**Additional file 1:** Niche differentiation of microbes and their functional signatures in Assam type tea (*Camellia sinensis* var. *assamica*)

pruned tea metagenome.tif

**Fig. S1.** Rarefaction curve of the Tea rhizosphere metagenome

Tea endosphere metagenome R1.tif

**Fig. S2.** Rarefaction curve of the Tea root endosphere Replicate 1 metagenome

Tea endosphere metagenome R2.tif

**Fig. S3.** Rarefaction curve of the Tea root endosphere Replicate 2 metagenome

**Table S1:** Additional file: Definition of the major KEGG pathways (>1.00%) in the three metagenomes

|  |  |
| --- | --- |
| Pathway | Definition |
| Glycolysis / Gluconeogenesis | ko00010 |
| Citrate cycle (TCA cycle) | ko00020 |
| Pentose phosphate pathway | ko00030 |
| Pentose and glucuronate interconversions | ko00040 |
| Fructose and mannose metabolism | ko00051 |
| Galactose metabolism | ko00052 |
| Ascorbate and aldarate metabolism | ko00053 |
| Fatty acid biosynthesis | ko00061 |
| Fatty acid metabolism | ko00071 |
| Steroid biosynthesis | ko00100 |
| Primary bile acid biosynthesis | ko00120 |
| Ubiquinone and other terpenoid-quinone biosynthesis | ko00130 |
| Steroid hormone biosynthesis | ko00140 |
| Oxidative phosphorylation | ko00190 |
| Photosynthesis | ko00195 |
| Purine metabolism | ko00230 |
| Caffeine metabolism | ko00232 |
| Pyrimidine metabolism | ko00240 |
| Alanine, aspartate and glutamate metabolism | ko00250 |
| Tetracycline biosynthesis | ko00253 |
| Glycine, serine and threonine metabolism | ko00260 |
| Cysteine and methionine metabolism | ko00270 |
| Valine, leucine and isoleucine degradation | ko00280 |
| Geraniol degradation | ko00281 |
| Valine, leucine and isoleucine biosynthesis | ko00290 |
| Lysine biosynthesis | ko00300 |
| Lysine degradation | ko00310 |
| Penicillin and cephalosporin biosynthesis | ko00311 |
| beta-Lactam resistance | ko00312 |
| Arginine and proline metabolism | ko00330 |
| Histidine metabolism | ko00340 |
| Tyrosine metabolism | ko00350 |
| 1,1,1-Trichloro-2,2-bis(4-chlorophenyl)ethane (DDT) degradation | ko00351 |
| Phenylalanine metabolism | ko00360 |
| Chlorocyclohexane and chlorobenzene degradation | ko00361 |
| Bisphenol degradation | ko00363 |
| Fluorobenzoate degradation | ko00364 |
| Tryptophan metabolism | ko00380 |
| Phenylalanine, tyrosine and tryptophan biosynthesis | ko00400 |
| Taurine and hypotaurine metabolism | ko00430 |
| Phosphonate and phosphinate metabolism | ko00440 |
| Selenocompound metabolism | ko00450 |
| Glutathione metabolism | ko00480 |
| Starch and sucrose metabolism | ko00500 |
| N-Glycan biosynthesis | ko00510 |
| Other glycan degradation | ko00511 |
| Various types of N-glycan biosynthesis | ko00513 |
| Other types of O-glycan biosynthesis | ko00514 |
| Amino sugar and nucleotide sugar metabolism | ko00520 |
| Streptomycin biosynthesis | ko00521 |
| Glycosaminoglycan degradation | ko00531 |
| Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate | ko00532 |
| Glycosaminoglycan biosynthesis - keratan sulfate | ko00533 |
| Glycosaminoglycan biosynthesis - heparan sulfate / heparin | ko00534 |
| Lipopolysaccharide biosynthesis | ko00540 |
| Peptidoglycan biosynthesis | ko00550 |
| Glycerolipid metabolism | ko00561 |
| Inositol phosphate metabolism | ko00562 |
| Glycosylphosphatidylinositol(GPI)-anchor biosynthesis | ko00563 |
| Glycerophospholipid metabolism | ko00564 |
| Ether lipid metabolism | ko00565 |
| Arachidonic acid metabolism | ko00590 |
| Linoleic acid metabolism | ko00591 |
| alpha-Linolenic acid metabolism | ko00592 |
| Sphingolipid metabolism | ko00600 |
| Glycosphingolipid biosynthesis - lacto and neolacto series | ko00601 |
| Pyruvate metabolism | ko00620 |
| Dioxin degradation | ko00621 |
| Xylene degradation | ko00621 |
| Polycyclic aromatic hydrocarbon degradation | ko00624 |
| Chloroalkane and chloroalkene degradation | ko00625 |
| Aminobenzoate degradation | ko00627 |
| Glyoxylate and dicarboxylate metabolism | ko00630 |
| Nitrotoluene degradation | ko00633 |
| Propanoate metabolism | ko00640 |
| Ethylbenzene degradation | ko00642 |
| Styrene degradation | ko00643 |
| Butanoate metabolism | ko00650 |
| C5-Branched dibasic acid metabolism | ko00660 |
| One carbon pool by folate | ko00670 |
| Methane metabolism | ko00680 |
| Carbon fixation pathways in prokaryotes | ko00720 |
| Thiamine metabolism | ko00730 |
| Riboflavin metabolism | ko00740 |
| Vitamin B6 metabolism | ko00750 |
| Nicotinate and nicotinamide metabolism | ko00760 |
| Pantothenate and CoA biosynthesis | ko00770 |
| Biotin metabolism | ko00780 |
| Lipoic acid metabolism | ko00785 |
| Folate biosynthesis | ko00790 |
| Atrazine degradation | ko00791 |
| Retinol metabolism | ko00830 |
| Porphyrin and chlorophyll metabolism | ko00860 |
| Terpenoid backbone biosynthesis | ko00900 |
| Diterpenoid biosynthesis | ko00904 |
| Carotenoid biosynthesis | ko00906 |
| Zeatin biosynthesis | ko00908 |
| Sesquiterpenoid and triterpenoid biosynthesis | ko00909 |
| Nitrogen metabolism | ko00910 |
| Sulfur metabolism | ko00920 |
| Caprolactam degradation | ko00930 |
| Phenylpropanoid biosynthesis | ko00940 |
| Flavonoid biosynthesis | ko00941 |
| Isoflavonoid biosynthesis | ko00943 |
| Flavone and flavonol biosynthesis | ko00944 |
| Stilbenoid, diarylheptanoid and gingerol biosynthesis | ko00945 |
| Tropane, piperidine and pyridine alkaloid biosynthesis | ko00960 |
| Glucosinolate biosynthesis | ko00966 |
| Aminoacyl-tRNA biosynthesis | ko00970 |
| Insect hormone biosynthesis | ko00981 |
| Drug metabolism - other enzymes | ko00983 |
| Steroid degradation | ko00984 |
| Biosynthesis of unsaturated fatty acids | ko01040 |
| Biosynthesis of siderophore group nonribosomal peptides | ko01053 |
| Biosynthesis of type II polyketide backbone | ko01056 |
| ABC transporters | ko02010 |
| Two-component system | ko02020 |
| Bacterial chemotaxis | ko02030 |
| Flagellar assembly | ko02040 |
| Phosphotransferase system (PTS) | ko02060 |
| Ribosome biogenesis in eukaryotes | ko03008 |
| Ribosome | ko03010 |
| RNA transport | ko03013 |
| mRNA surveillance pathway | ko03015 |
| RNA degradation | ko03018 |
| RNA polymerase | ko03020 |
| Basal transcription factors | ko03022 |
| DNA replication | ko03030 |
| Spliceosome | ko03040 |
| Proteasome | ko03050 |
| Protein export | ko03060 |
| Bacterial secretion system | ko03070 |
| PPAR signaling pathway | ko03320 |
| Base excision repair | ko03410 |
| Nucleotide excision repair | ko03420 |
| Mismatch repair | ko03430 |
| Homologous recombination | ko03440 |
| Non-homologous end-joining | ko03450 |
| MAPK signaling pathway | ko04010 |
| MAPK signaling pathway - yeast | ko04011 |
| ErbB signaling pathway | ko04012 |
| MAPK signaling pathway - fly | ko04013 |
| Calcium signaling pathway | ko04020 |
| NF-kappa B signaling pathway | ko04064 |
| HIF-1 signaling pathway | ko04066 |
| Phosphatidylinositol signaling system | ko04070 |
| Plant hormone signal transduction | ko04075 |
| Neuroactive ligand-receptor interaction | ko04080 |
| Cell cycle | ko04110 |
| Cell cycle - yeast | ko04111 |
| Cell cycle - Caulobacter | ko04112 |
| Meiosis - yeast | ko04113 |
| Oocyte meiosis | ko04114 |
| p53 signaling pathway | ko04115 |
| Ubiquitin mediated proteolysis | ko04120 |
| Sulfur relay system | ko04122 |
| SNARE interactions in vesicular transport | ko04130 |
| Regulation of autophagy | ko04140 |
| Protein processing in endoplasmic reticulum | ko04141 |
| Lysosome | ko04142 |
| Endocytosis | ko04144 |
| Phagosome | ko04145 |
| Peroxisome | ko04146 |
| mTOR signaling pathway | ko04150 |
| PI3K-Akt signaling pathway | ko04151 |
| Apoptosis | ko04210 |
| Cardiac muscle contraction | ko04260 |
| Wnt signaling pathway | ko04310 |
| Dorso-ventral axis formation | ko04320 |
| Notch signaling pathway | ko04330 |
| Hedgehog signaling pathway | ko04340 |
| Axon guidance | ko04360 |
| Osteoclast differentiation | ko04380 |
| Focal adhesion | ko04510 |
| Cell adhesion molecules (CAMs) | ko04514 |
| Adherens junction | ko04520 |
| Tight junction | ko04530 |
| Gap junction | ko04540 |
| Antigen processing and presentation | ko04612 |
| Renin-angiotensin system | ko04614 |
| NOD-like receptor signaling pathway | ko04621 |
| RIG-I-like receptor signaling pathway | ko04622 |
| Plant-pathogen interaction | ko04626 |
| Jak-STAT signaling pathway | ko04630 |
| Leukocyte transendothelial migration | ko04670 |
| Circadian rhythm - fly | ko04711 |
| Neurotrophin signaling pathway | ko04722 |
| Retrograde endocannabinoid signaling | ko04723 |
| Phototransduction - fly | ko04745 |
| Regulation of actin cytoskeleton | ko04810 |
| Insulin signaling pathway | ko04910 |
| Adipocytokine signaling pathway | ko04920 |
| Type I diabetes mellitus | ko04940 |
| Maturity onset diabetes of the young | ko04950 |
| Vasopressin-regulated water reabsorption | ko04962 |
| Proximal tubule bicarbonate reclamation | ko04964 |
| Pancreatic secretion | ko04972 |
| Protein digestion and absorption | ko04974 |
| Fat digestion and absorption | ko04975 |
| Bile secretion | ko04976 |
| Alzheimer's disease | ko05010 |
| Parkinson's disease | ko05012 |
| Amyotrophic lateral sclerosis (ALS) | ko05014 |
| Huntington's disease | ko05016 |
| Prion diseases | ko05020 |
| Cocaine addiction | ko05030 |
| Morphine addiction | ko05032 |
| Alcoholism | ko05034 |
| Bacterial invasion of epithelial cells | ko05100 |
| Vibrio cholerae infection | ko05110 |
| Vibrio cholerae pathogenic cycle | ko05111 |
| Epithelial cell signaling in Helicobacter pylori infection | ko05120 |
| Pathogenic Escherichia coli infection | ko05130 |
| Salmonella infection | ko05132 |
| Legionellosis | ko05134 |
| Leishmaniasis | ko05140 |
| Chagas disease (American trypanosomiasis) | ko05142 |
| African trypanosomiasis | ko05143 |
| Malaria | ko05144 |
| Amoebiasis | ko05146 |
| Staphylococcus aureus infection | ko05150 |
| Tuberculosis | ko05152 |
| Influenza A | ko05164 |
| Epstein-Barr virus infection | ko05169 |
| Pathways in cancer | ko05200 |
| Transcriptional misregulation in cancers | ko05202 |
| Viral carcinogenesis | ko05203 |
| Chemical carcinogenesis | ko05204 |
| Bladder cancer | ko05219 |
| Small cell lung cancer | ko05222 |
| Systemic lupus erythematosus | ko05322 |
| Primary immunodeficiency | ko05340 |
| Hypertrophic cardiomyopathy (HCM) | ko05410 |