# The dynamics of indigenous epiphytic bacterial and fungal communities of barley grains through the commercial malting process in Western Canada

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# *Supplementary Material*

## 1 Supplementary Figures and Tables

### 1.1 Supplementary Tables

**Supplementary Table S1. Synonyms of fungal genera.**

**Supplementary Table S2. Sequences and OTUs assigned to a known taxon at each taxonomic rank.**

**Supplementary Table S3. Metabolic pathways enriched or depleted through the malting process.**

**Supplementary Table S4: Topological properties of molecular ecological networks of microbial communities associated with field and steeped barley grains and the malt end product.**

### 1.2 Supplementary Figures

**Supplementary Figure S1. Fungal community taxonomic profile at the A) phylum, B) class, C) order, D) family, and E) genus levels.**

**Supplementary Figure S2. Bacterial community taxonomic profile at the A) phylum, B) class, C) order, D) family, and E) genus levels.**

**Supplementary Table S1. Fungal synonyms list.**

| Accepted generic name | Synonyms being substitued |
|---|---|
| Alternaria | Lewia |
| Ascocoryne | Coryne |
| Aspergillus | Eurotium,Emericella |
| Asterophora | Ugola |
| Bipolaris | Cochliobolus |
| Ceratobasidium | Ceratorhiza |
| Cladosporium | Davidiella |
| Claviceps | Sphacelia |
| Coprinellus | Ozonium |
| Coprinopsis | Hormographiella |
| Cristulariella | Nervostroma |
| Dendrocollybia | Tilachlidiopsis |
| Drechslera | Pyrenophora,Setosphaeria |
| Epichloe | Neotyphodium |
| Exobasidium | Tilletiopsis |
| Exserohilum | Setosphaeria |
| Fusarium | Gibberella |
| Ganoderma | Thermophymatospora |
| Grovesinia | Hinomyces |
| Hohenbuehelia | Nematoctonus |
| Microdochium | Monographella |
| Morchella | Costantinella |
| Nectria | Tubercularia |
| Onygena | Sporendonema |
| Penicillium | Eupenicillium |
| Pleurotus | Antromycopsis |
| Ramularia | Mycosphaerella |
| Termitomyces | Termitosphaera |
| Tolypocladium | Elaphocordyceps |
| Trichoderma | Hypocrea |
| Tulasnella | Epulorhiza |
| Ustilago | Pseudozyma |
| Valdensia | Valdensinia |
| Wolfiporia | Gemmularia |

**Supplementary Table S2. Sequences and OTUs assigned to a known taxon at each taxonomic rank**

| | ITS2 | | | | 16S | | | |
|---|---|---|---|---|---|---|---|---|
| | Total Reads | Total OTUs | % sequences identified | % OTUs identified | Total Reads | Total OTUs | % sequences identified | % OTUs identified |
| **Kingdom** | 587127 | 962 | 100.0 | 100.0 | 1399108.0 | 2566.0 | 100.0 | 100.0 |
| **Phylum** | | | 100.0 | 100.0 | | | 100.0 | 100.0 |
| **Class** | | | 98.8 | 97.7 | | | 100.0 | 100.0 |
| **Order** | | | 98.7 | 96.1 | | | 100.0 | 99.0 |
| **Family** | | | 46.0 | 44.8 | | | 99.3 | 92.9 |
| **Genus** | | | 93.6 | 68.9 | | | 57.2 | 64.3 |

## Supplementary Table S3. Metabolic pathways enriched or depleted through the malting proces

| Function | description | genus | Reference stage | Stage | Enriched/ Depleted | baseMean | log2Fold Change | lfcSE | padj |
|---|---|---|---|---|---|---|---|---|---|
| THREOCAT-PWY | superpathway of L-threonine metabolism | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Streptococcus; Leuconostocaceae; Sanguibacter | Field_Barley | Kilned | Enriched | 169.96 | 9.79 | 1.10 | 1.34E-17 |
| PWY-7013 | L-1,2-propanediol degradation | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Actinomycetales; Sphingobacterium; Streptococcus; Leuconostocaceae; Sanguibacter | Field_Barley | Kilned | Enriched | 301.49 | 7.97 | 0.90 | 2.72E-17 |
| PWY-5005 | biotin biosynthesis II | Corynebacterium; Arthrobacter; Micrococcaceae; Leuconostoc; Sphingobacterium; Actinomycetales; Streptococcus | Field_Barley | Kilned | Enriched | 101.77 | 7.96 | 0.85 | 2.74E-19 |
| P164-PWY | purine nucleobases degradation I (anaerobic) | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Streptococcus; Leuconostocaceae; Sanguibacter | Field_Barley | Kilned | Enriched | 286.44 | 7.84 | 0.88 | 1.55E-17 |
| PWY-5507 | adenosylcobalamin biosynthesis I (early cobalt insertion) | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Streptococcus; Leuconostocaceae; Sanguibacter | Field_Barley | Kilned | Enriched | 125.52 | 7.17 | 0.89 | 1.16E-14 |

| **Function** | **description** | **genus** | **Reference stage** | **Stage** | **Enriched/ Depleted** | **baseMean** | **log2Fold Change** | **lfcSE** | **padj** |
|---|---|---|---|---|---|---|---|---|---|
| LACTOSECAT-PWY | lactose and galactose degradation I | Arthrobacter; Micrococcaceae; Lactococcus; Streptococcus; Leuconostoc; Microbacterium; Actinomycetales | Field_Barley | Kilned | Enriched | 223.06 | 6.95 | 0.81 | 2.18E-16 |
| PWY-6470 | peptidoglycan biosynthesis V (&beta;-lactam resistance) | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Streptococcus; Leuconostocaceae; Sanguibacter | Field_Barley | Kilned | Enriched | 1126.54 | 6.71 | 0.54 | 2.86E-33 |
| HCAMHPDEG-PWY | 3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation to 2-oxopent-4-enoate | Micrococcaceae; Microbacterium; Arthrobacter; Corynebacterium; Actinomycetales | Field_Barley | Kilned | Enriched | 224.87 | 4.65 | 0.53 | 5.60E-17 |
| PWY-6690 | cinnamate and 3-hydroxycinnamate degradation to 2-oxopent-4-enoate | Micrococcaceae; Microbacterium; Arthrobacter; Corynebacterium; Actinomycetales | Field_Barley | Kilned | Enriched | 224.87 | 4.65 | 0.53 | 5.60E-17 |
| PWY-6339 | syringate degradation | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Actinomycetales; Leuconostoc; Leuconostocaceae; Streptococcus; Sanguibacter; Microbacterium | Field_Barley | Kilned | Enriched | 222.02 | 4.16 | 0.77 | 3.20E-07 |
| GLCMANNANAUT-PWY | superpathway of N-acetylglucosamine, N-acetylmannosamine and N-acetylneuraminate degradation | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Streptococcus; Leuconostocaceae; Sanguibacter | Field_Barley | Kilned | Enriched | 358.83 | 4.04 | 0.53 | 2.42E-13 |

| Function | description | genus | Reference stage | Stage | Enriched/ Depleted | baseMean | log2Fold Change | lfcSE | padj |
|---|---|---|---|---|---|---|---|---|---|
| PWY0-1277 | 3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation | Lactococcus; Micrococcaceae; Leuconostoc; Microbacterium; Arthrobacter; Actinomycetales; Streptococcus; Leuconostocaceae; Sanguibacter; Corynebacterium | Field_Barley | Kilned | Enriched | 490.33 | 3.78 | 0.45 | 6.52E-16 |
| P441-PWY | superpathway of N-acetylneuraminate degradation | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Streptococcus; Leuconostocaceae; Sanguibacter | Field_Barley | Kilned | Enriched | 879.26 | 3.59 | 0.47 | 2.65E-13 |
| GALLATE-DEGRADATION-I-PWY | gallate degradation II | Arthrobacter; Micrococcaceae; Microbacterium | Field_Barley | Kilned | Enriched | 143.56 | 3.23 | 0.59 | 2.06E-07 |
| METHYLGALLATE-DEGRADATION-PWY | methylgallate degradation | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Actinomycetales; Leuconostoc; Leuconostocaceae; Streptococcus; Sanguibacter; Microbacterium | Field_Barley | Kilned | Enriched | 177.52 | 3.21 | 0.58 | 1.85E-07 |
| PWY-5860 | superpathway of demethylmenaquinol-6 biosynthesis I | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Leuconostocaceae; Sanguibacter; Streptococcus | Field_Barley | Kilned | Enriched | 525.42 | 3.12 | 0.24 | 9.43E-36 |
| PWY-5862 | superpathway of demethylmenaquinol-9 biosynthesis | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Leuconostocaceae; Sanguibacter; Streptococcus | Field_Barley | Kilned | Enriched | 525.42 | 3.12 | 0.24 | 9.43E-36 |

| Function | description | genus | Reference stage | Stage | Enriched/ Depleted | baseMean | log2Fold Change | lfcSE | padj |
|---|---|---|---|---|---|---|---|---|---|
| P381-PWY | adenosylcobalamin biosynthesis II (late cobalt incorporation) | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Streptococcus; Leuconostocaceae; Sanguibacter | Field_Barley | Kilned | Enriched | 167.81 | 3.02 | 0.53 | 5.75E-08 |
| PWY-5845 | superpathway of menaquinol-9 biosynthesis | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Leuconostocaceae; Sanguibacter; Streptococcus | Field_Barley | Kilned | Enriched | 734.42 | 3.02 | 0.23 | 8.59E-37 |
| PWY-5850 | superpathway of menaquinol-6 biosynthesis I | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Leuconostocaceae; Sanguibacter; Streptococcus | Field_Barley | Kilned | Enriched | 734.42 | 3.02 | 0.23 | 8.59E-37 |
| PWY-5896 | superpathway of menaquinol-10 biosynthesis | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Leuconostocaceae; Sanguibacter; Streptococcus | Field_Barley | Kilned | Enriched | 734.42 | 3.02 | 0.23 | 8.59E-37 |
| P341-PWY | glycolysis V (Pyrococcus) | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Streptococcus; Leuconostocaceae; Sanguibacter | Field_Barley | Kilned | Enriched | 138.75 | 2.96 | 0.43 | 3.17E-11 |

| Function | description | genus | Reference stage | Stage | Enriched/ Depleted | baseMean | log2Fold Change | lfcSE | padj |
|---|---|---|---|---|---|---|---|---|---|
| HEXITOLDEGSUPER-PWY | superpathway of hexitol degradation (bacteria) | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Streptococcus; Leuconostocaceae; Sanguibacter | Field_Barley | Kilned | Enriched | 2064.62 | 2.27 | 0.26 | 4.95E-17 |
| TEICHOICACID-PWY | teichoic acid (poly-glycerol) biosynthesis | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Streptococcus; Leuconostocaceae; Sanguibacter | Field_Barley | Kilned | Enriched | 1808.39 | 2.03 | 0.22 | 2.68E-18 |
| PWY-1269 | CMP-3-deoxy-D-manno-octulosonate biosynthesis I | Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 551.14 | -2.10 | 0.30 | 1.81E-11 |
| PWY-5855 | ubiquinol-7 biosynthesis (prokaryotic) | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 1114.29 | -2.16 | 0.44 | 2.32E-06 |
| PWY-5856 | ubiquinol-9 biosynthesis (prokaryotic) | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 1114.29 | -2.16 | 0.44 | 2.32E-06 |
| PWY-5857 | ubiquinol-10 biosynthesis (prokaryotic) | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 1114.29 | -2.16 | 0.44 | 2.32E-06 |
| PWY-6708 | ubiquinol-8 biosynthesis (prokaryotic) | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 1114.29 | -2.16 | 0.44 | 2.32E-06 |
| PWY-5920 | superpathway of heme biosynthesis from glycine | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 1274.38 | -2.27 | 0.33 | 5.95E-11 |
| PWY-7328 | superpathway of UDP-glucose-derived O-antigen building blocks biosynthesis | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 987.48 | -2.28 | 0.26 | 6.44E-17 |

| Function | description | genus | Reference stage | Stage | Enriched/ Depleted | baseMean | log2Fold Change | lfcSE | padj |
|---|---|---|---|---|---|---|---|---|---|
| NAGLIPASYN-PWY | lipid IVA biosynthesis | Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 536.80 | -2.32 | 0.32 | 2.99E-12 |
| PWY0-862 | (5Z)-dodec-5-enoate biosynthesis | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 1419.47 | -2.33 | 0.31 | 1.21E-12 |
| PWY0-321 | phenylacetate degradation I (aerobic) | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 322.41 | -2.36 | 0.74 | 0.00303849 |
| PWY-5655 | L-tryptophan degradation IX | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 117.54 | -2.40 | 0.39 | 3.18E-09 |
| UBISYN-PWY | superpathway of ubiquinol-8 biosynthesis (prokaryotic) | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 870.54 | -2.43 | 0.41 | 1.83E-08 |
| PWY-7664 | oleate biosynthesis IV (anaerobic) | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 1494.96 | -2.45 | 0.33 | 7.61E-13 |
| GLUCOSE1PMETAB-PWY | glucose and glucose-1-phosphate degradation | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 900.17 | -2.48 | 0.30 | 1.51E-15 |
| PWYG-321 | mycolate biosynthesis | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 1576.31 | -2.50 | 0.34 | 1.20E-12 |
| PWY-6467 | Kdo transfer to lipid IVA III (Chlamydia) | Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 504.88 | -2.52 | 0.35 | 2.88E-12 |
| LEU-DEG2-PWY | L-leucine degradation I | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 738.50 | -2.59 | 0.35 | 7.47E-13 |
| PWY-6282 | palmitoleate biosynthesis I (from (5Z)-dodec-5-enoate) | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 1421.18 | -2.60 | 0.35 | 8.94E-13 |
| PWY-5989 | stearate biosynthesis II (bacteria and plants) | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 1502.88 | -2.64 | 0.35 | 7.27E-13 |

| Function | description | genus | Reference stage | Stage | Enriched/ Depleted | baseMean | log2Fold Change | lfcSE | padj |
|---|---|---|---|---|---|---|---|---|---|
| PWY-6731 | starch degradation III | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 360.48 | -2.68 | 0.38 | 1.38E-11 |
| PWY-5181 | toluene degradation III (aerobic) (via p-cresol) | Intrasporangiaceae; Xanthomonas; Xanthomonadaceae; Luteimonas; Pedobacter | Field_Barley | Kilned | Depleted | 399.47 | -2.74 | 0.76 | 0.000774206 |
| PWY-6182 | superpathway of salicylate degradation | Intrasporangiaceae; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 307.90 | -2.74 | 0.62 | 2.68E-05 |
| BIOTIN-BIOSYNTHESIS-PWY | biotin biosynthesis I | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 964.31 | -2.77 | 0.46 | 7.75E-09 |
| PWY-7315 | dTDP-N-acetylthomosamine biosynthesis | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 121.36 | -2.82 | 0.40 | 1.95E-11 |
| FASYN-INITIAL-PWY | superpathway of fatty acid biosynthesis initiation (E. coli) | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 1549.95 | -2.87 | 0.37 | 1.69E-13 |
| PWY-5417 | catechol degradation III (ortho-cleavage pathway) | Intrasporangiaceae; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 314.23 | -2.88 | 0.63 | 1.81E-05 |
| PWY-5431 | aromatic compounds degradation via &beta;-ketoadipate | Intrasporangiaceae; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 314.23 | -2.88 | 0.63 | 1.81E-05 |
| PWY-6630 | superpathway of L-tyrosine biosynthesis | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 1168.54 | -3.07 | 0.84 | 0.000665029 |
| PWY-6185 | 4-methylcatechol degradation (ortho cleavage) | Intrasporangiaceae; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 298.98 | -3.07 | 0.80 | 0.000343752 |
| PWY-6628 | superpathway of L-phenylalanine biosynthesis | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 1181.62 | -3.08 | 0.84 | 0.000641244 |
| PWY-6519 | 8-amino-7-oxononanoate biosynthesis I | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 1044.36 | -3.16 | 0.49 | 5.91E-10 |

| Function | description | genus | Reference stage | Stage | Enriched/ Depleted | baseMean | log2Fold Change | lfcSE | padj |
|---|---|---|---|---|---|---|---|---|---|
| PWY-5654 | 2-amino-3-carboxymuconate semialdehyde degradation to 2-oxopentenoate | Intrasporangiaceae; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 214.29 | -3.19 | 0.44 | 2.81E-12 |
| PWY-5647 | 2-nitrobenzoate degradation I | Intrasporangiaceae; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 231.32 | -3.33 | 0.44 | 2.78E-13 |
| NAD-BIOSYNTHESIS-II | NAD salvage pathway II | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 397.99 | -3.45 | 0.91 | 0.000440583 |
| NADSYN-PWY | NAD biosynthesis II (from tryptophan) | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 587.75 | -3.61 | 0.59 | 4.39E-09 |
| PWY-5651 | L-tryptophan degradation to 2-amino-3-carboxymuconate semialdehyde | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 456.17 | -3.84 | 0.61 | 2.35E-09 |
| TYRFUMCAT-PWY | L-tyrosine degradation I | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 452.27 | -3.86 | 0.74 | 7.53E-07 |
| PPGPPMET-PWY | ppGpp biosynthesis | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 706.97 | -4.07 | 0.80 | 1.26E-06 |
| PWY0-1479 | tRNA processing | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 122.95 | -4.43 | 0.83 | 4.95E-07 |
| PWY-5028 | L-histidine degradation II | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Kilned | Depleted | 330.26 | -4.67 | 0.56 | 1.99E-15 |
| THREOCAT-PWY | superpathway of L-threonine metabolism | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Streptococcus; Leuconostocaceae; Sanguibacter | Field_Barley | Steeped | Enriched | 169.96 | 8.60 | 1.19 | 7.96E-11 |

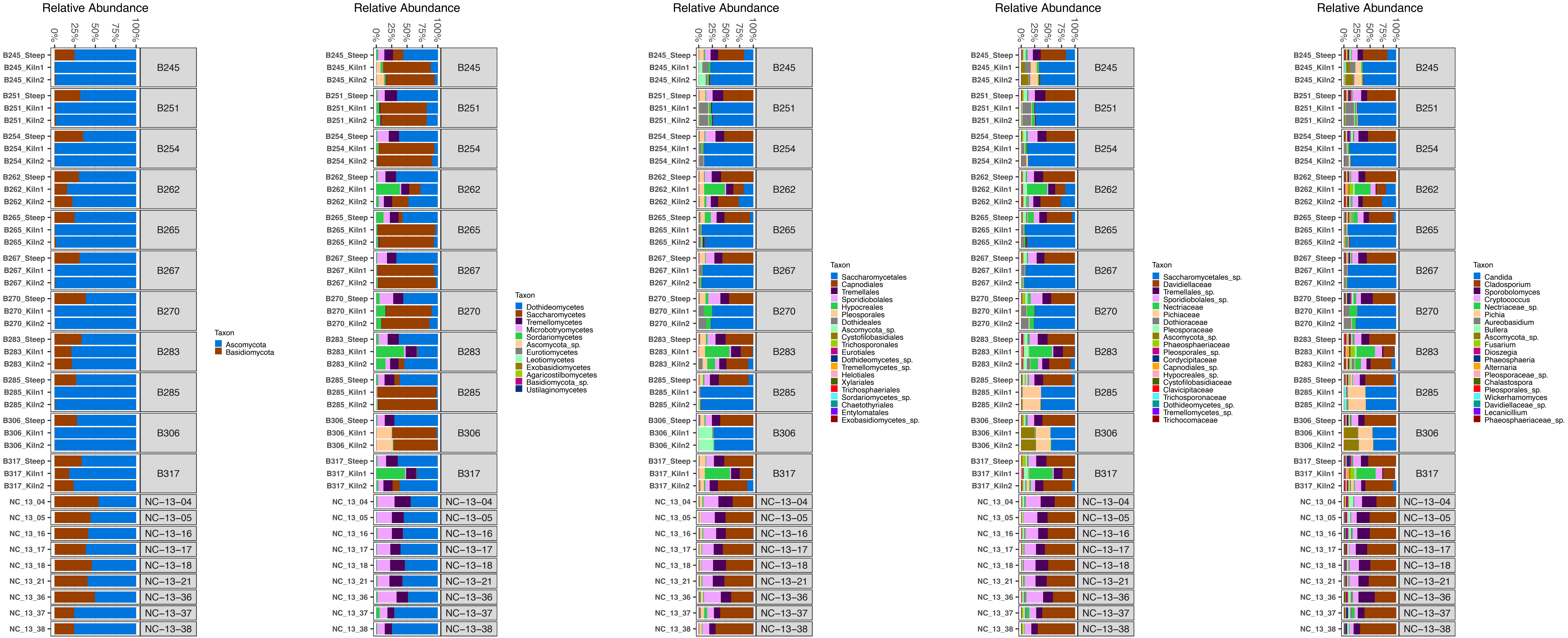
| Function | description | genus | Reference stage | Stage | Enriched/ Depleted | baseMean | log2Fold Change | lfcSE | padj |
|---|---|---|---|---|---|---|---|---|---|
| PWY-7013 | L-1,2-propanediol degradation | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Actinomycetales; Sphingobacterium; Streptococcus; Leuconostocaceae; Sanguibacter | Field_Barley | Steeped | Enriched | 301.49 | 7.00 | 1.01 | 4.06E-10 |
| P164-PWY | purine nucleobases degradation I (anaerobic) | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Streptococcus; Leuconostocaceae; Sanguibacter | Field_Barley | Steeped | Enriched | 286.44 | 6.45 | 0.99 | 4.08E-09 |
| PWY-5005 | biotin biosynthesis II | Corynebacterium; Arthrobacter; Micrococcaceae; Leuconostoc; Sphingobacterium; Actinomycetales; Streptococcus | Field_Barley | Steeped | Enriched | 101.77 | 6.00 | 0.92 | 4.08E-09 |
| PWY-5507 | adenosylcobalamin biosynthesis I (early cobalt insertion) | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Streptococcus; Leuconostocaceae; Sanguibacter | Field_Barley | Steeped | Enriched | 125.52 | 5.84 | 0.99 | 1.66E-07 |
| LACTOSECAT-PWY | lactose and galactose degradation I | Arthrobacter; Micrococcaceae; Lactococcus; Streptococcus; Leuconostoc; Microbacterium; Actinomycetales | Field_Barley | Steeped | Enriched | 223.06 | 5.83 | 0.91 | 8.33E-09 |
| PWY-6470 | peptidoglycan biosynthesis V (&beta;-lactam resistance) | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Streptococcus; Leuconostocaceae; Sanguibacter | Field_Barley | Steeped | Enriched | 1126.54 | 4.79 | 0.62 | 1.97E-12 |

| **Function** | **description** | **genus** | **Reference stage** | **Stage** | **Enriched/ Depleted** | **baseMean** | **log2Fold Change** | **lfcSE** | **padj** |
|---|---|---|---|---|---|---|---|---|---|
| PWY-6339 | syringate degradation | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Actinomycetales; Leuconostoc; Leuconostocaceae; Streptococcus; Sanguibacter; Microbacterium | Field_Barley | Steeped | Enriched | 222.02 | 3.26 | 0.87 | 0.002579709 |
| GLCMANNANAUT-PWY | superpathway of N-acetylglucosamine, N-acetylmannosamine and N-acetylneuraminate degradation | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Leuconostoc; Microbacterium; Sphingobacterium; Actinomycetales; Streptococcus; Leuconostocaceae; Sanguibacter | Field_Barley | Steeped | Enriched | 358.83 | 2.30 | 0.60 | 0.001824711 |
| GALLATE-DEGRADATION-I-PWY | gallate degradation II | Arthrobacter; Micrococcaceae; Microbacterium | Field_Barley | Steeped | Enriched | 143.56 | 2.29 | 0.67 | 0.004950516 |
| METHYLGALLATE-DEGRADATION-PWY | methylgallate degradation | Corynebacterium; Lactococcus; Arthrobacter; Micrococcaceae; Actinomycetales; Leuconostoc; Leuconostocaceae; Streptococcus; Sanguibacter; Microbacterium | Field_Barley | Steeped | Enriched | 177.52 | 2.27 | 0.66 | 0.004950516 |
| PWY0-1479 | tRNA processing | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Field_Barley | Steeped | Depleted | 122.95 | -2.84 | 0.95 | 0.013346605 |
| HCAMHPDEG-PWY | 3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation to 2-oxopent-4-enoate | Micrococcaceae; Microbacterium; Arthrobacter; Corynebacterium; Actinomycetales | Steeped | Kilned | Enriched | 224.87 | 2.65 | 0.49 | 1.43E-06 |
| PWY-6690 | cinnamate and 3-hydroxycinnamate degradation to 2-oxopent-4-enoate | Micrococcaceae; Microbacterium; Arthrobacter; Corynebacterium; Actinomycetales | Steeped | Kilned | Enriched | 224.87 | 2.65 | 0.49 | 1.43E-06 |

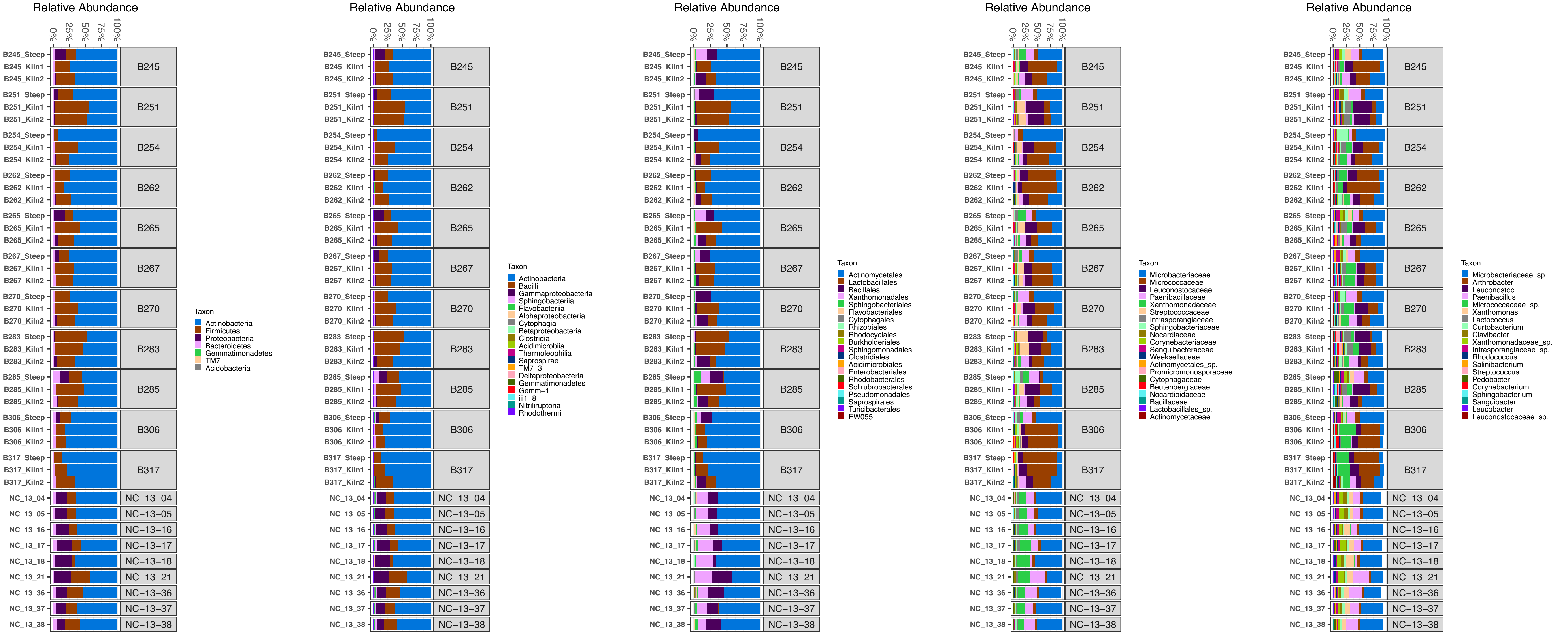
| **Function** | **description** | **genus** | **Reference stage** | **Stage** | **Enriched/ Depleted** | **baseMean** | **log2Fold Change** | **lfcSE** | **padj** |
|---|---|---|---|---|---|---|---|---|---|
| PWY0-1277 | 3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation | Lactococcus; Micrococcaceae; Leuconostoc; Microbacterium; Arthrobacter; Actinomycetales; Streptococcus; Leuconostocaceae; Sanguibacter; Corynebacterium | Steeped | Kilned | Enriched | 490.33 | 2.21 | 0.42 | 2.61E-06 |
| NAD-BIOSYNTHESIS-II | NAD salvage pathway II | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Steeped | Kilned | Depleted | 397.99 | -2.13 | 0.85 | 0.029022103 |
| NADSYN-PWY | NAD biosynthesis II (from tryptophan) | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Steeped | Kilned | Depleted | 587.75 | -2.23 | 0.55 | 0.000599512 |
| PWY-5651 | L-tryptophan degradation to 2-amino-3-carboxymuconate semialdehyde | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Steeped | Kilned | Depleted | 456.17 | -2.38 | 0.57 | 0.000430854 |
| TYRFUMCAT-PWY | L-tyrosine degradation I | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Steeped | Kilned | Depleted | 452.27 | -2.46 | 0.69 | 0.002307863 |
| PPGPPMET-PWY | ppGpp biosynthesis | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Steeped | Kilned | Depleted | 706.97 | -2.57 | 0.74 | 0.002919526 |
| PWY-5028 | L-histidine degradation II | Intrasporangiaceae; Pedobacter; Xanthomonas; Xanthomonadaceae; Luteimonas | Steeped | Kilned | Depleted | 330.26 | -3.17 | 0.53 | 9.75E-08 |

## Supplementary Table S4: Topological properties of molecular ecological networks of microbial communities associated with field and steeped barley grains and the malt end product.

| **Network Indexes** | **Field barley** | **Steeped** | **Malt** |
|---|---|---|---|
| Nodes | 380 | 537 | 307 |
| Edges | 3820 | 6558 | 483 |
| Average degree | 10.75 | 14.92 | 1.99 |
| Average path distance | 2.48 | 2.43 | 2.41 |
| Average clustering coefficient | 0.362 | 0.357 | 0.413 |
| Max degree | 98 | 98 | 19 |
| Node with max degree | Micrococcaceae sp. (in Actinobacteria) | Micrococcaceae sp. (in Actinobacteria) | *Cryptococcus* sp. (in Basidiomycota) |
| Max betweeness | 3663.45 | 3663.45 | 7851.11 |
| Node with max betweeness | Actinomycetales sp. (in Actinobacteria) | Actinomycetales sp. (in Actinobacteria) | *Corynebacterium* sp. (in Actinobacteria) |
| Max betweeness centrality | 1212.12 | 3394 | 2010.37 |
| Node with max betweeness centrality | Actinomycetales sp. (in Actinobacteria) | Bacteria sp. | *Corynebacterium* sp. (in Actinobacteria) |
| Closeness centrality | 7 | 7 | 6 |
| Node with max eigenvector centrality | Comamonadacea (in Proteobacteria) | NA | *Cryptococcus* sp. (in Basidiomycota) |
| Centralization of eigenvector centrality (CE) | 0.039 | 0.048 | 0.047 |



**Supplementary Figure S1. Fungal community taxonomic profile at the A) phylum, B) class, C) order, D) family, and E) genus levels.**



**Supplementary Figure S2. Bacterial community taxonomic profile at the A) phylum, B) class, C) order, D) family, and E) genus levels.**