWAY: ko01230: Biosynthesis of amino acids: This map presents a modular architecture of the biosynthesis pathways of twenty amino acids, which may be viewed as consisting of the core part and its extensions. The core part is the KEGG module for conversion of three-carbon compounds from glyceraldehyde-3P to pyruvate [MD:M00002], together with the pathways around serine and glycine. This KEGG module is the most conserved one in the KEGG MODULE database and is found in almost all the completely sequenced genomes. The extensions are the pathways containing the reaction modules RM001, RM033, RM032, and RM002 for biosynthesis of branched-chain amino acids (left) and basic amino acids (bottom), and the pathways for biosynthesis of histidine and aromatic amino acids (top right). It is interesting to note that the so-called essential amino acids that cannot be synthesized in human and other organisms generally appear in these extensions. Furthermore, the bottom extension of basic amino acids appears to be most divergent containing multiple pathways for lysine biosynthesis and multiple gene sets for arginine biosynthesis.
4759	SAYg11 62.t1	0.144833	GO:0006006: glucose metabolic process; GO:0016620: oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor; GO:0050661: NADP binding; GO:0051287: NAD binding; GO:0055114: oxidation-reduction process	KEGG Orthology: K00134: GAPDH, gapA: glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]; KEGG PATHWAY: ko00010: Glycolysis / Gluconeogenesis: Glycolysis is the process of converting glucose into pyruvate and generating small amounts of ATP (energy) and NADH (reducing power). It is a central pathway that produces important precursor metabolites: six-carbon compounds of glucose-6P and fructose-6P and three-carbon compounds of glyceraldehyde-3P, glycerate-3P, phosphoenolpyruvate, and pyruvate [MD:M00001]. Acetyl-CoA, another important precursor metabolite, is produced by oxidative decarboxylation of pyruvate [MD:M00307]. When the enzyme genes of this pathway are examined in completely sequenced genomes, the reaction steps of three-carbon compounds from glyceraldehyde-3P to pyruvate form a conserved core module [MD:M00002], which is found in almost all organisms and which sometimes contains operon structures in bacterial genomes. Gluconeogenesis is a synthesis pathway of glucose from noncarbohydrate precursors. It is essentially a reversal of glycolysis with minor variations of alternative paths [MD:M00003].; KEGG PATHWAY: ko00710: Carbon fixation in photosynthetic organisms: ; KEGG PATHWAY: ko01200: Carbon

				metabolism: Carbon metabolism is the most basic aspect of life. This map presents an overall view of central carbon metabolism, where the number of carbons is shown for each compound denoted by a circle, excluding a cofactor (CoA, CoM, THF, or THMPT) that is replaced by an asterisk. The map contains carbon utilization pathways of glycolysis (map00010), pentose phosphate pathway (map00030), and citrate cycle (map00020), and six known carbon fixation pathways (map00710 and map00720) as well as some pathways of methane metabolism (map00680). The six carbon fixation pathways are: (1) reductive pentose phosphate cycle (Calvin cycle) in plants and cyanobacteria that perform oxygenic photosynthesis, (2) reductive citrate cycle in photosynthetic green sulfur bacteria and some chemolithoautotrophs, (3) 3-hydroxypropionate bi-cycle in photosynthetic green nonsulfur bacteria, two variants of 4-hydroxybutyrate pathways in Crenarchaeota called (4) hydroxypropionate-hydroxybutyrate cycle and (5) dicarboxylate-hydroxybutyrate cycle, and (6) reductive acetyl-CoA pathway in methanogenic bacteria.; KEGG PATHWAY: ko01230: Biosynthesis of amino acids: This map presents a modular architecture of the biosynthesis pathways of twenty amino acids, which may be viewed as consisting of the core part and its extensions. The core part is the KEGG module for conversion of three-carbon compounds from glyceraldehyde-3P to pyruvate [MD:M00002], together with the pathways around serine and glycine. This KEGG module is the most conserved one in the KEGG MODULE database and is found in almost all the completely sequenced genomes. The extensions are the pathways containing the reaction modules RM001, RM033, RM032, and RM002 for biosynthesis of branched-chain amino acids (left) and basic amino acids (bottom), and the pathways for biosynthesis of histidine and aromatic amino acids (top right). It is interesting to note that the so-called essential amino acids that cannot be synthesized in human and other organisms generally appear in these extensions. Furthermore, the bottom extension of basic amino acids appears to be most divergent containing multiple pathways for lysine biosynthesis and multiple gene sets for arginine biosynthesis.; KEGG PATHWAY: ko04066: HIF-1 signaling pathway: Hypoxia-inducible factor 1 (HIF-1) is a transcription factor that functions as a master regulator of oxygen homeostasis. It consists of two subunits: an inducibly-expressed HIF-1alpha subunit and a constitutively-expressed HIF-1beta subunit. Under normoxia,
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				HIF-1 alpha undergoes hydroxylation at specific prolyl residues which leads to an immediate ubiquitination and subsequent proteasomal degradation of the subunit. In contrast, under hypoxia, HIF-1 alpha subunit becomes stable and interacts with coactivators such as p300/CBP to modulate its transcriptional activity. Eventually, HIF-1 acts as a master regulator of numerous hypoxia-inducible genes under hypoxic conditions. The target genes of HIF-1 encode proteins that increase O₂ delivery and mediate adaptive responses to O₂ deprivation. Despite its name, HIF-1 is induced not only in response to reduced oxygen availability but also by other stimulants, such as nitric oxide, or various growth factors.; KEGG PATHWAY: ko05010: Alzheimer's disease: Alzheimer's disease (AD) is a chronic disorder that slowly destroys neurons and causes serious cognitive disability. AD is associated with senile plaques and neurofibrillary tangles (NFTs). Amyloid-beta (Abeta), a major component of senile plaques, has various pathological effects on cell and organelle function. The extracellular Abeta oligomers may activate caspases through activation of cell surface death receptors. Alternatively, intracellular Abeta may contribute to pathology by facilitating tau hyperphosphorylation, disrupting mitochondria function, and triggering calcium dysfunction. To date genetic studies have revealed four genes that may be linked to autosomal dominant or familial early onset AD (FAD). These four genes include: amyloid precursor protein (APP), presenilin 1 (PS1), presenilin 2 (PS2) and apolipoprotein E (ApoE). All mutations associated with APP and PS proteins can lead to an increase in the production of Abeta peptides, specifically the more amyloidogenic form, Abeta42. FAD-linked PS1 mutation downregulates the unfolded protein response and leads to vulnerability to ER stress.
4760	5AYg28 7.t1	0.138824	GO:0003677: DNA binding; GO:0030261: chromosome condensation	KEGG Orthology: K03530: hupB: DNA-binding protein HU-beta
4761	5AYg67 7.t1	0.137328	GO:0005524: ATP binding; GO:0005737: cytoplasm; GO:0016491: oxidoreductase activity; GO:0042026: protein refolding; GO:0051082: unfolded protein binding; GO:0055114: oxidation-reduction process	KEGG Orthology: K04077: groEL, HSPD1: chaperonin GroEL; KEGG PATHWAY: ko03018: RNA degradation: The correct processing, quality control and turnover of cellular RNA molecules are critical to many aspects in the expression of genetic information. In eukaryotes, two major pathways of mRNA decay exist and both pathways are initiated by poly(A) shortening of the mRNA. In the 5' to 3' pathway, this is followed by decapping which then permits the 5' to 3' exonucleolytic degradation of transcripts. In the 3' to 5'

				pathway, the exosome, a large multisubunit complex, plays a key role. The exosome exists in archaeal cells, too. In bacteria, endoribonuclease E, a key enzyme involved in RNA decay and processing, organizes a protein complex called degradosome. RNase E or R interacts with the phosphate-dependent exoribonuclease polynucleotide phosphorylase, DEAD-box helicases, and additional factors in the RNA-degrading complex.; KEGG PATHWAY: ko04940: Type I diabetes mellitus: Type I diabetes mellitus is a disease that results from autoimmune destruction of the insulin-producing beta-cells. Certain beta-cell proteins act as autoantigens after being processed by antigen-presenting cell (APC), such as macrophages and dendritic cells, and presented in a complex with MHC-II molecules on the surface of the APC. Then immunogenic signals from APC activate CD4+ T cells, predominantly of the Th1 subset. Antigen-activated Th1 cells produce IL-2 and IFNgamma. They activate macrophages and cytotoxic CD8+ T cells, and these effector cells may kill islet beta-cells by one or both of two types of mechanisms: (1) direct interactions of antigen-specific cytotoxic T cells with a beta-cell autoantigen-MHC-I complex on the beta-cell, and (2) non-specific inflammatory mediators, such as free radicals/oxidants and cytokines (IL-1, TNFalpha, TNFbeta, IFNgamma).; KEGG PATHWAY: ko05134: Legionellosis: Legionellosis is a potentially fatal infectious disease caused by the bacterium Legionella pneumophila and other legionella species. Two distinct clinical and epidemiological syndromes are associated with Legionella species: Legionnaires' disease is the more severe form of the infection, which may involve pneumonia, and Pontiac fever is a milder respiratory illness.; KEGG PATHWAY: ko05152: Tuberculosis: Tuberculosis, or TB, is an infectious disease caused by Mycobacterium tuberculosis. One third of the world's population is thought to be infected with TB. About 90% of those infected result in latent infections, and about 10% of latent infections develop active diseases when their immune system is impaired due to the age, other diseases such as AIDS or exposure to immunosuppressive drugs. TB is transmitted through the air and primarily attacks the lungs, then it can spread by the circulatory system to other parts of body. Once TB bacilli have entered the host by the respiratory route and infected macrophages in the lungs, they interfere with phagosomal maturation, antigen presentation, apoptosis and host immune
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				system to establish persistent or latent infection.
4762	5AYg22 60.t1	0.135	GO:0043190: ATP-binding cassette (ABC) transporter complex; GO:0055085: transmembrane transport	KEGG Orthology: K12368: dppA: dipeptide transport system substrate-binding protein; KEGG PATHWAY: ko02010: ABC transporters: The ATP-binding cassette (ABC) transporters form one of the largest known protein families, and are widespread in bacteria, archaea, and eukaryotes. They couple ATP hydrolysis to active transport of a wide variety of substrates such as ions, sugars, lipids, sterols, peptides, proteins, and drugs. The structure of a prokaryotic ABC transporter usually consists of three components; typically two integral membrane proteins each having six transmembrane segments, two peripheral proteins that bind and hydrolyze ATP, and a periplasmic (or lipoprotein) substrate-binding protein. Many of the genes for the three components form operons as in fact observed in many bacterial and archaeal genomes. On the other hand, in a typical eukaryotic ABC transporter, the membrane spanning protein and the ATP-binding protein are fused, forming a multi-domain protein with the membrane-spanning domain (MSD) and the nucleotide-binding domain (NBD).; KEGG PATHWAY: ko02030: Bacterial chemotaxis: Chemotaxis is the process by which cells sense chemical gradients in their environment and then move towards more favorable conditions. In chemotaxis, events at the receptors control autophosphorylation of the CheA histidine kinase, and the phosphohistidine is the substrate for the response regulator CheY, which catalyzes the transfer of the phosphoryl group to a conserved aspartate. The resulting CheY-P can interact with the switch mechanism in the motor. This interaction causes a change in behavior, such as in direction or speed of rotation of flagella.
4763	5AYg98 0.t1	0.133866	GO:0016021: integral component of membrane	KEGG Orthology: K16079: omp31: outer membrane immunogenic protein
4764	5AYg27 44.t1	0.131774	GO:0000413: protein peptidyl-prolyl isomerization; GO:0003755: peptidyl-prolyl cis-trans isomerase activity	KEGG Orthology: K03769: ppiC: peptidyl-prolyl cis-trans isomerase C [EC:5.2.1.8]
4765	5AYg25 75.t1	0.130147	GO:0003735: structural constituent of ribosome; GO:0005840: ribosome; GO:0006412: translation; GO:0019843: rRNA binding	KEGG Orthology: K02899: RP-L27, MRPL27, rpmA: large subunit ribosomal protein L27; KEGG PATHWAY: ko03010: Ribosome:
4766	5AYg67 6.t1	0.128736	GO:0005524: ATP binding; GO:0005737: cytoplasm; GO:0006457: protein	KEGG Orthology: K04078: groES, HSPE1: chaperonin GroES

			folding	
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SYM01004 versus SYM00091

Table 705: Differential secreted protein abundance between SYM01004 and SYM00091.

This table describes the differential protein expression between pairs of orthologous proteins from a genus, where one member of the pair has a beneficial effect on plant growth and the other has a neutral effect. "A.mean" represents the average normalized spectral counts between biological replicates of the beneficial member of the pair. "B.mean" represents the average normalized spectral counts between biological replicates of the neutral member of the pair. "Fold change" represents the fold change difference between the two organisms. "FDR q-value" represents the false discovery rate corrected q-value.

	SEQ ID Beneficial	A.protein	SEQ ID Neutral	B.protein	KEGG	GO	A.mean	B.mean	Fold-change	FDR q-value
4734	5AYg1329.t1	4671	5BYg3790.t1		ade, Purine metabolism	adenine catabolic process, adenine deaminase activity	0.057	0	5.9	3.9 0E-02
4735	5AYg1185.t1	4672	5BYg649.t1		Biosynthesis of amino acids, Carbon metabolism, Glycine, serine and threonine metabolism, Methane metabolism, serA, PHGDH	L-serine biosynthetic process, NAD binding, oxidation-reduction process, phosphoglycerate dehydrogenase activity	0	0.009	-3.3	4.9 0E-02
4736	5AYg1107.t1	4673	5BYg1291.t1		ABC transporters, ABC.MS.S, msmX, msmK, malk, sugC, ggtA, msiK	ATP binding, ATP-binding cassette (ABC) transporter complex, ATPase activity, carbohydrate transport, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, metabolic process, transmembrane transport, transporter activity	0.008	0	3.2	4.4 0E-02
4737	5AYg1262.t1	4674	5BYg1034.t1		None	integral component of membrane, transport, transporter activity	0	0.007	-3.1	4.0 0E-02

4738	5AYg1075.t1	4675	5BYg577.t1	E2.4.1.1, glgP, PYG, Insulin signaling pathway, Starch and sucrose metabolism	carbohydrate metabolic process, glycogen phosphorylase activity, pyridoxal phosphate binding	0	0.007	-2.9	3.0 0E-02
4739	5AYg1184.t1	4676	5BYg648.t1	Biosynthesis of amino acids, Carbon metabolism, Glycine, serine and threonine metabolism, Methane metabolism, serC, PSAT1, Vitamin B6 metabolism	cytoplasm, L-serine biosynthetic process, O-phospho-L-serine:2-oxoglutarate aminotransferase activity	0.036	0.005	2.7	4.9 0E-02
4740	5AYg126.t1	4677	5BYg3243.t1	Carbon metabolism, GLDC, gcvP, Glycine, serine and threonine metabolism	glycine decarboxylation via glycine cleavage system, glycine dehydrogenase (decarboxylating) activity, lyase activity, oxidation-reduction process	0.032	0.006	2.2	3.9 0E-02
4741	5AYg124.t1	4678	5BYg3241.t1	K09796	None	0.019	0.004	2.1	3.9 0E-02

[0118] A total of 1390 proteins were detected across all *Agrobacterium* samples with two or more unique peptides at the false discovery rates indicated above.

KEGG Pathway enrichment of beneficial fungi versus neutral fungi

Table 706: KEGG Pathway enrichment of beneficial fungi versus neutral fungi

Category	KEGG ID	Name	Description	SEQ ID Beneficial	A.Protein.ID	SEQ ID Neutral	B.Protein.ID	FDR q-value
KEGG PATHWAY	ko00500	Starch and sucrose metabolism	none	643; 2293; 2292; 874; 480; 2288; 487; 2285; 580; 2279; 4543; 4515; 4669; 4668; 4666; 4615; 4573; 4661; 4659; 4571	1AXg13171.t 1, 1AXg2246.t1, 1AXg2742.t1, 1AXg2815.t1, 1AXg3149.t1, 1AXg4053.t1, 1AXg5358.t1, 1AXg5538.t1, 1AXg5751.t1, 1AXg8814.t1, 3AXg10791.t 1, 3AXg10862.t 1, 3AXg1436.t1, 3AXg192.t1, 3AXg2790.t1, 3AXg4536.t1, 3AXg4810.t1, 3AXg6314.t1, 3AXg7872.t1, 3AXg9121.t1	4104; 4126; 4125; 2443; 4097; 4122; 2349; 4118; 2382; 2436; 2377; 2350; 2721; 2470; 4508; 4413; 4507; 4505; 4422; 4500; 4433; 4410; 4423; 4491; 4487; 4442; 4346; 4484	1BXg10106.t1 , 1BXg10460.t1 , 1BXg10656.t1 , 1BXg1289.t1, 1BXg135.t1, 1BXg1561.t1, 1BXg2692.t1, 1BXg3232.t1, 1BXg3531.t1, 1BXg4362.t1, 1BXg4998.t1, 1BXg5592.t1, 1BXg9114.t1, 1BXg9824.t1, 3BXg11320.t1 , 3BXg14385.t1 , 3BXg1864.t1, 3BXg2317.t1, 3BXg3121.t1, 3BXg3387.t1, 3BXg6481.t1, 3BXg6843.t1, 3BXg6890.t1, 3BXg7356.t1, 3BXg928.t1, 3BXg9632.t1, 3BXg9786.t1, 3BXg9960.t1	2.92E -10
KEGG Orthology	K08257	E3.2.1.101	mannan endo-1,6-alpha-mannosidase [EC:3.2.1.101]	2277; 528; 623; 2278; 4663; 4585	1AXg10033.t 1, 1AXg4291.t1, 1AXg459.t1, 1AXg9931.t1, 3AXg512.t1, 3AXg7050.t1	2457; 4121; 4112; 2422; 4391; 4499; 4492	1BXg12075.t1 , 1BXg1595.t1, 1BXg6031.t1, 1BXg8019.t1, 3BXg10636.t1 , 3BXg3817.t1, 3BXg7176.t1	2.62E -05
KEGG Orthology	K18576	XEG	xyloglucan-specific endo-beta-1,4-glucanase [EC:3.2.1.151]	2273; 1249; 4540	1AXg6048.t1, 1AXg9842.t1, 3AXg10237.t 1	2390; 4109; 3093; 4509; 4343	1BXg307.t1, 1BXg8240.t1, 1BXg9770.t1, 3BXg10794.t1 , 3BXg1101.t1	4.04E -05

KEGG PATHWAY	ko00040	Pentose and glucuronate interconversi ons	none	480; 4515; 4666; 4571	1AXg3149.t1, 3AXg10862.t 1, 3AXg2790.t1, 3AXg9121.t1	4099; 2377; 4106; 4442	1BXg12260.t1 , 1BXg4998.t1, 1BXg941.t1, 3BXg9632.t1	0.000 335
KEGG Orthology	K00505	TYR	tyrosinase [EC:1.14.18.1]	2275; 4609; 4528; 4660	1AXg11951.t 1, 3AXg2591.t1, 3AXg2961.t1, 3AXg6319.t1	4096; 4113; 4415; 4501; 4369; 4498; 4495; 4394; 4488	1BXg5424.t1, 1BXg5696.t1, 3BXg1833.t1, 3BXg3225.t1, 3BXg390.t1, 3BXg3977.t1, 3BXg6039.t1, 3BXg8171.t1, 3BXg8955.t1	0.002 931
KEGG PATHWAY	ko00052	Galactose metabolism	none	874; 2291; 4669; 4615; 4661	1AXg2815.t1, 1AXg325.t1, 3AXg1436.t1, 3AXg4536.t1, 3AXg6314.t1	4097; 2382; 2350; 2721; 4508; 4422; 4496; 4494; 4410; 4491; 4484	1BXg135.t1, 1BXg3531.t1, 1BXg5592.t1, 1BXg9114.t1, 3BXg11320.t1 , 3BXg3121.t1, 3BXg5975.t1, 3BXg6701.t1, 3BXg6843.t1, 3BXg7356.t1, 3BXg9960.t1	0.003 136

KEGG PATHWAY	ko00965	Betalain biosynthesis	Betalains are water-soluble nitrogen-containing pigments that are present in plants belonging to the order Caryophyllales (such as cactus and amaranth families) and in higher fungi. They contain betalamic acid as the chromophore and are classified into two types: betacyanins and betaxanthins. Betacyanins contain a cyclo-DOPA residue and exhibit red/violet coloration, while betaxanthins contain different amino acids or amino side chains and exhibit a yellow/orange coloration. The condensation of betalamic acid with amino acids (including cyclo-DOPA or amines) in plants is a spontaneous reaction, not an enzyme-catalyzed reaction.	2275; 4609; 4528; 4660	1AXg11951.t1, 3AXg2591.t1, 3AXg2961.t1, 3AXg6319.t1	4096; 4113; 4415; 4501; 4369; 4498; 4495; 4394; 4488	1BXg5424.t1, 1BXg5696.t1, 3BXg1833.t1, 3BXg3225.t1, 3BXg390.t1, 3BXg3977.t1, 3BXg6039.t1, 3BXg8171.t1, 3BXg8955.t1	0.003 618
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KEGG PATHWAY	ko04916	Melanogenesis is	Cutaneous melanin pigment plays a critical role in camouflage, mimicry, social communication, and protection against harmful effects of solar radiation. Melanogenesis is under complex regulatory control by multiple agents. The most important positive regulator of melanogenesis is the MC1 receptor with its ligands melanocortic peptides. MC1R activates the cyclic AMP (cAMP) response-element binding protein (CREB). Increased expression of MITF and its activation by phosphorylation (P) stimulate the transcription of tyrosinase (TYR), tyrosinase-related protein 1 (TYRP1), and dopachrome tautomerase (DCT), which produce melanin. Melanin synthesis takes place within specialized intracellular organelles named melanosomes. Melanin-containing melanosomes then move from the perinuclear region to the dendrite tips and are transferred to keratinocytes by a still not well-characterized mechanism.	2275; 665; 4609; 4528; 4660	1AXg11951.t1, 1AXg4299.t1, 3AXg2591.t1, 3AXg2961.t1, 3AXg6319.t1	2320; 4096; 4113; 4415; 4501; 4369; 4498; 4495; 4394; 4488	1BXg11664.t1, 1BXg5424.t1, 1BXg5696.t1, 3BXg1833.t1, 3BXg3225.t1, 3BXg390.t1, 3BXg3977.t1, 3BXg6039.t1, 3BXg8171.t1, 3BXg8955.t1	0.005636
				424				

KEGG PATHWAY	ko04142	Lysosome	Lysosomes are membrane-delimited organelles in animal cells serving as the cell's main digestive compartment to which all sorts of macromolecules are delivered for degradation. They contain more than 40 hydrolases in an acidic environment (pH of about 5). After synthesis in the ER, lysosomal enzymes are decorated with mannose-6-phosphate residues, which are recognized by mannose-6-phosphate receptors in the trans-Golgi network. They are packaged into clathrin-coated vesicles and are transported to late endosomes. Substances for digestion are acquired by the lysosomes via a series of processes including endocytosis, phagocytosis, and autophagy.	521; 2295; 608; 2290; 2289; 2286; 2282; 4559; 4670; 4665; 4525; 4526; 4624	1AXg11059.t1, 1, 1AXg12307.t1, 1, 1AXg1785.t1, 1AXg3652.t1, 1AXg3653.t1, 1AXg5534.t1, 1AXg7972.t1, 3AXg10485.t1, 1, 3AXg10865.t1, 1, 3AXg3114.t1, 3AXg5987.t1, 3AXg8810.t1, 3AXg9670.t1	4102; 4124; 2407; 4116; 4111; 4107; 4506; 4353; 4497; 4432; 4386; 4362; 4485	1BXg10249.t1, , 1BXg11338.t1, , 1BXg1175.t1, 1BXg4075.t1, 1BXg7402.t1, 1BXg9090.t1, 3BXg2203.t1, 3BXg4014.t1, 3BXg4508.t1, 3BXg5175.t1, 3BXg5319.t1, 3BXg821.t1, 3BXg9634.t1	0.009 426
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KEGG PATHWAY	ko00950	Isoquinoline alkaloid biosynthesis	Isoquinoline alkaloids are tyrosine-derived plant alkaloids with an isoquinoline skeleton. Among them benzylisoquinoline alkaloids form an important group with potent pharmacological activity, including analgesic compounds of morphine and codeine, and anti-infective agents of berberine, palmatine, and magnoflorine. Biosynthesis of isoquinoline alkaloids proceeds via decarboxylation of tyrosine or DOPA to yield dopamine, which together with 4-hydroxyphenylacetaldehyde, an aldehyde derived from tyrosine, is converted to reticuline, an important precursor of various benzylisoquinoline alkaloids.	2275; 1342; 4609; 4528; 4660	1AXg11951.t1, 1AXg7766.t1, 3AXg2591.t1, 3AXg2961.t1, 3AXg6319.t1	4098; 4119; 4096; 4113; 4108; 3185; 4415; 4501; 4369; 4498; 4495; 4493; 4394; 4488	1BXg12278.t1, 1BXg2903.t1, 1BXg5424.t1, 1BXg5696.t1, 1BXg8510.t1, 1BXg886.t1, 3BXg1833.t1, 3BXg3225.t1, 3BXg390.t1, 3BXg3977.t1, 3BXg6039.t1, 3BXg6827.t1, 3BXg8171.t1, 3BXg8955.t1	0.011 241
KEGG PATHWAY	ko00630	Glyoxylate and dicarboxylate metabolism	none	2272; 4638; 4658	1AXg6636.t1, 3AXg457.t1, 3AXg9876.t1	4103; 2315; 4110; 4490	1BXg10186.t1, 1BXg2840.t1, 1BXg7797.t1, 3BXg7921.t1	0.011 241

KEGG PATHWAY	ko00740	Riboflavin metabolism	none	2275; 485; 496; 663; 2283; 2280; 4609; 4528; 4660	1AXg11951.t1, 1, 1AXg1240.t1, 1AXg13882.t1, 1, 1AXg4563.t1, 1AXg5998.t1, 1AXg8556.t1, 3AXg2591.t1, 3AXg2961.t1, 3AXg6319.t1	4100; 4123; 4117; 2464; 4096; 4114; 2477; 4113; 4415; 4503; 4501; 4369; 4498; 4469; 4495; 4489; 4394; 4488	1BXg11698.t1, 1BXg11921.t1, 1BXg3956.t1, 1BXg4094.t1, 1BXg5424.t1, 1BXg5433.t1, 1BXg5689.t1, 1BXg5696.t1, 3BXg1833.t1, 3BXg246.t1, 3BXg3225.t1, 3BXg390.t1, 3BXg3977.t1, 3BXg443.t1, 3BXg6039.t1, 3BXg8118.t1, 3BXg8171.t1, 3BXg8955.t1	0.011 241
KEGG PATHWAY	ko00520	Amino sugar and nucleotide sugar metabolism	none	2276; 2296; 608; 2294; 2287; 2284; 2281; 2279; 4559; 4667; 4664; 4662; 4602	1AXg10429.t1, 1, 1AXg11997.t1, 1, 1AXg1785.t1, 1AXg2013.t1, 1AXg5017.t1, 1AXg5996.t1, 1AXg8113.t1, 1AXg8814.t1, 3AXg10485.t1, 1, 3AXg2394.t1, 3AXg407.t1, 3AXg618.t1, 3AXg9481.t1	4101; 2407; 4122; 2483; 4120; 2382; 2322; 4115; 2350; 4105; 4408; 4505; 4502; 4410; 4362; 4486	1BXg11696.t1, 1BXg1175.t1, 1BXg1561.t1, 1BXg2454.t1, 1BXg2483.t1, 1BXg3531.t1, 1BXg3931.t1, 1BXg4950.t1, 1BXg5592.t1, 1BXg9514.t1, 3BXg11985.t1, 3BXg2317.t1, 3BXg251.t1, 3BXg6843.t1, 3BXg821.t1, 3BXg9283.t1	0.041 684
KEGG PATHWAY	ko00350	Tyrosine metabolism	none	2275; 1342; 4609; 4528; 4660	1AXg11951.t1, 1, 1AXg7766.t1, 3AXg2591.t1, 3AXg2961.t1, 3AXg6319.t1	4098; 4119; 4096; 4113; 4108; 3185; 4415; 4501; 4369; 4498; 4495; 4493; 4394; 4488	1BXg12278.t1, 1BXg2903.t1, 1BXg5424.t1, 1BXg5696.t1, 1BXg8510.t1, 1BXg886.t1, 3BXg1833.t1, 3BXg3225.t1, 3BXg390.t1, 3BXg3977.t1, 3BXg6039.t1, 3BXg6827.t1, 3BXg8171.t1, 3BXg8955.t1	0.045 141

KEGG PATHWAY	ko00240	Pyrimidine metabolism	none	2274; 1124; 662; 4648	1AXg2750.t1, 1AXg5630.t1, 1AXg7452.t1, 3AXg4651.t1	2968; 2326; 2352; 2463; 4504	1BXg1133.t1, 1BXg4339.t1, 1BXg5639.t1, 1BXg6885.t1, 3BXg2357.t1	0.064 093
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Gene Ontology enrichment of beneficial fungi versus neutral fungi

Table 707: GO enrichment of beneficial fungi versus neutral fungi

GO Term	Description	SEQ ID Beneficial	A.Protein.ID	SEQ ID Neutral	B.Protein.ID	FDR q- value
GO:0005 576	extracellular region	478; 4917; 4918; 874; 633; 2291; 2287; 2285; 2284; 4947; 2281; 667; 497; 4948; 4877; 4919; 4878; 4559; 4879; 4920; 4515; 4880; 4921; 4666; 4650; 4922; 4923; 4881; 4525; 4510; 4661; 4882; 4924; 4925; 4571; 4883; 4658; 4642	1AXg10805.t1, 1AXg1317.t1, 1AXg21242.t1, 1AXg2815.t1, 1AXg3175.t1, 1AXg325.t1, 1AXg5017.t1, 1AXg5538.t1, 1AXg5996.t1, 1AXg8019.t1, 1AXg8113.t1, 1AXg9193.t1, 1AXg9750.t1, 1AXg9874.t1, 3AXg10204.t1, 3AXg10215.t1, 3AXg10410.t1, 3AXg10485.t1, 3AXg10796.t1, 3AXg10814.t1, 3AXg10862.t1, 3AXg2666.t1, 3AXg2755.t1, 3AXg2790.t1, 3AXg2954.t1, 3AXg5176.t1, 3AXg5370.t1, 3AXg5893.t1, 3AXg5987.t1, 3AXg6236.t1, 3AXg6314.t1, 3AXg7257.t1, 3AXg7674.t1, 3AXg8315.t1, 3AXg9121.t1, 3AXg9736.t1, 3AXg9876.t1, 3AXg9889.t1	4926; 2435; 4101; 4099; 4859; 4927; 4858; 2345; 4928; 4929; 4115; 2377; 4895; 4930; 4896; 4109; 2468; 2721; 4932; 4897; 4356; 4898; 4933; 4468; 4934; 4351; 4935; 4899; 4900; 4386; 4936; 4901; 4428; 4902; 4490; 4362; 4937; 4442; 4938	1BXg1054.t1, 1BXg11562.t1, 1BXg11696.t1, 1BXg12260.t1, 1BXg1692.t1, 1BXg177.t1, 1BXg2047.t1, 1BXg2053.t1, 1BXg4311.t1, 1BXg4617.t1, 1BXg4950.t1, 1BXg4998.t1, 1BXg6497.t1, 1BXg6576.t1, 1BXg7924.t1, 1BXg8240.t1, 1BXg8760.t1, 1BXg9114.t1, 3BXg10428.t1, 3BXg10792.t1, 3BXg11001.t1, 3BXg11147.t1, 3BXg11837.t1, 3BXg12052.t1, 3BXg14356.t1, 3BXg2216.t1, 3BXg2769.t1, 3BXg3018.t1, 3BXg3920.t1, 3BXg5319.t1, 3BXg5448.t1, 3BXg6241.t1, 3BXg7066.t1, 3BXg7579.t1, 3BXg7921.t1, 3BXg821.t1, 3BXg9358.t1, 3BXg9632.t1, 3BXg9781.t1	1.82E-14
GO:0008 812	choline dehydrogen ase activity	4608; 4582; 4555; 4594; 4562; 4829; 4560	3AXg1008.t1, 3AXg10624.t1, 3AXg3404.t1, 3AXg3931.t1,	4387; 4365; 4358; 4811;	3BXg1050.t1, 3BXg3212.t1, 3BXg4400.t1, 3BXg5049.t1,	3.00E-06

			3AXg6329.t1, 3AXg8145.t1, 3AXg8514.t1	4363	3BXg7997.t1	
GO:0005 618	cell wall	4939; 614; 934; 4571; 4940	1AXg12959.t1, 1AXg2047.t1, 1AXg6047.t1, 3AXg9121.t1, 3AXg9980.t1	2413; 4475; 4341	1BXg2549.t1, 3BXg11145.t1, 3BXg3303.t1	1.22E-05
GO:0016 614	oxidoreductase activity, acting on CH-OH group of donors	4803; 4876; 4865; 4864; 4863; 4840; 4527; 4518; 4570; 4884; 4885; 4886; 4572; 4887; 4888; 4538	1AXg11202.t1, 1AXg1148.t1, 1AXg7074.t1, 1AXg7314.t1, 1AXg8008.t1, 3AXg10359.t1, 3AXg1658.t1, 3AXg2998.t1, 3AXg3962.t1, 3AXg5234.t1, 3AXg5286.t1, 3AXg6307.t1, 3AXg6312.t1, 3AXg7030.t1, 3AXg7536.t1, 3AXg8418.t1	2433; 4857; 4844; 4843; 4824; 4466; 4823; 4479; 4906; 4907; 4908; 4909; 4910; 4417; 4399; 4911	1BXg11481.t1, 1BXg3389.t1, 1BXg8979.t1, 1BXg9251.t1, 3BXg10091.t1, 3BXg1035.t1, 3BXg10533.t1, 3BXg13120.t1, 3BXg3860.t1, 3BXg5594.t1, 3BXg7349.t1, 3BXg7537.t1, 3BXg8146.t1, 3BXg8641.t1, 3BXg8643.t1, 3BXg9353.t1	2.62E-05
GO:0000 272	polysaccharide catabolic process	2293; 2284; 2273; 667; 1249; 4540; 4668; 4941; 4923	1AXg2246.t1, 1AXg5996.t1, 1AXg6048.t1, 1AXg9193.t1, 1AXg9842.t1, 3AXg10237.t1, 3AXg192.t1, 3AXg2760.t1, 3AXg5370.t1	4125; 2435; 4101; 2349; 4928; 2468; 3093; 4509; 4356; 4343; 4500; 4942; 4423; 4460	1BXg10656.t1, 1BXg11562.t1, 1BXg11696.t1, 1BXg2692.t1, 1BXg4311.t1, 1BXg8760.t1, 1BXg9770.t1, 3BXg10794.t1, 3BXg11001.t1, 3BXg1101.t1, 3BXg3387.t1, 3BXg6628.t1, 3BXg6890.t1, 3BXg9765.t1	3.30E-05
GO:0045 490	pectin catabolic process	4948; 4666; 4943; 4571	1AXg9874.t1, 3AXg2790.t1, 3AXg5277.t1, 3AXg9121.t1	4099; 4937; 4449	1BXg12260.t1, 3BXg9358.t1, 3BXg9608.t1	3.30E-05
GO:0004 252	serine-type endopeptidase activity	4804; 652; 4947; 666; 4670; 4921; 4577; 4834; 4922; 4525; 4526	1AXg11086.t1, 1AXg7771.t1, 1AXg8019.t1, 1AXg9261.t1, 3AXg10865.t1, 3AXg2755.t1, 3AXg2995.t1, 3AXg3480.t1, 3AXg5176.t1, 3AXg5987.t1, 3AXg8810.t1	2467; 4850; 2452; 4814; 4497; 4386; 4936; 4355; 4944; 4381; 4485; 4945	1BXg10439.t1, 1BXg782.t1, 1BXg7838.t1, 3BXg1720.t1, 3BXg4508.t1, 3BXg5319.t1, 3BXg5448.t1, 3BXg6263.t1, 3BXg6633.t1, 3BXg8638.t1, 3BXg9634.t1, 3BXg9880.t1	3.92E-05
GO:0006 979	response to oxidative	2272; 4626; 4635	1AXg6636.t1, 3AXg10815.t1	4103; 4860;	1BXg10186.t1, 1BXg11947.t1	1.11E-04

	stress		3AXg2285.t1	4946	3BXg8947.t1	
GO:0030 248	cellulose binding	478; 4917; 4918; 633; 2291; 2287; 2285; 2281; 497; 4920; 4924; 4925	1AXg10805.t1, 1AXg1317.t1, 1AXg21242.t1, 1AXg3175.t1, 1AXg325.t1, 1AXg5017.t1, 1AXg5538.t1, 1AXg8113.t1, 1AXg9750.t1, 3AXg10814.t1, 3AXg7674.t1, 3AXg8315.t1	4926; 4927; 2345; 4929; 4115; 4930; 4933; 4934; 4935; 4428; 4938	1BXg1054.t1, 1BXg177.t1, 1BXg2053.t1, 1BXg4617.t1, 1BXg4950.t1, 1BXg6576.t1, 3BXg11837.t1, 3BXg14356.t1, 3BXg2769.t1, 3BXg7066.t1, 3BXg9781.t1	1.51E-04
GO:0016 788	hydrolase activity, acting on ester bonds	4805; 4873; 496; 645; 4836; 4539; 4569	1AXg10964.t1, 1AXg1296.t1, 1AXg13882.t1, 1AXg13885.t1, 3AXg1785.t1, 3AXg6767.t1, 3AXg8951.t1	2489; 4862; 2445; 2477; 4852; 4847; 4818; 4467; 4469; 4905	1BXg11282.t1, 1BXg11329.t1, 1BXg12241.t1, 1BXg5689.t1, 1BXg6844.t1, 1BXg8700.t1, 3BXg12041.t1, 3BXg3959.t1, 3BXg443.t1, 3BXg5704.t1	3.35E-04
GO:0004 190	aspartic- type endopeptida se activity	482; 494; 673; 2252; 4919; 4529; 4833; 4581; 4894	1AXg10578.t1, 1AXg6959.t1, 1AXg6960.t1, 1AXg9542.t1, 3AXg10215.t1, 3AXg1976.t1, 3AXg3738.t1, 3AXg573.t1, 3AXg9318.t1	2439; 4853; 4076; 2323; 2474; 4842; 4932; 4347; 4472; 4385; 4483; 4904	1BXg12089.t1, 1BXg5763.t1, 1BXg6565.t1, 1BXg7026.t1, 1BXg9737.t1, 1BXg9738.t1, 3BXg10428.t1, 3BXg11695.t1, 3BXg4394.t1, 3BXg5286.t1, 3BXg8935.t1, 3BXg9882.t1	3.46E-04
GO:0004 650	polygalactur onase activity	4515; 4666; 4943	3AXg10862.t1, 3AXg2790.t1, 3AXg5277.t1	2377; 4937; 4442	1BXg4998.t1, 3BXg9358.t1, 3BXg9632.t1	3.46E-04
GO:0004 185	serine-type carboxypept idase activity	587; 2282; 4838; 4837; 4827; 4826; 4624	1AXg11050.t1, 1AXg7972.t1, 3AXg10866.t1, 3AXg1190.t1, 3AXg891.t1, 3AXg9023.t1, 3AXg9670.t1	4102; 2386; 4825; 4812; 4353; 4432; 4810; 4807	1BXg10249.t1, 1BXg2887.t1, 3BXg10049.t1, 3BXg3887.t1, 3BXg4014.t1, 3BXg5175.t1, 3BXg5715.t1, 3BXg9635.t1	0.000484
GO:0016 798	hydrolase activity, acting on glycosyl bonds	530; 2296; 4875; 477; 4872; 2292; 480; 2290; 2289; 487; 4891; 4667; 4892; 4893	1AXg10268.t1, 1AXg11997.t1, 1AXg12212.t1, 1AXg13463.t1, 1AXg15301.t1, 1AXg2742.t1, 1AXg3149.t1, 1AXg3652.t1, 1AXg3653.t1, 1AXg5358.t1,	4800; 3811; 2483; 4949; 2352; 4849; 2300; 4813; 4480	1BXg10455.t1, 1BXg10918.t1, 1BXg2454.t1, 1BXg4330.t1, 1BXg5639.t1, 1BXg817.t1, 1BXg8757.t1, 3BXg2207.t1, 3BXg8858.t1	0.000484

			1AXg7786.t1, 3AXg2394.t1, 3AXg7003.t1, 3AXg8007.t1			
GO:0005 507	copper ion binding	4802; 1342; 4632; 4597; 4595; 4831	1AXg12235.t1, 1AXg7766.t1, 3AXg1263.t1, 3AXg3686.t1, 3AXg3946.t1, 3AXg5094.t1	2539; 4098; 4856; 3185; 4427; 4817; 4403	1BXg10115.t1, 1BXg12278.t1, 1BXg3746.t1, 1BXg886.t1, 3BXg10410.t1, 3BXg12053.t1, 3BXg689.t1	0.000489
GO:0008 810	cellulase activity	4918; 1249; 4540; 4839; 4941; 4532	1AXg21242.t1, 1AXg9842.t1, 3AXg10237.t1, 3AXg10372.t1, 3AXg2760.t1, 3AXg6046.t1	4927; 4929; 4930; 4109; 3093; 4509; 4343; 4934; 4942; 4903	1BXg177.t1, 1BXg4617.t1, 1BXg6576.t1, 1BXg8240.t1, 1BXg9770.t1, 3BXg10794.t1, 3BXg1101.t1, 3BXg14356.t1, 3BXg6628.t1, 3BXg9093.t1	0.000644
GO:0071 555	cell wall organization	4939; 614; 934; 4515; 4666; 4659; 4940	1AXg12959.t1, 1AXg2047.t1, 1AXg6047.t1, 3AXg10862.t1, 3AXg2790.t1, 3AXg7872.t1, 3AXg9980.t1	4099; 2413; 2482; 2377; 4475; 4487; 4937; 4442	1BXg12260.t1, 1BXg2549.t1, 1BXg264.t1, 1BXg4998.t1, 3BXg11145.t1, 3BXg928.t1, 3BXg9358.t1, 3BXg9632.t1	0.001751
GO:0008 081	phosphoric diester hydrolase activity	4520; 4950; 4951	3AXg3348.t1, 3AXg429.t1, 3AXg8372.t1	2343; 4952; 4953; 4954; 4388	1BXg6110.t1, 3BXg10729.t1, 3BXg10989.t1, 3BXg1818.t1, 3BXg5195.t1	0.003097
GO:0004 601	peroxidase activity	4626; 4635	3AXg10815.t1, 3AXg2285.t1	2539; 4808; 4946	1BXg10115.t1, 3BXg8361.t1, 3BXg8947.t1	0.003136
GO:0044 238	primary metabolic process	501; 4835; 4630; 4830; 4828	1AXg11043.t1, 3AXg3154.t1, 3AXg6318.t1, 3AXg8054.t1, 3AXg8258.t1	4798	3BXg2943.t1	0.008701
GO:0006 629	lipid metabolic process	4520; 4950; 4832; 4951	3AXg3348.t1, 3AXg429.t1, 3AXg4906.t1, 3AXg8372.t1	2339; 2343; 4822; 4952; 4953; 4954; 4388	1BXg11161.t1, 1BXg6110.t1, 3BXg10687.t1, 3BXg10729.t1, 3BXg10989.t1, 3BXg1818.t1, 3BXg5195.t1	0.022235
GO:0030 246	carbohydrat e binding	4801; 487; 4615	1AXg4233.t1, 1AXg5358.t1, 3AXg4536.t1	4097; 4949; 4854; 2332; 4815; 4422; 4489;	1BXg135.t1, 1BXg4330.t1, 1BXg5733.t1, 1BXg9970.t1, 3BXg144.t1, 3BXg3121.t1, 3BXg8118.t1,	0.022419

				4484	3BXg9960.t1	
GO:0008233	peptidase activity	567; 489; 1013; 2286	1AXg1909.t1, 1AXg3273.t1, 1AXg3484.t1, 1AXg5534.t1	4124; 4861; 2858; 4846; 4809	1BXg11338.t1, 1BXg11861.t1, 1BXg2151.t1, 1BXg8705.t1, 3BXg7109.t1	0.026107
GO:0016311	dephosphorylation	485; 602; 4870; 4869; 4868; 4867; 4866; 4841; 4889; 4623; 4618; 4646; 4890	1AXg1240.t1, 1AXg12610.t1, 1AXg2072.t1, 1AXg2679.t1, 1AXg3651.t1, 1AXg5280.t1, 1AXg7026.t1, 3AXg10295.t1, 3AXg2325.t1, 3AXg2688.t1, 3AXg6634.t1, 3AXg8755.t1, 3AXg9415.t1	2329; 2401; 4855; 4114; 2478; 4821; 4439; 4816; 4912; 4503; 4913; 4914; 4915; 4425	1BXg1583.t1, 1BXg3489.t1, 1BXg4136.t1, 1BXg5433.t1, 1BXg6623.t1, 3BXg10709.t1, 3BXg11186.t1, 3BXg12884.t1, 3BXg23.t1, 3BXg246.t1, 3BXg383.t1, 3BXg4227.t1, 3BXg5208.t1, 3BXg5671.t1	0.028109
GO:0005886	plasma membrane	484; 4874; 4871; 649; 665; 658; 651; 4641; 4521; 4955; 4956; 4514; 4957	1AXg11973.t1, 1AXg12543.t1, 1AXg20005.t1, 1AXg2148.t1, 1AXg4299.t1, 1AXg4879.t1, 1AXg9624.t1, 3AXg10151.t1, 3AXg1507.t1, 3AXg1833.t1, 3AXg3620.t1, 3AXg7460.t1, 3AXg7667.t1	2336; 2431; 2451; 4851; 4848; 4845; 4820; 4819; 4916; 4473	1BXg1674.t1, 1BXg3283.t1, 1BXg7238.t1, 1BXg7733.t1, 1BXg8189.t1, 1BXg8837.t1, 3BXg11471.t1, 3BXg11779.t1, 3BXg11859.t1, 3BXg8700.t1	0.120452
GO:0008168	methyltransferase activity	4799; 4663; 4662	3AXg3246.t1, 3AXg512.t1, 3AXg618.t1	4797; 4492	3BXg5144.t1, 3BXg7176.t1	0.14079

[0119] These data suggest that numerous biological processes are different in beneficial endophytes, for example as compared to neutral endophytes. Some of these processes include cell wall degradation, starch and sucrose metabolism, and protection from oxidative stress.

[0120] One mechanism of entry of endophytes into intact plant tissue is by enzymatic processes involving degradation of cell walls. Beneficial endophytes used in this example show increased levels of secreted proteins that may be involved in such degradation, for example those that fall within the following gene ontology annotations: GO:0005618 (cell wall), GO:0000272 (polysaccharide catabolic process), GO:0045490 (pectin catabolic process), GO:0030248 (cellulose binding), GO:0004650 (polygalacturonase activity),

GO:0008810 (cellulase activity), GO:0071555 (cell wall organization), GO:0004185 (serine-type carboxypeptidase activity), GO:0016798 (hydrolase activity, acting on glycosyl bonds), and GO:0030246 (carbohydrate binding). Certain of the proteins that fall within these gene ontology annotations may also be involved in starch and sucrose metabolism.

- 5 **[0121]** Beneficial endophytes of the invention secreted proteins that may provide a benefit to the plant, such as proteins involved in protection against oxidative stress (GO:0016614 (oxidoreductase activity, acting on CH-OH group of donors); GO:0006979 (response to oxidative stress); GO:0005507 (copper ion binding), and GO:0004601 (peroxidase activity)).

Example 8: Greenhouse Characterization**Setup and watering conditions**

[0122] A sandy loam growth substrate is mixed in the greenhouse and consisting of 60% loam and 40% mortar sand (Northeast Nursery, Peabody, MA). Prior to mixing, loam is sifted
5 through a 3/8" square steel mesh screen to remove larger particles and debris. Half of the appropriate fertilizers and soil treatments to be applied during the season is added to the soil mixture prior to sowing. The remaining components are provided dissolved in irrigation water at the onset of the reproductive stages of development. Substrate surface area per pot is calculated based on pot diameter in order to approximate the "acreage" of individual pots. An
10 equivalent volume of fertilized soil is then gently added to each pot in order to minimize compaction of the soil. The substrate is saturated with water 3-4 hours before sowing.

[0123] Commercially available seeds (e.g., seeds described herein) are coated with microbial treatments using the formulation used for field trials and described herein. Treatments included microbial coatings and two controls (non-treated and formulation).
15 Three seeds are sown evenly spaced at the points of a triangle. Soil is then overlaid atop the seeds and an additional 200 mL water was added to moisten the overlaying substrate.

Midseason measurements and harvest

[0124] Emergence percentage is observed. Further, at various times through the growing season, plants are assessed for onset of and recovery from stress symptoms, for example but
20 not limited to: leaf senescence, anthesis-silking interval, leaf chlorophyll content, grain weight, and total yield.

[0125] To compare treated plants to controls, a fully Bayesian robust t-test is performed. Briefly, R (R Core Team, 2015) was used with the BEST package (Kruschke and Meredith, 2015) and JAGS (Plummer, 2003) to perform a Markov Chain Monte Carlo estimation of the
25 posterior distribution the likely differences between the two experimental groups. A 95% highest density interval (HDI) is overlaid onto this distribution to aid in the interpretation of whether the two biological groups truly differ.

Tissue collection and processing for transcriptomics, hormone, and metabolomics analysis

[0126] In order to assess the effects of endophyte treatment on plant growth at the
30 transcriptomic, phytohormone, and metabolomic levels, plants are harvested. Three pots from each treatment are selected. Once separated, the tissues (roots, stems, leaves, other plant elements as appropriate) from the three pots of each treatment are pooled. For collection, first

all loosely attached substrate is removed from the roots by gently tapping and shaking the roots. Any adherent substrate is removed by submerging the roots in water and manually dislodging attached soil and debris. The roots are then blotted dry before being cut from the aerial tissue, followed by separating petioles and leaves from the stem. As tissues are removed from the plant they are immediately bagged and frozen in liquid nitrogen. All harvested tissues are kept in liquid nitrogen or stored at -80°C until further processing.

[0127] To prepare for analyses, the tissues are ground with liquid nitrogen using a pre-chilled mortar and pestle. Approximately 100-200 micrograms of each ground sample pool is transferred to a chilled 1.5 mL microtube for RNA extraction and subsequent transcriptome, phytohormone and metabolite analysis. For proteomic analysis, 3 g of each ground sample pool is used. The remaining ground tissue is then transferred to a chilled 50 mL conical tube and stored in liquid nitrogen or at -80°C until shipment for further analyses.

Example 9: Assessment of Plant Colonization

[0128] The protocols described in this section allow confirmation of successful colonization of plants by endophytes, for example by direct recovery of viable colonies from various tissues of the inoculated plant.

Recovery of viable colonies from seeds

[0129] Seeds are surface-sterilized by exposing them to chlorine gas overnight, using the methods described elsewhere. Sterile seeds are then inoculated with submerged in 0.5 OD overnight cultures (Tryptic Soy Broth, TSB) of bacteria and allowed to briefly air dry. The seeds are then placed in tubes filled partially with a sterile sand-vermiculite mixture [(1:1 wt:wt)] and covered with 1 inch of the mixture, watered with sterile water, sealed and incubated in a greenhouse for 7 days. After incubation, various tissues of the plants are harvested and used as donors to isolate bacteria by placing tissue section in a homogenizer (TSB 20%) and mechanical mixing. The slurry is then serially diluted in 10-fold steps to 10⁻³ and dilutions 1 through 10⁻³ are plated on TSA 20% plates (1.3% agar). Plates are incubated overnight and pictures are taken of the resulting plates as well as colony counts for CFU. Bacteria are identified visually by colony morphotype and molecular methods described herein. Representative colony morphotypes are also used in colony PCR and sequencing for isolate identification via ribosomal gene sequence analysis as described herein. These trials are repeated twice per experiment, with 5 biological samples per treatment.

Culture-independent methods to confirm colonization of the plant or seeds by bacteria or fungi.

[0130] One way to detect the presence of endophytes on or within plants or seeds is to use quantitative PCR (qPCR). Internal colonization by the endophyte can be demonstrated by using surface-sterilized plant tissue (including seed) to extract total DNA, and isolate-specific fluorescent MGB probes and amplification primers are used in a qPCR reaction. An increase in the product targeted by the reporter probe at each PCR cycle therefore causes a proportional increase in fluorescence due to the breakdown of the probe and release of the reporter. Fluorescence is measured by a quantitative PCR instrument and compared to a standard curve to estimate the number of fungal or bacterial cells within the plant.

Experimental Description

[0131] The design of both species-specific amplification primers, and isolate-specific fluorescent probes are well known in the art. Plant tissues (seeds, stems, leaves, flowers, etc.) are pre-rinsed and surface sterilized using the methods described herein.

[0132] Total DNA is extracted using methods known in the art, for example using commercially available Plant-DNA extraction kits, or the following method.

1. Tissue is placed in a cold-resistant container and 10-50mL of liquid nitrogen is applied. Tissues are then macerated to a powder.
2. Genomic DNA is extracted from each tissue preparation, following a chloroform:isoamyl alcohol 24:1 protocol (Sambrook et al., 1989).

[0133] Quantitative PCR is performed essentially as described by Gao et al. (2010) with primers and probe(s) specific to the desired isolate using a quantitative PCR instrument, and a standard curve is constructed by using serial dilutions of cloned PCR products corresponding to the specie-specific PCR amplicon produced by the amplification primers. Data are analyzed using instructions from the quantitative PCR instrument's manufacturer software.

[0134] As an alternative to qPCR, Terminal Restriction Fragment Length Polymorphism, (TRFLP) can be performed, essentially as described in Johnston-Monje and Raizada (2011). Group specific, fluorescently labelled primers are used to amplify a subset of the microbial population, especially bacteria, especially fungi, especially archaea, especially viruses. This fluorescently labelled PCR product is cut by a restriction enzyme chosen for heterogeneous distribution in the PCR product population. The enzyme cut mixture of fluorescently labelled

and unlabeled DNA fragments is then submitted for sequence analysis on a Sanger sequence platform such as the Applied Biosystems 3730 DNA Analyzer.

Immunological methods to detect microbes in seeds and vegetative tissues

5 [0135] A polyclonal antibody is raised against specific bacteria X or fungus Y strains via standard methods. A polyclonal antibody is also raised against specific GUS and GFP proteins via standard methods. Enzyme-linked immunosorbent assay (ELISA) and immunogold labeling is also conducted via standard methods, briefly outlined below.

10 [0136] Immunofluorescence microscopy procedures involve the use of semi-thin sections of plant element or adult plant tissues transferred to glass objective slides and incubated with blocking buffer (20 mM Tris (hydroxymethyl)-aminomethane hydrochloride (TBS) plus 2 % bovine serum albumin, pH 7.4) for 30 min at room temperature. Sections are first coated for 30 min with a solution of primary antibodies and then with a solution of secondary antibodies (goat anti-rabbit antibodies) coupled with fluorescein isothiocyanate (FITC) for 30 min at room temperature. Samples are then kept in the dark to eliminate breakdown of the light-sensitive FITC. After two 5-min washings with sterile potassium phosphate buffer (PB) (pH 7.0) and one with double-distilled water, sections are sealed with mounting buffer (100 mL 0.1 M sodium phosphate buffer (pH 7.6) plus 50 mL double-distilled glycerine) and observed under a light microscope equipped with ultraviolet light and a FITC Texas-red filter.

20 [0137] Ultrathin (50- to 70-nm) sections for TEM microscopy are collected on pioloform-coated nickel grids and are labeled with 15-nm gold-labeled goat anti-rabbit antibody. After being washed, the slides are incubated for 1 h in a 1:50 dilution of 5-nm gold-labeled goat anti-rabbit antibody in IGL buffer. The gold labeling is then visualized for light microscopy using a BioCell silver enhancement kit. Toluidine blue (0.01%) is used to lightly counterstain the gold-labeled sections. In parallel with the sections used for immunogold silver enhancement, serial sections are collected on uncoated slides and stained with 1% toluidine blue. The sections for light microscopy are viewed under an optical microscope, and the ultrathin sections are viewed by TEM.

Example 10: Assessment of Improved Plant Characteristics: Differentially Regulated Hormones

30 Methods

[0138] For hormone analysis, 100 ± 10 mg tissue is measured into microtubes (chilled with liquid nitrogen), and sent on dry ice to a vendor. Plant hormone analysis is performed per

Christiansen *et al.* (2014) with slight modification. Briefly, hormones are extracted from 100 ± 10 mg of frozen tissue and tissue weights are recorded for quantification. A mixture containing 10 microliters of 2.5 microMolar internal standards and 500 microliters of extraction buffer [1-propanol/H₂O/concentrated HCl (2:1:0.002, vol/vol/vol) is added to each sample and vortexed until thawed. Samples are agitated for 30 min at 4°C, then 500 microliters of dichloromethane (CH₂Cl₂) is added. Samples are agitated again for 30 min at 4°C, and then centrifuged at 13,000 x g for 5 min. in darkness. The lower organic layer is removed into a glass vial and the solvent is evaporated by drying samples for 30-40 min under a N₂ stream. Samples are re-solubilized in 150 microliters of MeOH, shaken for 1 min and centrifuged at 14,000 x g for 2 min. A supernatant of 90 microliters is transferred into the autosampler vial and hormones are analyzed by ultraperformance liquid chromatography, coupled to mass spectrometry (UPLC-MS/MS). Ascentis Express C-18 Column (3 cm x 2.1 mm, 2.7 cm) is connected to an API 3200 using electrospray ionization-tandem mass spectrometry (MS/MS) with scheduled multiple reaction monitoring (SMRM). The injection volume is 5 microliters and has a 300 microliters/min mobile phase consisting of Solution A (0.05% acetic acid in water) and Solution B (0.05% acetic acid in acetonitrile) with a gradient consisting of (time – %B): 0.3 – 1%, 2 – 45%, 5 – 100%, 8 – 100%, 9 – 1%, 11 – stop. Quantitation is carried out with Analyst software (AB Sciex), using the internal standards as a reference for extraction recovery. Leaf, root, and/or other tissue is saved in -62°C and saved for subsequent gene expression analysis.

[0139] Mass spectra of plant hormones are obtained. Fold changes between control and treated samples are calculated by dividing the mass spectrum value from the treated sample by the value from the control sample.

[0140] Modulation of hormones related to growth as well as related to resistance to abiotic and biotic stresses are found in plants treated with endophytes as compared to isoline plants lacking such treatment.

Example 11: Assessment of Improved Plant Characteristics and Differentially Regulated Metabolites

Methods

[0141] For metabolite analysis, 150 ± 10 mg of each sample is transferred into 1.5mL microtubes (chilled in liquid nitrogen) and sent on dry ice to the Proteomics and Metabolomics Facility at Colorado State University. Metabolomics data acquisition is performed per the following methods provided by Dr. Corey Broeckling at CSU. To prepare the samples for analysis, phytohormones are extracted from ground plant material using a

biphasic protocol. One mL of a methyl tert-butyl ether (MTBE): methanol:water mixture (6:3:1) is added to each sample then shaken for 1 hour. Next, 250 microliters cold water and a mix of internal standards are added to each sample to promote phase separation. Samples are shaken again for 5 minutes. Samples are then centrifuged at 2,095 x g at 4°C for 15 minutes.

5 The organic top phase is removed for hormone analysis, dried under an inert nitrogen environment, then re-suspended in 400 microliters of 50% acetonitrile. Extracts are then directly analyzed by LC-MS.

[0142] For GC-MS, the polar (lower phase) extract is dried using a speedvac, resuspended in 50 microliters of pyridine containing 50 mg/mL of methoxyamine hydrochloride, 10 incubated at 60°C for 45 min, sonicated for 10 min, and incubated for an additional 45 min at 60°C. Next, 25 microliters of N-methyl-N-trimethylsilyltrifluoroacetamide with 1% trimethylchlorosilane (MSTFA + 1% TMCS, Thermo Scientific) is added and samples re incubated at 60°C for 30 min, centrifuged at 3000 x g for 5 min, cooled to room temperature, and 80 microliters of the supernatant is transferred to a 150 microliters glass insert in a GC- 15 MS autosampler vial. Metabolites are detected using a Trace GC Ultra coupled to a Thermo ISQ mass spectrometer (Thermo Scientific). Samples are injected in a 1:10 split ratio twice in discrete randomized blocks. Separation occurs using a 30 m TG-5MS column (Thermo Scientific, 0.25 mm i.d., 0.25 micrometer film thickness) with a 1.2 mL/min helium gas flow rate, and the program consists of 80°C for 30 sec, a ramp of 15°C per min to 330°C, and an 8 20 min hold. Masses between 50-650 m/z re scanned at 5 scans/sec after electron impact ionization. The ionization source is cleaned and retuned and the injection liner replaced between injection replicates. Analysis for plant hormones is performed by UPLC-MS/MS as follows.

[0143] Metabolites are detected and mass spectra annotated by comparing to libraries of 25 known spectra including an in-house database at CSU (LC-MS only), the National Institute of Standards and Technology databases, Massbank MS database, and the Golm Metabolite Database. Initial annotation is automated, followed by manual validation of annotations. Following annotation, compounds are identified. After removal of technical artifacts (e.g. siloxane), and ambiguous or vague annotations (e.g. carbohydrate or saccharide), identified 30 compounds remain for analysis. These compounds are assessed for fold change over control plants. Metabolites are grouped by pathways (e.g. carbohydrate metabolism or alkaloid biosynthesis) and the KEGG database and literature are manually referenced to identify pertinent shifts in metabolic patterns in plants treated with microbes. Any compound without

an appreciable shift compared to that observed in control plants is removed from further analysis.

[0144] Modulation of metabolites related to growth as well as related to resistance to abiotic and biotic stresses are found in plants treated with endophytes as compared to isoline plants lacking such treatment.

Example 12: Efficacy Testing of Endophytes in Crop Production

Method

[0145] Whole plants or plant elements, such as seeds, roots, or leaves, from any of the crops useful in the invention are treated with endophytes as described in Examples 3, 4, or 8. They are then sown in a variety in different growing regions for efficacy testing. Trials consist of ten replicate plots for each treatment and control respectively arranged in a spatially balanced randomized complete block design (Van Es et al. 2007). In addition to measuring total yield, metrics such as seedling emergence, normalized difference vegetation index (NDVI) and time to flowering are assessed. Endophytes are applied alone as a seed treatment, as well as in combination with other endophytes.

Results

[0146] Crop plants that have been treated with the endophyte(s) of the present invention demonstrate improvements in one or more agronomically-important characteristic, for example but not limited to: disease resistance, drought tolerance, heat tolerance, cold tolerance, salinity tolerance, metal tolerance, herbicide tolerance, chemical tolerance, improved water use efficiency, improved nitrogen utilization, improved nitrogen fixation, pest resistance, herbivore resistance, pathogen resistance, increased yield, increased yield under water-limited conditions, health enhancement, vigor improvement, growth improvement, photosynthetic capability improvement, nutrition enhancement, altered protein content, altered oil content, increased biomass, increased shoot length, increased root length, improved root architecture, improved plant standability, increased plant element weight, altered plant element carbohydrate composition, altered plant element oil composition, number of pods, delayed senescence, stay-green, and altered plant element protein composition.

Example 13: Generating/Isolating Endophytes Compatible With Agrochemicals

[0147] The application of pesticides against fungal pathogens of agriculturally-relevant plants is a common practice in agriculture to ensure higher yields. One method of pesticide delivery is to cover the seeds with a coating with pesticides. Although pesticides are meant to

deter the growth and propagation of pathogenic microorganisms, they may also affect endophyte populations residing inside of the seed. For this purpose, conferring compatibility mechanisms to endophytic fungi providing beneficial properties which are sensitive to these compounds is desirable for the maintenance of endophytes in the seeds.

5 [0148] Compatibility with pesticides can be intrinsic (naturally pesticide compatible fungi, for example) or acquired (due to mutations in the genetic material of the microorganism, or to the introduction of exogenous DNA by natural DNA transfer).

[0149] Fungicides used as protectants are effective only on the seed surface, providing protection against seed surface-borne pathogens and providing some level of control of soil-borne pathogens. These products generally have a relatively short residual. Protectant
10 fungicides such as captan, maneb, thiram, or fludioxonil help control many types of soil-borne pathogens, except root rotting organisms. Systemic fungicides are absorbed into the emerging seedling and inhibit or kill susceptible fungi inside host plant tissues. Systemic fungicides used for seed treatment include the following: azoxystrobin, carboxin,
15 mefenoxam, metalaxyl, thiabendazole, trifloxystrobin, and various triazole fungicides, including difenoconazole, ipconazole, tebuconazole, and triticonazole. Mefenoxam and metalaxyl are primarily used to target the oomycetes such as species of *Pythium* and *Phytophthora*.

[0150] Strobilurin analogues, such as azoxystrobin, inhibit mitochondrial respiration by
20 blocking electron transfer at the cytochrome bcl complex. Phenylamides, including metalaxyl, interfere with RNA synthesis in target fungi. Oxathiin systemic fungicides like carboxin inhibits the incorporation of phenylalanine into protein and of uracil into RNA. Azole fungicides BAS 480F, flusilazole, and tebuconazole are inhibitors of sterol 14 α -demethylase, and block sterol biosynthesis.

25 *I. Determination of intrinsic resilience against agrochemicals of bacteria cultured from seeds*

[0151] To test the intrinsic resilience pesticides of bacteria isolated as described herein, minimum inhibitory concentration (MIC) assays are performed on all isolated bacteria of interest, as described in Wiegand, Irith, Kai Hilpert, and Robert EW Hancock. Nature
30 protocols 3.2 (2008): 163-175, which is incorporated herein by reference in its entirety. Briefly, known concentrations of bacterial cells or spores are used to inoculate plates containing solid media with different concentrations of the pesticide, or to inoculate liquid

media containing different concentrations of the pesticide (in a 96-well plate). The pesticides are used at the concentration recommended by the manufacturer for seed coating, and two-fold dilutions down to 0.000125 (12 two-fold dilutions). Growth is assessed after incubation for a defined period of time (16–20 h) and compared to cultures grown in the same manner without any pesticides as control. The MIC value is determined as described in Wiegand, Irith, Kai Hilpert, and Robert EW Hancock. Nature protocols 3.2 (2008): 163-175.

II. Determination of intrinsic resilience against agrochemicals of fungi cultured from seeds

[0152] To test the intrinsic resilience against pesticides of the fungi isolated as described in this application, minimum inhibitory concentration (MIC) assays are performed on all isolated fungi of interest, as described in Mohiddin, F. A., and M. R. Khan. African Journal of Agricultural Research 8.43 (2013): 5331-5334 (incorporated herein by reference in its entirety), with the following changes: Briefly, double strength potato dextrose agar is prepared containing different concentrations of each pesticide. The pesticides are applied at the concentration recommended by the manufacturer, and also in two fold dilutions to 0.000125X (12 two-fold dilutions). Thereafter, the plates are seeded centrally with a 3 mm disc of 4 days old culture of each fungus that had been centrifuged and rinsed twice in sterile phosphate buffer. PDA plates without a fungicide but inoculated with the fungi serve as a control. The inoculated plates are incubated at $25 \pm 2^\circ\text{C}$ for 5 days. The radial growth of the colony in each treatment is measured and the percent inhibition of growth is calculated as described by Mohiddin, F. A., and M. R. Khan. African Journal of Agricultural Research 8.43 (2013): 5331-5334 (incorporated herein by reference in its entirety). Fungal isolates are classified as resilience against the particular pesticide if their maximum tolerance concentration (MTC) is 2x or above the concentration of pesticides recommended to be used in seed coatings.

III. Generating fungal species with compatibility with commercial pesticides coated onto seeds

[0153] When a fungal strain of interest that provides a beneficial property to its plant host is found to be sensitive to a commercially-relevant pesticide, pesticide-compatible variants of the strains need to be generated for use in this application. Generation of compatibility to multiple pesticides or cocktails of pesticides is accomplished by sequentially selecting compatible variants to each individual pesticide and then confirming compatibility with a

combination of the pesticides. After each round of selection, fungi are tested for their ability to form symbiotic relationships with the plants and to confirm that they provide a beneficial property on the plant as did the parental strain, with or without application of the pesticide product as described herein.

5 [0154] Generation and isolation of pesticide-compatible strains derived from endophytic strains isolated from seeds and shown to provide beneficiary traits to plants is performed as described by Shapiro-Ilan, David I., et al. Journal of invertebrate pathology 81.2 (2002): 86-93(incorporated herein by reference in its entirety), with some changes. Briefly, spores of the isolated fungi are collected and solutions containing between $\sim 1 \times 10^3$ spores are used to
10 inoculate potato dextrose agar (PDA) plates containing 2, 5, and 10 times the MTC of the particular strain. Plates are incubated for 1-5 days and a single colony from the highest concentration of pesticide which allows growth is inoculated onto a fresh plate with the same pesticide concentration 7 consecutive times. After compatibility has been established, the strain is inoculated onto PDA plates 3 consecutive times and then inoculated onto a PDA
15 plate containing the pesticide to confirm that the compatibility trait is permanent.

[0155] Alternatively, if this method fails to provide a compatible strain, a spore suspension is treated with ethyl methanesulfonate to generate random mutants, similarly as described by Leonard, Cory A., Stacy D. Brown, and J. Russell Hayman. International journal of microbiology 2013 (2013), Article ID 901697 (incorporated herein by reference in its
20 entirety) and spores from this culture are used in the experiment detailed above.

[0156] To develop fungal endophytes compatible with multiple pesticides or cocktails of pesticides, spores of a strain compatible with one or more pesticides are used to select for variants to a new pesticide as described above. Strains developed this way are tested for retention of the pesticide-compatibility traits by inoculating these strains onto PDA plates
25 containing each single pesticide or combinations of pesticides.

IV. Generating bacterial species with compatibility to commercial pesticides coated onto seeds

[0157] When a bacterial strain of interest is found to be sensitive to a commercially-relevant pesticide, generation of pesticide-compatible variants of the strains can be generated
30 for use in this application. Generation of compatible with multiple pesticides or cocktails of pesticides is accomplished by first sequentially selecting variants compatible with incrementally higher concentrations of each individual pesticide (as described by Thomas,

Louise, et al. *Journal of Hospital Infection* 46.4 (2000): 297-303, which is incorporated herein by reference in its entirety). To develop bacterial endophytes compatible with multiple pesticides or cocktails of pesticides, bacterial cells of a strain compatible with one or more pesticides is used to select for variants to a new pesticide as described above. Strains developed this way are tested for retention of the pesticide-compatible traits by inoculating these strains onto PDA plates containing each single pesticide or combinations of pesticides.

[0158] After each round of selection, bacteria are tested for their ability to live within plants and for their ability to provide the same beneficial property to the plant as did the parental strain, with or without application of the pesticide product to the plants as described herein.

V. Generation of pesticide-compatible bacteria by insertion of a resistance plasmid

[0159] Many bacterial plasmids that confer compatible pesticides have been described in the literature (Don, R. H., and J. M. Pemberton. *Journal of Bacteriology* 145.2 (1981): 681-686; and Fisher, P. R., J. Appleton, and J. M. Pemberton. *Journal of bacteriology* 135.3 (1978): 798-804, each of which is incorporated herein by reference in its entirety)

[0160] For cases in which obtaining naturally occurring compatible bacteria is not feasible, use of these plasmids is a possible way to develop endophytic strains compatible with multiple pesticides.

[0161] For example, a *Pseudomonas fluorescens* strain that provides anti-nematode properties to plants but is sensitive to the pesticides 2,4-dichlorophenoxyacetic acid and 4-chloro-2-methylphenoxyacetic can be transformed with the plasmid pJP2 (isolated from *Alcaligenes eutrophus*) which provides transmissible compatible with these compounds, as described by Don and Pemberton, 1981. Briefly, plasmids are transferred by conjugation to *Pseudomonas*, using the method described in Haas, Dieter, and Bruce W. Holloway. *Molecular and General Genetics* 144.3 (1976): 243-251 (incorporated herein by reference in its entirety).

[0162] After the generation of bacteria carrying pesticide-compatibility conferring plasmids, these endophytes are tested for their ability to live inside plant tissues and for their ability to provide the same beneficial property to the plant as it did for the parental strain, with or without application of the pesticide product to the plants as described herein.

VI. Growth and scale-up of bacteria for inoculation on solid media

[0163] The bacterial isolates are grown by loop-inoculation of a single colony into R2A broth (supplemented with appropriate antibiotics) in 100 mL flasks. The bacterial culture is incubated at 30 ± 2 °C for 2 days at 180 rpm in a shaking incubator (or under varying temperatures and shaking speeds as appropriate). This liquid suspension is then used to inoculate heat sterilized vermiculite powder that is premixed with sterile R2A broth (without antibiotics), resulting in a soil like mixture of particles and liquid. This microbial powder is then incubated for an additional couple of days at 30 ± 2 °C with daily handshaking to aerate the moist powder and allow bacterial growth. Microbially inoculated vermiculite powder is now ready for spreading on to soil or onto plant parts. Alternatively, the R2A broth is used to inoculate Petri dishes containing R2A or another appropriate nutrient agar where lawns of bacteria are grown under standard conditions and the solid colonies scraped off, resuspended in liquid and applied to plants as desired.

VII. Growth & scale-up of fungi for inoculation on solid media

[0164] Once a fungal isolate has been characterized, conditions are optimized for growth in the lab and scaled-up to provide sufficient material for assays. For example, the medium used to isolate the fungus is supplemented with nutrients, vitamins, co-factors, plant-extracts, and other supplements that can decrease the time required to grow the fungal isolate or increase the yield of mycelia and/or spores the fungal isolate produces. These supplements can be found in the literature or through screening of different known media additives that promote the growth of all fungi or of the particular fungal taxa.

[0165] To scale up the growth of fungal isolates, isolates are grown from a frozen stock on several Petri dishes containing media that promotes the growth of the particular fungal isolate and the plates are incubated under optimal environmental conditions (temperature, atmosphere, light). After mycelia and spore development, the fungal culture is scraped and resuspended in 0.05M Phosphate buffer (pH 7.2, 10mL/plate). Disposable polystyrene Bioassay dishes (500 cm², Thermo Scientific Nunc UX-01929-00) are prepared with 225mL of autoclaved media with any required supplements added to the media, and allowed to solidify. Plates are stored at room temperature for 2-5 days prior to inoculation to confirm sterility. 5mL of the fungal suspension is spread over the surface of the agar in the Bioassay plate in a biosafety cabinet, plates are allowed to dry for 1h, and they are then incubated for 2-5 days, or until mycelia and/or spores have developed.

[0166] A liquid fungal suspension is then created via the following. Fungal growth on the surface of the agar in the Bioassay plates are then scraped and resuspended in 0.05M Phosphate buffer (pH 7.2). OD₆₀₀ readings are taken using a spectrometer and correlated to previously established OD₆₀₀/CFU counts to estimate fungal population densities, and the volume adjusted with additional sodium phosphate buffer to result in 100 mL aliquots of fungi at a density of approximately 10⁶-10¹¹ spores/mL. This suspension may or may not be filtered to remove mycelia and can be used to create a liquid microbial formulation as described herein to apply the fungal isolate onto a plant, plant part, or seed.

VIII. Growth & scale-up of bacteria for inoculation in liquid media

[0167] Bacterial strains are grown by loop-inoculation of one single colony into R2A broth (amended with the appropriate antibiotics) in 100 mL flasks. The bacterial culture is incubated at 28±2 °C for 1 day at 180 rpm in a shaking incubator (or under varying temperatures and shaking speeds as appropriate). The bacteria are pelleted by centrifugation and resuspended in sterile 0.1 M sodium phosphate. OD₆₀₀ readings are taken using a spectrometer and correlated to previously established OD₆₀₀/CFU counts to estimate bacterial population densities, and the volume adjusted with additional sodium phosphate buffer to result in 100 mL aliquots of bacteria at a density of 1x10⁸ cells/mL. To help break surface tension, aid bacterial entry into plants and provide microbes for some energy for growth, 10 µL of Silwet L-77 surfactant and 1 g of sucrose is added to each 100 mL aliquot (resulting in 0.01% v/v and 1% v/v concentrations, respectively) in a similar way as in the protocol for *Agrobacterium*-mediated genetic transformation of *Arabidopsis thaliana* seed [Clough, S., Bent, A. (1999) The Plant Journal 16(6): 735-743].

IX. Growth & scale-up of fungi for inoculation in liquid media

[0168] Once a fungal isolate has been characterized, conditions are optimized for growth in the lab and scaled-up to provide enough material for assays. For example, the medium used to isolate the fungi is supplemented with nutrients, vitamins, co-factors, plant-extracts, and/or other supplements that can decrease the time required to grow the fungal isolate and/or increase the yield of mycelia and/or spores the fungal isolate produces. These supplements can be found in the literature or through screening of different known media additives that promote the growth of all fungi or of the particular fungal taxa.

[0169] To scale up the growth of fungal isolates, isolates are grown from a frozen stock on Petri dishes containing media that promotes the growth of the particular fungal isolate and the

plates are incubated under optimal environmental conditions (temperature, atmosphere, light). After mycelia and spore development, the fungal culture is scraped and resuspended in 0.05M Phosphate buffer (pH 7.2, 10mL/plate). 1 liter of liquid media selected to grow the fungal culture is prepared in 2L glass flasks and autoclaved and any required supplements added to the media. These are stored at room temperature for 2-5 days prior to inoculation to confirm sterility. 1mL of the fungal suspension is added aseptically to the media flask, which is then incubated for 2-5 days, or until growth in the liquid media has reached saturation. Spore counts are determined using hemacytometer and correlated to previously established OD₆₀₀/CFU counts to estimate fungal population densities, and the volume adjusted with additional sodium phosphate buffer to result in 100 mL aliquots of fungi at a density of approximately 10^6 - 10^{11} spores/mL. This suspension may or may not be filtered to remove mycelia and can be used to create a liquid microbial formulation as described herein to apply the fungal isolate onto a plant, plant part, or seed.

X. Creation of liquid microbial formulations or preparations for the application of microbes to plants

[0170] Bacterial or fungal cells are cultured in liquid nutrient broth medium to between 10^2 - 10^{12} CFU/mL. The cells are separated from the medium and suspended in another liquid medium if desired. The microbial formulation may contain one or more bacterial or fungal strains. The resulting formulation contains living cells, lyophilized cells, or spores of the bacterial or fungal strains. The formulation may also contain water, nutrients, polymers and binding agents, surfactants or polysaccharides such as gums, carboxymethylcellulose and polyalcohol derivatives. Suitable carriers and adjuvants can be solid or liquid and include natural or regenerated mineral substances, solvents, dispersants, wetting agents, tackifiers, thickeners, binders or fertilizers. Compositions can take the form of aqueous solutions, oil-in-water emulsions, or water-in-oil emulsions. Small amounts of insoluble material can optionally be present, for example in suspension in the medium, but it is generally preferred to minimize the presence of such insoluble material.

XI. Inoculation of plants by coating microbes directly onto seed

[0171] Seed is treated by coating it with a liquid microbial formulation (prepared as described herein) comprising microbial cells and other formulation components, directly onto the seed surface at the rate of 10^2 - 10^8 microbial CFU per seed. Seeds are soaked in liquid microbial formulation for 1, 2, 3, 5, 10, 12, 18 or 24 hours or 2, 3, or 5 days. After soaking in

microbial formulation, seeds are planted in growing containers or in an outdoor field. Seeds may also be coated with liquid microbial formulation by using an auger or a commercial batch treater. One or more microbial formulations or other seed treatments are applied concurrently or in sequence. Treatment is applied to the seeds using a variety of conventional treatment techniques and machines, such as fluidized bed techniques, augers, the roller mill method, rotostatic seed treaters, and drum coaters. Other methods, such as spouted beds may also be useful. The seeds are pre-sized before coating. Optionally the microbial formulation is combined with an amount of insecticide, herbicide, fungicide, bactericide, or plant growth regulator, or plant micro- or macro-nutrient prior to or during the coating process. After coating, the seeds are typically dried and then transferred to a sizing machine for grading before planting. Following inoculation, colonization of the plants or seeds produced therefrom is confirmed via any of the various methods described herein. Growth promotion or stress resilience benefits to the plant are tested via any of the plant growth testing methods described herein.

XII. Inoculation of plants with a combination of two or more microbes

[0172] Seeds can be coated with bacterial or fungal endophytes. This method describes the coating of seeds with two or more bacterial or fungal strains. The concept presented here involves simultaneous seed coating of two microbes (e.g., both a gram negative endophytic bacterium *Burkholderia phytofirmans* and a gram positive endophytic bacterium *Bacillus* *mojavensis*). Optionally, both microbes are genetically transformed by stable chromosomal integration as follows. *Bacillus mojavensis* are transformed with a construct with a constitutive promoter driving expression of a synthetic operon of GFPuv and spectinomycin resistance genes, while *Burkholderia phytofirmans* are transformed with a construct with a constitutive promoter driving expression of the lac operon with an appended spectinomycin resistance gene. Seeds are coated with a prepared liquid formulation of the two microbes the various methods described herein. Various concentrations of each endophyte in the formulation is applied, from 10^2 CFU/seed to about 10^8 CFU/seed. Following inoculation, colonization of the plants or seeds produced therefrom may be confirmed via any of the various methods described herein. Growth promotion or stress resilience benefits to the plant are tested via any of the plant growth testing methods described herein.

XIII. Culturing to confirm colonization of plant by bacteria

[0173] The presence in the seeds or plants of GFPuv or gusA-labeled endophytes can be detected by colony counts from mashed seed material and germinated seedling tissue using R2A plates amended with 5-Bromo-4-chloro-3-indolyl β -D-glucuronide (X-glcA, 50 μ g/mL), IPTG (50 μ g/mL) and the antibiotic spectinomycin (100 μ g/mL). Alternatively, bacterial or fungal endophytes not having received transgenes can also be detected by isolating microbes from plant, plant tissue or seed homogenates (optionally surface-sterilized) on antibiotic free media and identified visually by colony morphotype and molecular methods described herein. Representative colony morphotypes are also used in colony PCR and sequencing for isolate identification via ribosomal gene sequence analysis as described herein. These trials are repeated twice per experiment, with 5 biological samples per treatment.

XIV. Culture-independent methods to confirm colonization of the plant or seeds by bacteria or fungi

[0174] One way to detect the presence of endophytes on or within plants or seeds is to use quantitative PCR (qPCR). Internal colonization by the endophyte can be demonstrated by using surface-sterilized plant tissue (including seed) to extract total DNA, and isolate-specific fluorescent MGB probes and amplification primers are used in a qPCR reaction. An increase in the product targeted by the reporter probe at each PCR cycle therefore causes a proportional increase in fluorescence due to the breakdown of the probe and release of the reporter. Fluorescence is measured by a quantitative PCR instrument and compared to a standard curve to estimate the number of fungal or bacterial cells within the plant.

XV. Experimental Description

[0175] The design of both species-specific amplification primers, and isolate-specific fluorescent probes are well known in the art. Plant tissues (seeds, stems, leaves, flowers, etc.) are pre-rinsed and surface sterilized using the methods described herein.

[0176] Total DNA is extracted using methods known in the art, for example using commercially available Plant-DNA extraction kits, or the following method.

1. Tissue is placed in a cold-resistant container and 10-50mL of liquid nitrogen is applied. Tissues are then macerated to a powder.
2. Genomic DNA is extracted from each tissue preparation, following a chloroform:isoamyl alcohol 24:1 protocol (Sambrook, Joseph, Edward F. Fritsch, and Thomas Maniatis. *Molecular cloning*. Vol. 2. New York: Cold spring harbor laboratory press, 1989.).

[0177] Quantitative PCR is performed essentially as described by Gao, Zhan, et al. *Journal of clinical microbiology* 48.10 (2010): 3575-3581 with primers and probe(s) specific to the desired isolate using a quantitative PCR instrument, and a standard curve is constructed by using serial dilutions of cloned PCR products corresponding to the specie-specific PCR amplicon produced by the amplification primers. Data are analyzed using instructions from the quantitative PCR instrument's manufacturer software.

[0178] As an alternative to qPCR, Terminal Restriction Fragment Length Polymorphism, (TRFLP) can be performed, essentially as described in Johnston-Monje D, Raizada MN (2011) PLoS ONE 6(6): e20396. Group specific, fluorescently labelled primers are used to amplify a subset of the microbial population, especially bacteria, especially fungi, especially archaea, especially viruses. This fluorescently labelled PCR product is cut by a restriction enzyme chosen for heterogeneous distribution in the PCR product population. The enzyme cut mixture of fluorescently labelled and unlabeled DNA fragments is then submitted for sequence analysis on a Sanger sequence platform such as the Applied Biosystems 3730 DNA Analyzer.

XVI. Immunological methods to detect microbes in seeds and vegetative tissues

[0179] A polyclonal antibody is raised against specific bacteria X or fungus Y strains via standard methods. A polyclonal antibody is also raised against specific GUS and GFP proteins via standard methods. Enzyme-linked immunosorbent assay (ELISA) and immunogold labeling is also conducted via standard methods, briefly outlined below.

[0180] Immunofluorescence microscopy procedures involve the use of semi-thin sections of seed or seedling or adult plant tissues transferred to glass objective slides and incubated with blocking buffer (20 mM Tris (hydroxymethyl)-aminomethane hydrochloride (TBS) plus 2 % bovine serum albumin, pH 7.4) for 30 min at room temperature. Sections are first coated for 30 min with a solution of primary antibodies and then with a solution of secondary antibodies (goat anti-rabbit antibodies) coupled with fluorescein isothiocyanate (FITC) for 30 min at room temperature. Samples are then kept in the dark to eliminate breakdown of the light-sensitive FITC. After two 5-min washings with sterile potassium phosphate buffer (PB) (pH 7.0) and one with double-distilled water, sections are sealed with mounting buffer (100 mL 0.1 M sodium phosphate buffer (pH 7.6) plus 50 mL double-distilled glycerine) and observed under a light microscope equipped with ultraviolet light and a FITC Texas-red filter.

[0181] Ultra-thin (50- to 70-nm) sections for TEM microscopy are collected on pioloform-coated nickel grids and are labeled with 15-nm gold-labeled goat anti-rabbit antibody. After being washed, the slides are incubated for 1 h in a 1:50 dilution of 5-nm gold-labeled goat anti-rabbit antibody in IGL buffer. The gold labeling is then visualized for light microscopy using a BioCell silver enhancement kit. Toluidine blue (0.01%) is used to lightly counterstain the gold-labeled sections. In parallel with the sections used for immunogold silver enhancement, serial sections are collected on uncoated slides and stained with 1% toluidine blue. The sections for light microscopy are viewed under an optical microscope, and the ultrathin sections are viewed by TEM.

10 *XVII. Characterization of uniformity of endophytes in a population of seeds*

[0182] To test for the homogeneity of endophytes either on the surface or colonizing the interior tissues in a population of seeds, seeds are tested for the presence of the microbes by culture-dependent and/or –independent methods. Seeds are obtained, surface sterilized and pulverized, and the seed homogenate is divided and used to inoculate culture media or to extract DNA and perform quantitative PCR. The homogeneity of colonization in a population of seeds is assessed through detection of specific microbial strains via these methods and comparison of the culture-dependent and culture-independent results across the population of seeds. Homogeneity of colonization for a strain of interest is rated based on the total number of seeds in a population that contain a detectable level of the strain, on the uniformity across the population of the number of cells or CFU of the strain present in the seed, or based on the absence or presence of other microbial strains in the seed.

XVIII. Experimental Description

[0183] Surface sterilized seeds are obtained as described herein. For culture-dependent methods of microbial-presence confirmation, bacterial and fungi are obtained from seeds essentially as described herein with the following modification. Seed homogenate is used to inoculate media containing selective and/or differential additives that will allow to identification of a particular microbe.

[0184] For qPCR, total DNA of each seed is extracted using methods known in the art, as described herein.

30 *XIX. Characterization of homogeneity of colonization in population of plants*

[0185] To test for the homogeneity of microorganisms (including endophytes) colonizing the interior in a population of plants, tissues from each plant are tested for the presence of the

microbes by culture-dependent and/or -independent methods. Tissues are obtained, surface sterilized and pulverized, and the tissue material is divided and used to inoculate culture media or to extract DNA and perform quantitative PCR. The homogeneity of colonization in a population of plants is assessed through detection of specific microbial strains via these methods and comparison of the culture-dependent and culture-independent results across the population of plants or their tissues. Homogeneity of colonization for a strain of interest is rated based on the total number of plants in a population that contain a detectable level of the strain, on the uniformity across the population of the number of cells or CFU of the strain present in the plant tissue, or based on the absence or presence of other microbial strains in the plant.

XX. Experimental Description

[0186] Surface sterilized plant tissues are obtained as described herein. For culture-dependent methods of microbial-presence confirmation, bacterial and fungi are obtained from plant tissues essentially as described herein with the following modification. Plant tissue homogenate is used to inoculate media containing selective and/or differential additives that will allow identification of a particular microbe.

[0187] For qPCR, total DNA of each plant tissue is extracted using methods known in the art, as described herein.

[0188] Other embodiments will be apparent to those skilled in the art from consideration of the specification and practice of the embodiments. Consider the specification and examples as exemplary only, with a true scope and spirit being indicated by the following claims.

CLAIMS

1. A method for improving an agricultural trait in an agricultural plant, the method comprising:

- a. providing an agricultural plant, seed or tissue thereof,
- 5 b. contacting said plant, seed or tissue thereof with a formulation comprising an endophyte that is common to at least two donor plant types that is present in the formulation in an amount effective to colonize the plant, and
- c. growing the plants under conditions that allow the endophyte to improve a trait in the plant.

10 2. A method for improving an agricultural trait in an agricultural plant, the method comprising:

- a. providing a modern agricultural plant, seed or tissue thereof,
- b. contacting said plant, seed, or tissue thereof with a formulation comprising an endophyte derived from an ancestral plant in an amount effective to colonize the
15 plant, and
- c. allowing the plant to grow under conditions that allow the endophyte to colonize the plant.

3. A method for preparing a seed comprising an endophyte population, said method comprising applying to an exterior surface of a seed a formulation comprising an endophyte
20 population consisting essentially of an endophyte comprising a 16S rRNA or ITS rRNA nucleic acid sequence at least 95% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455.

4. A method for treating seedlings, the method comprising:

- a) contacting foliage or the rhizosphere of a plurality of agricultural plant
25 seedlings with a seed a formulation comprising an endophyte population consisting essentially of an endophyte comprising a 16S rRNA or ITS rRNA nucleic acid sequence at least 95% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455; and
- b) growing the contacted seedlings.

5. A method for modulating a plant trait comprising applying to vegetation or an area adjacent the vegetation, a seed a formulation comprising an endophyte population consisting essentially of an endophyte comprising a 16S rRNA or ITS rRNA nucleic acid sequence at least 95% identical to a nucleic acid sequence selected from the group consisting of SEQ ID
5 NOs: 1-455, wherein the formulation is capable of providing a benefit to the vegetation, or to a crop produced from the vegetation.

6. A method for modulating a plant trait comprising applying a formulation to soil, the seed a formulation comprising an endophyte population consisting essentially of an endophyte comprising a 16S rRNA or ITS rRNA nucleic acid sequence at least 95% identical
10 to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455, wherein the formulation is capable of providing a benefit to seeds planted within the soil, or to a crop produced from plants grown in the soil.

7. The method of claims 1 or 2, wherein the endophyte comprises a 16S rRNA or ITS rRNA nucleic acid sequence at least 95% identical to a nucleic acid sequence selected from
15 the group consisting of SEQ ID NOs: 1-455.

8. The method of any of claims 1-6, wherein the endophyte is capable of a function or activity selected from the group consisting of auxin production, nitrogen fixation, production of an antimicrobial compound, mineral phosphate solubilization, siderophore production, cellulase production, chitinase production, xylanase production, and acetoin production.

20 9. The method of claim 8, wherein the endophyte exhibits at least two of: auxin production, nitrogen fixation, production of an antimicrobial compound, mineral phosphate solubilization, siderophore production, cellulase production, chitinase production, xylanase production, and acetoin production.

10. The method of any of claims 1-6, wherein the endophyte is capable of metabolizing at
25 least one substrate selected from the group consisting of: a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid,
30 glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-

glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose.

11. The method of any of claims 1-6, wherein the endophyte is capable of metabolizing at
 5 least two substrates selected from the group consisting of: a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-
 10 cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline,
 15 salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose.

12. The method of any one of claims 1-6, wherein the endophyte is present at a concentration of at least 10² CFU or spores per seed on the surface of seeds after contacting.

13. The method of any one of claims 1-6, wherein the applying or contacting comprises spraying, immersing, coating, encapsulating, or dusting the seeds or seedlings with the
 20 formulation.

14. The method of any one of claims 1-6, wherein the benefit or agricultural trait is selected from the group consisting of: increased root biomass, increased root length, increased height, increased shoot length, increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency,
 25 increased overall biomass, increased grain yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance, increased salt tolerance, increased resistance to nematode stress, increased resistance to a fungal pathogen, increased resistance to a bacterial pathogen, increased resistance to a viral pathogen, a detectable modulation in the level of a metabolite, a detectable modulation in the transcriptome, and a detectable modulation in the
 30 proteome, relative to reference seeds or agricultural plants derived from reference seeds.

15. The method of any one of claims 1-6, wherein the benefit or agricultural trait comprises at least two benefits or agricultural traits selected from the group consisting of:

increased root biomass, increased root length, increased height, increased shoot length, increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency, increased overall biomass, increased grain yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance, increased salt tolerance, increased resistance to nematode stress, increased resistance to a fungal pathogen, increased resistance to a bacterial pathogen, increased resistance to a viral pathogen, a detectable modulation in the level of a metabolite, a detectable modulation in the transcriptome, and a detectable modulation in the proteome, relative to reference seeds or agricultural plants derived from reference seeds

16. The method of claims 14 or 15, wherein the benefit is increased tolerance to low nitrogen stress or increased nitrogen use efficiency, and the endophyte is non-diazotrophic.

17. The method of any one of claims 1-6, wherein the formulation comprises at least one member selected from the group consisting of an agriculturally compatible carrier, a tackifier, a microbial stabilizer, a fungicide, an antibacterial agent, an herbicide, a nematocide, an insecticide, a plant growth regulator, a rodenticide, and a nutrient.

18. The method of any one of claims 1-6, wherein the endophyte comprises a nucleic acid sequence that is at least 97% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455, wherein the endophyte is present in the formulation in an amount effective to colonize the mature agricultural plant.

19. The method of any one of claims 1-6, wherein the endophyte comprises a nucleic acid sequence that is at least 99% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455, wherein the endophyte is present in the formulation in an amount effective to colonize the mature agricultural plant.

20. The method of any one of claims 1-6, wherein the endophyte comprises a nucleic acid sequence that is at least 99.5% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455, wherein the endophyte is present in the formulation in an amount effective to colonize the mature agricultural plant.

21. The method of any one of claims 1-6, wherein the plant, seed or tissue thereof is contacted with at least 10 CFU or spores, at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or

spores, at least 30,000 CFU or spores, at least 100,000 CFU or spores, at least 300,000 CFU or spores, at least 1,000,000 CFU or spores, or more, of the endophyte.

22. The method of claim 1, wherein the two donor plants are of the same family.

23. The method of claim 1, wherein the two donor plants are of the same genus.

5 24. The method of claim 1, wherein the two donor plants are of the same species.

25. The method of claim 1, wherein the agricultural plant tissue is a seed.

26. The method of claim 25, wherein the population is disposed on the surface of the seed.

27. The method of any one of claims 1-6, wherein the formulation comprises at least two
10 endophytes comprising a nucleic acid sequence that is at least 97% identical, at least 98% identical, at least 99% identical, at least 99.5% identical, or 100% identical, to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455, wherein the at least two endophytes are present in the formulation in an amount effective to colonize the mature agricultural plant.

15 28. The method of claim 27, wherein the formulation comprises at least two endophytes provided in Table 1, Table 2, Table 7 and Table 8.

29. The method of any one of claims 1-6, wherein the plant is a monocot.

30. The method of claim 29, wherein the monocot is selected from the group consisting of corn, wheat, barley and rice.

20 31. The method of any one of claims 1-6, wherein the plant is a dicot.

32. The method of claim 31, wherein the dicot is selected from the group consisting of a soybean, peanut, canola, cotton, Brassica Napus, cabbage, lettuce, melon, strawberry, turnip, watermelon, tomato and pepper.

33. The method of any one of claims 1-6, wherein the endophyte is present in the
25 formulation in an amount effective to be detectable within a target tissue of the agricultural plant selected from a fruit, seed, leaf, root or portion thereof.

34. The method of any one of claims 1-6, wherein the endophyte is detected in an amount of at least 10 CFU or spores, at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores, at least

30,000 CFU or spores, at least 100,000 CFU or spores, at least 300,000 CFU or spores, at least 1,000,000 CFU or spores, or more, in the target tissue.

35. The method of any one of claims 1-6, wherein the endophyte is present in the formulation in an amount effective to increase the biomass and/or yield of the fruit or seed
5 produced by the plant by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, or more, when compared with the fruit or seed of a reference agricultural plant.

36. The method of any one of claims 1-6, wherein the endophyte is present in the
10 formulation in an amount effective to detectably increase the biomass of the plant or tissue thereof.

37. The method of claim 35, wherein the biomass of the plant, or tissue thereof is detectably increased by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least
15 80%, at least 90%, at least 100%, or more, when compared with a reference agricultural plant.

38. The method of any one of claims 1-6, wherein the endophyte is present in the formulation in an amount effective to detectably increase the rate of germination of the seed.

39. The method of claim 38, wherein the rate of germination of the seed is increased by at
20 least 0.5%, at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100% or more, when compared with a reference agricultural plant.

40. The method of any one of claims 1-6, wherein the endophyte is present in the formulation in an amount effective to detectably induce production of auxin in the plant.

25 41. The method of claim 40, wherein the production of auxin in the plant is increased by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100% or more, when compared with a reference agricultural plant.

42. An agricultural plant, or portion of tissue thereof, comprising a formulation
30 comprising an endophyte that is common to at least two donor plant types that is disposed on

an exterior surface of the plant or portion of tissue thereof, or within the plant or portion of tissue thereof, in an amount effective to colonize the plant, and in an amount effective to provide a benefit to the modern agricultural plant.

43. The plant of claim 42, wherein the endophyte comprises a nucleic acid sequence that
5 is at least 97% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455.

44. The plant of claim 43, wherein the endophyte comprises a nucleic acid sequence that is at least 99% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455.

10 45. The plant of claim 43, wherein the endophyte comprises a nucleic acid sequence that is at least 99.5% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455.

46. The plant of claim 42, wherein the endophyte is capable of a function or activity selected from the group consisting of auxin production, nitrogen fixation, production of an
15 antimicrobial compound, mineral phosphate solubilization, siderophore production, cellulase production, chitinase production, xylanase production, and acetoin production.

47. The plant of claim 42, wherein the endophyte exhibits at least two of: auxin production, nitrogen fixation, production of an antimicrobial compound, mineral phosphate solubilization, siderophore production, cellulase production, chitinase production, xylanase
20 production, and acetoin production.

48. The plant of claim 42, wherein the endophyte is capable of metabolizing at least one substrate selected from the group consisting of: a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-
30

acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose.

49. The plant of claim 42, wherein the endophyte is capable of metabolizing at least two substrates selected from the group consisting of: a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, 5 dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, 10 glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose.

15 50. The plant of claim 42, wherein the formulation is disposed on an exterior surface of the plant or portion of tissue thereof, or within the plant or portion of tissue thereof, by spraying, immersing, coating, encapsulating, or dusting the plant or portion of tissue thereof with the formulation.

51. The plant of claim 42, further comprising a formulation that comprises at least one 20 member selected from the group consisting of an agriculturally compatible carrier, a tackifier, a microbial stabilizer, a fungicide, an antibacterial agent, an herbicide, a nematicide, an insecticide, a plant growth regulator, a rodenticide, and a nutrient.

52. The plant of claim 42, wherein the benefit is selected from the group consisting of: increased root biomass, increased root length, increased height, increased shoot length, 25 increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency, increased overall biomass, increased yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance, increased salt tolerance, increased resistance to nematode stress, increased resistance to a fungal pathogen, increased resistance to a bacterial pathogen, increased resistance to a viral pathogen, 30 increased resistance to herbivory, a detectable modulation in the level of a metabolite, a detectable modulation in the proteome, and a detectable modulation in the transcriptome, relative to a reference agricultural plant.

53. The plant of claim 42, wherein the benefit comprises at least two benefits selected from the group consisting of increased: root biomass, increased root length, increased height, increased shoot length, increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency, increased overall biomass, increased yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance, increased salt tolerance, increased resistance to nematode stress, increased resistance to a fungal pathogen, increased resistance to a bacterial pathogen, increased resistance to a viral pathogen, increased resistance to herbivory, a detectable modulation in the level of a metabolite, a detectable modulation in the proteome, and a detectable modulation in the transcriptome, relative to a reference agricultural plant.
54. The plant of claim 52 or 53, wherein the benefit is increased tolerance to low nitrogen stress or increased nitrogen use efficiency, and the endophyte is non-diazotrophic.
55. The plant of claim 42, wherein the plant or portion of tissue thereof is contacted with at least 10 CFU or spores, at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores, at least 30,000 CFU or spores, at least 100,000 CFU or spores, at least 300,000 CFU or spores, at least 1,000,000 CFU or spores, or more, of the endophyte.
56. The plant of claim 42, wherein the plant tissue is a seed.
57. The plant of claim 56, wherein the endophyte is disposed on the surface of the seed.
58. The plant of claim 42, comprising at least two endophytes comprising a nucleic acid sequence that is at least 97% identical, at least 98% identical, at least 99% identical, at least 99.5% identical, or 100% identical, to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455 in an amount effective to colonize the mature agricultural plant.
59. The plant of claim 42, wherein the two endophytes are selected from the groups disclosed in Table 1, Table 2, Table 7 and Table 8.
60. The plant of claim 42, which is a monocot.
61. The plant of claim 60, wherein the monocot is selected from the group consisting of corn, wheat, barley and rice.
62. The plant of claim 42, which is a dicot.

63. The plant of claim 62, wherein the dicot is selected from the group consisting of a soybean, canola, cotton, Brassica Napus, tomato and pepper.

64. The plant of claim 42, wherein the endophyte is disposed in an amount effective to be detectable within a target tissue of the mature target tissue of the mature agricultural plant
5 selected from a fruit, seed, leaf, root or portion thereof.

65. The plant of claim 42, wherein the population is disposed in an amount effective to increase the rate of germination of the seed.

66. The plant of claim 65, wherein the rate of germination of the seed is increased by at least 0.5%, at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 20%, at
10 least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100% or more, when compared with a reference agricultural plant.

67. The plant of claim 42, wherein the population is disposed in an amount effective to be detectable within a target tissue of the mature plant.

68. The plant of claim 67, wherein the target tissue is selected from the group consisting
15 of the root, shoot, leaf, flower, fruit and seed.

69. The plant of claim 42, wherein the population is detected in an amount of at least 10 CFU or spores, at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores, at least 30,000 CFU or spores, at least 100,000 CFU or spores, at least 300,000 CFU or spores, at least 1,000,000
20 CFU or spores, or more, in the plant or target tissue thereof.

70. The plant of claim 42, wherein the population of is disposed in an amount effective to be detectable in the rhizosphere surrounding the plant.

71. The plant of claim 70, wherein the population is detected in an amount of at least 10 CFU or spores, at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores, at least 30,000 CFU or
25 spores, at least 100,000 CFU or spores, at least 300,000 CFU or spores, at least 1,000,000 CFU or spores, or more, in the rhizosphere surrounding the plant.

72. The plant of claim 42, wherein the population is disposed in an amount effective to detectably increase the biomass of the plant.

73. The plant of claim 72, wherein the biomass of the plant is detectably increased by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, or more, when compared with a reference agricultural plant.

5 74. The plant of claim 42, wherein the population is disposed in an amount effective to increase the biomass of a fruit or seed of the plant.

75. The plant of claim 74, wherein the biomass of the fruit or seed of the plant is detectably increased by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, or more, when compared with the fruit or seed of a reference agricultural plant.

76. The plant of claim 42, wherein the population is disposed in an amount effective to increase the height of the plant.

15 77. The plant of claim 76, wherein the height of the plant is increased by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, or more, when compared with the height of a reference agricultural plant.

78. The plant of claim 42, wherein the population is disposed in an amount effective to increase production of auxin in the plant.

20 79. The plant of claim 78, wherein the auxin production of the plant is increased by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, or more, when compared with the auxin production of a reference agricultural plant.

25 80. The plant of claim 42, wherein the population is disposed in an amount effective to increase production of acetoin in the plant.

81. The plant of claim 80, wherein the acetoin production of the plant is increased by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, or more, when compared with the acetoin production of a reference agricultural plant.

82. The plant of claim 42, wherein the population is disposed in an amount effective to increase production of siderophore in the plant.

83. The plant of claim 82, wherein the siderophore production of the plant is increased by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at
5 least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, or more, when compared with the siderophore production of a reference agricultural plant.

84. The plant of claim 42, wherein the population is disposed in an amount effective to increase resistance to one or more stress conditions selected from the group consisting of a
10 drought stress, heat stress, cold stress, salt stress, and low mineral stress.

85. The plant of claim 42, wherein the population is disposed in an amount effective to effective to increase resistance to one or more biotic stress conditions selected from the group consisting of a nematode stress, insect herbivory stress, fungal pathogen stress, bacterial pathogen stress, and viral pathogen stress.

15 86. A bag comprising at least 1,000 seeds according to claim 56, wherein said bag further comprises a label describing said seeds and/or said population.

87. An agricultural formulation comprising an endophyte comprising a nucleic acid sequence that is at least 97% identical, at least 98% identical, at least 99% identical, at least 99.5% identical, or 100% identical, to a nucleic acid sequence selected from the group
20 consisting of SEQ ID NOs: 1-455 that is present in an amount effective to colonize a mature agricultural plant, wherein the formulation further comprises at least one member selected from the group consisting of an agriculturally compatible carrier, a tackifier, a microbial stabilizer, a fungicide, an antibacterial agent, an herbicide, a nematicide, an insecticide, a plant growth regulator, a rodenticide, and a nutrient.

25 88. The formulation of claim 87, wherein the agricultural plant is a monocot.

89. The formulation of claim 88, wherein the agricultural plant is selected from the group consisting of maize, barley, rice and wheat.

90. The formulation of claim 87, wherein the agricultural plant is a dicot.

91. The formulation of claim 90, wherein the agricultural plant is selected from the group consisting of soybean, canola, cotton, Brassica Napus, tomato, squash, cucumber, pepper, peanut, sunflower, and sugar beet.

92. The formulation of claim 87, wherein the population consists essentially of an endophyte comprising a nucleic acid sequence that is at least 99% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455.

93. The formulation of claim 87, wherein the population consists essentially of an endophyte comprising a nucleic acid sequence that is at least 99.5% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455.

94. The formulation of claim 87, comprising at least two different endophytes each comprise a nucleic acid sequence that is at least 97% identical, at least 98% identical, at least 99% identical, at least 99.5% identical, or 100% identical, to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455.

95. The formulation of claim 87, wherein each of the two different endophytes comprises the nucleic acid sequence disclosed in Table 1, Table 2, Table 7, and Table 8.

96. The formulation of claim 87, wherein at least 1%, at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 75%, at least 80%, at least 90%, or at least 95% or more, of the population is in spore form.

97. The formulation of claim 87, wherein the endophytes were adapted to culture on growth medium.

98. The formulation of claim 87, wherein the preparation is substantially stable at temperatures between about 0 °C and about 50 °C for at least three days.

99. The formulation of claim 98, wherein the preparation is substantially stable at temperatures between about 4 °C and about 37 °C for at least thirty days.

100. The formulation of claim 87, formulated to provide a population of plants that demonstrates a substantially homogenous growth rate when introduced into agricultural production.

101. A method for making the plant of claim 42, comprising providing a modern agricultural plant, and applying to the plant a formulation comprising an endophyte comprising an endophytic microbe comprising a nucleic acid sequence that is at least 97%

identical, at least 98% identical, at least 99% identical, at least 99.5% identical, or 100% identical, to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455 that is present in an amount effective to colonize the plant.

102. A commodity plant product comprising the plant of claim 42, or a portion or part thereof.

103. The commodity plant product of claim 102, wherein the product is a grain, a flour, a starch, a syrup, a meal, an oil, a film, a packaging, a nutraceutical product, a pulp, an animal feed, a fish fodder, a bulk material for industrial chemicals, a cereal product, a processed human-food product, a sugar or an alcohol and protein.

104. A method of producing a commodity plant product, comprising:

a. obtaining a plant or plant tissue from the plant of claim 42, or progeny or derivative thereof, and

b. producing the commodity plant product therefrom.

105. A synthetic combination comprising a purified microbial population in association with a plurality of seeds or seedlings of an agricultural plant, wherein the purified microbial population comprises a first endophyte, wherein the first endophyte comprises a 16S rRNA or ITS rRNA nucleic acid sequence at least 97% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455, and wherein the first endophyte is present in the synthetic combination in an amount effective to provide a benefit to the seeds or seedlings or the plants derived from the seeds or seedlings.

106. The synthetic combination of claim 105, wherein the first endophyte is capable of at least one of: production of an auxin, nitrogen fixation, production of an antimicrobial, production of a siderophore, mineral phosphate solubilization, production of a cellulase, production of a chitinase, production of a xylanase, and production of acetoin, or a combination of two or more thereof.

107. The synthetic combination of claim 105, wherein the first endophyte is capable of metabolizing at least one substrate selected from the group consisting of: a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-

melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyrac acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose.

108. A synthetic combination comprising at least two endophytes associated with a seed, wherein at least the first endophyte is heterologous to the seed and wherein the first endophyte comprises a 16S rRNA or ITS rRNA nucleic acid sequence at least 97% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-455, wherein the endophytes are present in the formulation in an amount effective to provide a benefit to the seeds or seedlings or the plants derived from the seeds or seedlings.

109. The synthetic combination of claim 108, wherein the first endophyte is capable of metabolizing at least one substrate selected from the group of: a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyrac acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose.

110. The synthetic combination of claim 108 or 109, wherein both of the endophytes are heterologous to the seed.

111. The synthetic combination of any of claims 105-110, wherein the synthetic combination is disposed within a packaging material selected from a bag, box, bin, envelope, carton, or container.

112. The synthetic combination of any of claims 105-110, comprising 1000 seed weight amount of seeds, wherein the packaging material optionally comprises a desiccant, and wherein the synthetic combination optionally comprises an anti-fungal agent.

113. The synthetic combination of any of claims 105-110, wherein the first endophyte is localized on the surface of the seeds or seedlings.

114. The synthetic combination of any of claims 105-110, wherein the first endophyte is obtained from a plant species other than the seeds or seedlings of the synthetic combination.

115. The synthetic combination of any of claims 105-110, wherein the first endophyte is obtained from a plant cultivar different from the cultivar of the seeds or seedlings of the synthetic combination.

116. The synthetic combination of any of claims 105-110, wherein the first endophyte is obtained from a plant cultivar that is the same as the cultivar of the seeds or seedlings of the synthetic combination.

117. The synthetic combination of any of claims 105-107, wherein the microbial population further comprises a second endophyte.

118. The synthetic combination of claim 117, wherein the microbial population further comprises a second microbial endophyte having an 16S rRNA or ITS rRNA nucleic acid sequence that is less than 95% identical to that of the first microbial endophyte.

119. The synthetic combination of any of claims 105-109, wherein the first endophyte is a bacterial endophyte.

120. The synthetic combination of any of claims 108-109, wherein the second endophyte is a bacterial endophyte.

121. The synthetic combination of any of claims 108-109, wherein the second endophyte is a fungal endophyte.

122. The synthetic combination of any of claims 108-109, wherein the first endophyte is a fungal endophyte.

123. The synthetic combination of claim 122, wherein the second endophyte is a fungal endophyte.

124. The synthetic combination of claim 122, wherein the second endophyte is a bacterial endophyte.

125. The synthetic combination of claim 105, wherein the microbial population further comprises a second endophyte, and wherein the first and second endophytes are
5 independently capable of at least one of production of an auxin, nitrogen fixation, production of an antimicrobial, production of a siderophore, mineral phosphate solubilization, production of a cellulase, production of a chitinase, production of a xylanase, or production of acetoin, or a combination of two or more thereof.

126. The synthetic combination of claim 105, wherein the first and second endophytes are
10 independently capable of at least one of production of an auxin, nitrogen fixation, production of an antimicrobial, production of a siderophore, mineral phosphate solubilization, production of a cellulase, production of a chitinase, production of a xylanase, or production of acetoin, or a combination of two or more thereof.

127. The synthetic combination of claim 105, wherein the microbial population further
15 comprises a second endophyte, wherein the first and second endophytes are independently capable of metabolizing at least one substrate selected from the group consisting of: a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-
20 melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycy-L-aspartic acid, glycy-L-glutamic acid, glycy-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol,
25 maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose, or a combination of two or more thereof.

128. The synthetic combination of claim 108, wherein the first and second endophytes are
30 independently capable of metabolizing at least one substrate selected from the group consisting of: a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol,

D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycy-L-aspartic acid, glycy-L-glutamic acid, glycy-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose, or a combination of two or more thereof.

129. The synthetic combination of any of claims 105-109, wherein the first endophyte is capable of at least two of auxin production, nitrogen fixation, production of an antimicrobial compound, mineral phosphate solubilization, siderophore production, cellulase production, chitinase production, xylanase production, and acetoin production.

130. The synthetic combination of any of claims 105-109, wherein the first endophyte is capable of metabolizing at least two substrates selected from the group consisting of: a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycy-L-aspartic acid, glycy-L-glutamic acid, glycy-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose.

131. The synthetic combination of any of claims 105-109, wherein the benefit is selected from the group consisting of: increased root biomass, increased root length, increased height, increased shoot length, increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency, increased overall biomass, increased grain yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance, increased salt tolerance, increased resistance to nematode stress, increased resistance to a fungal pathogen, increased resistance to a bacterial pathogen, increased resistance to a viral pathogen, a detectable modulation in the level of a metabolite, a

detectable modulation in the transcriptome, and a detectable modulation in the proteome, relative to reference seeds or agricultural plants derived from reference seeds.

132. The synthetic combination of claim 131, wherein the benefit comprises at least two benefits selected from the group consisting of: increased root biomass, increased root length,
5 increased height, increased shoot length, increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency, increased overall biomass, increased grain yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance, increased salt tolerance, increased resistance to nematode stress, increased resistance to a fungal pathogen, increased resistance to a bacterial
10 pathogen, increased resistance to a viral pathogen, a detectable modulation in the level of a metabolite, a detectable modulation in the transcriptome, and a detectable modulation in the proteome, relative to reference seeds or agricultural plants derived from reference seeds.

133. The synthetic combination of any of claims 105-109, wherein the combination comprises seeds and the first endophyte is associated with the seeds as a coating on the
15 surface of the seeds.

134. The synthetic combination of any of claims 105-109, wherein the combination comprises seedlings and the first endophyte is contacted with the seedlings as a spray applied to one or more leaves and/or one or more roots of the seedlings.

135. The synthetic combination of any of claims 105-109, wherein the synthetic
20 combination further comprises one or more additional endophyte species.

136. The synthetic combination of any of claims 105-109, wherein the effective amount is at least 1×10^2 CFU or spores/per seed.

137. The synthetic combination of any of claims 105-109, wherein the effective amount is at least 1×10^3 CFU or spores/per seed.

25 138. The synthetic combination of any of claims 105-109, wherein the combination comprises seeds and the effective amount is from about 1×10^2 CFU or spores/per seed to about 1×10^8 CFU or spores/per seed.

139. The synthetic combination of any of claims 105-109, wherein said seed is a seed from an agricultural plant.

140. The synthetic combination of any of claims 105-109, wherein the first endophytes are present in an amount of at least 10 CFU or spores, at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores, at least 30,000 CFU or spores, at least 100,000 CFU or spores, at least
5 300,000 CFU or spores, or at least 1,000,000 CFU spores per seed.

141. The synthetic combination of any of claims 105-109, further comprising one or more of the following: a stabilizer, or a preservative, or a carrier, or a surfactant, an anticomplex agent, or any combination thereof.

142. The synthetic combination of any of claims 105-109, further comprising one or more
10 of the following: fungicide, nematocide, bactericide, insecticide, and herbicide.

143. The synthetic combination of any of claims 105-109, wherein said seed is a transgenic seed.

144. A plurality of synthetic combinations of any of claims 105-109, placed in a medium that promotes plant growth, said medium selected from the group consisting of: soil,
15 hydroponic apparatus, and artificial growth medium.

145. A plurality of synthetic combinations of any of claims 105-109, wherein the synthetic combinations are shelf-stable.

146. A plant grown from the synthetic combination of any of claims 105-109, said plant exhibiting an improved phenotype of agronomic interest, selected from the group consisting
20 of: increased root biomass, increased root length, increased height, increased shoot length, increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency, increased overall biomass, increased grain yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance, increased salt tolerance, increased resistance to nematode stress, increased resistance to a
25 fungal pathogen, increased resistance to a bacterial pathogen, increased resistance to a viral pathogen, a detectable modulation in the level of a metabolite, a detectable modulation in the transcriptome, and a detectable modulation in the proteome.

147. A method for preparing an agricultural seed composition, comprising contacting the surface of a plurality of seeds with a formulation comprising a purified microbial population
30 that comprises at least two endophytes that are heterologous to the seed, wherein the first endophyte is capable of metabolizing at least one of α -D-glucose, arabinose, arbutin, b-

methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose, wherein the endophytes are present in the formulation in an amount capable of modulating a trait of agronomic importance, as compared to isoline plants grown from seeds not contacted with said formulation.

148. A method for preparing an agricultural seed composition, comprising contacting the surface of a plurality of seeds with a formulation comprising a purified microbial population that comprises at least two endophytes that are heterologous to the seed, wherein the first endophyte is capable of at least one function or activity selected from the group consisting of auxin production, nitrogen fixation, production of an antimicrobial compound, mineral phosphate solubilization, siderophore production, cellulase production, chitinase production, xylanase production, and acetoin production, wherein the endophytes are present in the formulation in an amount capable of modulating a trait of agronomic importance, as compared to isoline plants grown from seeds not contacted with said formulation.

149. A method of improving a phenotype during water limited conditions of a plurality of host plants grown from a plurality of seeds, comprising treating the seeds with a formulation comprising at least two endophytes that are heterologous to the seeds, wherein the first endophyte is capable of metabolizing at least one of a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-

glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose, said phenotype improvement selected from the group consisting of: increased root biomass, increased root
 5 length, increased height, increased shoot length, increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency, increased overall biomass, increased grain yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance, increased salt tolerance, increased resistance to nematode stress, increased resistance to a fungal pathogen, increased resistance to a bacterial
 10 pathogen, increased resistance to a viral pathogen, a detectable modulation in the level of a metabolite, a detectable modulation in the transcriptome, and a detectable modulation in the proteome.

150. The method of any of claims 147-149, wherein the first endophyte is a bacterial endophyte.

15 151. The method of claim 150, wherein the second endophyte is a bacterial endophyte.

152. The method of claim 150, wherein the second endophyte is a fungal endophyte.

153. The method of any of claims 147-149, wherein the first endophyte is a fungal endophyte.

154. The method of claim 153, wherein the second endophyte is a fungal endophyte.

20 155. The method of claim 153, wherein the second endophyte is a bacterial endophyte.

156. The method of any of claims 147-149, wherein the first endophyte is capable of metabolizing at least two of a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-
 25 mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-
 30 proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-

acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose.

157. The method of any of claims 147-149, wherein the second endophyte is capable of metabolizing at least two of a-D-glucose, arabinose, arbutin, b-methyl-D-galactoside, b-methyl-D-glucoside, D-alanine, D-arabitol, D-aspartic acid, D-cellobiose, dextrin, D-fructose, D-galactose, D-gluconic acid, D-glucosamine, dihydroxyacetone, DL-malic acid, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-serine, D-threonine, D-trehalose, D-xylose, g-amino-N-butyric acid, g-cyclodextrin, gelatin, gentiobiose, glycogen, glycyl-L-aspartic acid, glycyl-L-glutamic acid, glycyl-L-proline, glyoxylic acid, i-erythritol, inosine, L-alanine, L-alanyl-glycine, L-arabinose, L-asparagine, L-aspartic acid, L-galactonic acid-g-lactone, L-glutamic acid, L-glutamine, L-histidine, L-proline, L-rhamnose, L-serine, L-threonine, maltitol, maltose, maltotriose, mannose, N-acetyl-D-glucosamine, oxalic acid, palatinose, pectin, proline, salicin, stachyose, sucrose, trehalose, turanose, tyramine, uridine, and xylose.

158. The method of any of claims 147-149, wherein the formulation comprises the purified microbial population at a concentration of at least about 1×10^2 CFU/ml or spores/ml in a liquid formulation or about 1×10^2 CFU/gm or spores/ml in a non-liquid formulation.

159. The method of claims 147 or 148, wherein said trait of agronomic importance is selected from the group consisting of: increased root biomass, increased root length, increased height, increased shoot length, increased leaf number, increased water use efficiency, increased tolerance to low nitrogen stress, increased nitrogen use efficiency, increased overall biomass, increased grain yield, increased photosynthesis rate, increased tolerance to drought, increased heat tolerance, increased salt tolerance, increased resistance to nematode stress, increased resistance to a fungal pathogen, increased resistance to a bacterial pathogen, increased resistance to a viral pathogen, a detectable modulation in the level of a metabolite, a detectable modulation in the transcriptome, and a detectable modulation in the proteome.

160. The method of any of claims 147-149, wherein at least one of the endophytes is capable of localizing in a plant element of a plant grown from said seed, said plant element selected from the group consisting of: whole plant, seedling, meristematic tissue, ground tissue, vascular tissue, dermal tissue, seed, leaf, root, shoot, stem, flower, fruit, stolon, bulb, tuber, corm, keikis, and bud.

161. The method of any of claims 147-149, wherein at least one of the endophytes is capable of colonizing a plant element of a plant grown from said seed, said plant element selected from the group consisting of: whole plant, seedling, meristematic tissue, ground tissue, vascular tissue, dermal tissue, seed, leaf, root, shoot, stem, flower, fruit, stolon, bulb, tuber, corm, keikis, and bud.

162. The method of any of claims 147-149, wherein said formulation further comprises one or more of the following: a stabilizer, or a preservative, or a carrier, or a surfactant, or an anticomplex agent, or any combination thereof.

163. The method of any of claims 147-149, wherein said formulation further comprises one or more of the following: fungicide, nematocide, bactericide, insecticide, and herbicide.

164. The method of any of claims 147-149, wherein said seed is a transgenic seed.

165. A plant derived from the agricultural seed preparation of claims 147 or 148, wherein said plant comprises in at least one of its plant elements said endophytes.

166. The progeny of a plant of claim 165, wherein said progeny comprises in at least one of its plant elements said endophytes.

167. The method of any one of claims 1-41, 101, or 147-166, wherein the endophyte expresses one or more genes encoding a protein whose amino acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 479, 483, 519, 532, 549, 557, 561, 562, 577, 578, 611, 626, 640, 656, 660, 666, 674, 676, 677, 678, 679, 680, 682, 683, 684, 685, 686, 688, 689, 690, 691, 692, 693, 696, 697, 698, 701, 704, 706, 710, 711, 716, 717, 718, 719, 720, 721, 722, 723, 724, 727, 728, 729, 730, 731, 732, 733, 734, 735, 737, 738, 741, 743, 744, 745, 746, 747, 748, 749, 751, 753, 756, 757, 759, 761, 762, 763, 764, 765, 766, 767, 768, 769, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 782, 783, 784, 785, 786, 788, 790, 793, 795, 796, 797, 798, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 815, 816, 817, 818, 819, 820, 822, 823, 824, 825, 826, 829, 830, 833, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 846, 848, 850, 851, 853, 854, 855, 856, 857, 858, 859, 860, 864, 865, 866, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 884, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 897, 898, 899, 901, 902, 903, 904, 905, 906, 907, 908, 910, 911, 912, 913, 914, 915, 916, 917, 918, 920, 921, 922, 923, 924, 926, 927, 928, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939,

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2253, 2254, 2255, 2257, 2258, 2259, 2261, 2262, 2265, 2267, 2268, 2269, and 2270.

168. The method of claim 167, wherein protein expression is modulated in response to the first endophyte contacting a plant element.

169. The method of claim 167, wherein protein expression is upregulated in response to the first endophyte contacting a plant element.

170. The method of claim 169, wherein the amino acid sequence of the upregulated protein is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 549, 640, 656, 676, 684, 690, 937, 1456, 1467, 1479, 1484, 1488, 1490, 1498, 1499, 1500, 1504, 1505, 1508, 1513, 1529, 1534, 1538, 1540, 1547, 1551, 1554, 1561, 1566, 1568, 1570, 1571, 1574, 1578, 1581, 1583, 1591, 1592, 1593, 1597, 1598, 1604, 1605, 1609, 1615, 1616, 1619, 1622, 1624, 1626, 1629, 1630, 1632, 1636, 1638, 1642, 1643, 1647, 1650, 1651, 1652, 1659, 1661, 1664, 1666, 1671, 1675, 1676, 1678, 1684, 1685, 1689, 1692, 1694, 1695, 1696, 1701, 1706, 1709, 1711, 1712, 1718, 1723, 1725, 1728, 1729, 1732, 1737, 1738, 1740, 1741, 1744, 1746, 1747, 1751, 1755, 1761, 1763, 1771, 1772, 1775, 1778, 1779, 1782, 1787, 1788, 1791, 1792, 1797, 1798, 1799, 1800, 1805, 1819, 1824, 1828, 1835, 1840, 1842, 1843, 1846, 1854, 1860, 1862, 1868, 1875, 1892, 1893, 1900, 1901, 1910, 1918, 1924, 1925, 1926, 1928, 1932, 1933, 1934, 1938, 1943, 1946, 1949, 1950, 1953, 1963, 1967, 1971, 1973, 1975, 1985, 1990, 1994, 1998, 2000, 2003, 2006, 2010, 2013, 2016, 2018, 2021, 2025, 2027, 2028, 2030, 2034, 2035, 2036, 2048, 2050, 2052, 2054, 2059, 2062, 2065, 2066, 2067, 2068, 2074, 2080, 2091, 2092, 2093, 2095, 2097, 2098, 2100, 2101, 2104, 2108, 2110, 2112, 2117, 2119, 2125, 2131, 2134, 2135, 2145, 2149, 2150, 2156, 2159, 2162, 2168, 2181, 2185, 2193, 2195, 2196, 2206, 2211, 2216, 2217, 2219, 2220, 2221, 2223, 2231, 2236, 2239, 2242, 2243, 2248, 2255, 2257, 2258, 2259, or 2262.

171. The method of claim 167, wherein protein expression is repressed in response to the first endophyte contacting a plant element.

172. The method of claim 171, wherein the repressed protein amino acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 479, 483, 519, 532, 557, 626, 674, 678, 680, 683, 685, 688, 690, 696, 697, 701, 704, 706, 710, 711, 717, 720, 722, 723, 724, 728, 729, 730, 732, 733, 734, 737, 741, 744, 745, 748, 749, 751, 753, 756, 757, 761, 764, 766, 768, 769, 772, 773, 774, 778, 779, 782, 783, 784, 788, 790, 793, 795, 796, 797, 800, 802, 803, 806, 807, 808, 810, 812, 817, 818, 819, 820, 822, 825, 826, 833, 836, 837, 839, 841, 846, 848, 851, 853, 854, 855, 856, 857, 860, 864, 865, 866, 870, 872, 874, 876, 878, 879, 880, 881, 882, 884, 886, 887, 890, 891, 893, 894, 895, 898, 901,

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10 1222, 1223, 1225, 1226, 1230, 1237, 1242, 1244, 1249, 1251, 1253, 1256, 1260, 1261, 1262,
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15 1399, 1400, 1402, 1405, 1408, 1411, 1412, 1418, 1420, 1422, 1427, 1428, 1431, 1433, 1438,
1439, 1440, 1442, 1444, 1445, 1449, or 1450.

173. The method of claim 167, wherein the protein is expressed with at least a two-fold
difference, at least a three-fold difference, at least a four-fold difference, at least a five-fold
difference, at least a six-fold difference, at least a seven-fold difference, at least an eight-fold
20 difference, at least a nine-fold difference, at least a ten-fold difference or more in expression
level as compared to the protein expression level of a reference microorganism.

174. The method of claim 173, wherein the difference in expression level is positive.

175. The method of claim 173, wherein the difference in expression level is negative.

176. The method of claim 167, wherein the protein is involved in at least one KEGG
25 pathway selected from the group consisting of: endocytosis, purine metabolism, inositol
phosphate metabolism, and peroxisome.

177. The method of claim 167, wherein the protein is involved in at least one KEGG
pathway selected from the group consisting of: ko00403 (indole diterpene alkaloid
biosynthesis), ko00522 (biosynthesis of 12-, 14- and 16-membered macrolides), ko00550
30 (peptidoglycan biosynthesis), ko00601 (glycosphingolipid biosynthesis – lacto and neolacto
series), ko0901 (indole alkaloid biosynthesis), ko01052 (type I polyketide structures),

ko010503 (biosynthesis of siderophore group nonribosomal peptides), ko01501 (beta-Lactam resistance), and ko04071 (sphingolipid signaling pathway).

178. The method of any one of claims 1-41, 101, or 147-166, wherein the plant, crop, seedling, or plant grown from the seed expresses one or more genes whose nucleic acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 4127, 4128, 4129, 4130, 4131, 4132, 4133, 4134, 4135, 4136, 4137, 4138, 4139, 4140, 4141, 4142, 4143, 4144, 4145, 4146, 4147, 4148, 4149, 4150, 4151, 4152, 4153, 4154, 4155, 4156, 4157, 4158, 4159, 4160, 4161, 4162, 4163, 4164, 4165, 4166, 4167, 4168, 4169, 4170, 4171, 4172, 4173, 4174, 4175, 4176, 4177, 4178, 4179, 4180, 4181, 4182, 4183, 4184, 4185, 4186, 4187, 4188, 4189, 4190, 4191, 4192, 4193, 4194, 4195, 4196, 4197, 4198, 4199, 4200, 4201, 4202, 4203, 4204, 4205, 4206, 4207, 4208, 4209, 4210, 4211, 4212, 4213, 4214, 4215, 4216, 4217, 4218, 4219, 4220, 4221, 4222, 4223, 4224, 4225, 4226, 4227, 4228, 4229, 4230, 4231, 4232, 4233, 4234, 4235, 4236, 4237, 4238, 4239, 4240, 4241, 4242, 4243, 4244, 4245, 4246, 4247, 4248, 4249, 4250, 4251, 4252, 4253, 4254, 4255, 4256, 4257, 4258, 4259, 4260, 4261, 4262, 4263, 4264, 4265, 4266, 4267, 4268, or 4269.

179. The method of claim 178, wherein the one or more plant genes are modulated in response to the first endophyte contacting the plant or plant element as compared to a reference microorganism contacting the plant or plant element.

180. The method of claim 178, wherein the one or more plant genes are upregulated in response to the first endophyte contacting a plant element as compared to a reference microorganism contacting the plant or plant element.

181. The method of claim 180, wherein the upregulated genes nucleic acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 4131, 4140, 4142, 4153, 4162, 4167, 4181, 4183, 4184, 4195, 4199, 4201, 4206, 4213, 4222, 4223, 4250, 4253, or 4269.

182. The method of claim 178, wherein the transcription of one or more genes are repressed in response to the first endophyte contacting a plant element as compared to a reference microorganism contacting the plant or plant element.

183. The method of claim 182, wherein the repressed genes nucleic acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 4150.

184. The method of claim 178, wherein the one or more genes are expressed with at least a
5 0.5-fold difference, at least a 0.6-fold difference, at least a 0.7-fold difference, at least a 0.8-fold difference, at least a 0.9-fold difference, at least a 1.0-fold difference, at least a 1.1-fold difference, at least a 1.2-fold difference, at least a 1.3-fold difference or more in expression level as compared to the gene expression level of a reference microorganism.

185. The method of claim 184, wherein the difference in expression level is positive.

10 186. The method of claim 184, wherein the difference in expression level is negative.

187. The method of claim 178, wherein the one or more genes has at least one gene function selected from the group consisting of: cell wall modification, defense response, oxidation-reduction process, biological process, regulation of transcription, metabolic process, glucosinolate biosynthetic process, response to karrikin, protein phosphorylation,
15 protein folding, response to chitin, proteolysis, response to auxin stimulus, DNA-dependent regulation of transcription, N-terminal protein myristoylation, response to oxidative stress, cellular component, leaf senescence, resistance gene-dependent defense response signaling pathway, zinc ion binding, response to cold, malate metabolic process, transport, catalytic activity, response to ozone, VQ motif, regulation of systemic acquired resistance, potassium
20 ion transport, anaerobic respiration, multicellular organismal development, response to heat, methyltransferase activity, response to wounding, oxidation-reduction process, monooxygenase activity, oxidation-reduction process, carbohydrate metabolic process, exocytosis, nuclear-transcribed mRNA poly(A) tail shortening, sodium ion transport, glycerol metabolic process, on willebrand factor A3, response to water deprivation, response to salt
25 stress, and chlorophyll biosynthetic process.

188. The method of claim 187, wherein the gene has a gene ontology (GO) identifier selected from the group consisting of: GO:0003824, GO, catalytic activity; GO:0006355, GO, regulation of transcription, DNA-dependent; GO:0009870, GO, defense response signaling pathway, resistance gene-dependent; GO:0008150, GO, biological_process;
30 GO:0010200, GO, response to chitin; GO:0006508, GO, proteolysis; GO:0010193, GO, response to ozone; GO:0006979, GO, response to oxidative stress; and GO:0005975, GO, carbohydrate metabolic process.

189. The method of claim 178, wherein the gene function is selected from the following group: single-stranded DNA specific endodeoxyribonuclease activity, sequence-specific DNA binding transcription factor activity, NAD⁺ ADP-ribosyltransferase activity, metalloendopeptidase activity, DNA catabolic process, cellular iron ion homeostasis, response to osmotic stress, metallopeptidase activity, zinc ion binding, response to wounding, camalexin biosynthetic process, endoribonuclease activity, producing 5'-phosphomonoesters, cellular response to heat, T/G mismatch-specific endonuclease activity, polyamine oxidase activity, flavin adenine dinucleotide binding, cellular heat acclimation, cellular response to ethylene stimulus, cellular response to nitric oxide, and reactive oxygen species metabolic process.

190. The method of any one of claims 167-189, wherein the endophyte comprises an ITS rRNA nucleic acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the nucleic acid sequence of SEQ ID NO: 344.

191. The method of any one of claims 1-41, 101, or 147-166, wherein the endophyte expresses one or more genes encoding a protein whose amino acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 477-501, 505, 514, 518, 521, 528, 530, 531, 550, 566, 567, 572, 579, 580, 581, 587, 593, 600, 602, 614, 623, 630, 635, 643, 645, 652, 657, 661, 662, 667, 670, 672, 673, 4510-4535, 4540, 4541, 4542, 4547, 4555, 4558, 4560, 4569, 4570, 4571, 4572, 4577, 4582, 4592, 4594, 4602, 4608, 4609, 4622, 4626, 4641, 4643, 4653, 4654, 4742-4766, 4734, 4739, 4740, 477, 478, 480, 482, 484, 485, 487, 489, 494, 496, 497, 501, 530, 567, 587, 602, 614, 633, 645, 649, 651, 652, 658, 665, 666, 667, 673, 874, 934, 1013, 1249, 1342, 2252, 2272, 2273, 2281, 2282, 2284, 2285, 2286, 2287, 2289, 2290, 2291, 2292, 2293, 2296, 4510, 4514, 4515, 4518, 4520, 4521, 4525, 4526, 4527, 4529, 4532, 4538, 4539, 4540, 4555, 4559, 4560, 4562, 4569, 4570, 4571, 4572, 4577, 4581, 4582, 4594, 4595, 4597, 4608, 4615, 4618, 4623, 4624, 4626, 4630, 4632, 4635, 4641, 4642, 4646, 4650, 4658, 4659, 4661, 4662, 4663, 4666, 4667, 4668, 4670, 4799, 4801, 4802, 4803, 4804, 4805, 4826, 4827, 4828, 4829, 4830, 4831, 4832, 4833, 4834, 4835, 4836, 4837, 4838, 4839, 4840, 4841, 4863, 4864, 4865, 4866, 4867, 4868, 4869, 4870, 4871, 4872, 4873, 4874, 4875, 4876, 4877, 4878, 4879, 4880, 4881, 4882, 4883, 4884, 4885, 4886, 4887, 4888, 4889, 4890, 4891, 4892, 4893, 4894, 4917, 4918, 4919, 4920, 4921, 4922, 4923, 4924, 4925, 4939, 4940, 4941, 4943, 4947, 4948, 4950, 4951, 4955, 4956, 4957, 2315, 2320, 2322, 2326, 2349, 2350, 2352, 2377, 2382, 2390, 2407, 2422, 2436, 2443, 2457, 2463, 2464, 2470, 2477,

2483, 2721, 2968, 3093, 3185, 4096, 4097, 4098, 4099, 4100, 4101, 4102, 4103, 4104, 4105, 4106, 4107, 4108, 4109, 4110, 4111, 4112, 4113, 4114, 4115, 4116, 4117, 4118, 4119, 4120, 4121, 4122, 4123, 4124, 4125, 4126, 4346, 4353, 4362, 4369, 4386, 4391, 4394, 4408, 4410, 4413, 4415, 4422, 4423, 4432, 4433, 4442, 4469, 4487, 4489, 4491, 4493, 4494, 4495, 4496, 5 4497, 4498, 4499, 4500, 4501, 4502, 4503, 4504, 4505, 4506, 4507, 4508, 4509, 4343, 4484, 4485, 4486, 4488, 4490, and 4492.

192. The method of any of claims 1-41, 101, 104, 147-166, and 191, wherein the endophyte expresses one or more genes involved in starch and sucrose metabolism, cell wall degradation, or protection from oxidative stress.

10 193. The method of claim 191, wherein the protein is expressed with at least a two-fold difference, at least a three-fold difference, at least a four-fold difference, at least a five-fold difference, at least a six-fold difference, at least a seven-fold difference, at least an eight-fold difference, at least a nine-fold difference, at least a ten-fold difference or more in expression level as compared to the protein expression level of a reference microorganism.

15 194. The method of claim 193, wherein the difference in expression level is positive.

195. The method of claim 193, wherein the difference in expression level is negative.

196. The method of any one of claims 191-195, wherein the wherein the endophyte comprises an ITS rRNA nucleic acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group
20 consisting of SEQ ID NOs: 344 and 447.

197. The method of any one of claims 191-195, wherein the wherein the endophyte comprises a 16S rRNA nucleic acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 439 or 441.

25 198. The composition of any one of claims 42-100, 102, 103 or 105-146, wherein the endophyte expresses one or more genes encoding a protein whose amino acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 479, 483, 519, 532, 549, 557, 561, 562, 577, 578, 611, 626, 640, 656, 660, 666, 674, 676, 677, 678, 679, 680,
30 682, 683, 684, 685, 686, 688, 689, 690, 691, 692, 693, 696, 697, 698, 701, 704, 706, 710, 711, 716, 717, 718, 719, 720, 721, 722, 723, 724, 727, 728, 729, 730, 731, 732, 733, 734,

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897, 898, 899, 901, 902, 903, 904, 905, 906, 907, 908, 910, 911, 912, 913, 914, 915, 916,
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10 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 952, 953, 954, 955, 956,
957, 958, 959, 960, 961, 962, 963, 964, 968, 969, 971, 974, 976, 978, 979, 980, 984, 985,
987, 988, 989, 992, 993, 994, 995, 996, 998, 1000, 1001, 1002, 1003, 1006, 1008, 1010,
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199. The composition of claim 198, wherein protein expression is modulated in response to the first endophyte contacting a plant element.

200. The composition of claim 198, wherein protein expression is upregulated in response to the first endophyte contacting a plant element.

201. The composition of claim 198, wherein the amino acid sequence of the upregulated protein is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 549, 640, 656, 676, 684, 690, 937, 1456, 1467, 1479, 1484, 1488, 1490, 1498, 1499, 1500, 1504, 1505, 1508, 1513, 1529, 1534, 1538, 1540, 1547, 1551, 1554, 1561, 1566, 1568, 1570, 1571, 1574, 1578, 1581, 1583, 1591, 1592, 1593, 1597, 1598, 1604, 1605, 1609, 1615, 1616, 1619, 1622, 1624, 1626, 1629, 1630, 1632, 1636, 1638, 1642, 1643, 1647, 1650, 1651, 1652, 1659, 1661, 1664, 1666, 1671, 1675, 1676, 1678, 1684, 1685, 1689, 1692, 1694, 1695, 1696, 1701, 1706, 1709, 1711, 1712, 1718, 1723, 1725, 1728, 1729, 1732, 1737, 1738, 1740, 1741, 1744, 1746, 1747, 1751, 1755, 1761, 1763, 1771, 1772, 1775, 1778, 1779, 1782, 1787, 1788, 1791, 1792, 1797, 1798, 1799, 1800, 1805, 1819, 1824, 1828, 1835, 1840, 1842, 1843, 1846, 1854, 1860, 1862, 1868, 1875, 1892, 1893, 1900, 1901, 1910, 1918, 1924, 1925, 1926, 1928, 1932, 1933, 1934, 1938, 1943, 1946, 1949, 1950, 1953, 1963, 1967, 1971, 1973, 1975, 1985, 1990, 1994, 1998, 2000, 2003, 2006, 2010, 2013, 2016, 2018, 2021, 2025, 2027, 2028, 2030, 2034, 2035, 2036, 2048, 2050, 2052, 2054, 2059, 2062, 2065, 2066, 2067, 2068, 2074, 2080, 2091, 2092, 2093, 2095, 2097, 2098, 2100, 2101, 2104, 2108, 2110, 2112, 2117, 2119, 2125, 2131, 2134, 2135, 2145, 2149, 2150, 2156, 2159, 2162, 2168, 2181, 2185, 2193, 2195, 2196, 2206, 2211, 2216, 2217, 2219, 2220, 2221, 2223, 2231, 2236, 2239, 2242, 2243, 2248, 2255, 2257, 2258, 2259, or 2262.

202. The composition of claim 198, wherein protein expression is repressed in response to the first endophyte contacting a plant element.

203. The composition of claim 198, wherein the repressed protein amino acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 479, 483, 519, 532, 557, 626, 674, 678, 680, 683, 685, 688, 690, 696, 697, 701, 704, 706, 710, 711, 717, 720, 722, 723, 724, 728, 729, 730, 732, 733, 734, 737, 741, 744, 745, 748, 749, 751, 753, 756, 757, 761, 764, 766, 768, 769, 772, 773, 774, 778, 779, 782, 783, 784, 788, 790, 793, 795, 796, 797, 800, 802, 803, 806, 807, 808, 810, 812, 817, 818, 819, 820, 822, 825, 826, 833, 836, 837, 839, 841, 846, 848, 851, 853, 854, 855, 856, 857, 860, 864, 865, 866, 870, 872, 874, 876, 878, 879, 880, 881, 882, 884, 886, 887, 890, 891, 893, 894, 895, 898, 901, 903, 905, 907, 908, 910, 911, 912, 913, 915, 917, 918, 921, 924, 926, 927, 928, 933, 934, 935, 936, 937, 938, 940, 942, 944, 945, 946, 947, 950, 952, 954, 955, 957, 960, 961, 962, 963, 964, 968, 971, 976, 978, 979, 985, 987, 989, 992, 1000, 1001, 1002, 1003, 1006, 1008, 1012, 1014, 1018, 1019, 1021, 1022, 1024, 1025, 1028, 1031, 1032, 1034, 1037, 1038, 1040, 1042, 1043, 1046, 1047, 1050, 1051, 1056, 1059, 1064, 1065, 1068, 1070, 1072, 1077, 1079, 1083, 1086, 1087, 1091, 1094, 1095, 1098, 1102, 1103, 1104, 1110, 1111, 1112, 1113, 1114, 1116, 1117, 1118, 1121, 1126, 1130, 1132, 1133, 1134, 1136, 1139, 1143, 1146, 1147, 1151, 1155, 1156, 1158, 1159, 1160, 1162, 1163, 1165, 1168, 1170, 1172, 1174, 1176, 1180, 1182, 1183, 1186, 1188, 1192, 1193, 1194, 1196, 1197, 1198, 1209, 1214, 1217, 1218, 1219, 1221, 1222, 1223, 1225, 1226, 1230, 1237, 1242, 1244, 1249, 1251, 1253, 1256, 1260, 1261, 1262, 1264, 1270, 1272, 1274, 1276, 1279, 1280, 1283, 1284, 1285, 1286, 1288, 1290, 1292, 1298, 1300, 1303, 1307, 1309, 1311, 1312, 1313, 1320, 1321, 1324, 1325, 1328, 1330, 1331, 1333, 1336, 1337, 1339, 1340, 1344, 1346, 1352, 1353, 1355, 1357, 1358, 1359, 1360, 1361, 1363, 1364, 1365, 1370, 1375, 1376, 1379, 1380, 1383, 1384, 1386, 1390, 1391, 1392, 1393, 1396, 1399, 1400, 1402, 1405, 1408, 1411, 1412, 1418, 1420, 1422, 1427, 1428, 1431, 1433, 1438, 1439, 1440, 1442, 1444, 1445, 1449, or 1450.

204. The composition of claim 198, wherein the protein is expressed with at least a two-fold difference, at least a three-fold difference, at least a four-fold difference, at least a five-fold difference, at least a six-fold difference, at least a seven-fold difference, at least an eight-fold difference, at least a nine-fold difference, at least a ten-fold difference or more in expression level as compared to the protein expression level of a reference microorganism.

205. The composition of claim 204, wherein the difference in expression level is positive.

206. The composition of claim 204, wherein the difference in expression level is negative.

207. The composition of claim 198, wherein the protein is involved in at least one KEGG pathway selected from the group consisting of: endocytosis, purine metabolism, inositol phosphate metabolism, and peroxisome.

208. The composition of claim 198, wherein the protein is involved in at least one KEGG
5 pathway selected from the group consisting of: ko00403 (indole diterpene alkaloid biosynthesis), ko00522 (biosynthesis of 12-, 14- and 16-membered macrolides), ko00550 (peptidoglycan biosynthesis), ko00601 (glycosphingolipid biosynthesis – lacto and neolacto series), ko0901 (indole alkaloid biosynthesis), ko01052 (type I polyketide structures), ko010503 (biosynthesis of siderophore group nonribosomal peptides), ko01501 (beta-Lactam
10 resistance), and ko04071 (sphingolipid signaling pathway).

209. The composition of any one of claims 42-100, 102, 103 or 105-146, wherein the plant, crop, seedling, or plant grown from the seed expresses one or more genes whose nucleic acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 4127,
15 4128, 4129, 4130, 4131, 4132, 4133, 4134, 4135, 4136, 4137, 4138, 4139, 4140, 4141, 4142, 4143, 4144, 4145, 4146, 4147, 4148, 4149, 4150, 4151, 4152, 4153, 4154, 4155, 4156, 4157, 4158, 4159, 4160, 4161, 4162, 4163, 4164, 4165, 4166, 4167, 4168, 4169, 4170, 4171, 4172, 4173, 4174, 4175, 4176, 4177, 4178, 4179, 4180, 4181, 4182, 4183, 4184, 4185, 4186, 4187, 4188, 4189, 4190, 4191, 4192, 4193, 4194, 4195, 4196, 4197, 4198, 4199, 4200, 4201, 4202,
20 4203, 4204, 4205, 4206, 4207, 4208, 4209, 4210, 4211, 4212, 4213, 4214, 4215, 4216, 4217, 4218, 4219, 4220, 4221, 4222, 4223, 4224, 4225, 4226, 4227, 4228, 4229, 4230, 4231, 4232, 4233, 4234, 4235, 4236, 4237, 4238, 4239, 4240, 4241, 4242, 4243, 4244, 4245, 4246, 4247, 4248, 4249, 4250, 4251, 4252, 4253, 4254, 4255, 4256, 4257, 4258, 4259, 4260, 4261, 4262, 4263, 4264, 4265, 4266, 4267, 4268, or 4269.

25 210. The composition of claim 209, wherein the one or more plant genes are modulated in response to the first endophyte contacting the plant or plant element as compared to a reference microorganism contacting the plant or plant element.

211. The composition of claim 209, wherein the one or more plant genes are upregulated in response to the first endophyte contacting a plant element as compared to a reference
30 microorganism contacting the plant or plant element.

212. The composition of claim 211, wherein the upregulated genes nucleic acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a

nucleic acid sequence selected from the group consisting of SEQ ID NOs: 4131, 4140, 4142, 4153, 4162, 4167, 4181, 4183, 4184, 4195, 4199, 4201, 4206, 4213, 4222, 4223, 4250, 4253, or 4269.

213. The composition of claim 209, wherein the transcription of one or more genes are repressed in response to the first endophyte contacting a plant element as compared to a reference microorganism contacting the plant or plant element.

214. The composition of claim 213, wherein the repressed genes nucleic acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 4150.

215. The composition of claim 209, wherein the one or more genes are expressed with at least a 0.5-fold difference, at least a 0.6-fold difference, at least a 0.7-fold difference, at least a 0.8-fold difference, at least a 0.9-fold difference, at least a 1.0-fold difference, at least a 1.1-fold difference, at least a 1.2-fold difference, at least a 1.3-fold difference or more in expression level as compared to the gene expression level of a reference microorganism.

216. The composition of claim 215, wherein the difference in expression level is positive.

217. The composition of claim 215, wherein the difference in expression level is negative.

218. The composition of claim 209, wherein the one or more genes has at least one gene function selected from the group consisting of: cell wall modification, defense response, oxidation-reduction process, biological process, regulation of transcription, metabolic process, glucosinolate biosynthetic process, response to karrikin, protein phosphorylation, protein folding, response to chitin, proteolysis, response to auxin stimulus, DNA-dependent regulation of transcription, N-terminal protein myristoylation, response to oxidative stress, cellular component, leaf senescence, resistance gene-dependent defense response signaling pathway, zinc ion binding, response to cold, malate metabolic process, transport, catalytic activity, response to ozone, VQ motif, regulation of systemic acquired resistance, potassium ion transport, anaerobic respiration, multicellular organismal development, response to heat, methyltransferase activity, response to wounding, oxidation-reduction process, monooxygenase activity, oxidation-reduction process, carbohydrate metabolic process, exocytosis, nuclear-transcribed mRNA poly(A) tail shortening, sodium ion transport, glycerol metabolic process, on willebrand factor A3, response to water deprivation, response to salt stress, and chlorophyll biosynthetic process.

219. The composition of claim 218, wherein the gene has a gene ontology (GO) identifier selected from the group consisting of: GO:0003824, GO, catalytic activity; GO:0006355, GO, regulation of transcription, DNA-dependent; GO:0009870, GO, defense response signaling pathway, resistance gene-dependent; GO:0008150, GO, biological_process;
5 GO:0010200, GO, response to chitin; GO:0006508, GO, proteolysis; GO:0010193, GO, response to ozone; GO:0006979, GO, response to oxidative stress; and GO:0005975, GO, carbohydrate metabolic process.

220. The composition of claim 209, wherein the gene function is selected from the following group: single-stranded DNA specific endodeoxyribonuclease activity, sequence-
10 specific DNA binding transcription factor activity, NAD⁺ ADP-ribosyltransferase activity, metalloendopeptidase activity, DNA catabolic process, cellular iron ion homeostasis, response to osmotic stress, metallopeptidase activity, zinc ion binding, response to wounding, camalexin biosynthetic process, endoribonuclease activity, producing 5'-phosphomonoesters, cellular response to heat, T/G mismatch-specific endonuclease activity, polyamine oxidase
15 activity, flavin adenine dinucleotide binding, cellular heat acclimation, cellular response to ethylene stimulus, cellular response to nitric oxide, and reactive oxygen species metabolic process.

221. The composition of any one of claims 198-220, wherein the endophyte comprises an ITS rRNA nucleic acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at
20 least 99%, or 100% identical to the nucleic acid sequence of SEQ ID NO: 344.

222. The composition of any one of claims 42-100, 102, 103 or 105-146, wherein the endophyte expresses one or more genes encoding a protein whose amino acid sequence is at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 477-501, 505, 514,
25 518, 521, 528, 530, 531, 550, 566, 567, 572, 579, 580, 581, 587, 593, 600, 602, 614, 623, 630, 635, 643, 645, 652, 657, 661, 662, 667, 670, 672, 673, 4510-4535, 4540, 4541, 4542, 4547, 4555, 4558, 4560, 4569, 4570, 4571, 4572, 4577, 4582, 4592, 4594, 4602, 4608, 4609, 4622, 4626, 4641, 4643, 4653, 4654, 4742-4766, 4734, 4739, 4740, 477, 478, 480, 482, 484, 485, 487, 489, 494, 496, 497, 501, 530, 567, 587, 602, 614, 633, 645, 649, 651, 652, 658,
30 665, 666, 667, 673, 874, 934, 1013, 1249, 1342, 2252, 2272, 2273, 2281, 2282, 2284, 2285, 2286, 2287, 2289, 2290, 2291, 2292, 2293, 2296, 4510, 4514, 4515, 4518, 4520, 4521, 4525, 4526, 4527, 4529, 4532, 4538, 4539, 4540, 4555, 4559, 4560, 4562, 4569, 4570, 4571, 4572,

4577, 4581, 4582, 4594, 4595, 4597, 4608, 4615, 4618, 4623, 4624, 4626, 4630, 4632, 4635, 4641, 4642, 4646, 4650, 4658, 4659, 4661, 4662, 4663, 4666, 4667, 4668, 4670, 4799, 4801, 4802, 4803, 4804, 4805, 4826, 4827, 4828, 4829, 4830, 4831, 4832, 4833, 4834, 4835, 4836, 4837, 4838, 4839, 4840, 4841, 4863, 4864, 4865, 4866, 4867, 4868, 4869, 4870, 4871, 4872, 4873, 4874, 4875, 4876, 4877, 4878, 4879, 4880, 4881, 4882, 4883, 4884, 4885, 4886, 4887, 4888, 4889, 4890, 4891, 4892, 4893, 4894, 4917, 4918, 4919, 4920, 4921, 4922, 4923, 4924, 4925, 4939, 4940, 4941, 4943, 4947, 4948, 4950, 4951, 4955, 4956, 4957, 2315, 2320, 2322, 2326, 2349, 2350, 2352, 2377, 2382, 2390, 2407, 2422, 2436, 2443, 2457, 2463, 2464, 2470, 2477, 2483, 2721, 2968, 3093, 3185, 4096, 4097, 4098, 4099, 4100, 4101, 4102, 4103, 4104, 4105, 4106, 4107, 4108, 4109, 4110, 4111, 4112, 4113, 4114, 4115, 4116, 4117, 4118, 4119, 4120, 4121, 4122, 4123, 4124, 4125, 4126, 4346, 4353, 4362, 4369, 4386, 4391, 4394, 4408, 4410, 4413, 4415, 4422, 4423, 4432, 4433, 4442, 4469, 4487, 4489, 4491, 4493, 4494, 4495, 4496, 4497, 4498, 4499, 4500, 4501, 4502, 4503, 4504, 4505, 4506, 4507, 4508, 4509, 4343, 4484, 4485, 4486, 4488, 4490, and 4492.

223. The composition of any of claims 42-100, 102, 103, 105-146, and 222, wherein the endophyte expresses one or more genes involved in starch and sucrose metabolism, cell wall degradation, or protection from oxidative stress.

224. The composition of claim 223, wherein the protein is expressed with at least a two-fold difference, at least a three-fold difference, at least a four-fold difference, at least a five-fold difference, at least a six-fold difference, at least a seven-fold difference, at least an eight-fold difference, at least a nine-fold difference, at least a ten-fold difference or more in expression level as compared to the protein expression level of a reference microorganism.

225. The composition of claim 224, wherein the difference in expression level is positive.

226. The composition of claim 224, wherein the difference in expression level is negative.

227. The composition of any one of claims 222-226, wherein the wherein the endophyte comprises an ITS rRNA nucleic acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 344 and 447.

228. The composition of any one of claims 222-226, wherein the wherein the endophyte comprises a 16S rRNA nucleic acid sequence at least 95%, at least 96%, at least 97%, at least

98%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 439 or 441.

FIG. 1

Glycolysis / Gluconeogenesis

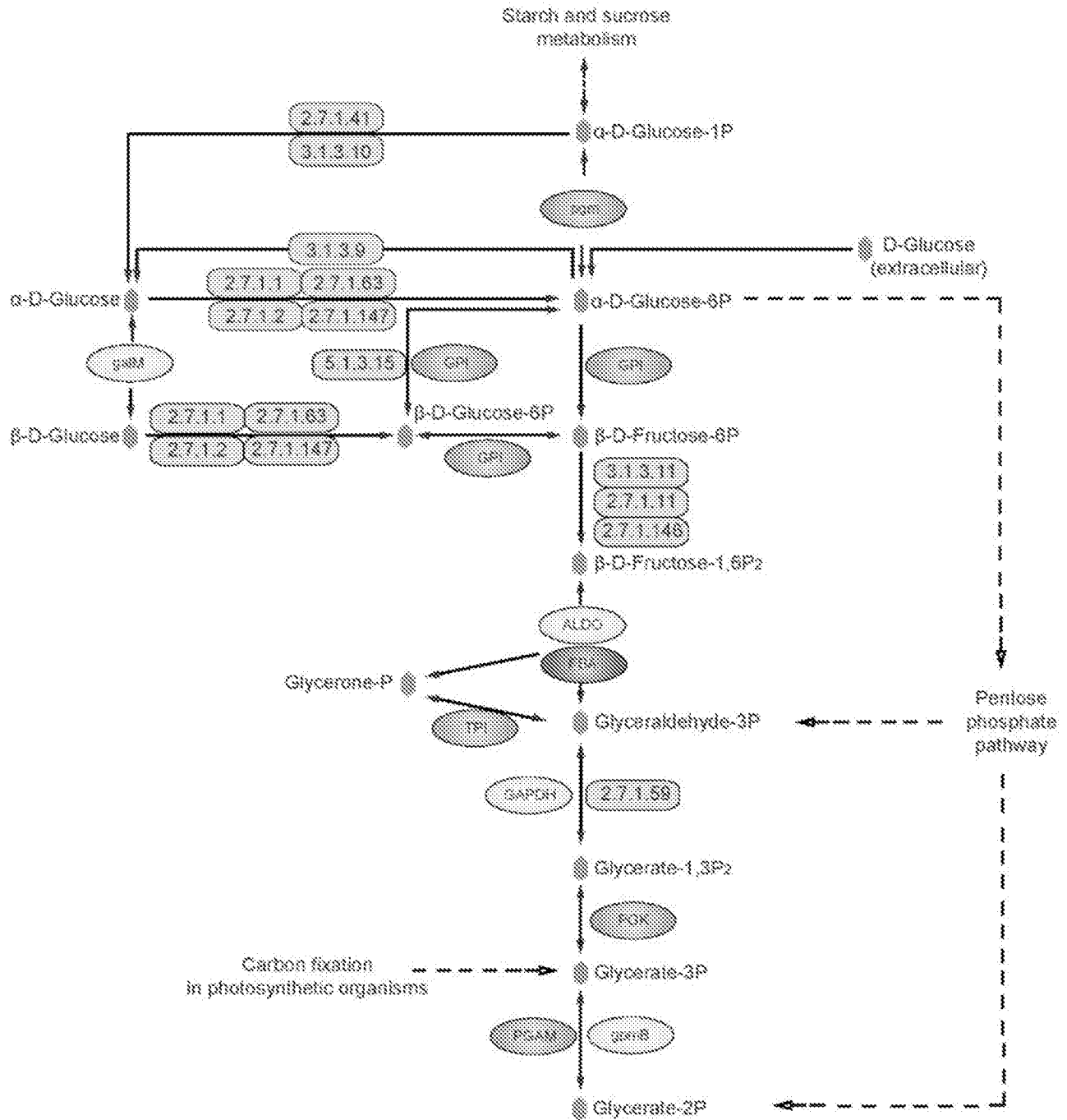


FIG. 1 Continued...

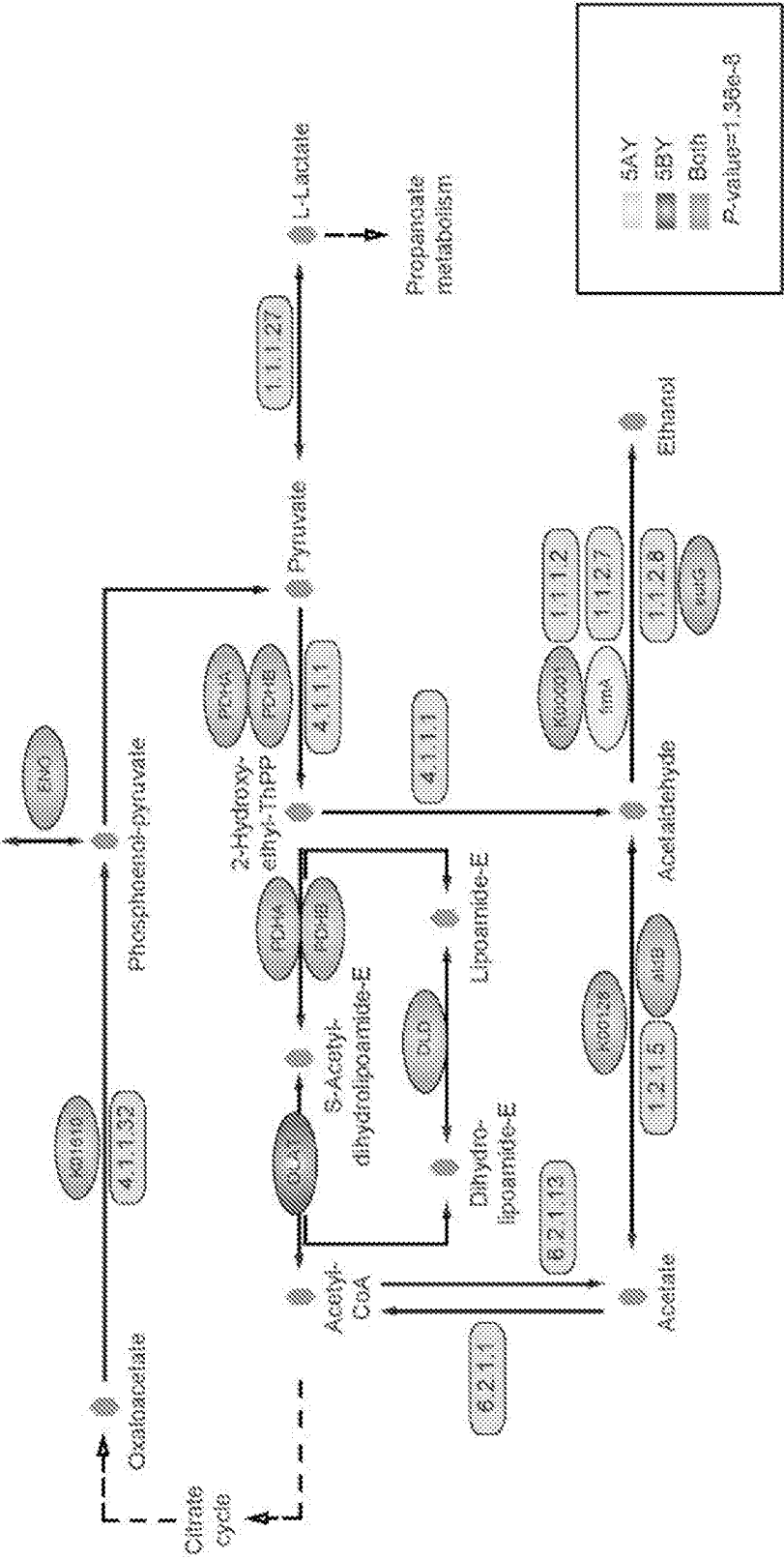


FIG. 2

