

SUPPLEMENTAL MATERIAL

The following supplementary material is available for this article on line:

Figure S1. Comparative analysis of relative abundance (peak height) of fungal (A) and bacterial (B) phylotypes significantly differed between wild type (Col-0) and *abcg30*. Negative control (T) (soil without plant) also included in this analysis. * indicates the values are statistically significant compared to wild type at $P < 0.05$.

Figure S2. ^1H NMR (A), 2D *J*-resolved (B), and projected 1D *J*-resolved (C) spectra of control *Arabidopsis* root exudates (Col 0) in the range of δ 6.0 – δ 8.7.

Figure S3. Loading plot of PC1 (A) and loading plot of PC2 (B) of principal component analysis of *Arabidopsis* root exudates using projected 1D *J*-resolved spectrum.

Figure S4. 2D *J*-resolved spectrum of wild type root exudates with compound assignments. (A) 1, salicylic acid; 2, shikimic acid; 3, (S)-(-)-tyrosine; 4, (S)-(-)-tryptophan; 5, phenylalanine; 6, naringenin; 7, naringin; 8, catechol; 9, benzoic acid; 10, cinnamic acid; 11, caffeic acid; 12, ferulic acid; 13, syringic acid; 14, cyanidin; 15, indole-3-acetic acid; 16, flavonoid-7-glycoside; 17, sinapic acid; 18, formic acid. (B) 19, glucose (α - form); 20, raffinose; 21, sinapoyl malate.

Figure S5. 2D *J*-resolved spectrum of wild type root exudates with compound assignments. (A) 19, glucose (β –form); 22, galactose; 23, tartaric acid. (B) 24, fructose; 25, mannitol.

Figure S6. 2D *J*-resolved spectrum of wild type root exudates with compound assignments. 26, acetic acid; 27, succinic acid; 28, malic acid; 29, L-methionine; 30, valine; 31, alanine; 32, α -linolenic acid; 33, lactic acid; 34, threonine.

Figure S7. Comparison of one dimensional projected *J*-resolved spectra of *Arabidopsis* wild type and mutant's root exudates in the range of δ 8.6 – δ 5.7. 1: Col-0, 2: *abcg30*, 3: *abcg34*, 4: *abcg35*, 5: *abcb1*, 6: *abcb4*, 7: *abcc2*, 8: *abca7*.

Figure S8. Comparison of one dimensional projected *J*-resolved spectra of *Arabidopsis* wild type and mutant's root exudates in the range of δ 5.6 – δ 4.3. 1: Col-0, 2: *abcg30*, 3: *abcg34*, 4: *abcg35*, 5: *abcb1*, 6: *abcb4*, 7: *abcc2*, 8: *abca7*.

Figure S9. Comparison of one dimensional projected *J*-resolved spectra of *Arabidopsis* wild type and mutant's root exudates in the range of δ 4.3 – δ 3.0. 1: Col-0, 2: *abcg30*, 3: *abcg34*, 4: *abcg35*, 5: *abcb1*, 6: *abcb4*, 7: *abcc2*, 8: *abca7*.

Figure S10. Comparison of one dimensional projected J-resolved spectra of Arabidopsis wild type and mutant's root exudates in the range of δ 3.0 – δ 0.5. 1: Col-0, 2: *abcg30*, 3: *abcg34*, 4: *abcg35*, 5: *abcb1*, 6: *abcb4*, 7: *abcc2*, 8: *abca7*.

Figure S11. Percentages of genes belonging to different functional categories were significantly up-regulated and down-regulated in *abcg30* root tissues compared with wild type (Col-0) by whole genome expression analyses. The differentially expressed genes are statistically significant at a P value below 0.01 and show more than 1.5-fold induction.

Figure S12. Phylogenetic tree showing the evolutionary relationships of 66 taxa of the group alpha-proteobacteria based on rDNA sequences. The evolutionary history was inferred using the Neighbor-Joining method. The bootstrap consensus tree inferred from 1000 replicates is taken to represent the evolutionary history of the taxa analyzed. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. All positions containing alignment gaps and missing data were eliminated only in pairwise sequence comparisons (Pairwise deletion option). There were a total of 1577 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4.

Table S1. Multi-response permutation procedures (MRPP) analysis comparing the microbial community associated with each Arabidopsis ABC transporter mutant. Each row (sample) was relativized by its total and each column (phylotype) was arcsine transformed. Generations were analyzed separately. The values in bold are statistically significant at $P \leq 0.05$, $n = 3$.

Table S2. Pair wise comparisons (compared to wild type (Col-0) from MRPP analysis comparing the microbial community associated with each Arabidopsis ABC transporter mutant. Each row (samples) was relativized by its total and each column (phylotype) was arcsine transformed. Generations were analyzed separately. The values in bold are statistically significant at $P \leq 0.05$, $n = 3$. Col, Col-0 (wildtype); *Ler*, Landsberg ecotype; T, negative control (soil without plant); *tt4*, *abca7*, *abcg30*, *abcg34*, *abcg35*, *abcc2*, *abcb1*, *abcb4*.

Table S3. Relative NMR intensity of changed metabolites in Col-0 and *abcg30* using projected *J*-resolved spectra (signals are normalized to 1000 of internal standard (TMSP) at δ 0.0. Values represented are the mean values of two independent experiments in triplicate (n=6).

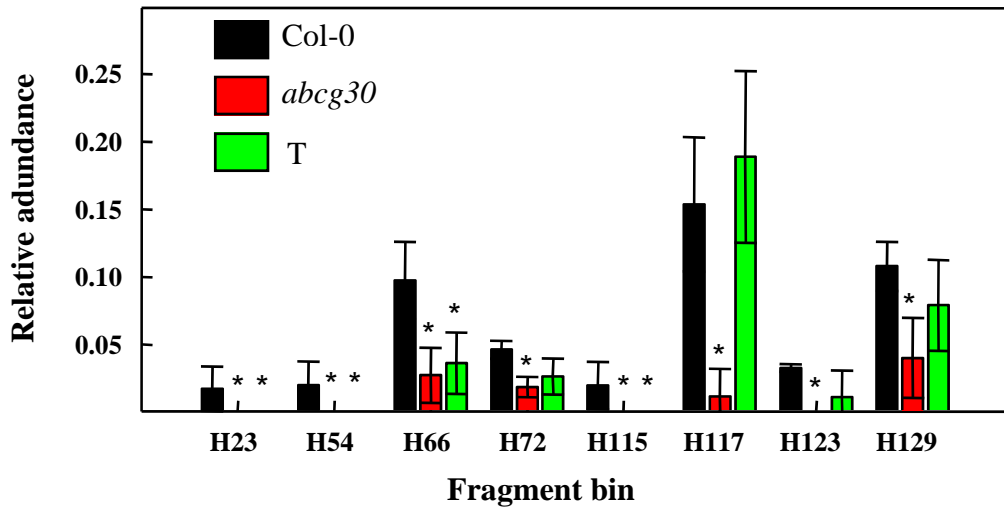
Table S4: Select list of genes differentially expressed in *abcg30* roots compared with wild type. The genes represented in this list are significantly up- and down-regulated at the value of $P < 0.01$.

Table S5. *In vitro* analysis of the Arabidopsis wild type (Col-0), *abcg30* root exudates and MS liquid media (control) effect on Arabidopsis soil microbes by plate counting assay. Values represented are the mean values of three independent experimental results. The readings were taken at two time points 24 and 48 hrs after plating. The values represent in parentheses are counts observed at 48 hr.

Table S6. List of ABC transporters and their T-DNA KO mutants used in this study.

Figure S1

A



B

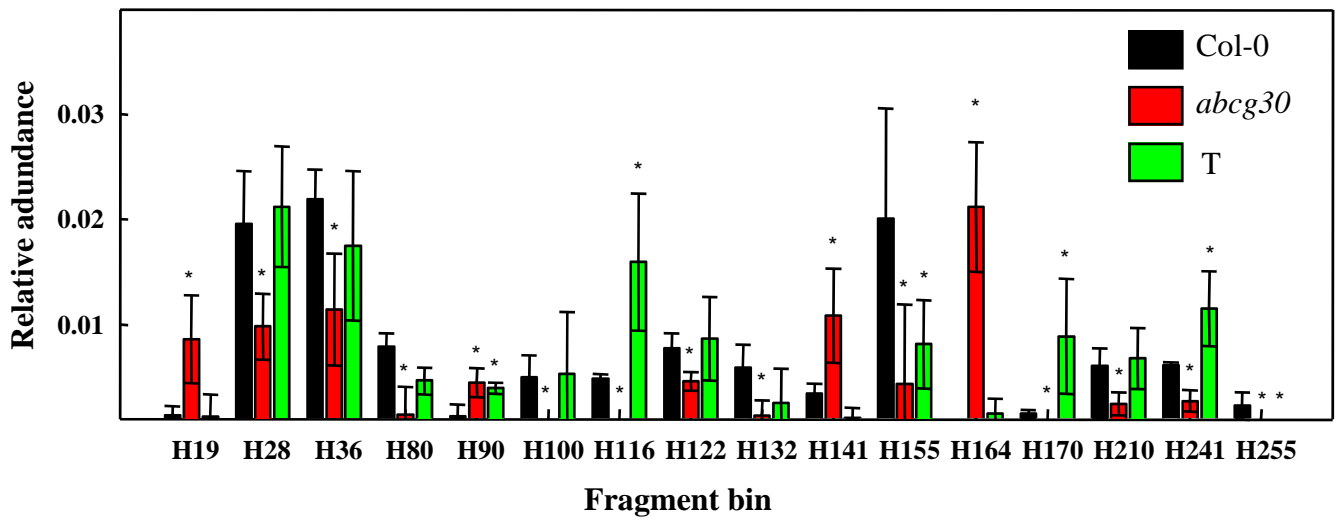
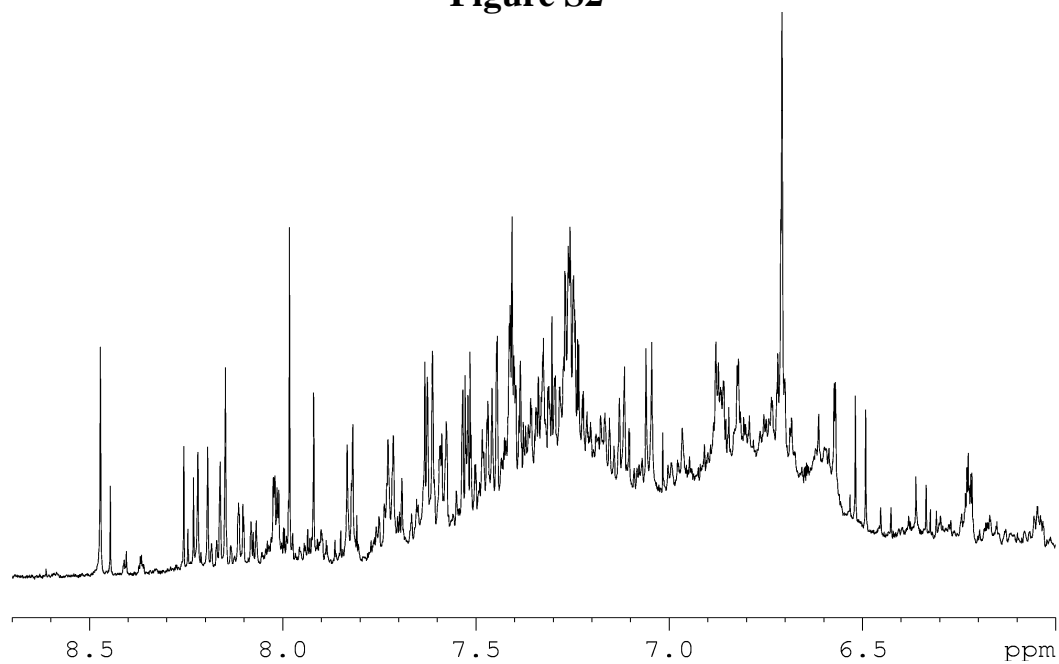
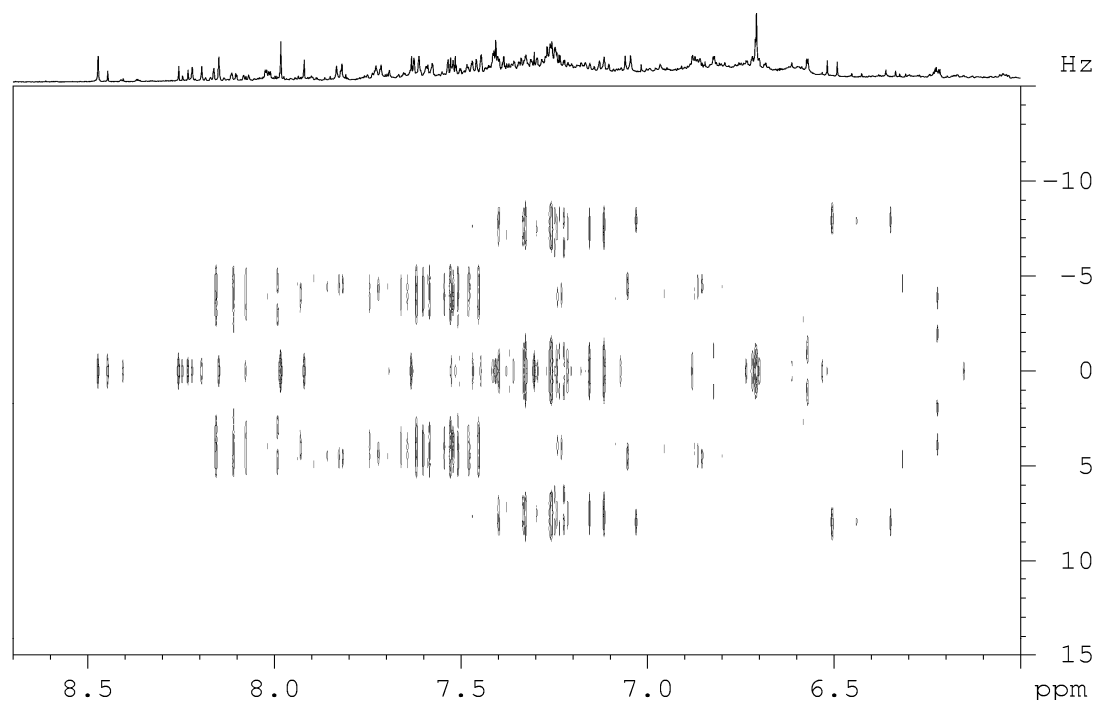


Figure S2

A



B



C

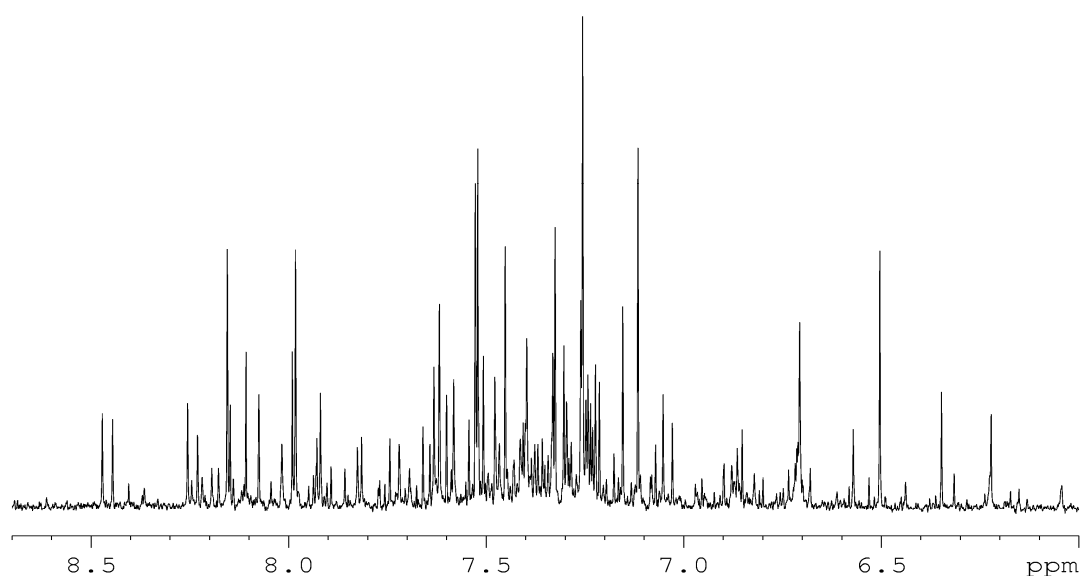
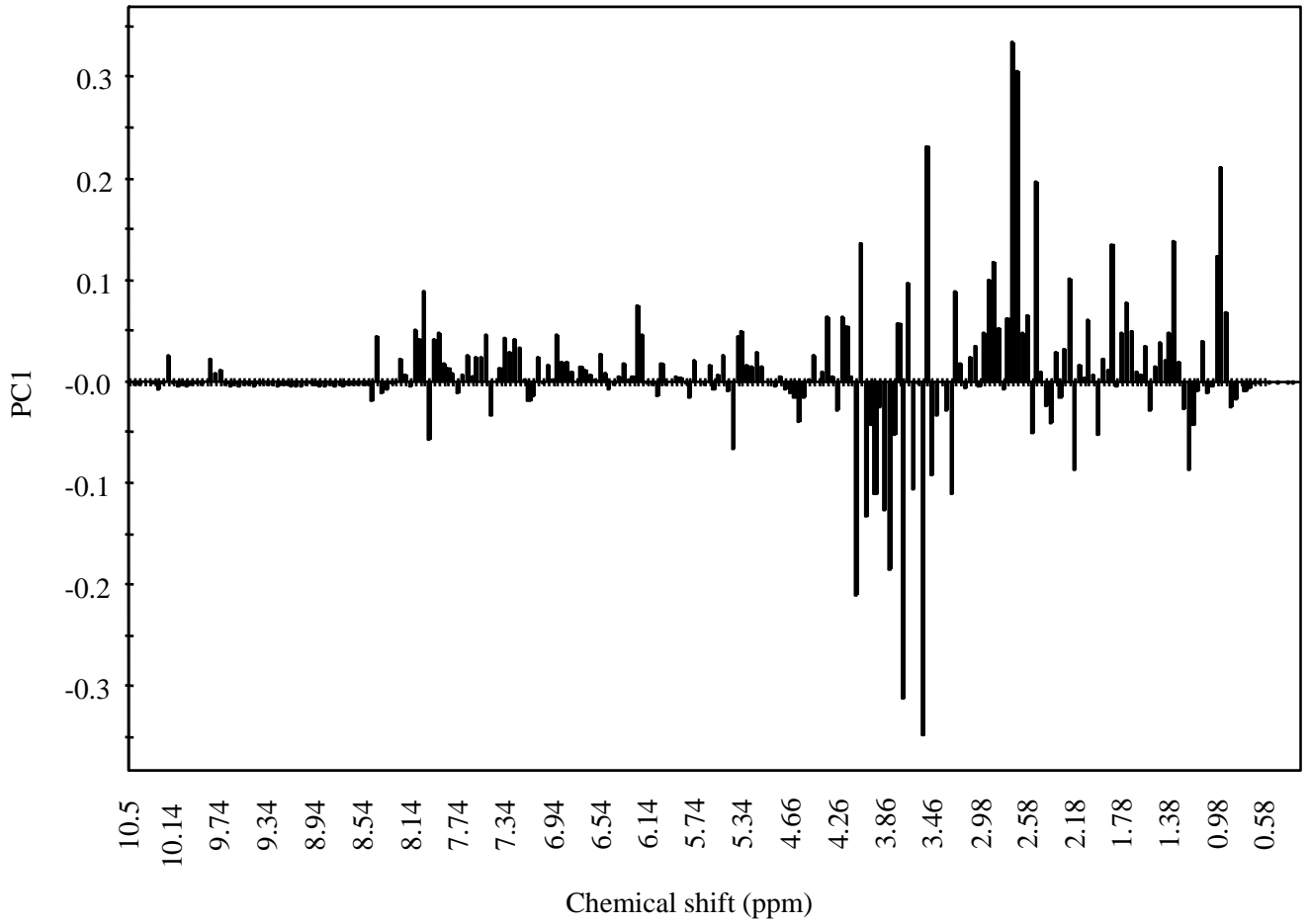


Figure S3

A



B

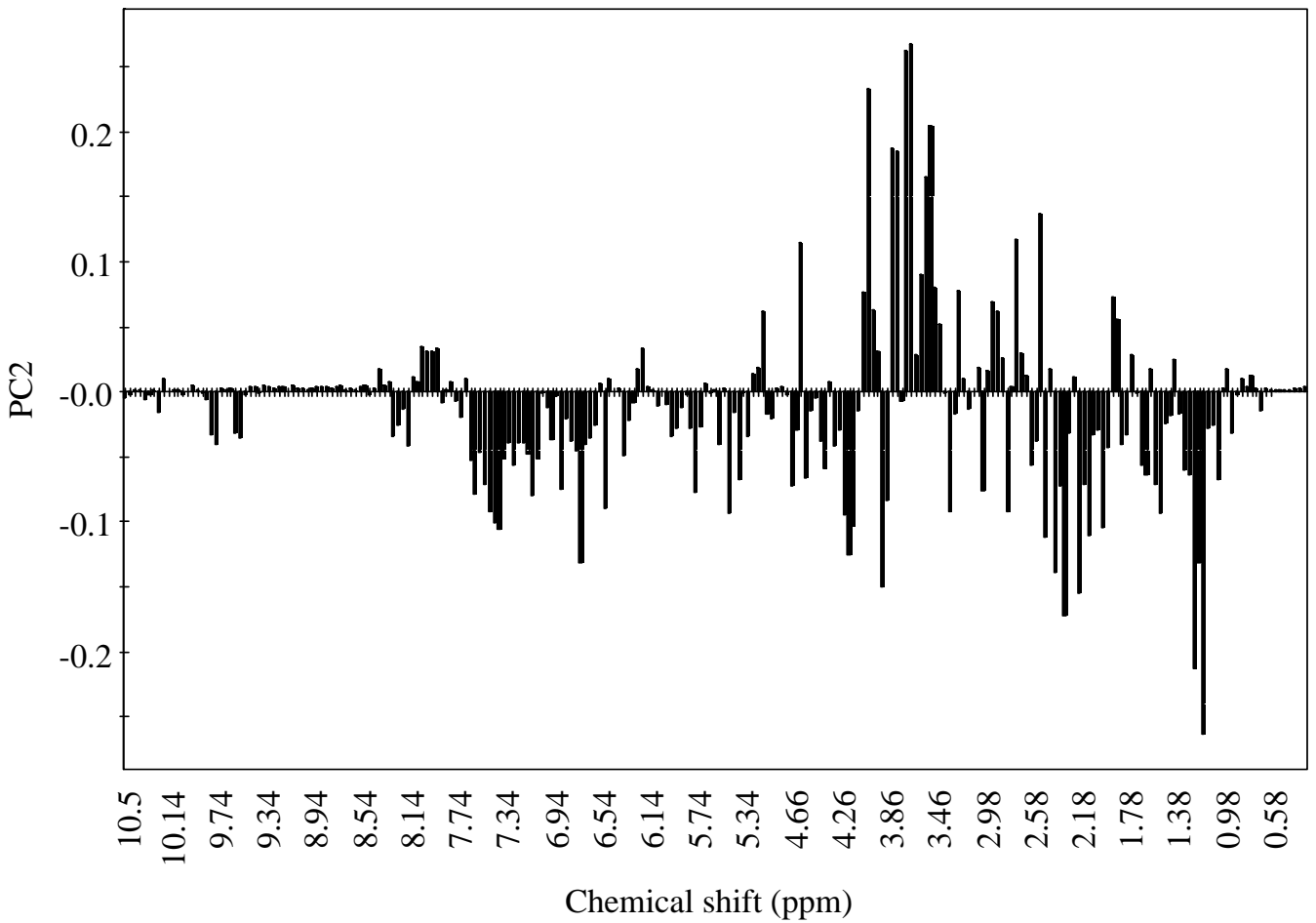
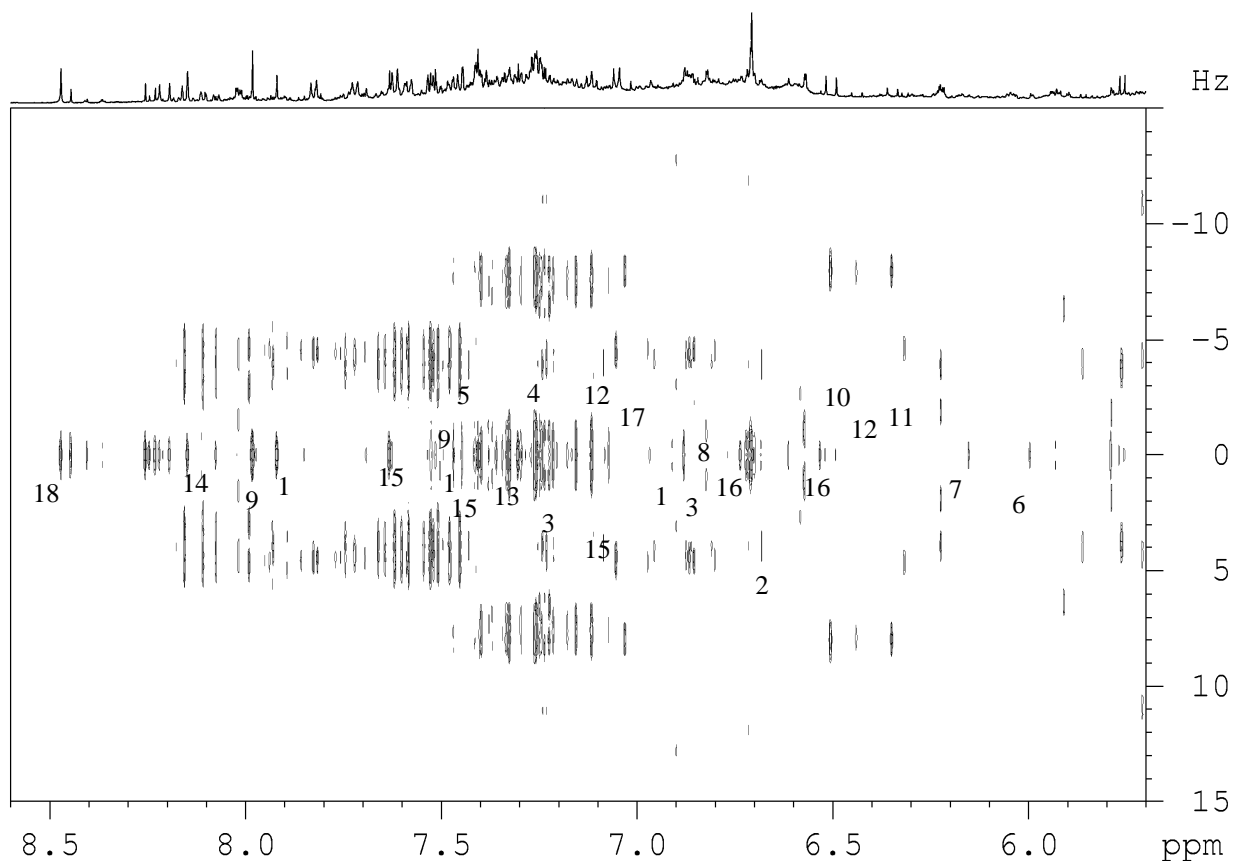


Figure S4

A



B

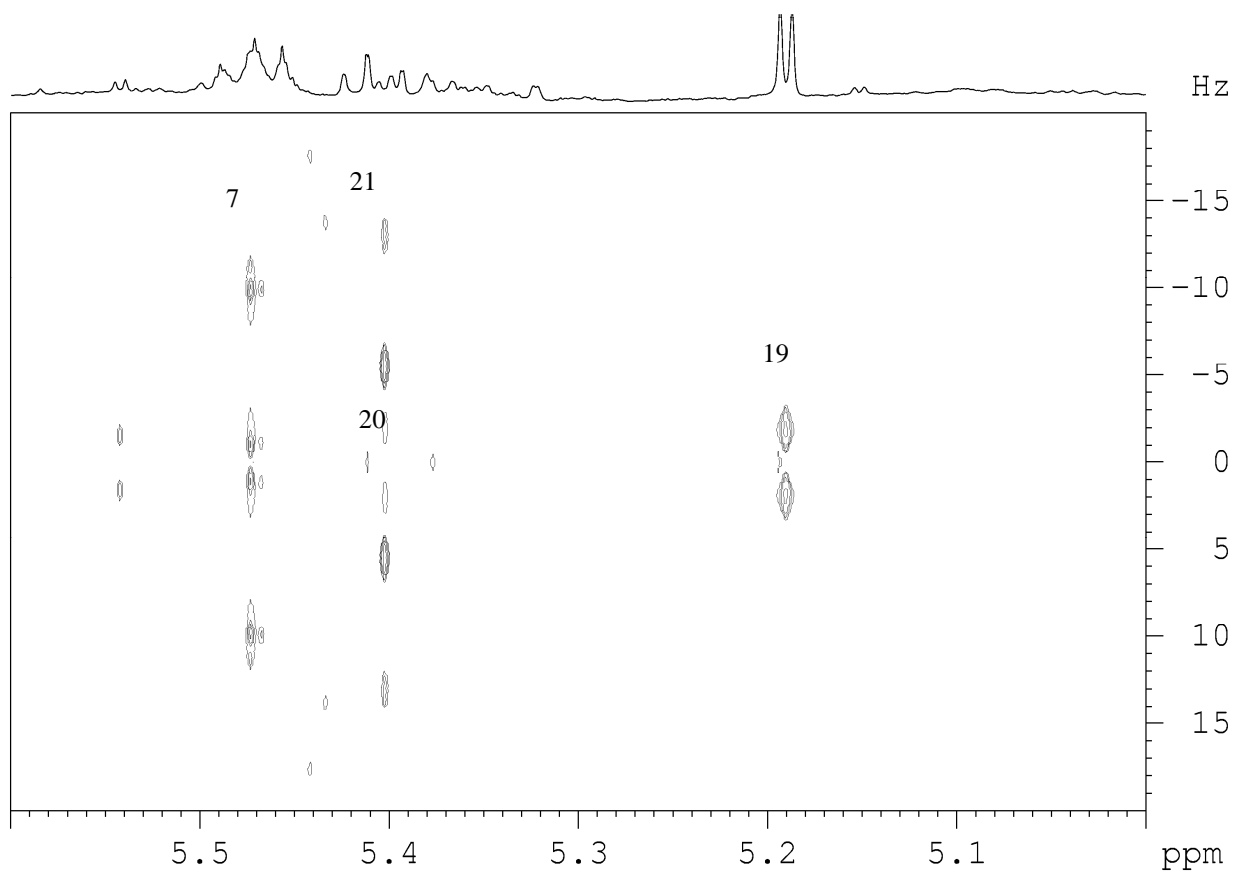
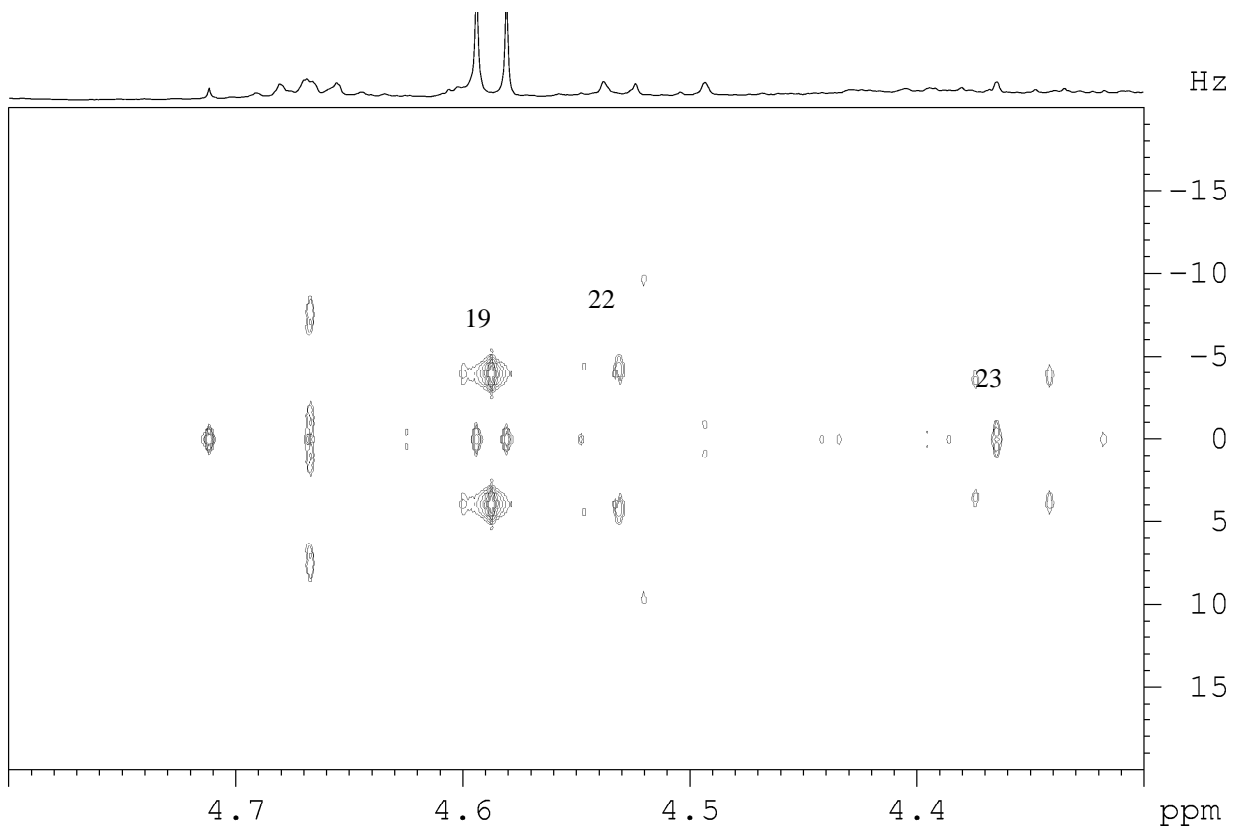


Figure S5

A



B

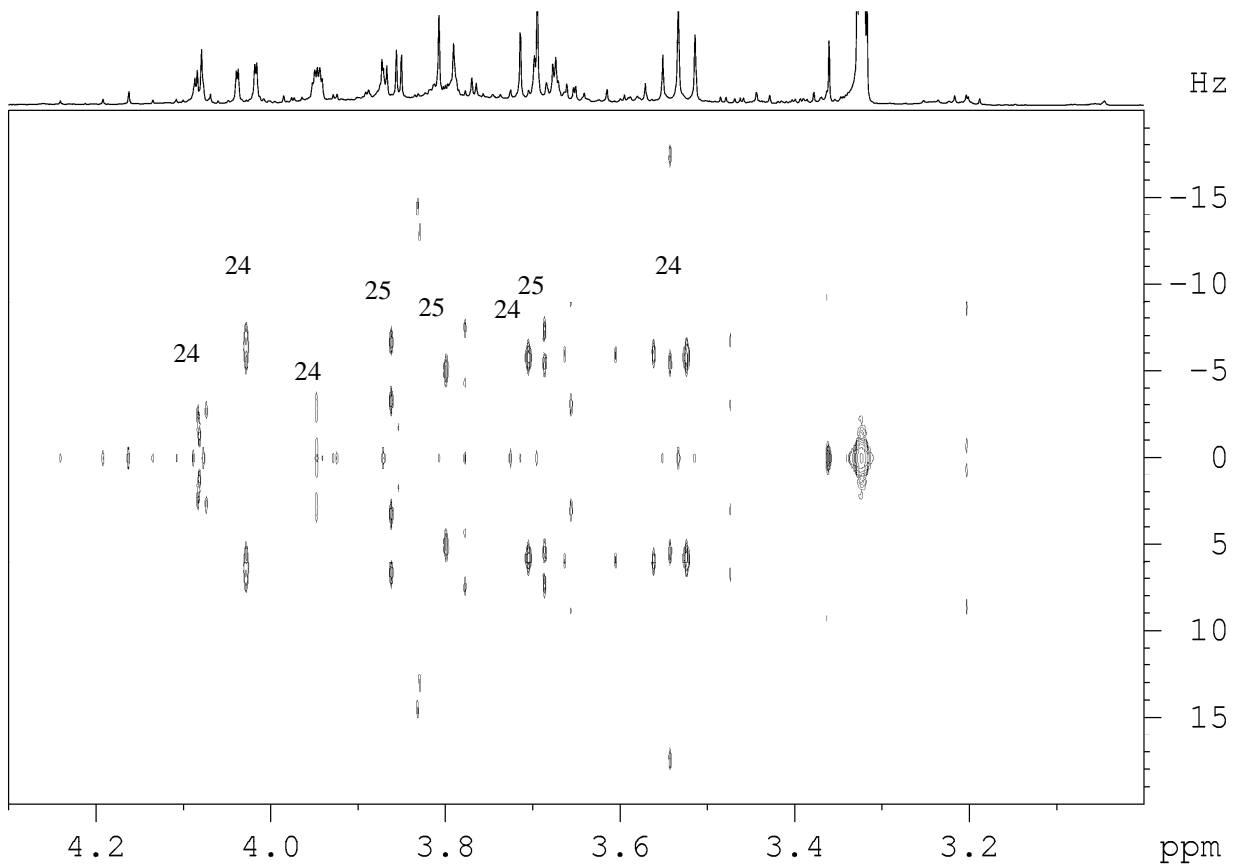


Figure S6

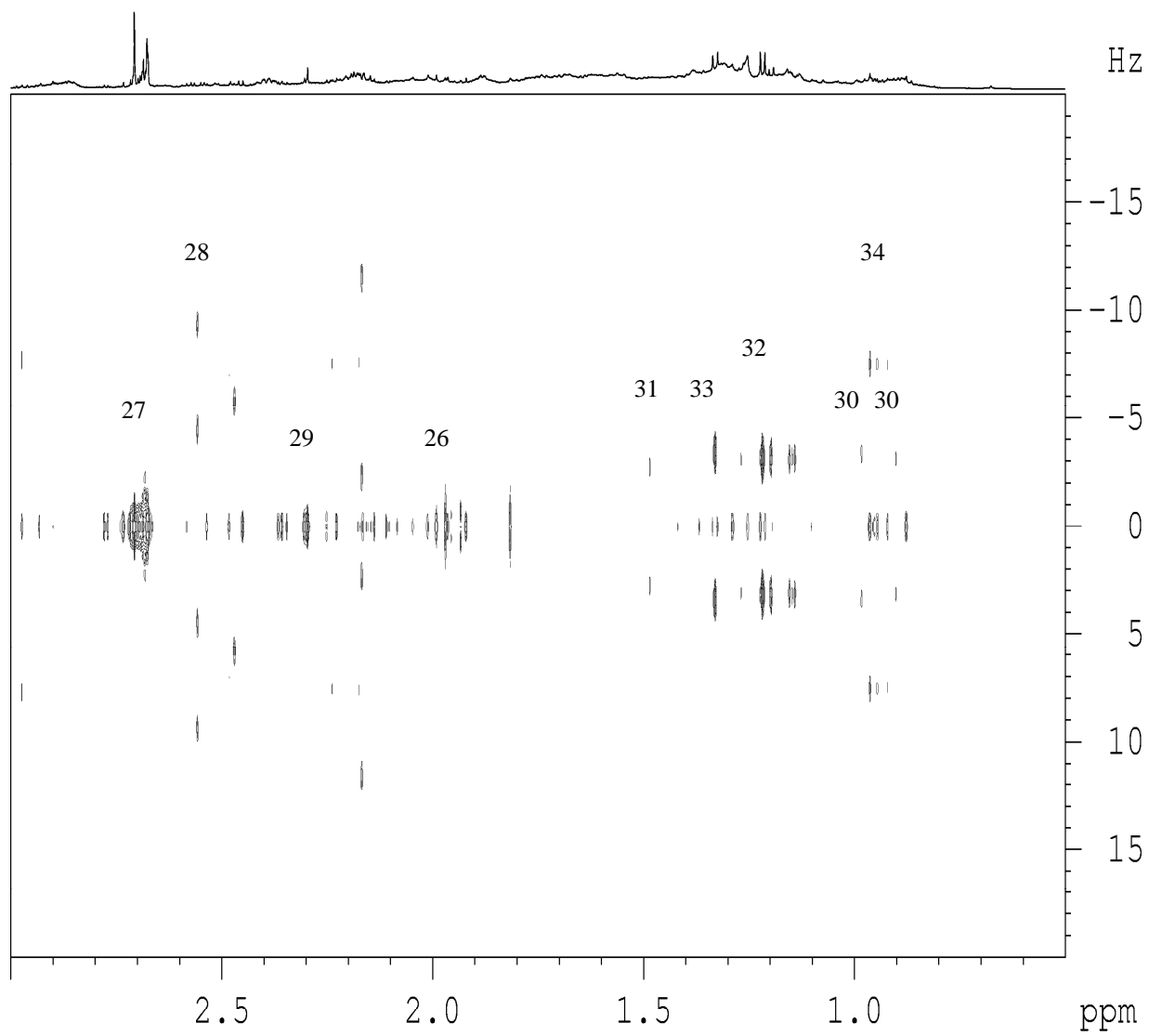


Figure S7

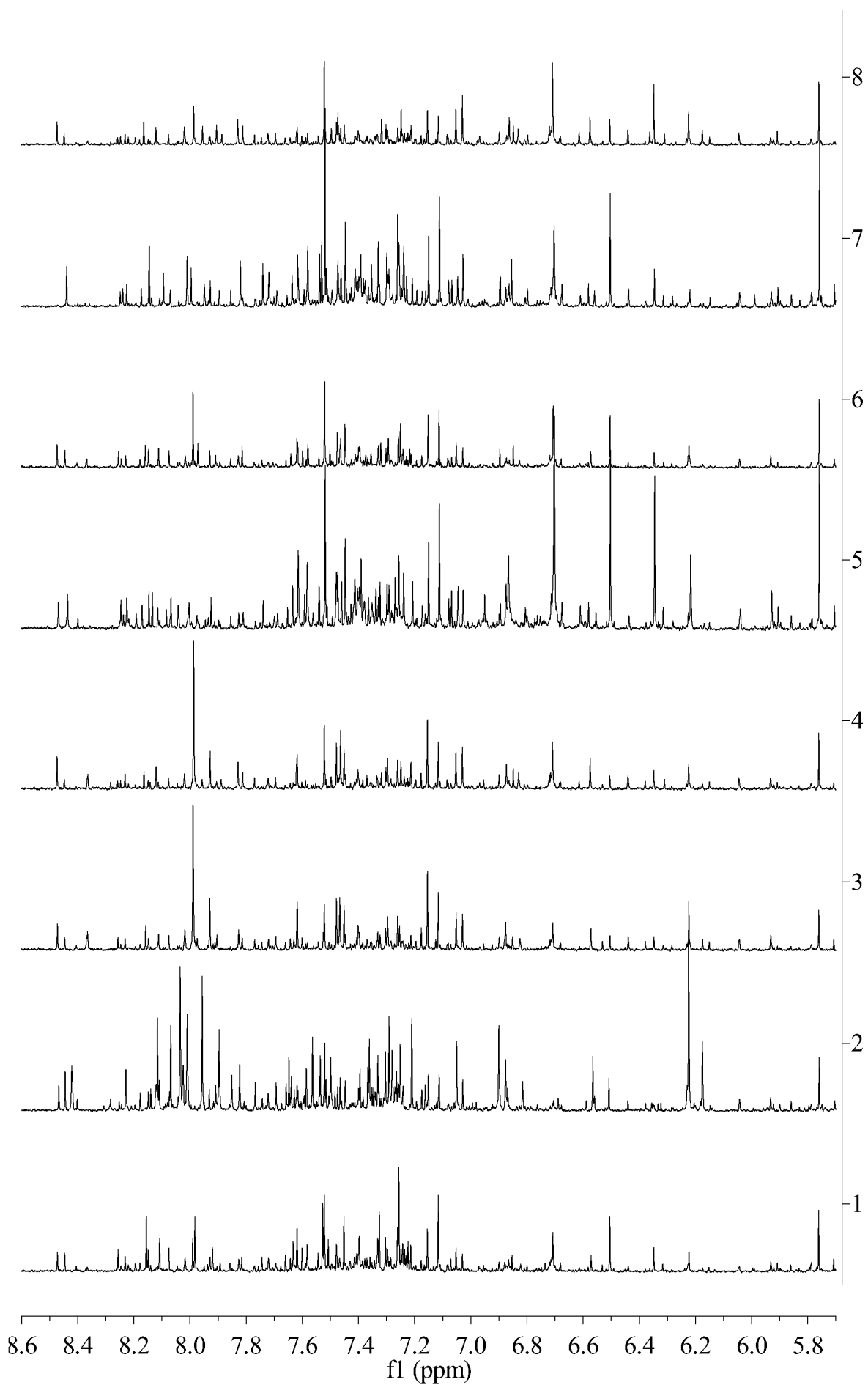


Figure S8

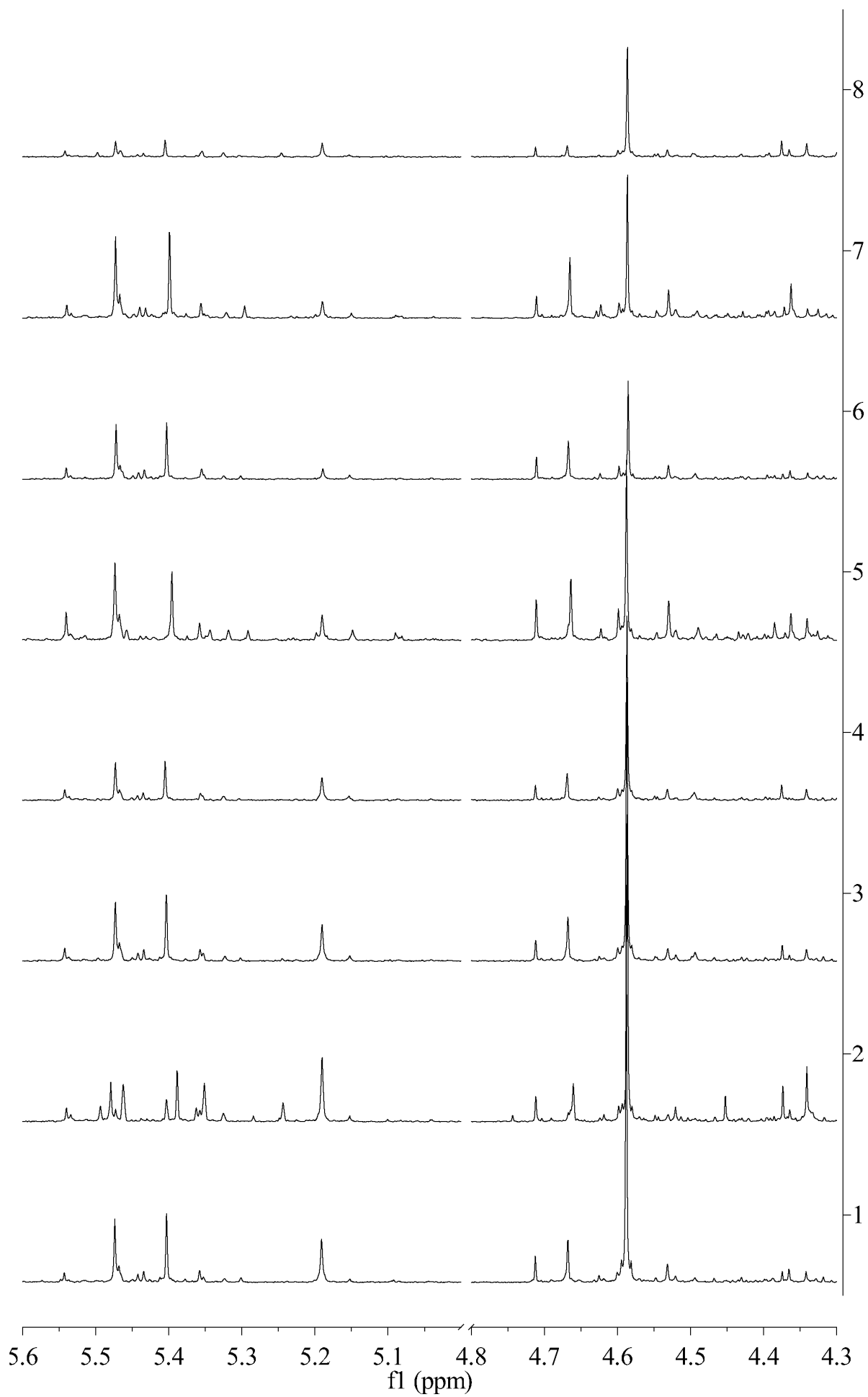


Figure S9

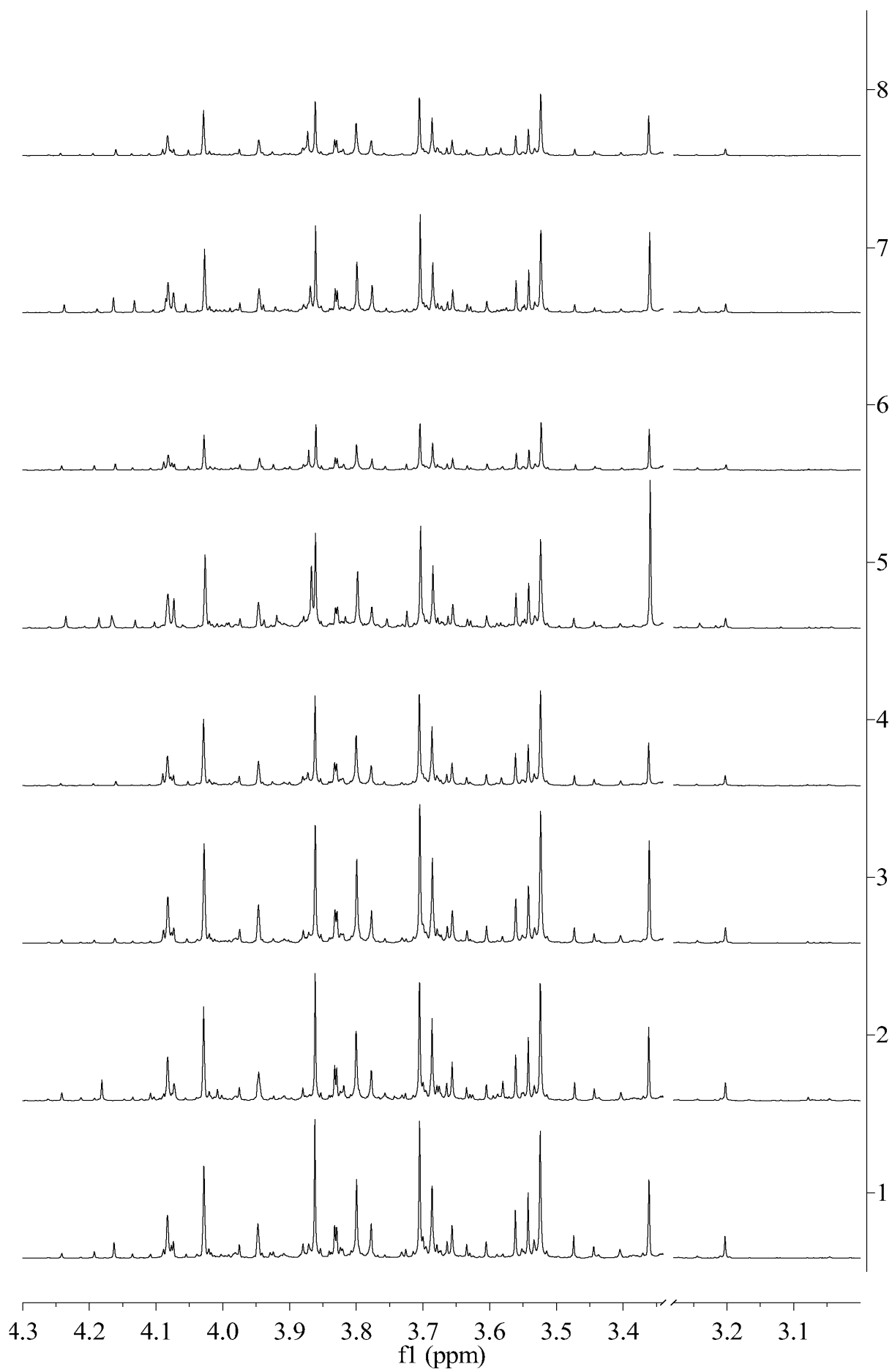


Figure S10

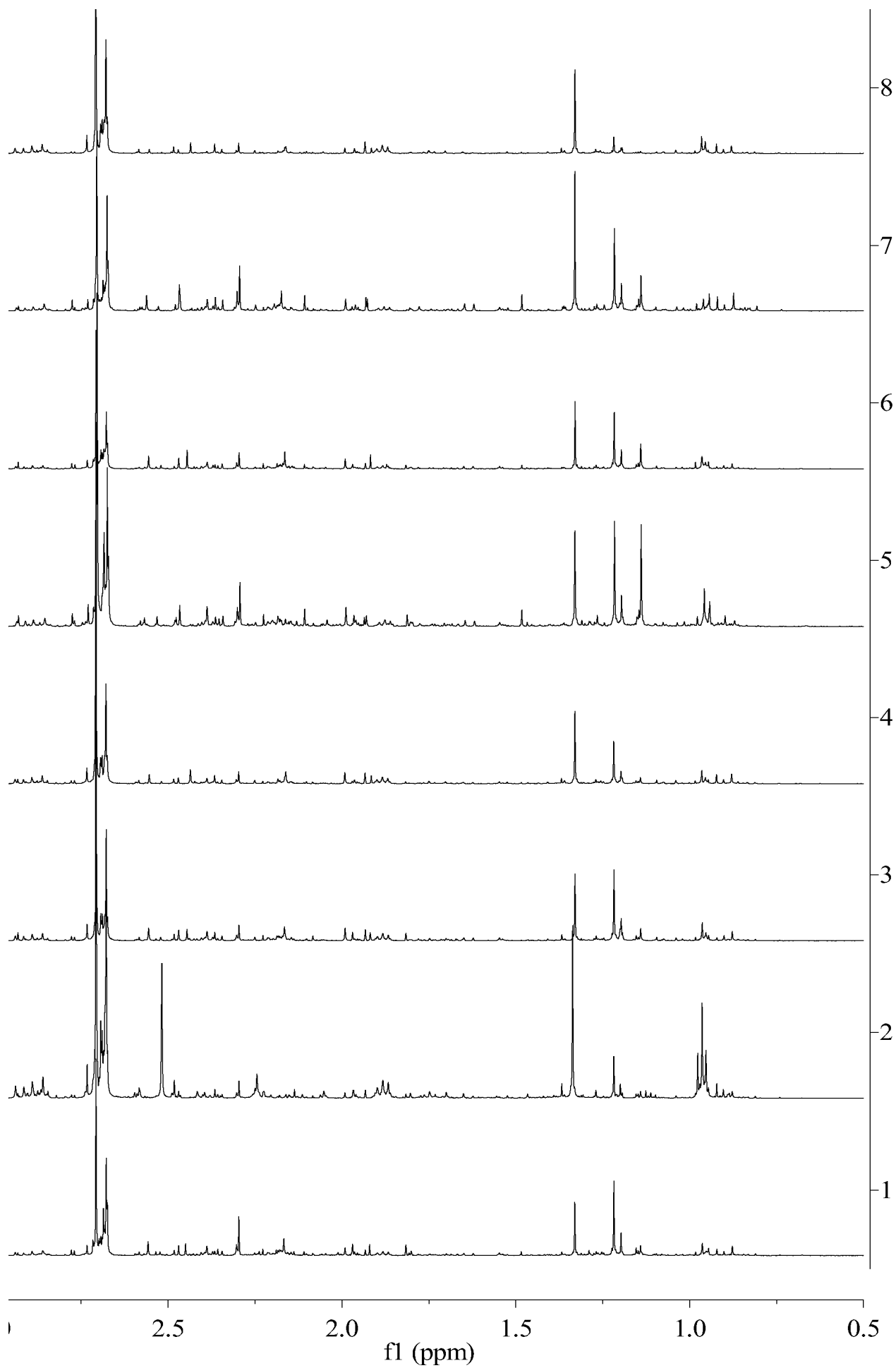
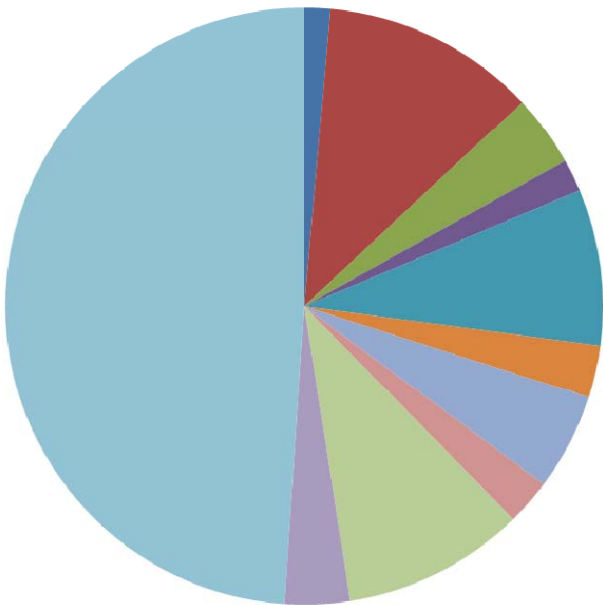
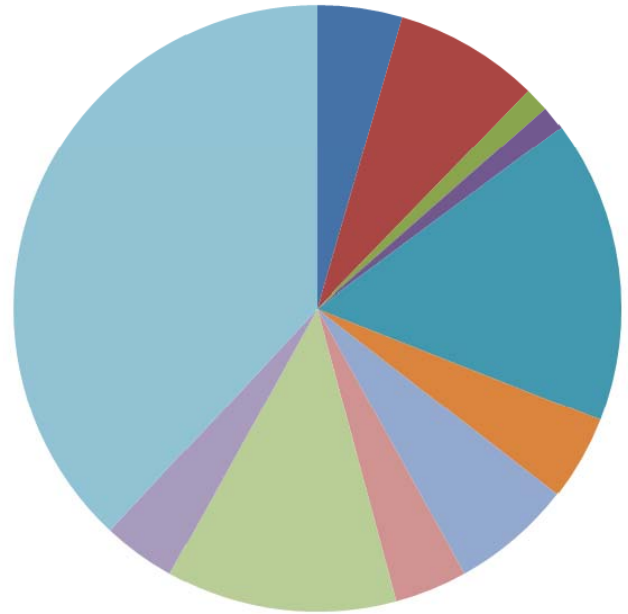


Figure S11

Up-regulated genes

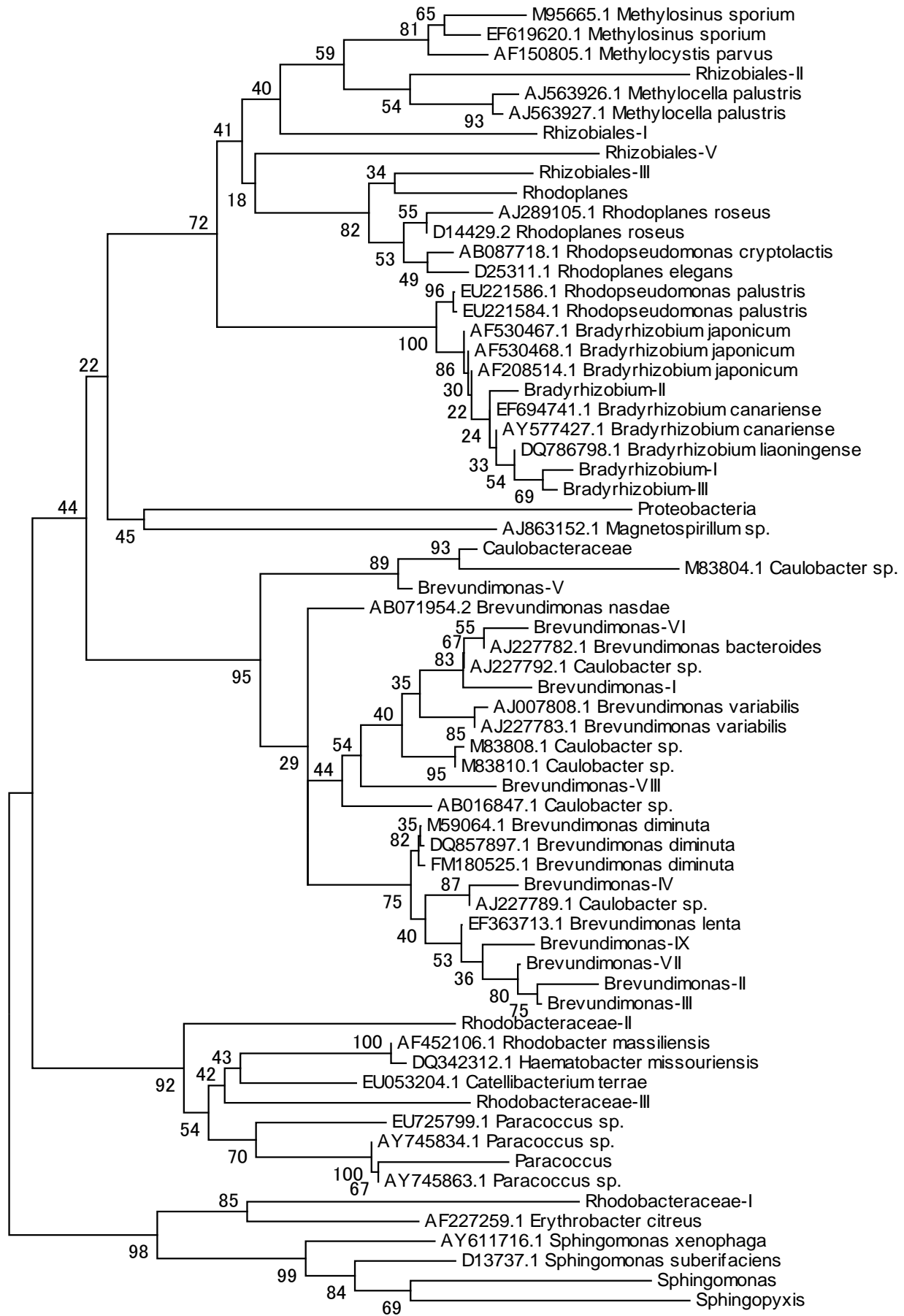


Down-regulated genes



■ Cell Growth, Cell Division and DNA Synthesis	(1.4/4.5)
■ Cell Rescue, Defense, Cell Death and Ageing	(11.6/7.7)
■ Cell Wall	(3.9/1.3)
■ Phytohormone Synthesis and Response	(1.8/1.3)
■ Primary Metabolism	(8.5/16.1)
■ Protein Fate	(2.8/4.5)
■ Secondary metabolism	(5.3/6.5)
■ Signal Transduction	(2.5/3.9)
■ Transcription factor	(9.9/12.3)
■ Transport	(3.5/3.9)
■ Unknown	(48.9/38.1)

Figure S12



0.01

Table S1. Multi-response permutation procedures (MRPP) analysis comparing the microbial community associated with each Arabidopsis ABC transporter mutant. Each row (sample) was relativized by its total and each column (phylotype) was arcsine transformed. Generations were analyzed separately. The values in bold are statistically significant at $P \leq 0.05$, $n = 3$.

	Relative Sorenson Distance ¹	MRPP Analysis ²		
		A-value	t-statistic	p-value
Fungi				
Gen 0	0.707	0.093	-4.88	0.000
Gen 1	0.585	0.025	-1.36	0.090
Gen 2	0.619	0.039	-1.82	0.049
Bacteria				
Gen 0	0.482	0.142	-7.44	0.000
Gen 1	0.418	0.019	-1.16	0.124
Gen 2	0.492	0.036	-2.33	0.015

¹Sorenson distance is the average distance between all samples ($n = 33$) within each generation. ²MRPP analysis (relative Sorenson distance) was conducted for each generation to compare differences between Arabidopsis ABC transporter mutants.

Table S2. Pair wise comparisons (compared to wild type (Col-0) from MRPP analysis comparing the microbial community associated with each Arabidopsis ABC transporter mutant. Each row (samples) was relativized by its total and each column (phylotype) was arcsine transformed. Generations were analyzed separately. The values in bold are statistically significant at $P \leq 0.05$, $n = 3$. *Ler*, Landsberg ecotype; T, negative control (soil without plant).

Mutant	Fungi			Bacteria		
	Gen 0	Gen 1	Gen 2	Gen 0	Gen 1	Gen 2
<i>Ler</i>	0.399	0.053	0.258	0.050	0.055	0.571
T	0.050	0.088	0.748	0.040	0.211	0.353
<i>tt4</i>	0.026	0.762	0.803	0.140	0.277	0.914
<i>abca7</i>	0.022	0.640	0.072	0.024	0.741	0.871
<i>abcg30</i>	0.042	0.791	0.027	0.052	0.383	0.036
<i>abcg34</i>	0.297	0.811	0.552	0.039	0.775	0.798
<i>abcg35</i>	0.096	0.139	0.606	0.138	0.222	0.972
<i>abcc2</i>	0.033	0.583	0.192	0.056	0.166	0.055
<i>abcb1</i>	0.182	0.697	0.309	0.181	0.105	0.436
<i>abcb4</i>	0.053	0.451	0.141	0.037	0.145	0.219

Table S3. Relative NMR intensity of changed metabolites in Col-0 and *abcg30* using projected *J*-resolved spectra (signals are normalized to 1000 of internal standard (TMSP) at δ 0.0*).

Metabolite	Target signal (ppm)	Intensity \pm S.D.		<i>P</i> value
		Col-0	<i>abcg30</i>	
Benzoic acid	7.89	0.28 \pm 0.10	1.26 \pm 0.13	<0.001
Salicylic acid	7.84	0.37 \pm 0.04	0.70 \pm 0.09	<0.001
Syringic acid	7.31	1.19 \pm 0.06	1.88 \pm 0.45	0.025
Tartaric acid	4.36	0.45 \pm 0.02	1.98 \pm 0.05	<0.001
Lactic acid	1.32	8.29 \pm 0.08	22.30 \pm 0.56	<0.001
α -linolenic acid	0.97	4.11 \pm 0.05	21.20 \pm 0.83	<0.001
cyanidin	8.08	0.47 \pm 0.11	1.53 \pm 0.24	<0.001
Sinapic acid and Sinapoyl malate	6.90	0.20 \pm 0.01	1.15 \pm 0.19	<0.001
Valine	1.00	3.08 \pm 0.04	9.22 \pm 0.84	<0.001
Indole-3-acetic acid	7.58	0.81 \pm 0.04	0.89 \pm 0.03	0.026
Raffinose	5.40	2.42 \pm 0.19	0.19 \pm 0.04	<0.001
Glucose	4.58	10.04 \pm 0.08	6.89 \pm 0.20	<0.001
Fructose	4.02	46.31 \pm 0.81	35.97 \pm 1.45	<0.001
Mannitol	3.85	61.64 \pm 0.22	41.69 \pm 1.00	<0.001

* All experiments are based on four replicates.

Table S4. Select list of genes differentially expressed in *abcg30* roots compared with wild type. The genes represented in this list are significantly up- and down-regulated at the value of $P < 0.01$.

Locus ID	Description	Fold-change
Up-regulated genes		
<i>Transport</i>		
At4g22460	Protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	2.16
At3g22120	Protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	2.14
At2g34390	Major intrinsic family protein / MIP family protein	2.03
At3g24290	Ammonium transporter, putative	2.00
At1g07290	Nucleotide-sugar transporter family protein	1.80
At3g27170	Chloride channel protein (CLC-b)	1.76
At1g12110	Nitrate/chlorate transporter (NRT1.1) (CHL1)	1.74
At5g44110	ABC transporter family protein (AtABCI21/AtNAP2)	1.74
At1g76520	Auxin efflux carrier family protein	1.61
At2g26910	ABC transporter family protein (AtABCG32/AtPDR4)	1.53
<i>Secondary metabolism</i>		
At1g47600	Glycosyl hydrolase family 1 protein	3.10
At2g23910	Cinnamoyl-CoA reductase-related	2.65
At3g45130	Cycloartenol synthase, putative	2.24
At2g43840	UDP-glucuronosyl/UDP-glucosyl transferase family protein	2.06
At3g55120	Chalcone-flavanone isomerase / chalcone isomerase (CHI)	2.02
At5g08640	Flavonol synthase 1 (FLS1)	1.88
At3g21560	UDP-glucosyltransferase, putative	1.86

At5g05270	Chalcone-flavanone isomerase family protein	1.80
At1g67980	Caffeoyl-CoA 3-O-methyltransferase, putative	1.79
At2g43820	UDP-glucuronosyl/UDP-glucosyl transferase family protein	1.75
At1g78480	Prenyltransferase/squalene oxidase repeat-containing protein	1.67
At5g13930	Chalcone synthase / naringenin-chalcone synthase	1.65
At5g04950	Nicotianamine synthase, putative	1.62

Transcription factors

At1g06160	Ethylene-responsive factor, putative	2.25
At5g25810	AP2 domain-containing transcription factor TINY (TINY)	2.05
At5g53980	Homeobox-leucine zipper family protein	1.90
At3g56980	Basic helix-loop-helix (bHLH) family protein	1.83
At5g42200	Zinc finger (C3HC4-type RING finger) family protein	1.81
At5g13910	AP2/EREBP-like transcription factor LEAFY PETIOLE, putative	1.80
At5g17800	Myb family transcription factor (MYB56)	1.75
At2g47520	AP2 domain-containing transcription factor, putative	1.74
At3g10910	Zinc finger (C3HC4-type RING finger) family protein	1.71
At1g02220	No apical meristem (NAM) family protein	1.69
At5g53200	Myb family transcription factor (TRIPTYCHON)	1.69
At1g68880	bZIP transcription factor family protein	1.68
At3g46640	Myb family transcription factor	1.68
At2g47460	Myb family transcription factor (MYB12)	1.66
At2g02740	Transcription factor, putative	1.65
At1g50420	Scarecrow-like transcription factor 3 (SCL3)	1.65
At2g17040	No apical meristem (NAM) family protein	1.64

At4g14465	DNA-binding protein-related	1.63
At2g23340	AP2 domain-containing transcription factor, putative	1.63
At1g18400	Basic helix-loop-helix (bHLH) family protein	1.61
At5g01520	Zinc finger (C3HC4-type RING finger) family protein	1.59
At4g11360	Zinc finger (C3HC4-type RING finger) family protein (RHA1b)	1.59
At1g09540	Myb family transcription factor (MYB61)	1.59
At1g13600	bZIP transcription factor family protein	1.57
At1g48000	Myb family transcription factor	1.57
At5g50820	No apical meristem (NAM) family protein	1.56
At5g42140	Zinc finger protein, putative / regulator of chromosome condensation (RCC1) family protein	1.53
At1g15100	Zinc finger (C3HC4-type RING finger) family protein	1.50

Down-regulated genes

Transport

At5g65990	Amino acid transporter family protein	0.48
At4g36670	Mannitol transporter, putative	0.46
At5g02170	Amino acid transporter family protein	0.40
At3g60160	ABC transporter family protein (AtABCC9/AtMRP9)	0.38
At1g08920	Sugar transporter, putative	0.35
At4g04760	Sugar transporter family protein	0.34

Secondary metabolism

At1g64910	Glycosyltransferase family protein	0.50
At3g51450	Strictosidine synthase family protein	0.49

At1g49530	Geranylgeranyl pyrophosphate synthase (GGPS6) / farnesyltranstransferase	0.47
At4g20230	Terpene synthase/cyclase family protein	0.47
At3g31415	Terpene synthase/cyclase family protein	0.47
At4g15340	Pentacyclic triterpene synthase (04C11)	0.45
At3g22250	UDP-glucuronosyl/UDP-glucosyl transferase family protein	0.41
At4g15280	UDP-glucuronosyl/UDP-glucosyl transferase family protein	0.41
At5g42600	Pentacyclic triterpene synthase, putative	0.30

Transcription factors

At2g22750	Basic helix-loop-helix (bHLH) family protein	0.49
At1g71200	Basic helix-loop-helix (bHLH) family protein	0.49
At1g74930	AP2 domain-containing transcription factor, putative	0.48
At4g22950	MADS-box protein (AGL19)	0.45
At1g65920	Regulator of chromosome condensation (RCC1) family protein / zinc finger protein-related	0.43
At1g69490	No apical meristem (NAM) family protein	0.43
At3g57920	Squamosa promoter-binding protein, putative	0.42
At1g19210	AP2 domain-containing transcription factor, putative	0.38
At2g44840	Ethylene-responsive element-binding protein, putative	0.35
At4g34410	AP2 domain-containing transcription factor, putative	0.34
At3g53600	Zinc finger (C2H2 type) family protein	0.31
At1g35625	Protease-associated zinc finger (C3HC4-type RING finger) family protein	0.27
At2g46510	Basic helix-loop-helix (bHLH) family protein	0.19

Table S5. *In vitro* analysis of the Arabidopsis wild type (Col-0), *abcg30* root exudates and MS liquid media (control) effect on Arabidopsis soil microbes by plate counting assay. Values represented are the mean values of three independent experimental results. The readings were taken at two time points 24 and 48 hrs after plating. The values represent in parentheses are counts observed at 48 hr.

Soil dilutions	Col-0 root exudates	<i>abcg30</i> root exudates	MS media
10 ⁻²	BL (BL)	BL (BL)	42±7(68±8)
10 ⁻³	BL (BL)	BL (BL)	3±1 (12±3)
10 ⁻⁴	BL (BL)	BL (BL)	0±0 (0±)
10 ⁻⁵	280±15 (BL)	0±0 (71±14)	0±0 (0±)

BL, bacterial lawn

Table S6. List of ABC transporters and their T-DNA KO mutants used in this study.

Locus ID	New synthetic name	Synonym	Mutant name	Reference
At4g15230	<i>abcg30</i>	<i>AtPDR2</i>	garlic_811_F08*	Badri et al., (2008)
At2g36380	<i>abcg34</i>	<i>AtPDR6</i>	garlic_627_F11*	Badri et al., (2008)
At1g15210	<i>abcg35</i>	<i>AtPDR7</i>	Salk_134725	Badri et al., (2008)
At2g34660	<i>abcc2</i>	<i>AtMRP2</i>	Salk_128332	Badri et al., (2008)
At3g47780	<i>abca7</i>	<i>AtATH6</i>	Salk_104795	Badri et al., (2008)
At2g36910	<i>abcb1</i>	<i>AtPgp1</i>	Salk_046440	Badri et al., (2008)
At2g47000	<i>abcb4</i>	<i>AtPgp4</i>	Salk_010207	Santelia et al., (2005)

*Currently named as SAIL lines; All T-DNA KO lines are in Arabidopsis wild type (Col-0) background.