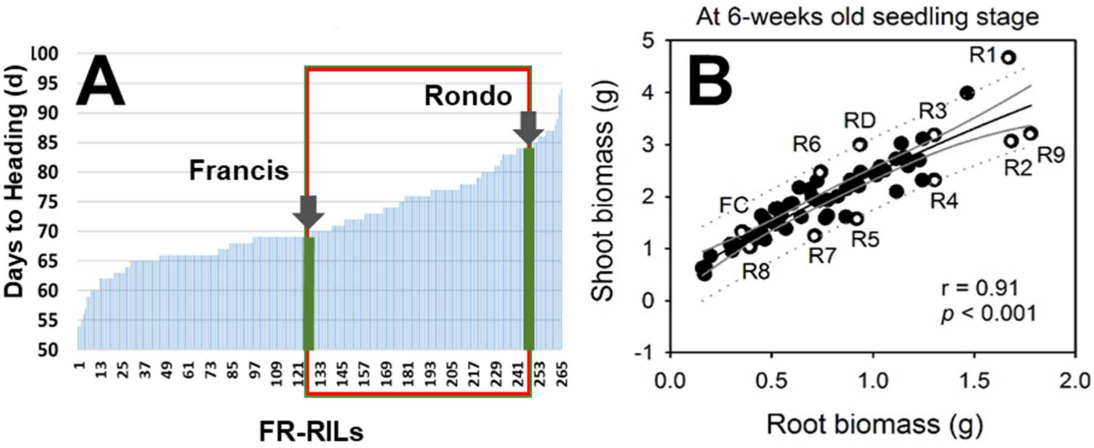

Figure S1. Rice genotype selection based on shoot and root biomass. 62 FR-RIL selected from mapping population (shown by red box) based on similar developmental stage as determined by days to heading in a field study (**A**). Shoot biomass as a function of root biomass among 62 FR-RILs evaluated as 6-week old seedlings in the greenhouse and selection of nine FR-RILs (R1-R9) and parents, Francis (FC) and Rondo (RD), for the soil microbiome study (**B**).

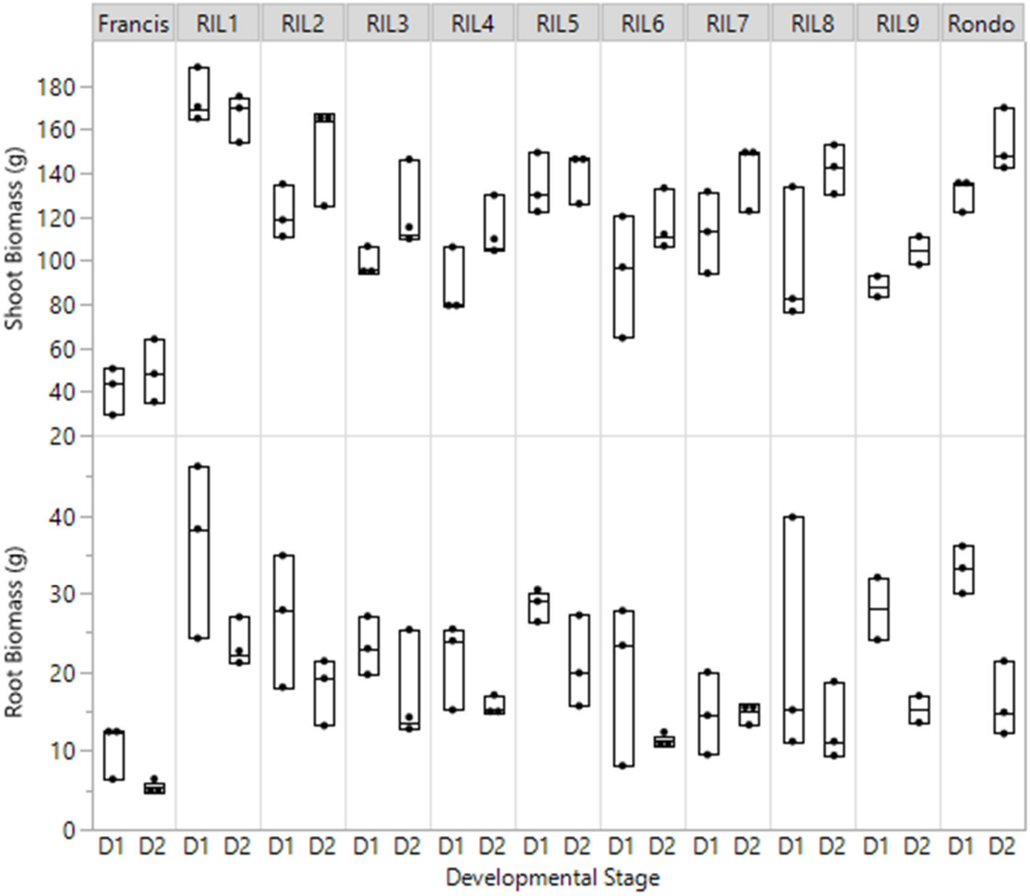

Figure S2. Biomass trends of nine rice genotypes. Root and shoot biomass of nine selected FR-RILs, and parents Francis and Rondo, at two developmental stages heading (D1) and physiological maturity (D2).

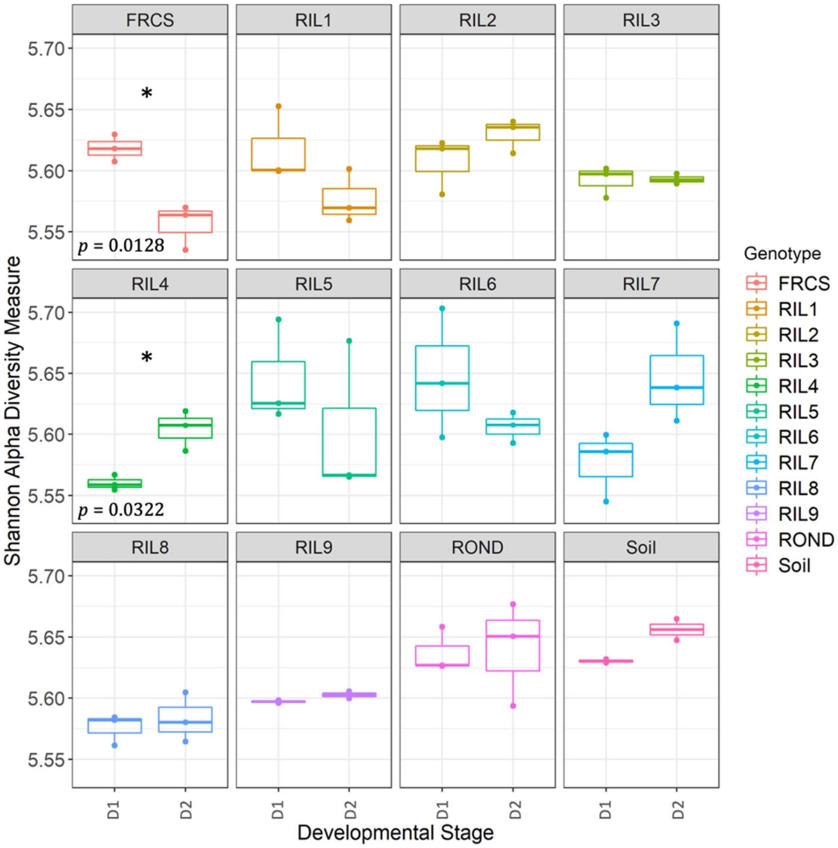

Figure S3. Shannon alpha diversity. Alpha diversity as measured by Shannon index for samples by genotype (Francis, Rondo, RILs 1-9, and control soil) for developmental stages heading (D1) and maturity (D2). Asterisks indicate significant differences by Welch's t-test at a significance level of $p = 0.05$.

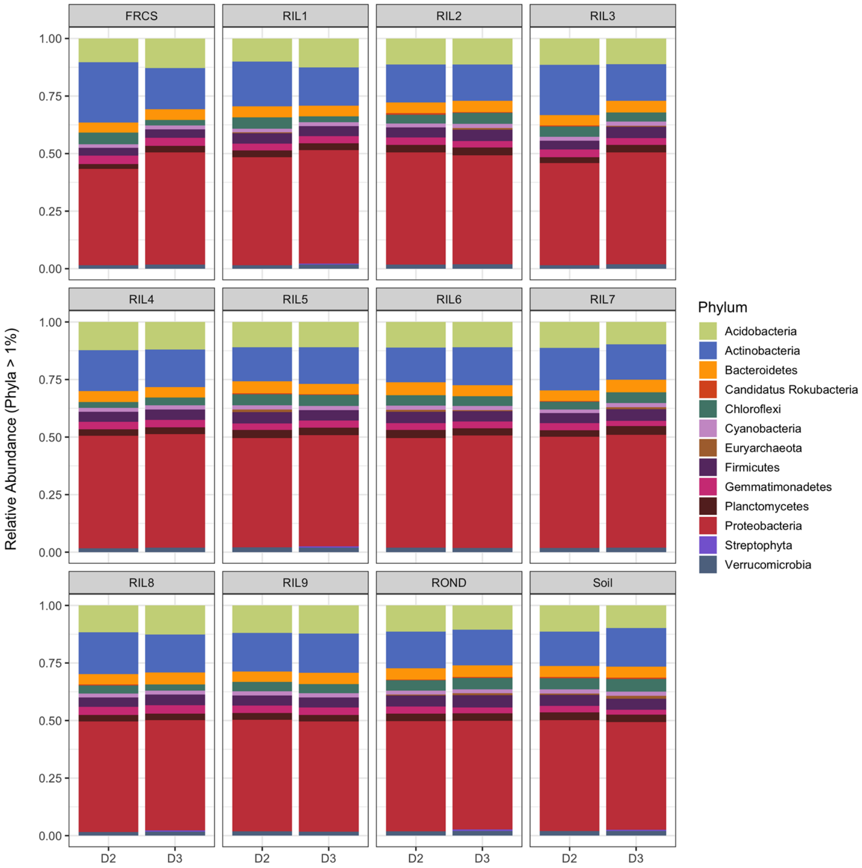

Figure S4. Relative abundance of the top 1% of phyla. Samples are shown by genotype, Francis (FRCS), Rondo (ROND), RILs 1-9, and control soil for developmental stages heading (D1) and maturity (D2).

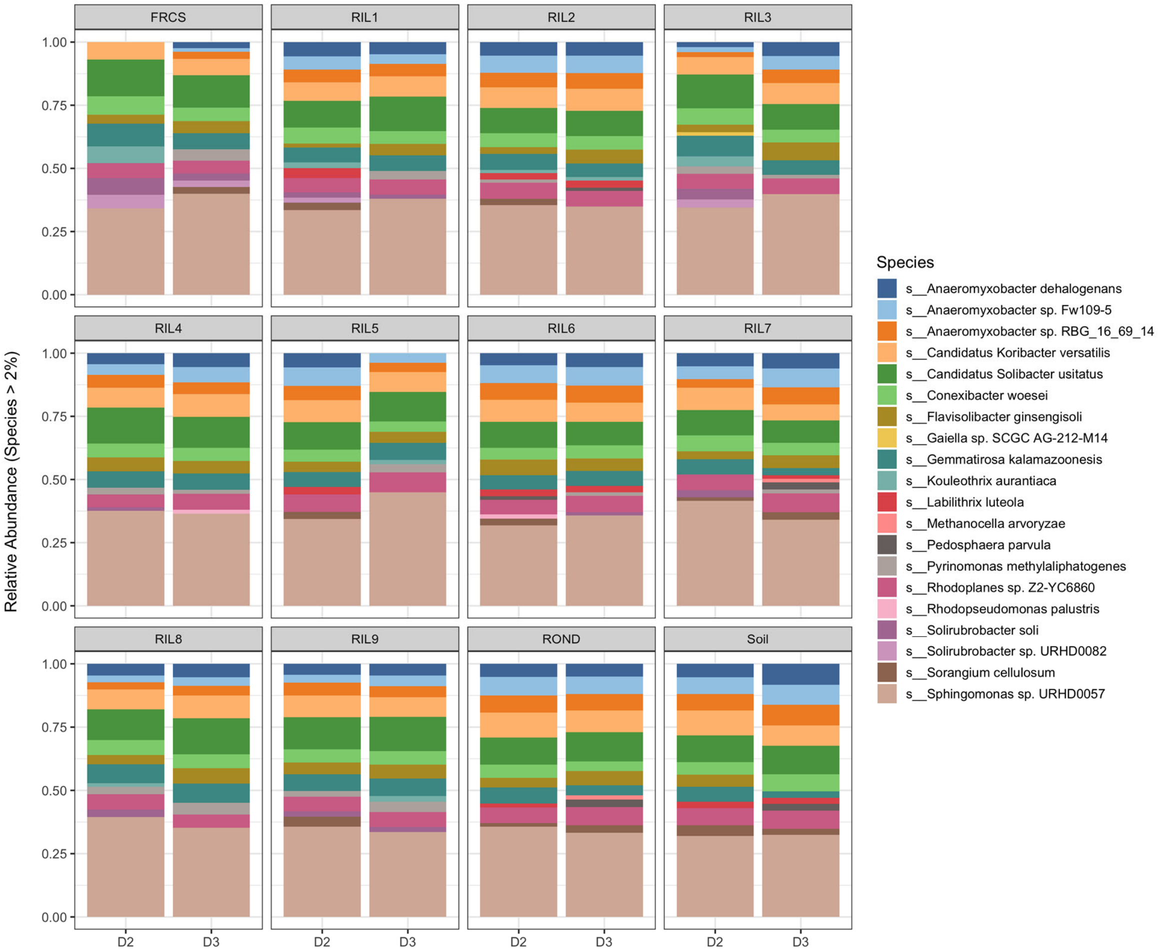

Figure S5. Relative abundance of the top 2% of species. Samples are shown by genotype, Francis (FRCS), Rondo (ROND), RILs 1-9, and control soil for developmental stages heading (D1) and maturity (D2).

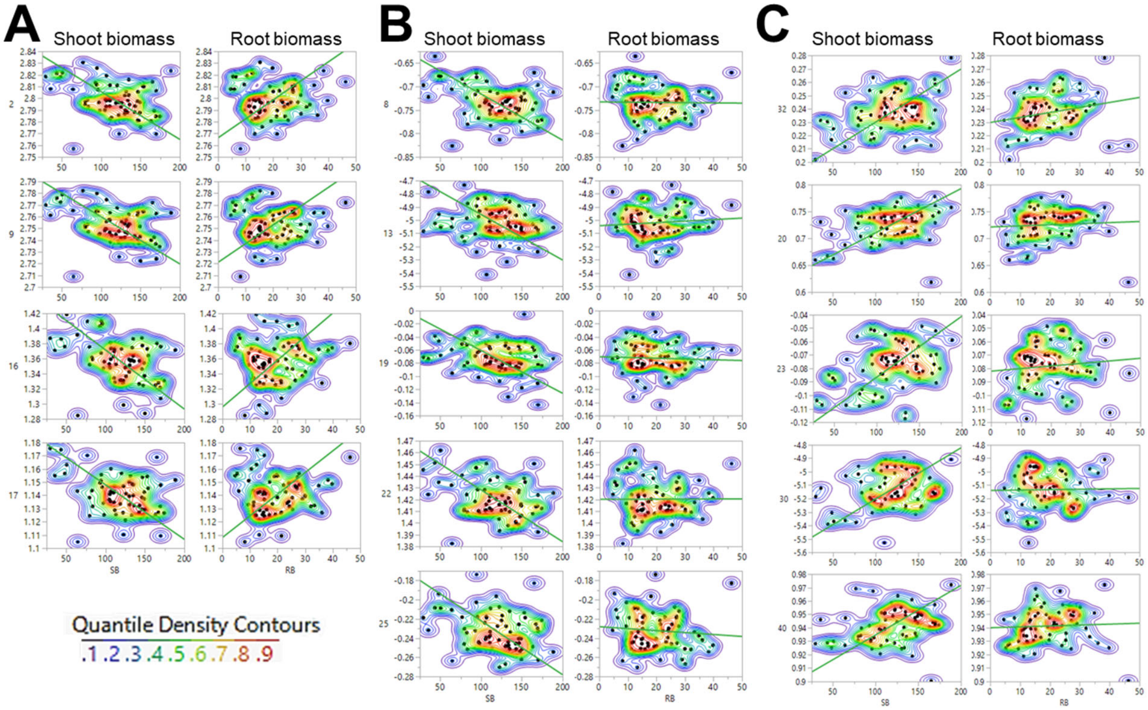

Figure S6. Linear regressions of biomass traits and metabolic function abundance. Linear regression of CLR transformed count data of metabolic functions (Y-axis) identified by PLS and passing $p < 0.01$ with shoot biomass and/or root biomass dry weights (X-axis). Functions showing negative correlations with shoot biomass and positive correlations with root biomass (**A**) or no correlation with root biomass (**B**) and microbial functions with positive correlations to shoot biomass but no correlation to root biomass (**C**). Contour lines indicate quantile density at 5% intervals. This means that approximately 5% of points generated from the estimated nonparametric distribution are below the lowest contour, 10% are below the next contour, and so on. The highest contour has about 95% of the points below it.

Table S1. Genes correlated to biomass traits. All genes identified as significantly correlated with shoot biomass (SB) and root biomass (RB). Gene names as well as numerical IDs (gene ID) used for coefficient plots are shown. *p*-values are reported for SB and RB. Variable importance in projection (VIP) scores greater than 0.8 are considered significantly different by responses, i.e., biomass traits and developmental stages, in the model.

Gene Cluster	Gene Description	ID	RB Coefficient	SB Coefficient
GC1	2-methylcitrate dehydratase FeS dependent (EC 4.2.1.79)	23	0.0185	-0.0078
	Arginine ABC transporter, permease protein ArtM	36	0.0274	-0.0103
	Ornithine aminotransferase (EC 2.6.1.13)	63	0.0208	-0.0045
	3,5-diaminohexanoate dehydrogenase (EC 1.4.1.11)	401	0.0224	-0.0062
	L-threonine transporter, anaerobically inducible	555	0.0166	-0.0114
	2-ketogluconate kinase (EC 2.7.1.13)	626	0.0286	-0.0116
	Maltose operon transcriptional repressor MalR, LacI family	1439	0.0242	-0.0067
	Putative regulator of the mannose operon, ManO	1509	0.0235	-0.0097
	poly(beta-D-mannuronate) lyase (EC 4.2.2.3)	1899	0.0226	-0.0073
	Substrate-specific component YkoE of thiamin-regulated ECF transporter for HydroxyMethylPyrimidine	2442	0.0143	-0.0083
	DNA polymerase-like protein MT3142	2904	0.0160	-0.0103
	Polyketide beta-ketoacyl synthase WhiE-KS paralog	3131	0.0163	-0.0080
	Phytoene desaturase, neurosporene or lycopene producing (EC 1.3.-.-)	3246	0.0192	-0.0108
	Fatty acyl-coenzyme A elongase	3263	0.0268	-0.0094
	Acyl carrier protein (ACP1)	3331	0.0287	-0.0107
	FIG027190: Putative transmembrane protein	3338	0.0196	-0.0065
	Triacylglycerol lipase precursor (EC 3.1.1.3)	3372	0.0120	-0.0088
	UPF0225 protein YchJ	3385	0.0208	-0.0078
	Haemin uptake system permease protein	3422	0.0242	-0.0112
	Probable Lysine n(6)-hydroxylase associated with siderophore S biosynthesis (EC 1.14.13.59)	3502	0.0204	-0.0060
	Dipeptide transport system permease protein DppC (TC 3.A.1.5.2)	3605	0.0190	-0.0036
	Transcriptional regulator of fimbriae expression FimZ (LuxR/UhpA family)	3791	0.0199	-0.0119
	Phenylacetaldehyde dehydrogenase (EC 1.2.1.39)	3929	0.0187	-0.0068
	Vanillate O-demethylase oxygenase subunit (EC 1.14.13.82)	4059	0.0182	-0.0051
	Protein gp47, recombination-related [Bacteriophage A118]	4705	0.0204	-0.0060
	Uncharacterized transporter, similarity to citrate transporter	4969	0.0150	-0.0080
	SSU ribosomal protein S10p (S20e), chloroplast	5339	0.0204	-0.0060
	SSU ribosomal protein S13p (S18e), mitochondrial	5382	0.0286	-0.0089
	Putative succinate dehydrogenase cytochrome b subunit	6059	0.0141	-0.0074
	Sigma factor RpoE negative regulatory protein RseB precursor	6373	0.0250	-0.0056
	tRNA methylase YGL050w homolog Wyeosine biosynthesis	6399	0.0204	-0.0060
	Diaminobutyrate-pyruvate aminotransferase (EC 2.6.1.46)	6476	0.0250	-0.0078
	Glutaredoxin 1	6486	0.0215	-0.0102
	RsbS, negative regulator of sigma-B	6603	0.0276	-0.0054
GC2	(GlcNAc)2 ABC transporter, permease component 2	621	0.0350	-0.0152
	Alpha-N-acetylglucosaminidase (EC 3.2.1.50)	811	0.0386	-0.0122
	Cyanate ABC transporter, ATP-binding protein	4406	0.0415	-0.0124
	Phage capsid and scaffold	4639	0.0375	-0.0123
	Autoinducer 2 (AI-2) ABC transport system, membrane channel protein LsrC	5486	0.0431	-0.0177
	High-affinity choline uptake protein BetT	6461	0.0323	-0.0128
GC3	3-isopropylmalate dehydrogenase (EC 1.1.1.85)	158	0.0042	1.1198
	2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I beta (EC 2.5.1.54)	179	0.0051	1.1988

	Arogenate dehydrogenase (EC 1.3.1.43)	190	-0.0064	0.9244
	Glycine cleavage system H protein	288	0.0069	0.9609
	Histidinol dehydrogenase (EC 1.1.1.23)	305	0.0020	0.8879
	Alcohol dehydrogenase (EC 1.1.1.1)	653	0.0010	0.9469
	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)	1041	0.0041	0.8290
	Pyruvate kinase (EC 2.7.1.40)	1049	0.0005	0.8530
	Glycerol kinase (EC 2.7.1.30)	1155	0.0014	0.8330
	Pseudouridine synthase family protein	1880	-0.0009	0.8058
	Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3.A.5.1.1)	1886	0.0008	0.9866
	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanine ligase (EC 6.3.2.10)	2125	0.0022	0.8193
	Iron-sulfur cluster regulator SufR	2560	-0.0063	0.8940
	Menaquinone-specific isochorismate synthase (EC 5.4.4.2)	2614	-0.0045	0.8975
	Recombination protein RecR	2876	0.0023	0.8047
	Cardiolipin synthetase (EC 2.7.8.-)	3217	0.0013	1.1016
	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)	3287	0.0020	0.8831
	Ferrous iron transport peroxidase EfeB	3433	-0.0037	1.2535
	Protein-L-isoaspartate O-methyltransferase (EC 2.1.1.77)	3804	0.0017	1.0299
	Cytochrome c oxidase polypeptide II (EC 1.9.3.1)	4276	0.0011	1.0269
	Deacetylases, including yeast histone deacetylase and acetoin utilization protein	4542	0.0060	0.9878
	Nucleoside diphosphate kinase (EC 2.7.4.6)	4576	0.0002	0.9320
	Xanthine dehydrogenase, molybdenum binding subunit (EC 1.17.1.4)	4597	0.0073	0.8507
	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	4917	0.0015	0.8848
	SSU ribosomal protein S7p (S5e)	5336	0.0053	0.8785
	WhiB-type transcription regulator	5688	-0.0024	1.0349
	Formate dehydrogenase putative subunit (EC 1.2.1.2)	5873	-0.0056	0.9771
	Permease of the drug/metabolite transporter (DMT) superfamily	6197	0.0044	1.1094
	Glycine betaine ABC transport system, ATP-binding protein OpuAA (EC 3.6.3.32)	6455	-0.0029	0.8410
	NADPH-dependent mycothiol reductase Mtr	6496	-0.0056	1.0215
	Outer membrane component of tripartite multidrug resistance system	6818	0.0060	1.0047
	Glutamine synthetase, clostridia type (EC 6.3.1.2)	257	0.0068	0.8157
	Archaeal DNA polymerase II small subunit (EC 2.7.7.7)	2978	0.0037	1.0251
	DNA primase large subunit (EC 2.7.7.-)	2980	0.0083	0.9626
	Possible subunit variant of phosphoribosylaminoimidazolecarboxamide formyltransferase [alternate form]	4534	0.0066	0.9626
	COG3269, Predicted RNA-binding protein, contains TRAM domain	6314	0.0081	1.0873
	tRNA nucleotidyltransferase, archaeal type (EC 2.7.7.21) (EC 2.7.7.25)	6387	0.0044	1.1832
GC4	Shikimate kinase II (EC 2.7.1.71)	197	0.0076	1.2748
	D-glycerate transporter (predicted)	875	0.0076	2.0098
	Formylmethanofuran dehydrogenase (tungsten) subunit C (EC 1.2.99.5)	1529	0.0149	1.5134
	DNA primase small subunit (EC 2.7.7.-)	2981	0.0106	1.5681
	Origin of replication recognition protein	2983	0.0074	1.9695
	Replication factor C large subunit	2985	0.0132	1.6176
	Proteasome-activating AAA-ATPase (PAN), archaeal	5091	0.0144	2.3503
	LSU ribosomal protein L8e (L2p)	5292	0.0080	1.9316
	CO dehydrogenase/acetyl-CoA synthase subunit epsilon, CO dehydrogenase subcomplex (EC 1.2.99.2)	5807	0.0105	1.5500
	CO dehydrogenase/acetyl-CoA synthase subunit gamma, corrinoid iron-sulfur subcomplex large subunit	5808	0.0081	1.3784
	Coenzyme F420 hydrogenase alpha subunit (FrcA) (EC 1.12.98.1)	5825	0.0109	1.5820

	Putative coenzyme F420-dependent oxidoreductase MJ1349	5833	0.0056	1.7134
	Energy-conserving hydrogenase (ferredoxin), subunit A	5848	0.0078	1.7037
	Energy-conserving hydrogenase (ferredoxin), subunit B	5849	0.0168	1.9770
	Archaeal transcription factor E	6230	0.0130	1.4273
GC5	Threonine dehydratase biosynthetic (EC 4.3.1.19)	166	0.0117	0.8579
	2-amino-3-ketobutyrate coenzyme A ligase (EC 2.3.1.29)	282	0.0095	0.9356
	Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (EC 5.3.1.16)	314	0.0184	1.4991
	Homoserine dehydrogenase (EC 1.1.1.3)	364	0.0100	1.1726
	3-hydroxybutyryl-CoA dehydratase (EC 4.2.1.55)	403	0.0145	1.1762
	Cystathionine gamma-synthase (EC 2.5.1.48)	435	0.0153	1.3358
	Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1)	495	0.0149	1.3261
	Fumarate hydratase class I, aerobic (EC 4.2.1.2)	683	0.0158	1.4098
	N-acetylglucosamine kinase of eukaryotic type (EC 2.7.1.59)	826	0.0152	0.8877
	2-ketoaldonate reductase, broad specificity (EC 1.1.1.215) (EC 1.1.1.-)	942	0.0116	0.8611
	Glucose 1-dehydrogenase (EC 1.1.1.47)	953	0.0088	0.9791
	Aldose 1-epimerase (EC 5.1.3.3)	1025	0.0178	1.2783
	4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)	1186	0.0175	1.3195
	Glycolate oxidase (EC 1.1.3.15)	1202	0.0122	0.9126
	Trehalose-6-phosphate phosphatase (EC 3.1.3.12)	1752	0.0137	1.0797
	Phosphopantothenoylcysteine decarboxylase (EC 4.1.1.36)	2467	0.0127	1.1586
	3-polyprenyl-4-hydroxybenzoate carboxy-lyase UbiX (EC 4.1.1.-)	2756	0.0128	1.0558
	Riboflavin synthase eubacterial/eukaryotic (EC 2.5.1.9)	2767	0.0081	0.9227
	Putative hydrolase in cluster with formaldehyde/S-nitrosomycothiol reductase MscR	2814	0.0039	0.8847
	Crossover junction endodeoxyribonuclease RuvC (EC 3.1.22.4)	3013	0.0102	1.0338
	Ferric reductase (1.6.99.14)	3394	0.0078	1.1035
	3-oxoadipate CoA-transferase subunit B (EC 2.8.3.6)	3977	0.0157	1.0626
	Lauroyl/myristoyl acyltransferase involved in lipid A biosynthesis (Lauroyl/myristoyl acyltransferase)	4238	0.0018	0.9441
	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	4305	0.0085	0.9310
	Nitrate/nitrite response regulator protein	4450	0.0112	0.8153
	Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6)	4528	0.0114	1.1648
	Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family	4593	0.0137	1.0765
	SSU ribosomal protein S6p	5335	0.0142	1.2624
	Ribonuclease Z (EC 3.1.26.11)	6391	0.0132	1.0048
	COG0613, Predicted metal-dependent phosphoesterases (PHP family)	6402	0.0110	0.9133
	Plasmin(ogen) receptor	6996	0.0082	1.1222
	Replication factor C small subunit	2986	0.0110	1.1432
GC6	Arginine deiminase (EC 3.5.3.6)	40	-0.0082	0.9847
	Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12)	56	-0.0083	0.8206
	N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18)	84	-0.0108	0.8982
	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)	98	-0.0074	0.8719
	Quinate/shikimate dehydrogenase [Pyrroloquinoline-quinone] (EC 1.1.99.25)	195	-0.0136	1.0901
	Cysteine synthase A (EC 2.5.1.47)	230	-0.0113	0.8750
	Glutamine synthetase type I (EC 6.3.1.2)	254	-0.0050	0.8482
	Glutamine synthetase family protein in hypothetical Actinobacterial gene cluster	272	-0.0126	1.3269
	Pyruvate,phosphate dikinase (EC 2.7.9.1)	281	-0.0052	0.8851
	Imidazole glycerol phosphate synthase amidotransferase subunit (EC 2.4.2.-)	309	-0.0059	1.0504
	Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)	311	-0.0059	0.8243

	Butyryl-CoA dehydrogenase (EC 1.3.99.2)	341	-0.0082	0.8143
	Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase (EC 1.8.1.4)	680	-0.0099	0.8947
	Gluconolactonase (EC 3.1.1.17)	1040	-0.0078	1.0147
	NAD(P) transhydrogenase subunit beta (EC 1.6.1.2)	1088	-0.0096	0.8447
	Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	1162	-0.0096	0.8370
	Aldehyde dehydrogenase B (EC 1.2.1.22)	1580	-0.0122	0.9542
	Protein acetyltransferase	1676	-0.0126	1.0163
	Rod shape-determining protein MreB	1833	-0.0100	0.8848
	Endonuclease III (EC 4.2.99.18)	1843	-0.0068	1.0067
	Signal recognition particle, subunit Ffh SRP54 (TC 3.A.5.1.1)	1887	-0.0061	0.8478
	5-FCL-like protein	2299	-0.0046	0.8503
	oxidoreductase of aldo/keto reductase family, subgroup 1	2540	-0.0104	0.8706
	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase (EC 2.2.1.9)	2612	-0.0136	1.1637
	Menaquinone via futalosine step 3	2624	-0.0114	0.9179
	Fumarylacetoacetate hydrolase family protein	2731	-0.0087	0.8672
	Homogentisate 1,2-dioxygenase (EC 1.13.11.5)	2732	-0.0106	0.8960
	Dihydroorotase (EC 3.5.2.3)	2796	-0.0073	0.8511
	Transcriptional regulator, FUR family	2820	-0.0090	0.9651
	ATP-dependent DNA ligase (EC 6.5.1.1) clustered with Ku protein, LigD	2884	-0.0066	0.8929
	DNA polymerase II (EC 2.7.7.7)	2887	-0.0091	0.8375
	Excinuclease ABC subunit A paralog of unknown function	2971	-0.0130	1.1397
	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	3196	-0.0090	0.8218
	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase (EC 1.17.7.1)	3285	-0.0077	0.8527
	2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (EC 3.7.1.-)	3966	-0.0101	0.8339
	Transcriptional regulator, IclR family	4013	-0.0122	0.9377
	FIG049476: HIT family protein	4236	-0.0091	0.9216
	Nitrite reductase [NAD(P)H] large subunit (EC 1.7.1.4)	4455	-0.0137	1.1419
	putative cytochrome P450 hydroxylase	4473	-0.0094	0.9657
	Beta-lactamase (EC 3.5.2.6)	4737	-0.0112	0.9271
	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)	4920	-0.0068	0.8112
	Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7)	4992	-0.0089	0.8223
	Alpha-aspartyl dipeptidase Peptidase E (EC 3.4.13.21)	5018	-0.0130	1.0777
	Bacterial proteasome-activating AAA-ATPase (PAN)	5085	-0.0107	0.9684
	Proteasome subunit beta (EC 3.4.25.1), bacterial	5090	-0.0085	1.0714
	Peptide deformylase (EC 3.5.1.88)	5448	-0.0107	0.8950
	Cytochrome c heme lyase subunit CcmF	5755	-0.0079	0.8183
	NAD-dependent formate dehydrogenase gamma subunit	5899	-0.0098	0.9837
	Cytochrome c551/c552	6110	-0.0129	1.3332
	Predicted transcriptional regulator of sulfate adenylyltransferase, Rrf2 family	6310	-0.0087	0.8164
	rRNA small subunit methyltransferase I	6331	-0.0071	0.8562
	Redox-sensitive transcriptional activator SoxR	6573	-0.0103	1.2450
	NPQTN specific sortase B	2212	-0.0054	0.8374
	LSU ribosomal protein L27Ae (L15p)	5275	-0.0043	0.9147
	Transcription initiation factor B	6232	-0.0040	1.0545
GC7	Leucine dehydrogenase (EC 1.4.1.9)	145	-0.0070	0.8191

	Seryl-tRNA synthetase (EC 6.1.1.11)	298	-0.0021	0.9538
	Acetyl-coenzyme A synthetase (EC 6.2.1.1)	346	-0.0033	0.8582
	Gamma-glutamyltranspeptidase (EC 2.3.2.2)	481	-0.0007	0.8533
	Threonine dehydrogenase and related Zn-dependent dehydrogenases	566	-0.0030	0.8095
	Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1)	692	-0.0023	0.8172
	Phosphoglycerate kinase (EC 2.7.2.3)	793	-0.0029	0.9111
	Beta-hexosaminidase (EC 3.2.1.52)	812	-0.0007	0.8382
	Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32)	850	-0.0008	0.9331
	Malate synthase (EC 2.3.3.9)	1079	-0.0035	0.8045
	Isoquinoline 1-oxidoreductase beta subunit (EC 1.3.99.16)	2497	-0.0025	0.8360
	FolM Alternative dihydrofolate reductase 1	2584	-0.0029	0.8183
	Aspartate carbamoyltransferase (EC 2.1.3.2)	2795	-0.0014	0.9487
	DinG family ATP-dependent helicase YoaA	2930	-0.0035	0.9313
	Holliday junction DNA helicase RuvA	3028	-0.0030	0.8134
	mandelate racemase/muconate lactonizing enzyme family protein	3981	-0.0002	0.9821
	Adenylosuccinate lyase (EC 4.3.2.2)	4523	-0.0016	0.9344
	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)	5034	-0.0015	0.9350
	ATP-dependent protease La (EC 3.4.21.53) Type I	5099	-0.0023	0.9588
	tRNA:Cm32/Um32 methyltransferase	6319	-0.0004	0.9128
	RNA polymerase sigma-70 factor	6370	-0.0078	0.8742
GC8	Arginine pathway regulatory protein ArgR, repressor of arg regulon	44	-0.0142	0.0025
	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	406	-0.0131	0.0040
	Methionyl-tRNA formyltransferase (EC 2.1.2.9)	2587	-0.0160	0.0064
	O-succinylbenzoate synthase (EC 4.2.1.113)	2616	-0.0143	0.0030
	Phosphoribosylaminoimidazole carboxylase catalytic subunit (EC 4.1.1.21)	4527	-0.0135	0.0045
	Pyridine nucleotide-disulphide oxidoreductase associated with reductive pyrimidine catabolism	4616	-0.0181	0.0035
	Glutamyl-tRNA(Gln) amidotransferase subunit B (EC 6.3.5.7)	4993	-0.0142	0.0043
	LSU ribosomal protein L5p (L11e)	5240	-0.0110	0.0055
	UbiD family decarboxylase, MJ1133 type	412	-0.0052	0.0108
	Lacto-N-biose phosphorylase (EC 2.4.1.211)	1381	-0.0058	0.0113
	Putative DNA-binding protein in cluster with Type I restriction-modification system	3047	-0.0109	0.0125
	Dipicolinate synthase subunit B	3076	-0.0111	0.0100
	Spore germination protein GerKB	3109	-0.0120	0.0084
	Stage IV sporulation protein A	3177	-0.0050	0.0126
	LSU ribosomal protein L18e	5267	-0.0124	0.0094
	LSU ribosomal protein L23Ae (L23p)	5271	-0.0087	0.0111
	LSU ribosomal protein L30e	5276	-0.0114	0.0116
	SSU ribosomal protein S27e	5362	-0.0152	0.0071
	DNA-directed RNA polymerase II second largest subunit (EC 2.7.7.6)	6261	-0.0154	0.0072
GC9	Rhodanese-like domain required for thiamine synthesis	2440	-0.0001	1.9343
	Stage V sporulation protein T, AbrB family transcriptional regulator (SpoVT)	3143	0.0021	1.5411
	Stage II sporulation protein required for processing of pro-sigma-E (SpoIIR)	3174	-0.0017	1.3223
	Disulfide bond chaperones of the HSP33 family	4118	-0.0014	1.3688
	LSU ribosomal protein L17e (L22p)	5265	-0.0021	1.2768
	LSU ribosomal protein L9e (L6p)	5293	0.0001	1.0543
	SSU ribosomal protein S28e	5363	-0.0007	1.4913
	coenzyme F420-reducing hydrogenase, beta subunit homolog	5832	-0.0014	1.3059
	[Fe] hydrogenase, HymA subunit, putative	5962	0.0017	1.2039

	Glutathione biosynthesis bifunctional protein gshF (EC 6.3.2.2)(EC 6.3.2.3)	6501	-0.0040	1.3590
GC10	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	374	-0.0228	0.0148
	S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50), prokaryotic class 1A	502	-0.0173	0.0093
	Predicted cellobiose ABC transport system, ATP-binding protein 1	764	-0.0324	0.0102
	Multiple sugar ABC transporter, substrate-binding protein	1123	-0.0242	0.0123
	Predicted regulator of fructose utilization, DeoR family	1138	-0.0221	0.0110
	Predicted L-rhamnose permease RhaY	1341	-0.0219	0.0102
	Formylmethanofuran dehydrogenase (tungsten) operon gene G	1526	-0.0198	0.0101
	Potassium uptake protein, integral membrane component, KtrB	4938	-0.0153	0.0116
	Similar to ribosomal large subunit pseudouridine synthase D, CAC1266-type	5215	-0.0257	0.0088
	SSU ribosomal protein S4p (S9e), mitochondrial	5397	-0.0211	0.0092
	Signal peptidase, type IV - prepilin/preflagellin	5413	-0.0167	0.0116
	Coenzyme F(420)H(2) dehydrogenase (methanophenazine) subunit FpoM	5845	-0.0216	0.0130
	Sulfhydrogenase II subunit g	5959	-0.0267	0.0139
	Conjugative transfer protein TrbG	6889	-0.0288	0.0142
GC11	IcmB (DotO) protein	3646	-0.0383	0.0169
	Possible alpha/beta hydrolase superfamily, slr1917 homolog	4225	-0.0341	0.0126
	photosystem I subunit XI (PsaL)	4833	-0.0370	0.0154
	Phycobilisome rod-core linker polypeptide, phycocyanin-associated	4871	-0.0382	0.0122
	Conjugative signal peptidase TrhF	6881	-0.0396	0.0122
	Inclusion membrane protein-52	6958	-0.0343	0.0148

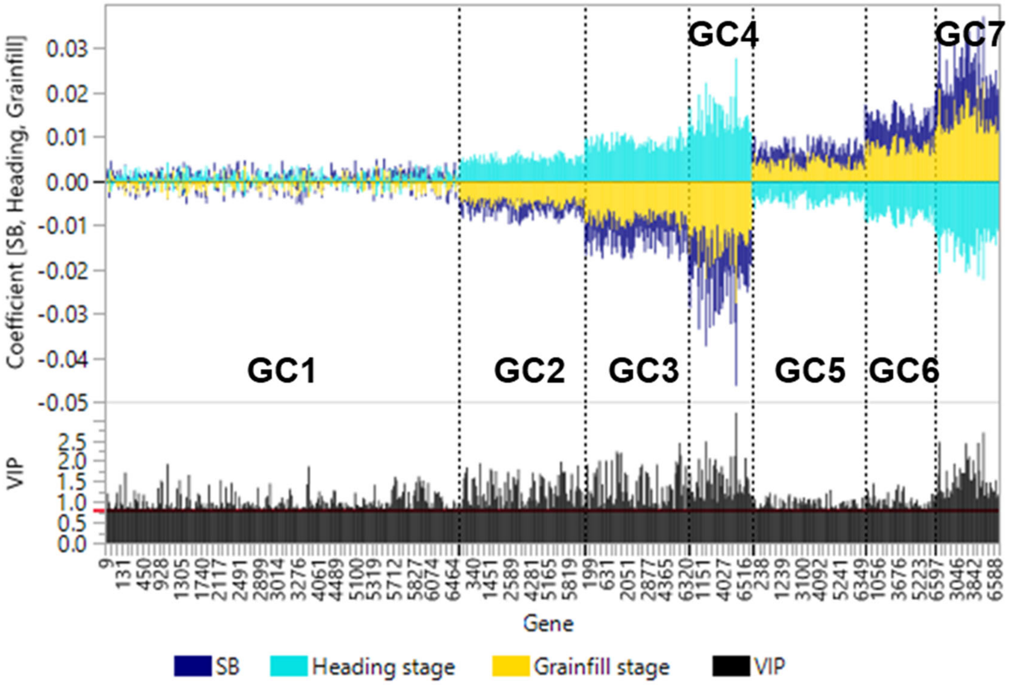

Figure S7. Partial least squares results for genes related to shoot biomass. Coefficients for genes significantly related to shoot biomass alone identified by PLS analysis and their relationship to heading and maturity stage, presented in a stacked bar plot. Variance in importance projection (VIP) scores are shown to indicate importance in the model (VIP > 0.8 are considered a significant contributor to the model).

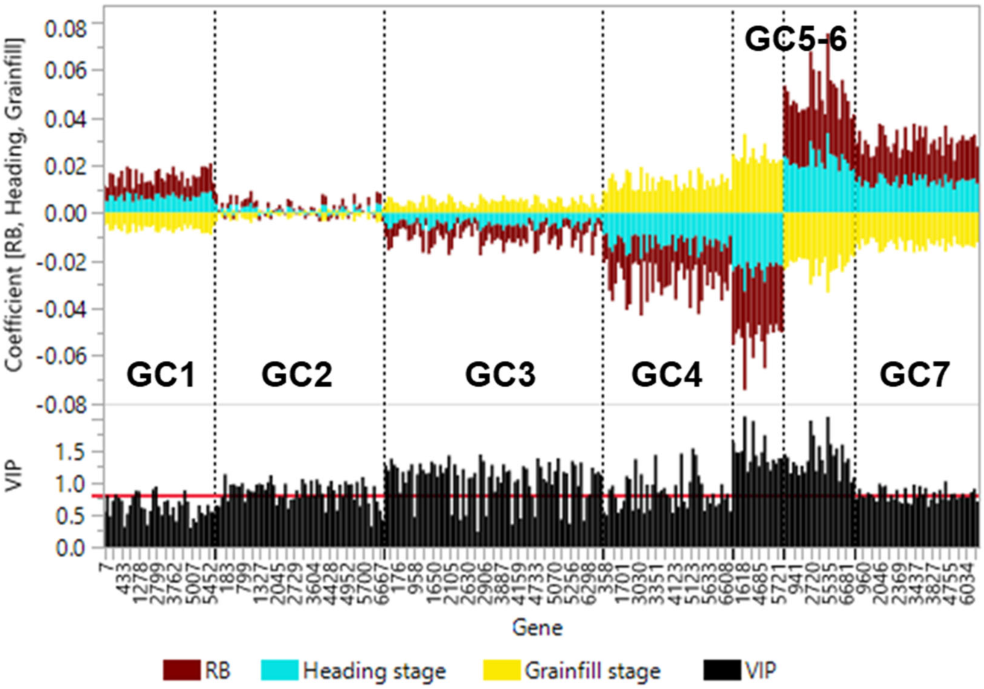

Figure S8. Partial least squares results for genes related to root biomass. Coefficients for genes significantly related to root biomass alone identified by PLS analysis and their relationship to heading and maturity stage, presented in a stacked bar plot. Variance in importance projection (VIP) scores are shown to indicate importance in the model (VIP > 0.8 are considered a significant contributor to the model).