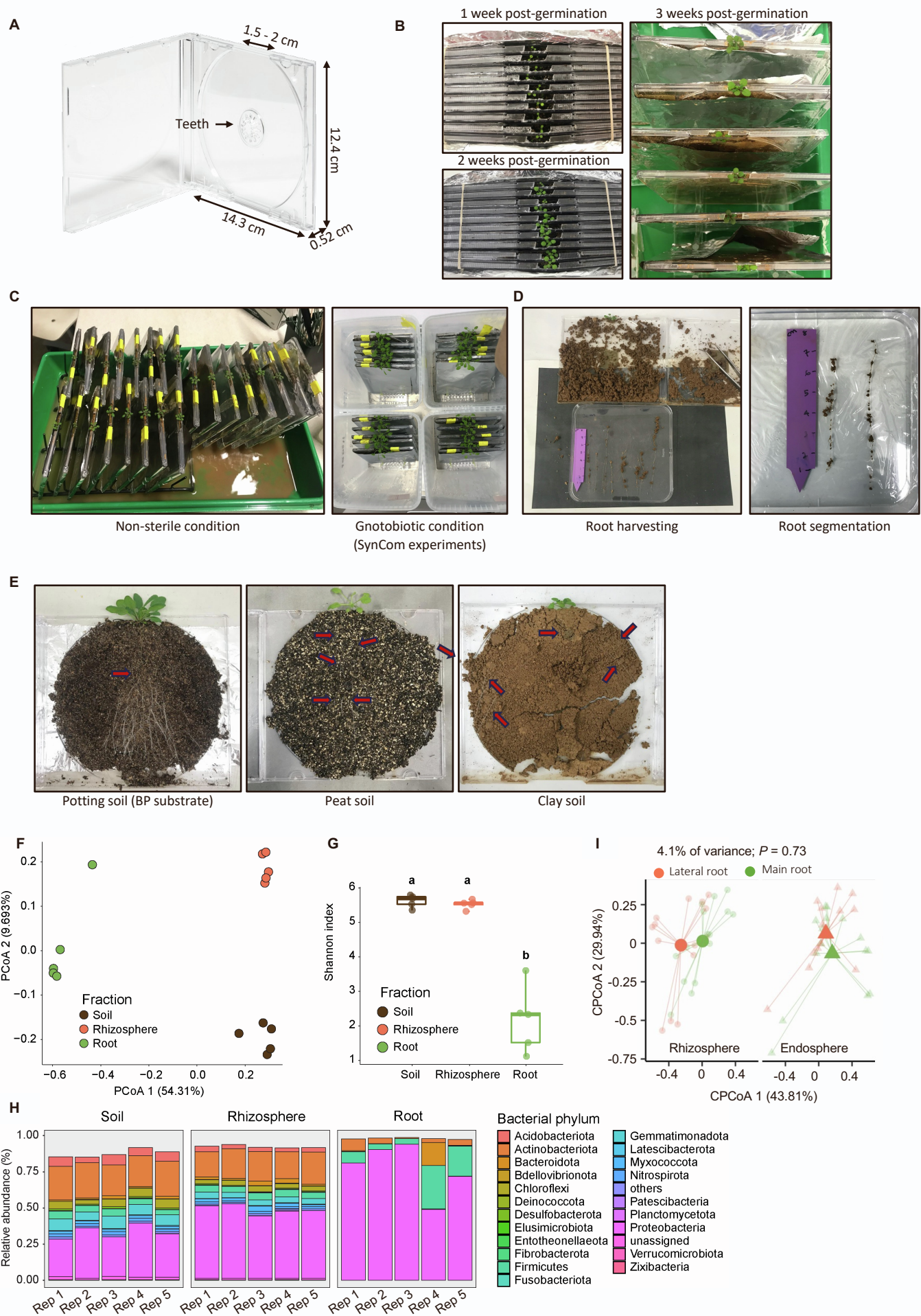


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## Supplemental information

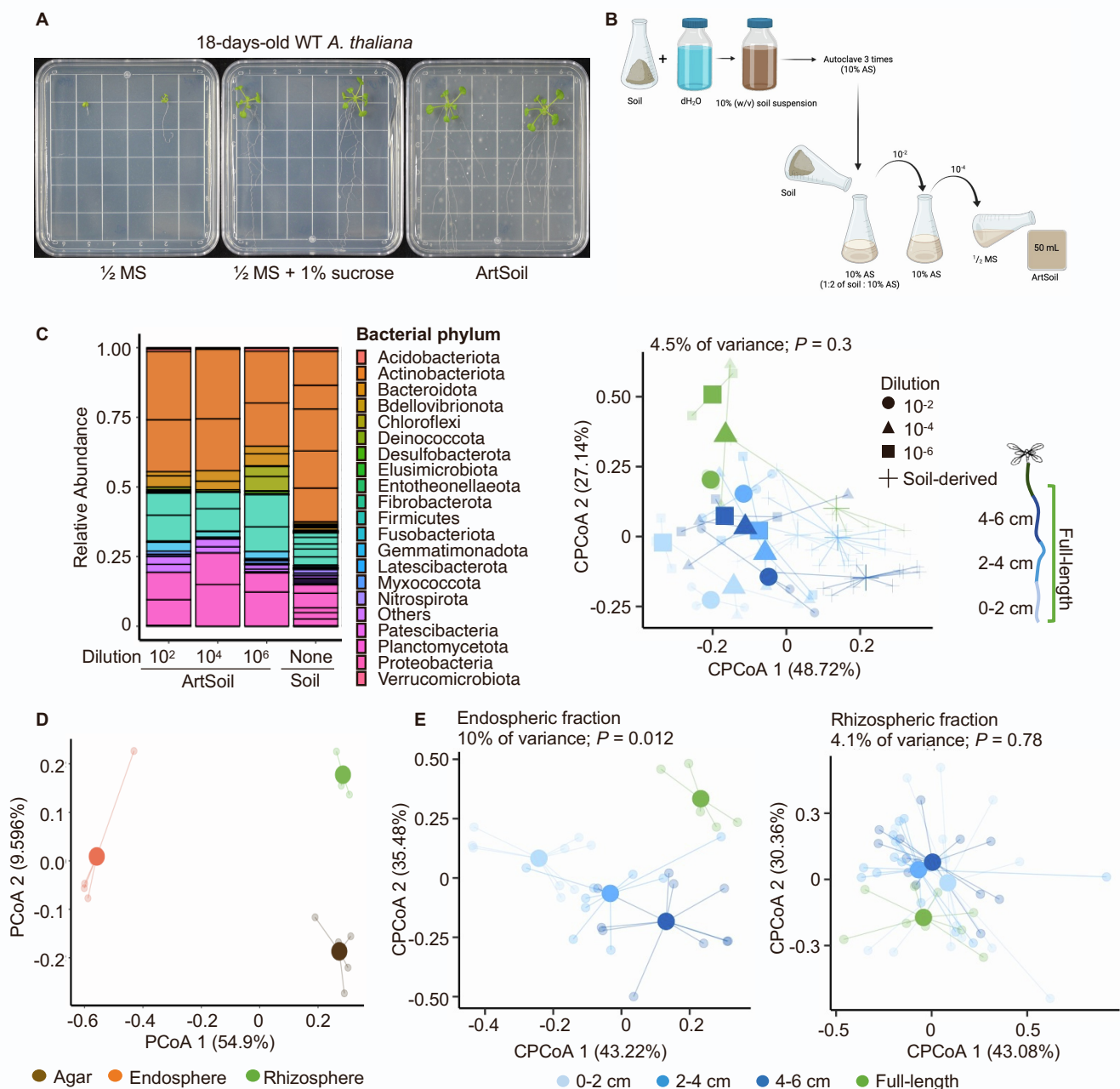
**Sugar transporters spatially organize microbiota  
colonization along the longitudinal  
root axis of *Arabidopsis***

**Eliza P.-I. Loo, Paloma Durán, Tin Yau Pang, Philipp Westhoff, Chen Deng, Carlos Durán, Martin Lercher, Ruben Garrido-Oter, and Wolf B. Frommer**



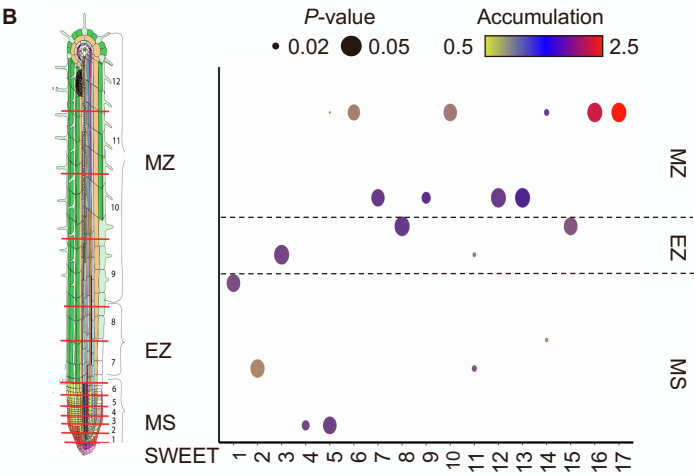
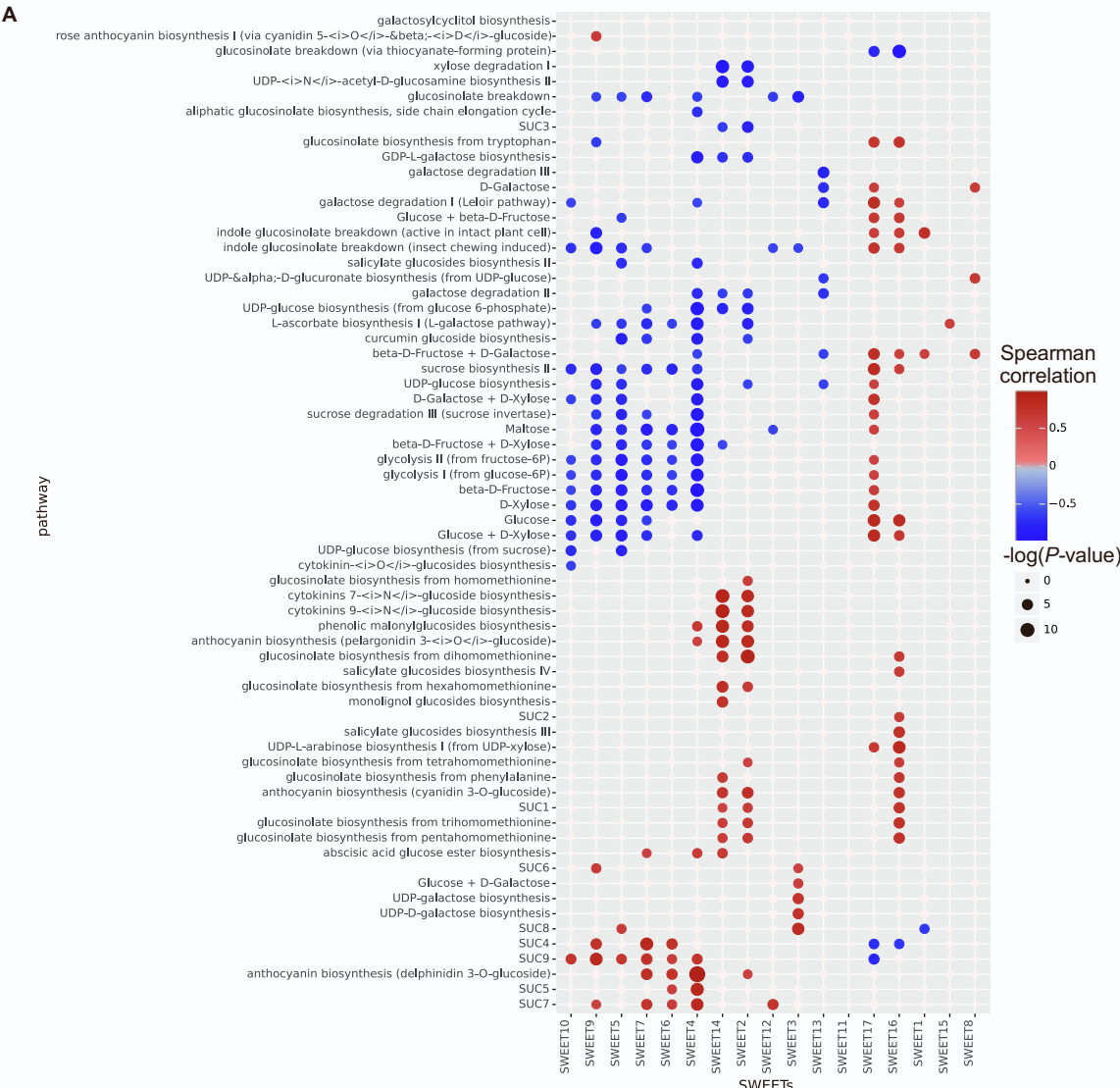
**Figure S1: Development of CD-Rhizotron to study spatial colonization of root bacteria (related to Figure 1 and STAR Methods)**

- A) Construction of CD-Rhizotron, with dimensions indicated.
- B) Phenotype of *A. thaliana* plants grown *via* CD-Rhizotron at different growth stages. Sterilized *A. thaliana* seeds were sown directly on the soil through the top opening. CD-Rhizotron was wrapped with aluminium foil to ensure root growth in darkness.
- C) Growth set-up for *A. thaliana* seedlings *via* CD-Rhizotron for non-sterile and gnotobiotic SynCom (CD-Rhizotron grown in sterile microboxes) experiments.
- D) Process of harvesting roots from CD-Rhizotron and the resulting roots harvested for subsequent sectioning and microbiota profiling.
- E) Growth of *A. thaliana* on different soil types in CD-Rhizotron. Examples of individual strands of root (except for potting soil) indicated with arrows.
- F) Bray-Curtis dissimilarity analysis of root bacterial community from *A. thaliana* grown *via* CD-Rhizotron. The fraction ‘soil’ refers to bacterial communities derived from bulk soil without the presence of plants, ‘rhizosphere’ refers to bacterial communities derived from soil tightly attached to roots, ‘endosphere’ refers to bacterial communities derived from root tissues.
- G) Shannon diversity of root bacterial community from *A. thaliana* grown *via* CD-Rhizotron.
- H) Relative abundance of root bacterial community from *A. thaliana* grown *via* CD-Rhizotron. ASVs with relative abundance <0.5% were filtered. Each bar represents the average relative abundance of biological replicates from 5 independent experiments.
- I) Bray-Curtis dissimilarity analysis of endospheric and rhizospheric bacterial community derived from lateral and main roots of *A. thaliana* grown on CD-Rhizotron.



**Figure S2: ArtSoil- a simple-to-assemble plant growth system for soil-like growth conditions (related to Figure 1 and STAR Methods)**

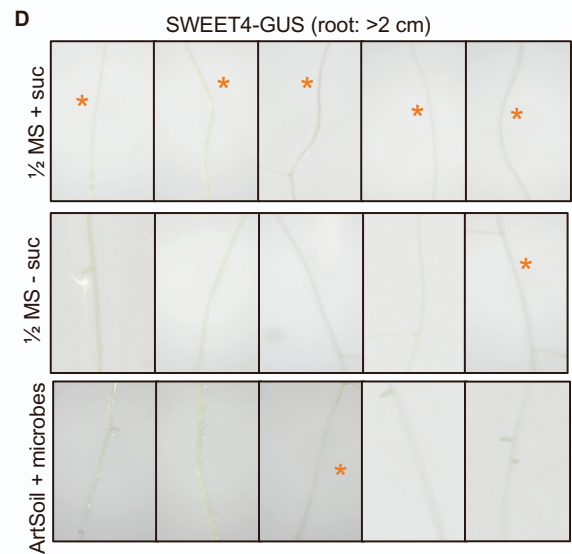
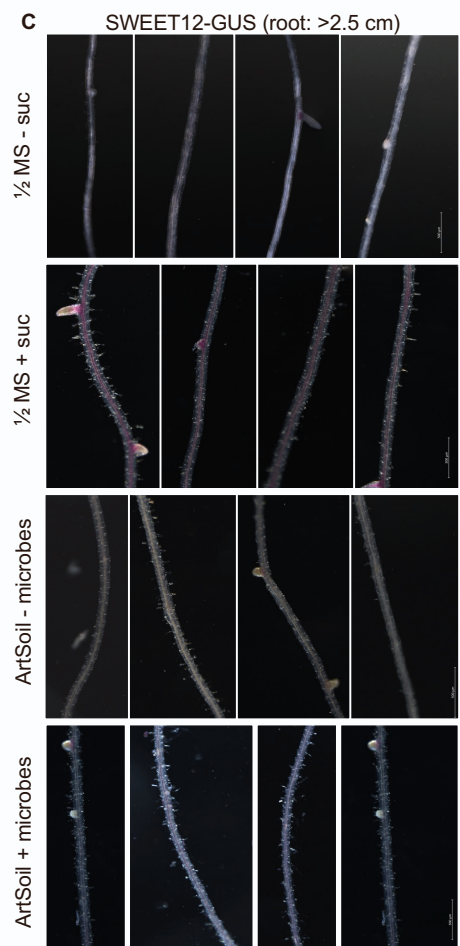
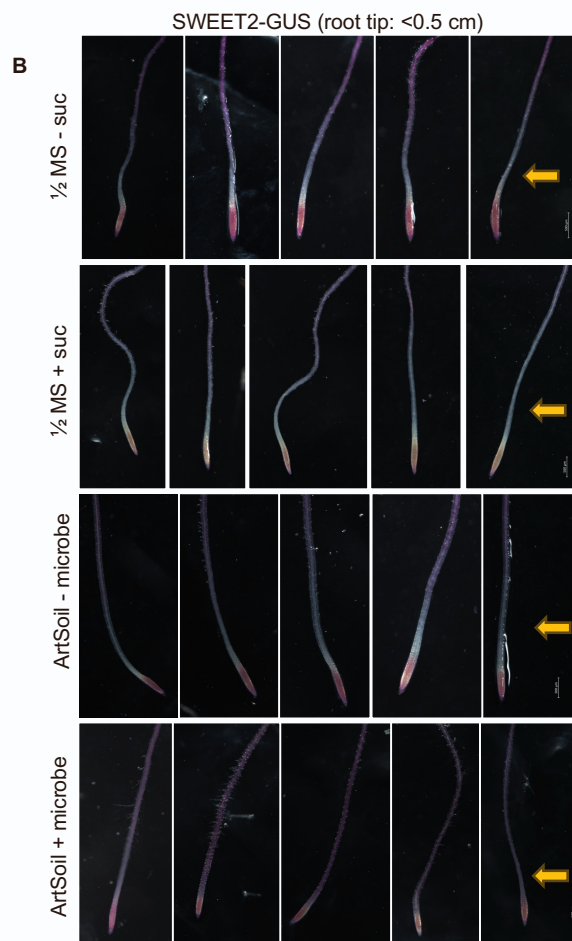
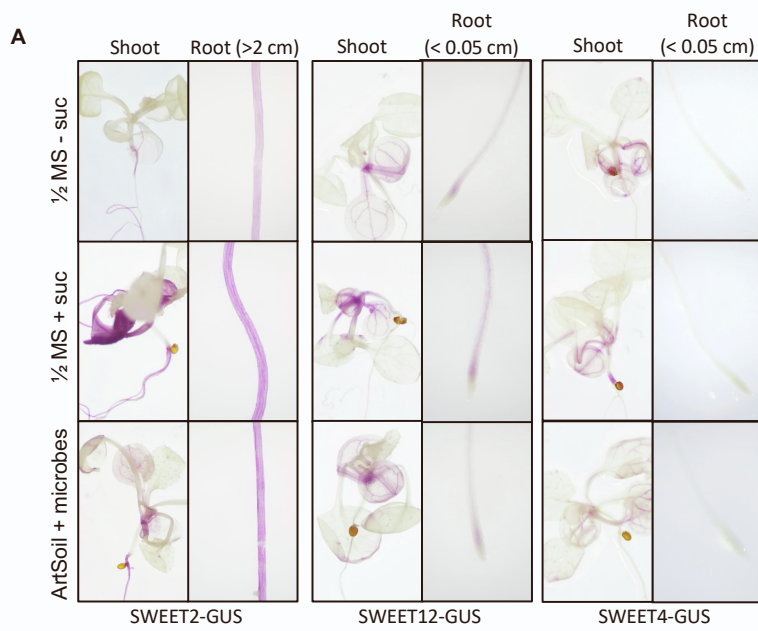
- A) Phenotype of *A. thaliana* seedlings grown on  $\frac{1}{2}$  MS-salt,  $\frac{1}{2}$  MS-salt supplemented with 1% sucrose, and ArtSoil.
- B) Step-by-step illustration for the preparation of ArtSoil. AS- Autoclave soil suspension. Image created with Biorender.
- C) Relative abundance and Bray-Curtis dissimilarity analysis of endospheric bacterial community derived from roots of soil-grown *A. thaliana* or plants grown on ArtSoil with 10<sup>-2</sup>, 10<sup>-4</sup>, and 10<sup>-6</sup> dilutions of soil.
- D) Bray-Curtis dissimilarity analysis of root bacterial community from *A. thaliana* grown on ArtSoil. The fraction ‘agar’ refers to bacterial communities derived from bulk agar containing soil suspension without the presence of plants, ‘rhizosphere’ refers to bacterial communities derived from soil tightly attached to roots, ‘endosphere’ refers to bacterial communities derived from root tissues.
- E) Bray-Curtis dissimilarity analysis of root bacterial community from *A. thaliana* grown in soil inoculated with SynCom. The fraction ‘0-2 cm’, ‘2-4 cm’, and ‘4-6 cm’ refers to bacterial communities derived from indicated locations of the root, ‘full-length’ refers to bacterial communities derived from the entire length of the root.



**Figure S3: Bioinformatics prediction of *SWEETs*' involvement in root sugar metabolic pathways (related to Figure 2)**

- A) Correlation between each member of *SWEET* and sugar-related metabolic pathway in the root. Color indicates positive or negative correlation between each *SWEET* with a particular metabolic pathway; size of circle indicates statistical significance of the correlation.
- B) Average accumulation of respective *SWEET* mRNA transcripts along the root axis. MS- meristematic zone (<0.25 mm), EZ- elongation zone (0.25-0.5 mm), MZ- maturation zone (>0.5 mm). Color indicates the relative amount of mRNA accumulation; the size of circle indicates statistical significance of the mRNA accumulation in indicated root zones.

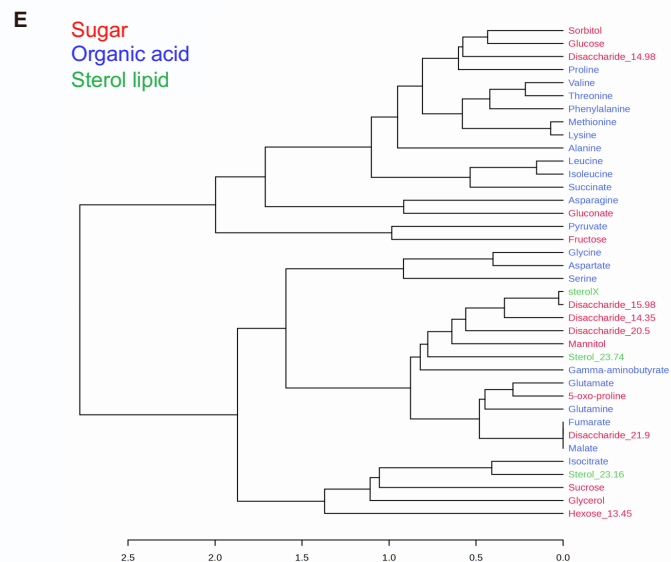
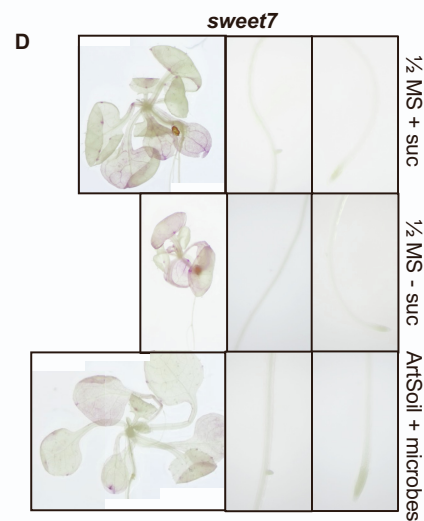
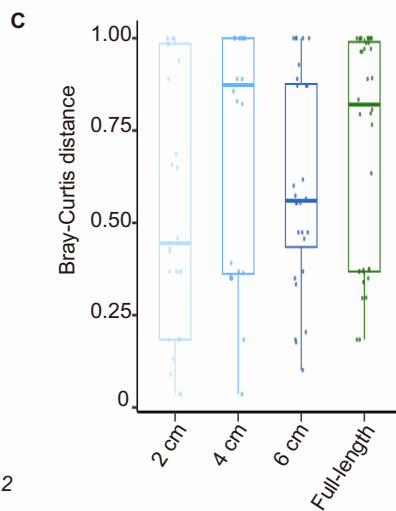
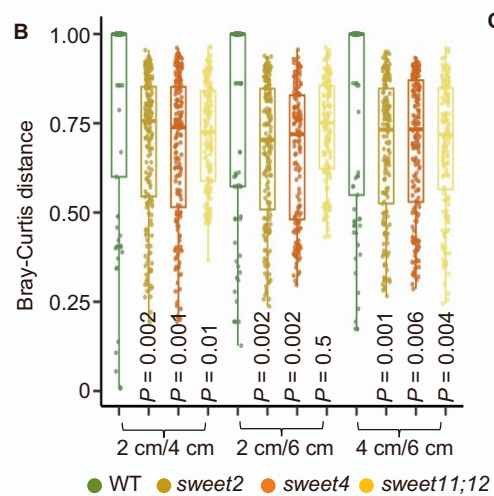
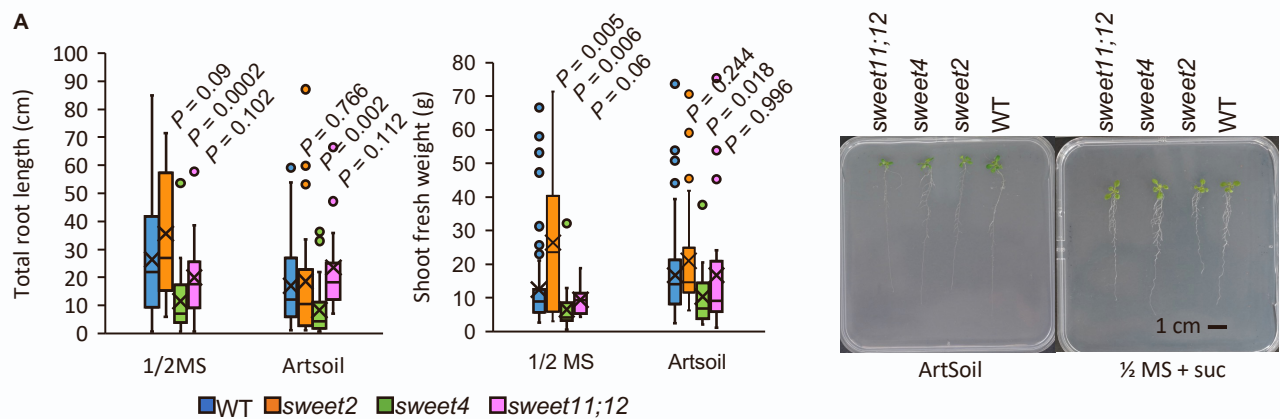




**Figure S4: Accumulation of SWEET2-GUS, SWEET12-GUS, and SWEET4-GUS in plants grown on  $\frac{1}{2}$  MS  $\pm$  suc or ArtSoil with heat-killed or live microbes (related to Figure 3)**

- A) Unaltered spatial accumulation of SWEET2-GUS, SWEET12-GUS and SWEET4-GUS in the shoot and indicated regions of the root in plants grown on indicated media. Representative image from  $N > 10$ . Individual images are shown in Figure S4B-D.
- B) Accumulation of SWEET2-GUS in the region just above the root tip ( $<0.05$  cm) is observed only in plants grown ArtSoil with live microbes. Yellow arrows indicate the (accumulation) zone of interest. Scale bar: 500  $\mu$ m.
- C) Accumulation of SWEET12-GUS in the regions above 2 cm from the root tip is observed in the vasculature of plants grown on  $\frac{1}{2}$  MS + suc and ArtSoil with live microbes. Scale bar: 500  $\mu$ m.
- D) Patchy accumulation of SWEET4-GUS in the regions above 2 cm from the root tip is observed only in plants grown on  $\frac{1}{2}$  MS + suc. Scale bar: 500  $\mu$ m.  $\frac{1}{2}$  MS - suc:  $\frac{1}{2}$  MS media without sucrose supplementation,  $\frac{1}{2}$  MS + suc:  $\frac{1}{2}$  MS media with sucrose supplementation, ArtSoil - microbes: ArtSoil inoculated with heat-killed soil microbes, ArtSoil + microbes: ArtSoil inoculated with soil microbes. All experiments above were repeated at least 3 times, each time  $N > 6$ .





**Figure S5: Phenotypes, spatial metabolite and microbiota profiles of *sweet* knock-out lines (related to Figures 4 and 5)**

- A) Total root length and shoot fresh weight of WT, *sweet2*, *sweet4*, and *sweet11;12* knock-out lines grown on  $\frac{1}{2}$  MS or ArtSoil + microbes. *P*-values were calculated using Welch's ANOVA. The experiment was repeated twice,  $N > 20$ .
- B) Pairwise comparison between Bray-Curtis distances of root microbiota derived from root segments of each genotype. X-axis indicates the root segments compared. Colors indicate plant genotype. *P*-values (Student's t-test) for *sweets* calculated against WT plants. See also Tables S1-S3.
- C) Bray-Curtis dissimilarities distances of root microbiota derived from each root segment compared to the full-length root of *sweet7* knock-out plants. Different colors represent respective root segments or full-length root samples as depicted in the cartoon on the left.
- D) Histochemical staining of SWEET7-GUS seedlings grown on  $\frac{1}{2}$  MS-salt  $\pm$  suc or ArtSoil + microbes.  $N > 10$ .
- E) Dendrogram depicting ranking of metabolite correlation with microbes (at class level) based on Spearman average linkage hierarchical clustering. Colors indicate classes of metabolites.

**Table S1: Statistical analyses for beta-diversity analyses. *P*-values calculated using PERMANOVA (related to Figure 1 and Figure 5B)**

Root segment pair	Corresponding figure	<i>P</i> -value
WT: 2 cm vs 4 cm	Figure 1A (Endosphere)	0.005
WT: 2 cm vs 6 cm	Figure 1A (Endosphere)	0.002
WT: 4 cm vs 6 cm	Figure 1A (Endosphere)	0.007
WT: 2 cm vs 4 cm	Figure 1A (Rhizosphere)	0.015
WT: 2 cm vs 6 cm	Figure 1A (Rhizosphere)	0.037
WT: 4 cm vs 6 cm	Figure 1A (Rhizosphere)	0.007
WT: 2 cm vs 4 cm	Figure 1B (Endosphere)	0.01
WT: 2 cm vs 6 cm	Figure 1B (Endosphere)	0.05
WT: 4 cm vs 6 cm	Figure 1B (Endosphere)	0.2
WT: 2 cm vs 4 cm	Figure 1B (Rhizosphere)	0.24
WT: 2 cm vs 6 cm	Figure 1B (Rhizosphere)	0.69
WT: 4 cm vs 6 cm	Figure 1B (Rhizosphere)	0.72
sweet2: 2 cm vs 4 cm	Figure 5B	0.67
sweet2: 2 cm vs 6 cm	Figure 5B	0.2
sweet2: 4 cm vs 6 cm	Figure 5B	0.65
sweet4: 2 cm vs 4 cm	Figure 5B	0.2
sweet4: 2 cm vs 6 cm	Figure 5B	0.04
sweet4: 4 cm vs 6 cm	Figure 5B	0.6
sweet11;12: 2 cm vs 4 cm	Figure 5B	0.003
sweet11;12: 2 cm vs 6 cm	Figure 5B	0.05
sweet11;12: 4 cm vs 6 cm	Figure 5B	0.04
2 cm: WT vs sweet2	Figure 5B	0.6
2 cm: WT vs sweet4	Figure 5B	0.7
2 cm: WT vs sweet11/12	Figure 5B	0.05
2 cm: sweet2 vs sweet4	Figure 5B	0.5
2 cm: sweet2 vs sweet11/12	Figure 5B	0.02
2 cm: sweet4 vs sweet11/12	Figure 5B	0.02
4 cm: WT vs sweet2	Figure 5B	0.3
4 cm: WT vs sweet4	Figure 5B	0.01
4 cm: WT vs sweet11/12	Figure 5B	0.3
4 cm: sweet2 vs sweet4	Figure 5B	0.11
4 cm: sweet2 vs sweet11/12	Figure 5B	0.46
4 cm: sweet4 vs sweet11/12	Figure 5B	0.1
6 cm: WT vs sweet2	Figure 5B	0.8
6 cm: WT vs sweet4	Figure 5B	0.8
6 cm: WT vs sweet11/12	Figure 5B	0.9
6 cm: sweet2 vs sweet4	Figure 5B	0.18
6 cm: sweet2 vs sweet11/12	Figure 5B	0.12
6 cm: sweet4 vs sweet11/12	Figure 5B	0.41

**Table S2: Bray-Curtis distance of each root segment for each genotype (Related to Figure 5B)**

<b>Root segment 1</b>	<b>Root segment 2</b>	<b>Mean Bray-Curtis distance</b>	<b>Standard error</b>
2 cm WT	4 cm WT	0.814	0.033
2 cm WT	6 cm WT	0.761	0.032
4 cm WT	6 cm WT	0.798	0.031
2 cm <i>sweet11/12</i>	2 cm <i>sweet11/12</i>	0.742	0.012
2 cm <i>sweet11/12</i>	4 cm <i>sweet11/12</i>	0.713	0.011
2 cm <i>sweet11/12</i>	6 cm <i>sweet11/12</i>	0.729	0.011
4 cm <i>sweet11/12</i>	6 cm <i>sweet11/12</i>	0.688	0.014
2 cm <i>sweet2</i>	6 cm <i>sweet2</i>	0.69	0.015
2 cm <i>sweet2</i>	4 cm <i>sweet2</i>	0.671	0.015
4 cm <i>sweet2</i>	6 cm <i>sweet2</i>	0.676	0.015
2 cm <i>sweet4</i>	4 cm <i>sweet4</i>	0.676	0.016
2 cm <i>sweet4</i>	6 cm <i>sweet4</i>	0.665	0.015
4 cm <i>sweet4</i>	4 cm <i>sweet4</i>	0.692	0.014

**Table S3: Statistical analyses on pairwise comparison of Bray-Curtis distances between root segments of each genotype (Related to Figure 5B)**

Root segment pair 1	Root segment pair 2	N pair 1	N pair 2	Test statistic	Degree of freedom	p	p.adj	p.adj.signif
2 cm WT vs. 4 cm WT	2 cm <i>sweet11/12</i> vs. 4 cm <i>sweet11/12</i>	81	169	2.864735846	98.2315757	0.005	0.010	**
2 cm WT vs. 4 cm WT	2 cm <i>sweet11/12</i> vs. 6 cm <i>sweet11/12</i>	81	169	2.441034521	97.18186883	0.016	0.029	*
2 cm WT vs. 4 cm WT	2 cm <i>sweet2</i> vs. 4 cm <i>sweet2</i>	81	182	3.40435836	113.0133652	0.001	0.002	**
2 cm WT vs. 4 cm WT	2 cm <i>sweet2</i> vs. 6 cm <i>sweet2</i>	81	182	3.920134494	112.6121207	0.000	0.000	***
2 cm WT vs. 4 cm WT	2 cm <i>sweet4</i> vs. 4 cm <i>sweet4</i>	81	168	3.735804971	117.5454259	0.000	0.001	***
2 cm WT vs. 4 cm WT	2 cm <i>sweet4</i> vs. 6 cm <i>sweet4</i>	81	156	4.063475204	113.4537742	0.000	0.000	***
2 cm WT vs. 4 cm WT	4 cm <i>sweet11/12</i> vs. 2 cm <i>sweet11/12</i>	81	169	2.864735846	98.2315757	0.005	0.010	**
2 cm WT vs. 4 cm WT	4 cm <i>sweet11/12</i> vs. 6 cm <i>sweet11/12</i>	81	169	3.504299554	108.3338739	0.001	0.001	**
2 cm WT vs. 4 cm WT	4 cm <i>sweet2</i> vs. 6 cm <i>sweet2</i>	81	169	3.76172002	113.4357328	0.000	0.001	***
2 cm WT vs. 4 cm WT	4 cm <i>sweet4</i> vs. 6 cm <i>sweet4</i>	81	182	3.364632907	110.6614455	0.001	0.002	**
2 cm WT vs. 6 cm WT	2 cm <i>sweet11/12</i> vs. 4 cm <i>sweet11/12</i>	81	169	1.382449213	99.56724944	0.170	0.248	ns
2 cm WT vs. 6 cm WT	2 cm <i>sweet11/12</i> vs. 6 cm <i>sweet11/12</i>	81	169	0.941018543	98.44033626	0.349	0.456	ns
2 cm WT vs. 6 cm WT	2 cm <i>sweet2</i> vs. 4 cm <i>sweet2</i>	81	182	1.992994247	115.4339219	0.049	0.082	ns
2 cm WT vs. 6 cm WT	2 cm <i>sweet2</i> vs. 6 cm <i>sweet2</i>	81	182	2.522507494	115.0038529	0.013	0.024	*
2 cm WT vs. 6 cm WT	2 cm <i>sweet4</i> vs. 4 cm <i>sweet4</i>	81	168	2.349954042	120.2662808	0.020	0.036	*
2 cm WT vs. 6 cm WT	2 cm <i>sweet4</i> vs. 6 cm <i>sweet4</i>	81	156	2.673995089	115.8720671	0.009	0.017	*
2 cm WT vs. 6 cm WT	4 cm <i>sweet11/12</i> vs. 2 cm <i>sweet11/12</i>	81	169	1.382449213	99.56724944	0.170	0.248	ns
2 cm WT vs. 6 cm WT	4 cm <i>sweet11/12</i> vs. 6 cm <i>sweet11/12</i>	81	169	2.079938776	110.4055996	0.040	0.068	ns
2 cm WT vs. 6 cm WT	4 cm <i>sweet2</i> vs. 6 cm <i>sweet2</i>	81	169	2.362761347	115.8711254	0.020	0.036	*
2 cm WT vs. 6 cm WT	4 cm <i>sweet4</i> vs. 6 cm <i>sweet4</i>	81	182	1.943936991	112.912498	0.054	0.089	ns
4 cm WT vs. 6 cm WT	4 cm <i>sweet11/12</i> vs. 2 cm <i>sweet11/12</i>	81	169	2.552494521	101.2373283	0.012	0.022	*
4 cm WT vs. 6 cm WT	4 cm <i>sweet11/12</i> vs. 6 cm <i>sweet11/12</i>	81	169	3.237768258	112.9913376	0.002	0.004	**
4 cm WT vs. 6 cm WT	4 cm <i>sweet2</i> vs. 6 cm <i>sweet2</i>	81	169	3.512329433	118.9060431	0.001	0.001	**
4 cm WT vs. 6 cm WT	4 cm <i>sweet4</i> vs. 6 cm <i>sweet4</i>	81	182	3.089418103	115.7231696	0.003	0.006	**

**Table S4: Metabolites and their retention times identified from root tissues using untargeted GC/MS (related to Figure 2)**

Metabolite	Superclass (MetFR)	Subclass (according to the Human Metabolome Database)	mass/fragment	Retention time (s)
Sterol_23.74	Sterol Lipids	Stigmastanes and derivatives	396	23.74
5-oxo-proline	Carbohydrates	Carbohydrates and carbohydrate conjugates	156.1	11.172
Alanine	Organic acids	Amino acids, peptides, and analogues	116.09	6.618
Ketoglutarate	Organic acids	Dicarboxylic acids and derivatives	198.06	11.668
Asparagine	Organic acids	Amino acids, peptides, and analogues	116.085	12.579
Aspartate	Organic acids	Amino acids, peptides, and analogues	232.119	11.155
Sterol_23.16	Sterol Lipids	Ergostane steroids	382	23.16
Isocitrate	Organic acids	Tricarboxylic acids and derivatives	273.098	13.925
Dimethylolpropanoic acid	(Internal standard)	(Internal standard)	148	11.668
Fructose	Carbohydrates	Carbohydrates and carbohydrate conjugates	307	14.444
Fumarate	Organic acids	Dicarboxylic acids and derivatives	245.067	9.28
Gamma-aminobutyrate	Organic acids	Amino acids, peptides, and analogues	304.1	11.233
Disaccharide_21.9	Carbohydrates	Carbohydrates and carbohydrate conjugates	204	21.9
Hexose	Carbohydrates	Carbohydrates and carbohydrate conjugates	387	17.8
Gluconate	Carbohydrates	Carbohydrates and carbohydrate conjugates	333.138	15.42
Glucose	Carbohydrates	Carbohydrates and carbohydrate conjugates	205.108	14.663
Glutamate	Organic acids	Amino acids, peptides, and analogues	246.135	12.09
Glutamine	Organic acids	Amino acids, peptides, and analogues	156.1	13.45
Glycerate	Carbohydrates	Carbohydrates and carbohydrate conjugates	189.077	9.189
Glycerol	Carbohydrates	Carbohydrates and carbohydrate conjugates	205.108	8.561
Glycine	Organic acids	Amino acids, peptides, and analogues	174.113	8.926
Isoleucine	Organic acids	Amino acids, peptides, and analogues	158.137	8.774
Disaccharide_21.5	Carbohydrates	Carbohydrates and carbohydrate conjugates	204	21.5
Disaccharide_14.71	Carbohydrates	Carbohydrates and carbohydrate conjugates	204	14.716
Leucine	Organic acids	Amino acids, peptides, and analogues	158.137	8.527
Lysine	Organic acids	Amino acids, peptides, and analogues	174.113	14.714
Malate	Organic acids	Dicarboxylic acids and derivatives	233.103	10.835
Disaccharide_20.5	Carbohydrates	Carbohydrates and carbohydrate conjugates	361.169	20.515
Mannitol	Carbohydrates	Monosaccharide	205.108	14.927
Disaccharide_14.98	Carbohydrates	Carbohydrates and carbohydrate conjugates	217	14.98
Methionine	Organic acids	Amino acids, peptides, and analogues	176.093	11.135
Myoinositol	Carbohydrates	Monosaccharide	305.1425	16.158
Phenylalanine	Organic acids	Amino acids, peptides, and analogues	192.12	12.181
Proline	Organic acids	Amino acids, peptides, and analogues	142.1	8.818
Pyruvate	Organic acids	Alpha-keto acids and derivatives	174.0586	6.025
Raffinose	Carbohydrates	Carbohydrates and carbohydrate conjugates	437.203	24.574
Ribitol	(Internal standard)	(Internal standard)	217	13.165
Serine	Organic acids	Amino acids, peptides, and analogues	204.124	9.509
Shikimate	Organic oxygen compounds	Alcohols and polyols	204.1	13.783
Sorbitol	Carbohydrates	Monosaccharide	319.158	14.991
Succinate	Organic acids	Dicarboxylic acids and derivatives	247.082	8.939
Sucrose	Carbohydrates	Carbohydrates and carbohydrate conjugates	361.169	19.886
Hexose_13.45	Carbohydrates	Carbohydrates and carbohydrate conjugates	217	13.45
Uk_11.60	Carbohydrates	Carbohydrates and carbohydrate conjugates	292.1	11.671
Threonine	Organic acids	Amino acids, peptides, and analogues	219.11	9.806
Disaccharide_14.35	Carbohydrates	Carbohydrates and carbohydrate conjugates	361	14.354
Disaccharide_15.98	Carbohydrates	Carbohydrates and carbohydrate conjugates	361	15.98
Valine	Organic acids	Amino acids, peptides, and analogues	144.121	7.91

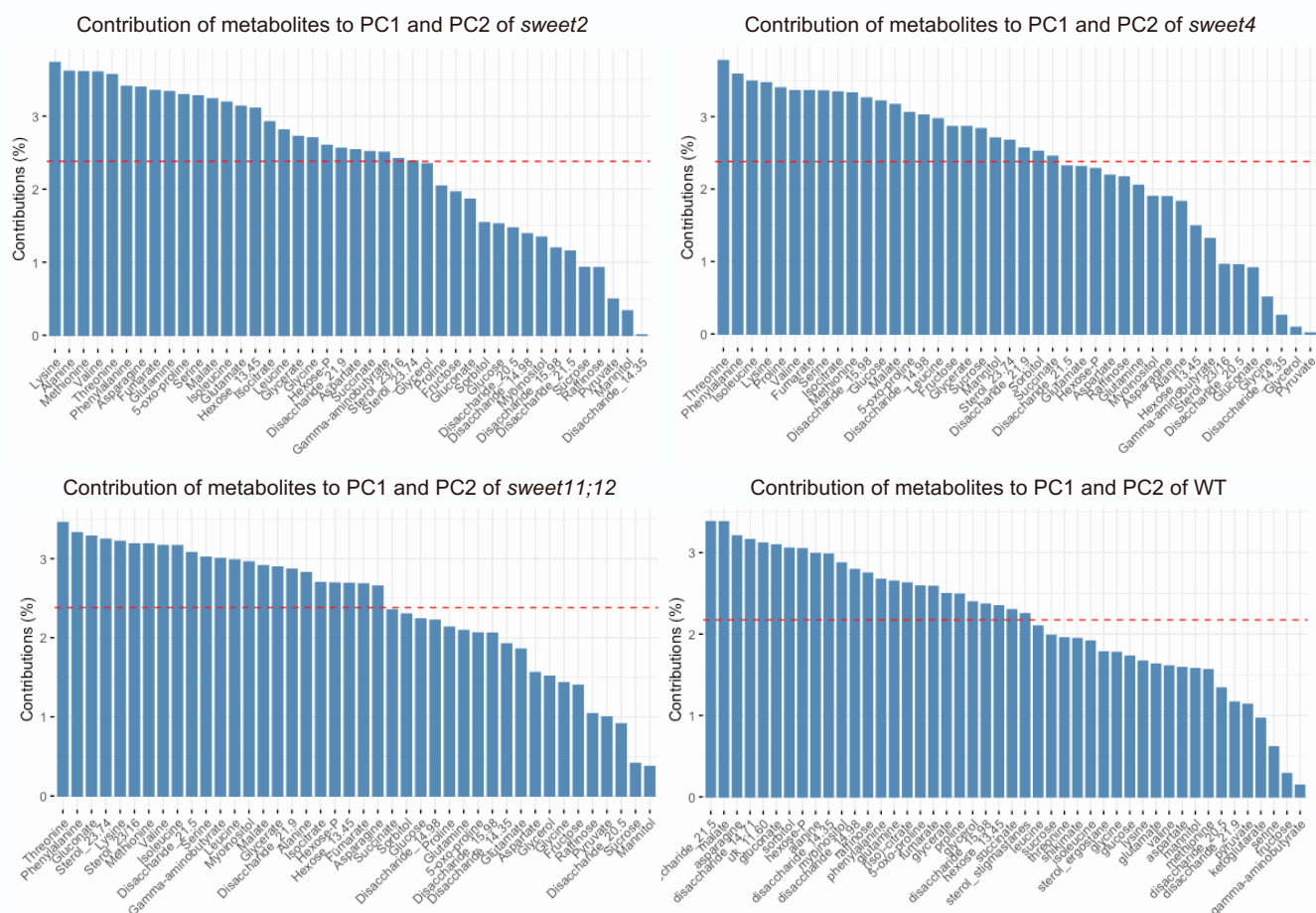


**Table S5: Information for members of Syncom used in this study (related to STAR Methods)**

Syncom member ID	Kingdom	Phylum	Class	Order	Family	Genus
Root151	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides
Root562	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Root61	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rhodanobacter
Root136	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Nocardia
Root123D2	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Afipia
Root1298	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Rhizobium
Root672	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium
Root154	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	(unknown)
Root436	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	(unknown)
Root190	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides
Root265	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium
Root608	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas
Root708	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Rhizobium
Root404	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	(unknown)
Root85	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	(unknown)
Root1444	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	(unknown)
Root720	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
Root224	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides
Root670	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	(unknown)
Root685	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	(unknown)
Root63	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces
Root52	Bacteria	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus
Root405	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	(unknown)
Root444D2	Bacteria	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus
Root494	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	(unknown)
Root413D1	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	(unknown)
Root1280	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter
Root66D1	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces
Root101	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Janibacter
Root1310	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces
Root480	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	(unknown)
Root170	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	Achromobacter
Root186	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Root342	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter
Root954	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Rhizobium
Root29	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	(unknown)
Root690	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	(unknown)
Root655	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter
Root71	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Root332	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	(unknown)
Root236	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Aeromicrobium
Root695	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	Mesorhizobium
Root149	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Rhizobium
Root700	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	(unknown)
Root81	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Agromyces
Root241	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
Root1257	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides
Root553	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	(unknown)
Root1237	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	(unknown)
Root181	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	(unknown)
Root1462	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	(unknown)
Root83	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	Achromobacter
Root239	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus
Root1485	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia
Root135	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium
Root73	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Rhizobium
Root930	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	(unknown)
Root131	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus
Root274	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	(unknown)
Root418	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium

Table S6: Genes in the pathways defined based on metabolic modeling (related to STAR Methods)

Pathway	Gene ID
Maltose	AT1G01090 // AT1G02640 // AT1G04410 // AT1G05610 // AT1G08480 // AT1G11720 // AT1G12900 // AT1G13440 // AT1G16300 // AT1G20860 // AT1G23190 // AT1G24180 // AT1G26560 // AT1G27680 // AT1G30120 // AT1G32380 // AT1G32440 // AT1G34430 // AT1G42970 // AT1G47420 // AT1G47840 // AT1G48030 // AT1G53240 // AT1G54220 // AT1G56190 // AT1G59900 // AT1G61800 // AT1G70730 // AT1G70820 // AT1G71750 // AT1G79530 // AT1G79550 // AT2G01140 // AT2G05710 // AT2G17130 // AT2G18450 // AT2G19860 // AT2G20420 // AT2G21170 // AT2G21330 // AT2G21770 // AT2G22480 // AT2G22780 // AT2G25540 // AT2G34590 // AT2G35390 // AT2G36390 // AT2G36460 // AT2G42910 // AT2G44350 // AT2G44450 // AT2G44480 // AT2G44530 // AT2G46390 // AT2G46505 // AT2G47510 // AT3G01180 // AT3G04050 // AT3G04120 // AT3G12780 // AT3G13930 // AT3G15020 // AT3G16950 // AT3G17240 // AT3G17940 // AT3G18080 // AT3G25960 // AT3G26650 // AT3G27380 // AT3G27800 // AT3G47000 // AT3G47050 // AT3G47520 // AT3G47800 // AT3G47833 // AT3G49160 // AT3G52200 // AT3G52930 // AT3G52990 // AT3G53900 // AT3G55410 // AT3G55440 // AT3G55650 // AT3G55810 // AT4G16155 // AT4G17090 // AT4G18240 // AT4G18780 // AT4G24620 // AT4G26270 // AT4G26390 // AT4G26520 // AT4G26530 // AT4G26910 // AT4G26970 // AT4G29130 // AT4G29220 // AT4G32210 // AT4G32410 // AT4G32840 // AT4G35830 // AT4G37840 // AT4G38970 // AT4G39210 // AT4G39350 // AT5G03650 // AT5G03690 // AT5G05170 // AT5G08300 // AT5G08570 // AT5G09600 // AT5G09660 // AT5G09870 // AT5G12860 // AT5G15140 // AT5G17420 // AT5G17520 // AT5G17630 // AT5G19220 // AT5G20830 // AT5G23250 // AT5G24300 // AT5G33320 // AT5G42260 // AT5G42740 // AT5G43330 // AT5G44030 // AT5G44640 // AT5G48300 // AT5G49190 // AT5G50850 // AT5G50950 // AT5G51820 // AT5G52920 // AT5G54800 // AT5G55070 // AT5G56350 // AT5G56630 // AT5G56720 // AT5G57655 // AT5G58330 // AT5G61580 // AT5G62575 // AT5G63680 // AT5G64740 // AT5G65685 // AT5G66570 // AT5G66760
Glucose	AT1G02640 // AT1G26560 // AT2G21770 // AT2G25540 // AT2G44450 // AT2G44480 // AT3G17940 // AT3G18080 // AT3G43190 // AT3G47000 // AT3G47050 // AT3G47800 // AT4G18780 // AT4G32410 // AT4G39350 // AT5G05170 // AT5G09870 // AT5G15140 // AT5G17420 // AT5G20830 // AT5G42260 // AT5G44030 // AT5G44640 // AT5G49190 // AT5G57655 // AT5G64740
beta-D-Fructose	AT1G01090 // AT1G04410 // AT1G08480 // AT1G12240 // AT1G21270 // AT1G23190 // AT1G24180 // AT1G27450 // AT1G30120 // AT1G32380 // AT1G34430 // AT1G47420 // AT1G47840 // AT1G47960 // AT1G48030 // AT1G53240 // AT1G54220 // AT1G59900 // AT1G61800 // AT1G62660 // AT1G70730 // AT1G70820 // AT1G71750 // AT1G80050 // AT2G05710 // AT2G17130 // AT2G18450 // AT2G19860 // AT2G20420 // AT2G22780 // AT2G34590 // AT2G35390 // AT2G36190 // AT2G42910 // AT2G44350 // AT2G44530 // AT2G46390 // AT2G46505 // AT2G47510 // AT3G13790 // AT3G13930 // AT3G15020 // AT3G16950 // AT3G17240 // AT3G27380 // AT3G47520 // AT3G47833 // AT3G52200 // AT3G55410 // AT3G41240 // AT4G16155 // AT4G22570 // AT4G23900 // AT4G24620 // AT4G26910 // AT4G26970 // AT4G29130 // AT4G32210 // AT4G35830 // AT4G37840 // AT5G08300 // AT5G09600 // AT5G09660 // AT5G11160 // AT5G12860 // AT5G17310 // AT5G17630 // AT5G20280 // AT5G23250 // AT5G23500 // AT5G42740 // AT5G43330 // AT5G50850 // AT5G50950 // AT5G51820 // AT5G54800 // AT5G55070 // AT5G56720 // AT5G58330 // AT5G62575 // AT5G63310 // AT5G64620 // AT5G65750 // AT5G66760
D-Galactose	AT1G12780 // AT1G23190 // AT1G30620 // AT1G47840 // AT1G63180 // AT1G64440 // AT1G70730 // AT1G70820 // AT2G19860 // AT2G34850 // AT3G06580 // AT3G10700 // AT3G43190 // AT4G23920 // AT4G29130 // AT4G37840 // AT5G17310 // AT5G18200 // AT5G20830 // AT5G49190 // AT5G51820 // AT5G57655
D-Xylose	AT1G02640 // AT1G06030 // AT1G12230 // AT1G26560 // AT1G47840 // AT1G63290 // AT1G66430 // AT1G71100 // AT2G01140 // AT2G01290 // AT2G19860 // AT2G21170 // AT2G21330 // AT2G22480 // AT2G31390 // AT2G36460 // AT2G44450 // AT2G44480 // AT2G45290 // AT3G01850 // AT3G04790 // AT3G17940 // AT3G18080 // AT3G43190 // AT3G47000 // AT3G47050 // AT3G47800 // AT3G52930 // AT3G55440 // AT3G59480 // AT3G60750 // AT4G10260 // AT4G26270 // AT4G26520 // AT4G26530 // AT4G29130 // AT4G29220 // AT4G32840 // AT4G37840 // AT4G38970 // AT5G03690 // AT5G13420 // AT5G15140 // AT5G42260 // AT5G44640 // AT5G49190 // AT5G49650 // AT5G51830 // AT5G56630 // AT5G57655 // AT5G61410 // AT5G61580
Glucose + beta-D-Fructose	AT1G12240 // AT1G21270 // AT1G47960 // AT1G62660 // AT5G64620
Glucose + D-Galactose	AT1G12780 // AT1G30620 // AT1G63180 // AT1G64440 // AT2G34850 // AT3G06580 // AT3G10700 // AT3G43190 // AT4G23920 // AT5G18200 // AT5G20830 // AT5G49190 // AT5G57655
Glucose + D-Xylose	AT1G02640 // AT1G12230 // AT1G26560 // AT1G63290 // AT1G71100 // AT2G01140 // AT2G01290 // AT2G21170 // AT2G21330 // AT2G21770 // AT2G22480 // AT2G25540 // AT2G36460 // AT2G44450 // AT2G44480 // AT2G45290 // AT3G01850 // AT3G04790 // AT3G17940 // AT3G18080 // AT3G43190 // AT3G47000 // AT3G47050 // AT3G47800 // AT3G52930 // AT3G55440 // AT3G60750 // AT4G18780 // AT4G26270 // AT4G26520 // AT4G26530 // AT4G29220 // AT4G32410 // AT4G32840 // AT4G38970 // AT4G39350 // AT5G03690 // AT5G05170 // AT5G09870 // AT5G13420 // AT5G15140 // AT5G17420 // AT5G20830 // AT5G42260 // AT5G44030 // AT5G44640 // AT5G49190 // AT5G49650 // AT5G56630 // AT5G57655 // AT5G61410 // AT5G61580 // AT5G64740
beta-D-Fructose + D-Galactose	AT1G06030 // AT1G12240 // AT1G12780 // AT1G21270 // AT1G23190 // AT1G30620 // AT1G47840 // AT1G47960 // AT1G62660 // AT1G63180 // AT1G64440 // AT1G66430 // AT1G70730 // AT1G70820 // AT2G19860 // AT2G31390 // AT2G34850 // AT3G06580 // AT3G10700 // AT3G59480 // AT4G10260 // AT4G23920 // AT4G24620 // AT4G29130 // AT4G37840 // AT5G17310 // AT5G18200 // AT5G42740 // AT5G51820 // AT5G51830 // AT5G57655 // AT5G64620
beta-D-Fructose + D-Xylose	AT1G01090 // AT1G04410 // AT1G06030 // AT1G08480 // AT1G09780 // AT1G12230 // AT1G12240 // AT1G12900 // AT1G13440 // AT1G16300 // AT1G16350 // AT1G21270 // AT1G23190 // AT1G24180 // AT1G30120 // AT1G32380 // AT1G32440 // AT1G34430 // AT1G42970 // AT1G47420 // AT1G47840 // AT1G47960 // AT1G48030 // AT1G53240 // AT1G54220 // AT1G56190 // AT1G59900 // AT1G62660 // AT1G63290 // AT1G66430 // AT1G70730 // AT1G70820 // AT1G71100 // AT1G71750 // AT1G74030 // AT1G79470 // AT1G79530 // AT1G79550 // AT2G01140 // AT2G01290 // AT2G05710 // AT2G17130 // AT2G18450 // AT2G19860 // AT2G20420 // AT2G21170 // AT2G21330 // AT2G22480 // AT2G22780 // AT2G31390 // AT2G34590 // AT2G35390 // AT2G36460 // AT2G36530 // AT2G42910 // AT2G44350 // AT2G44530 // AT2G46390 // AT2G46505 // AT2G47510 // AT3G01850 // AT3G04050 // AT3G04120 // AT3G04790 // AT3G08590 // AT3G12780 // AT3G13930 // AT3G15020 // AT3G16950 // AT3G17240 // AT3G25960 // AT3G26650 // AT3G27380 // AT3G43190 // AT3G47520 // AT3G47833 // AT3G49160 // AT3G50520 // AT3G52200 // AT3G52930 // AT3G52990 // AT3G55410 // AT3G55440 // AT3G55650 // AT3G55810 // AT3G59480 // AT3G60750 // AT4G10260 // AT4G16155 // AT4G23900 // AT4G26270 // AT4G26390 // AT4G26520 // AT4G26530 // AT4G26910 // AT4G26970 // AT4G29130 // AT4G29220 // AT4G32210 // AT4G32840 // AT4G35830 // AT4G37840 // AT4G38970 // AT5G03690 // AT5G08300 // AT5G08570 // AT5G09600 // AT5G09660 // AT5G09870 // AT5G12860 // AT5G13420 // AT5G17310 // AT5G20830 // AT5G23250 // AT5G43330 // AT5G47840 // AT5G49190 // AT5G49650 // AT5G50370 // AT5G50850 // AT5G50950 // AT5G51820 // AT5G51830 // AT5G52920 // AT5G55070 // AT5G56350 // AT5G56630 // AT5G56720 // AT5G57655 // AT5G58330 // AT5G61410 // AT5G61580 // AT5G62575 // AT5G63310 // AT5G63680 // AT5G64620 // AT5G65750 // AT5G66760
D-Galactose + D-Xylose	AT1G06030 // AT1G12230 // AT1G12240 // AT1G12780 // AT1G21270 // AT1G23190 // AT1G30620 // AT1G47840 // AT1G47960 // AT1G62660 // AT1G63180 // AT1G63290 // AT1G66430 // AT1G66430 // AT1G70730 // AT1G70820 // AT1G71100 // AT2G01140 // AT2G01290 // AT2G19860 // AT2G21170 // AT2G21330 // AT2G22480 // AT2G31390 // AT2G34850 // AT2G36460 // AT2G45290 // AT3G01850 // AT3G04790 // AT3G06580 // AT3G10700 // AT3G52930 // AT3G55440 // AT3G59480 // AT4G10260 // AT4G23920 // AT4G24620 // AT4G26270 // AT4G26520 // AT4G26530 // AT4G29130 // AT4G29220 // AT4G32840 // AT4G37840 // AT4G38970 // AT5G03690 // AT5G13420 // AT5G17310 // AT5G18200 // AT5G42740 // AT5G49650 // AT5G51820 // AT5G51830 // AT5G56630 // AT5G57655 // AT5G61410 // AT5G61580 // AT5G64620
SWEET1	AT1G21460
SWEET2	AT3G14770
SWEET3	AT5G53190
SWEET4	AT3G28007
SWEET5	AT5G62850
SWEET6	AT1G66770
SWEET7	AT4G10850
SWEET8	AT5G40260
SWEET9	AT2G39060
SWEET10	AT5G50790
SWEET11	AT3G48740
SWEET12	AT5G23660
SWEET13	AT5G50800
SWEET14	AT4G25010
SWEET15	AT5G13170
SWEET16	AT3G16690
SWEET17	AT4G15920
SUC1	AT1G71880
SUC2	AT1G22710
SUC3	AT2G02860
SUC4	AT1G09960
SUC5	AT1G71890
SUC6	AT5G43610
SUC7	AT1G66570
SUC8	AT2G14670
SUC9	AT5G06170



Data S1: Contribution of each metabolite to the two principle components that explain the largest variation (PC1 and PC2) of PCA for each plant genotype (related to Figure 4)