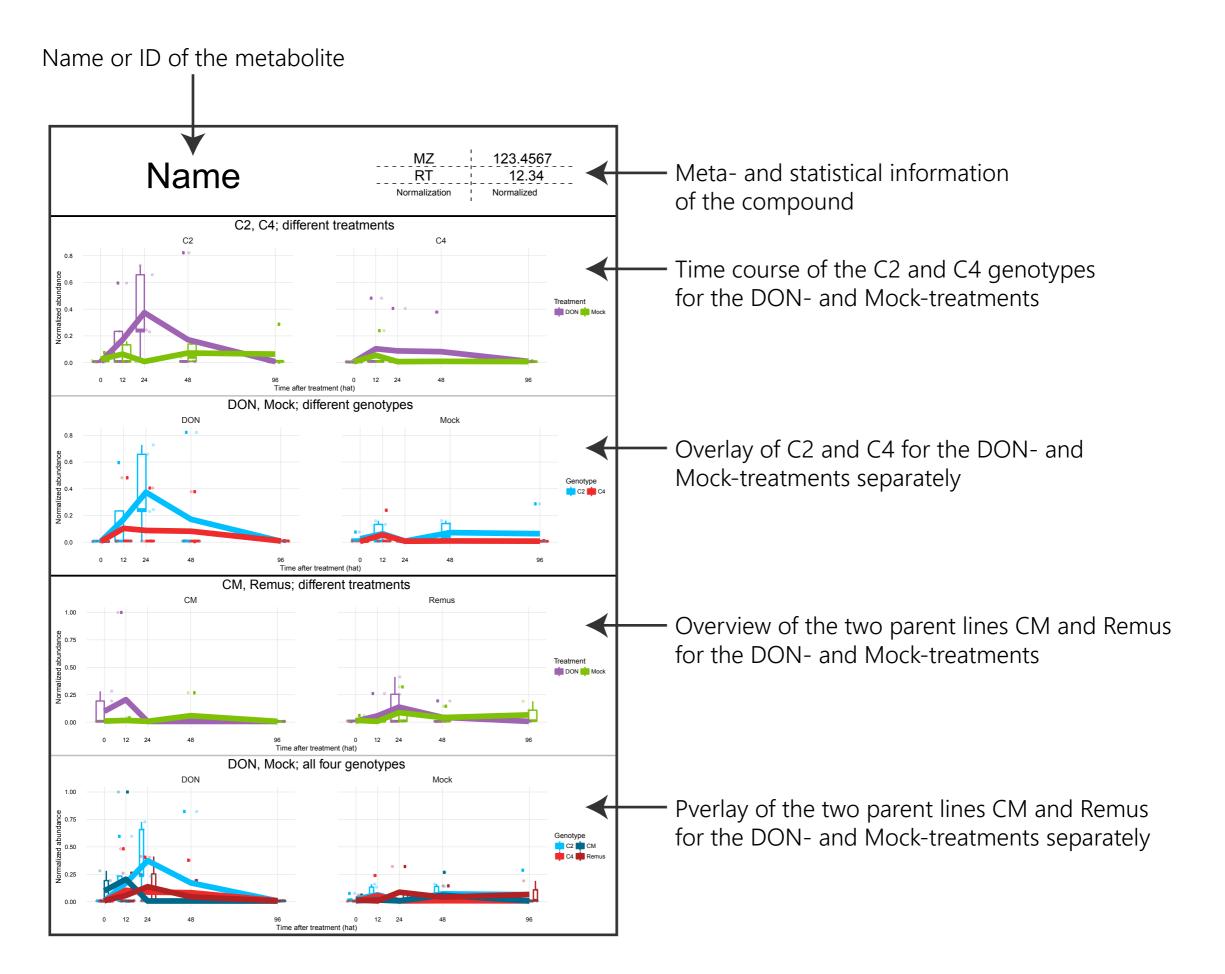
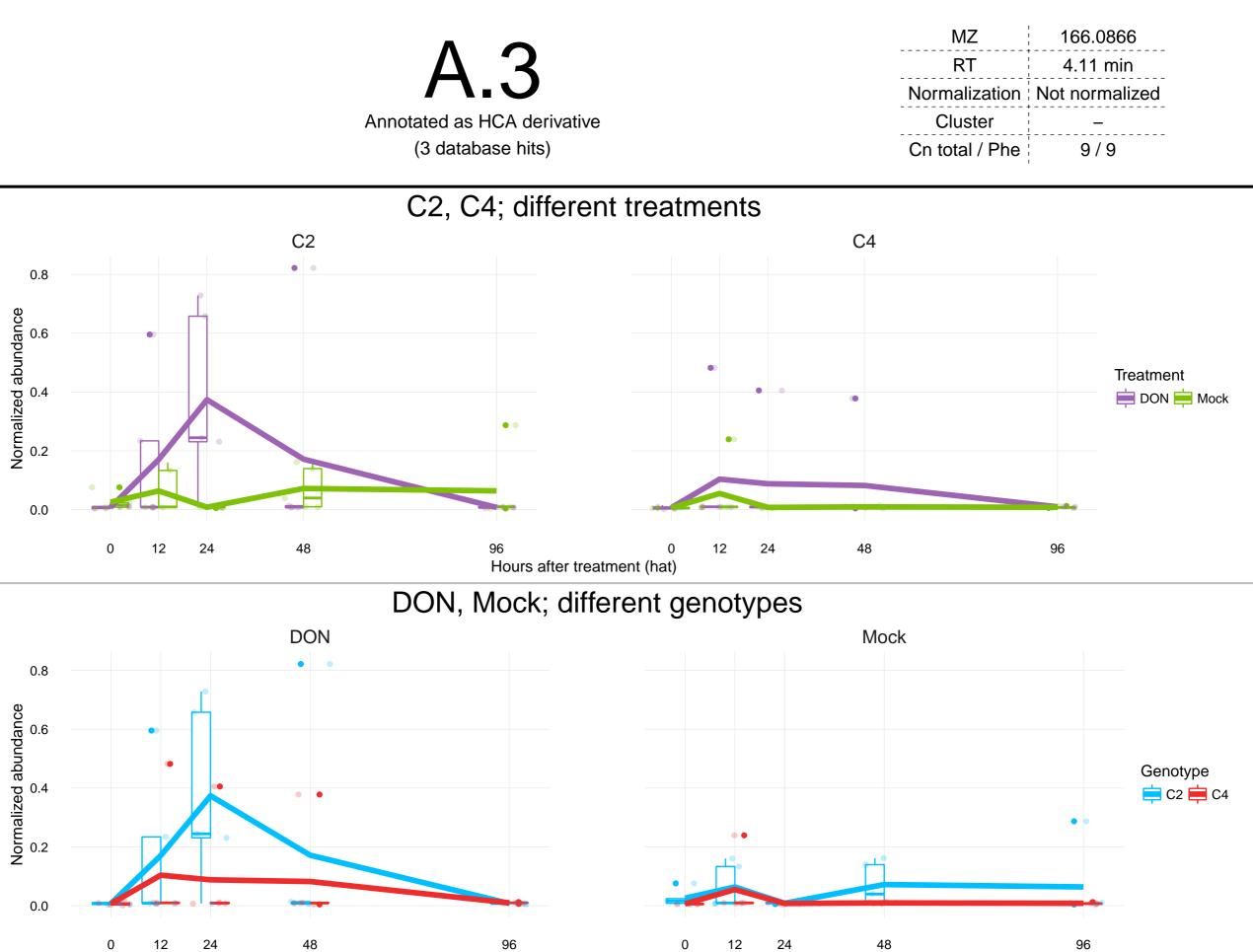
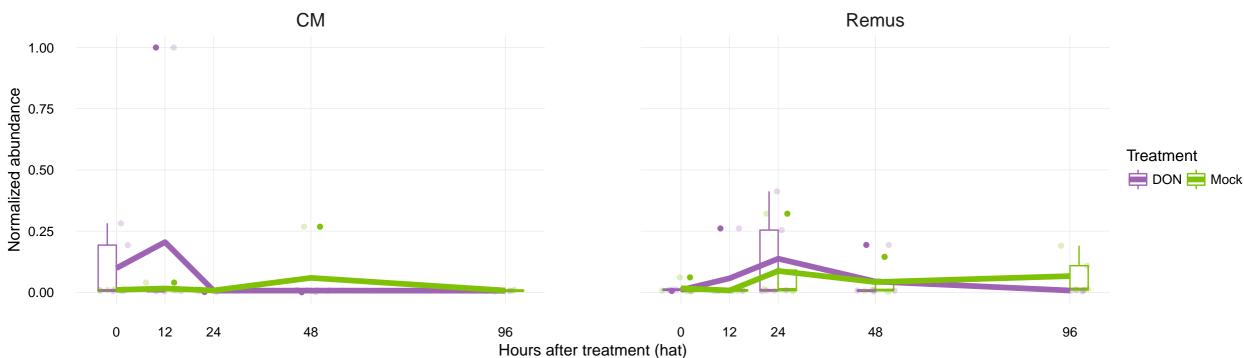
Supplementary Information 1:

This supplementary figure shows an overview of all Phe-derived metabolites (n=172) detected in the above shown publication. Each page illustrates the time course (mean values) of the metabolite abundances in the different treatments and/or genotypes respectively. Moreover, "QTL" or "TR+/-" labels indicate if there is a significant difference between the time points and/or genotypes. Please refer to the materials and methods part of the main text for the calculation of these indicator labels.

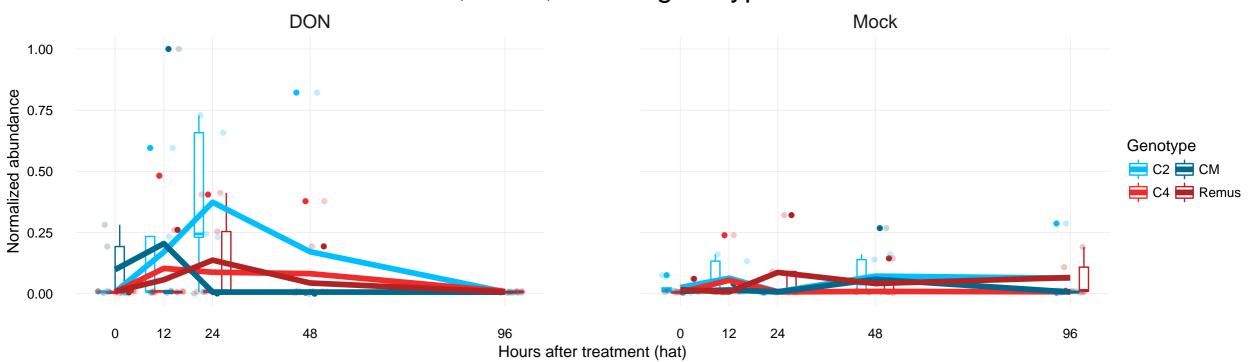




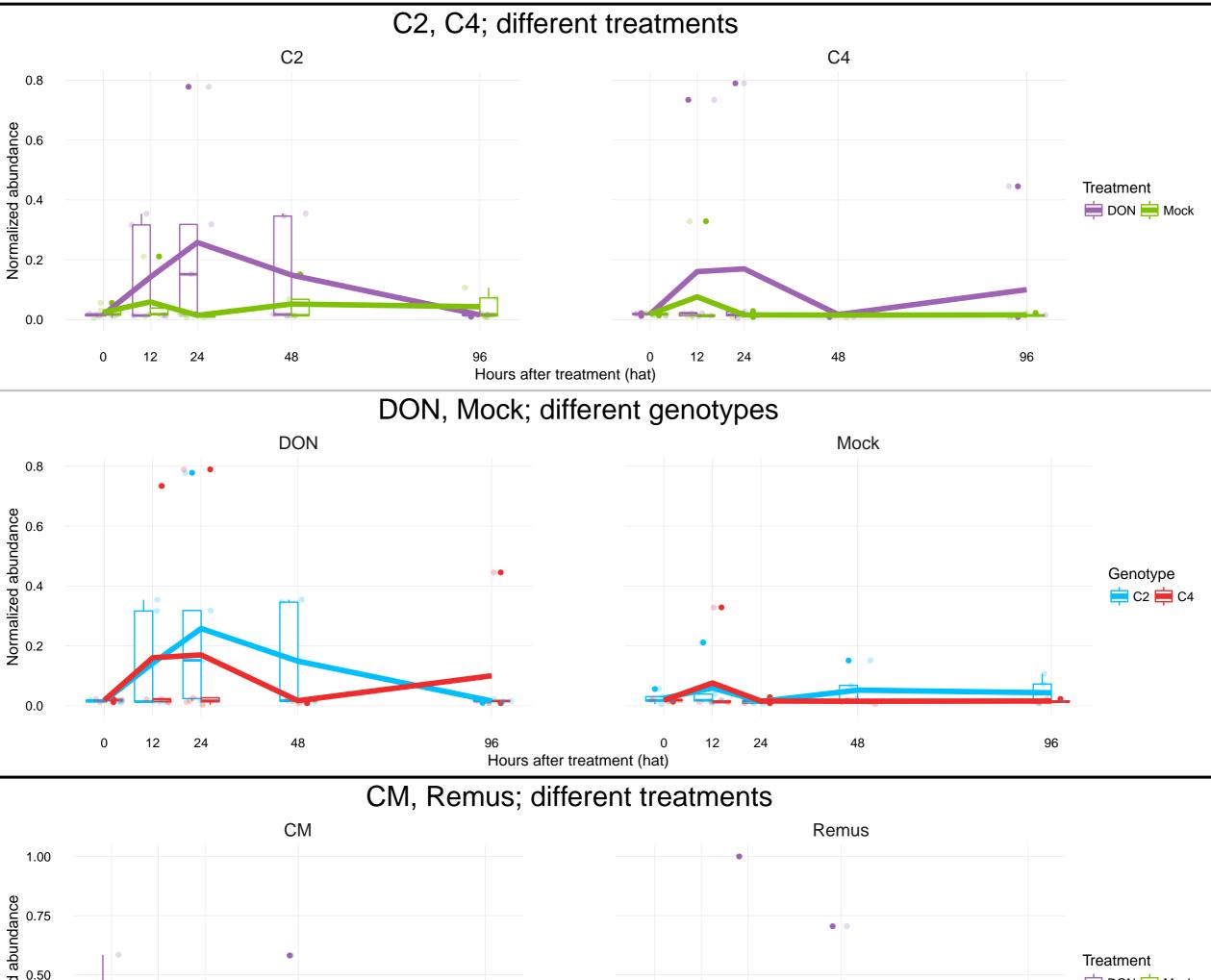
CM, Remus; different treatments

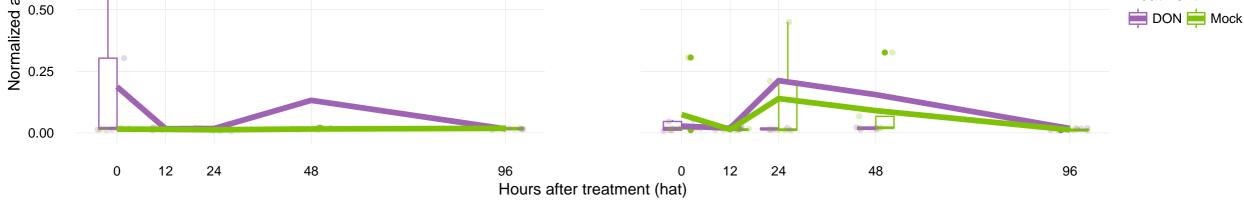


DON, Mock; all four genotypes

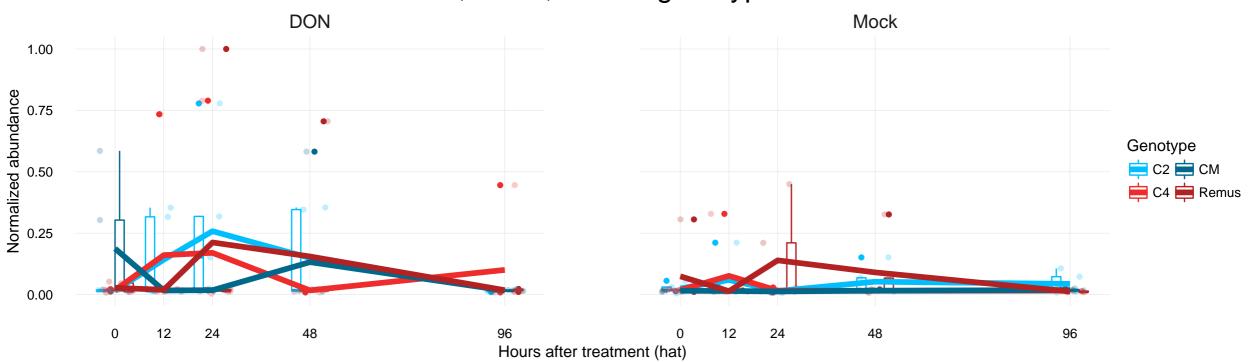


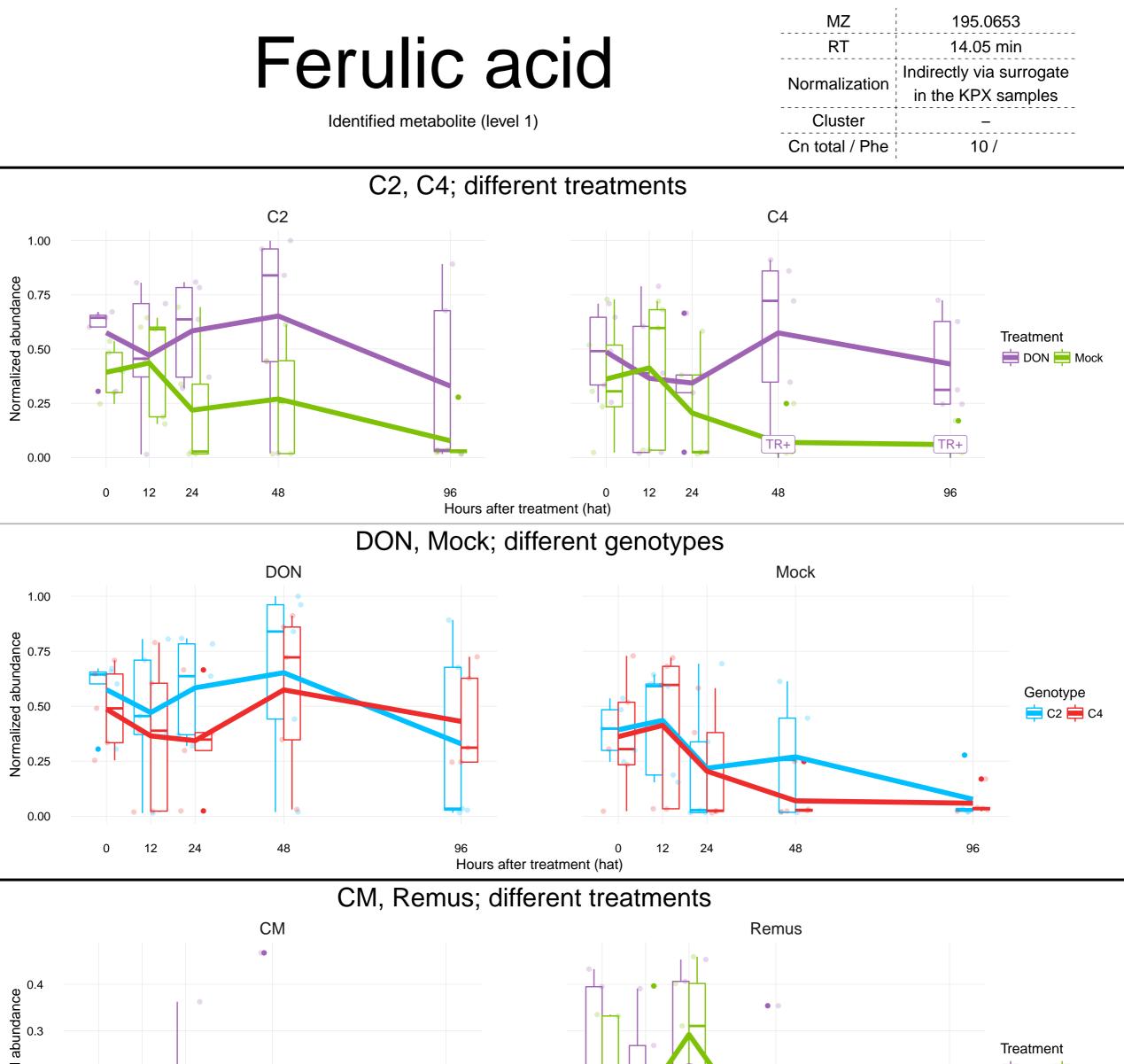


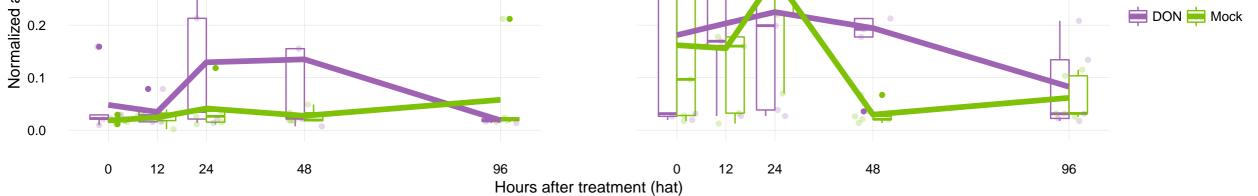




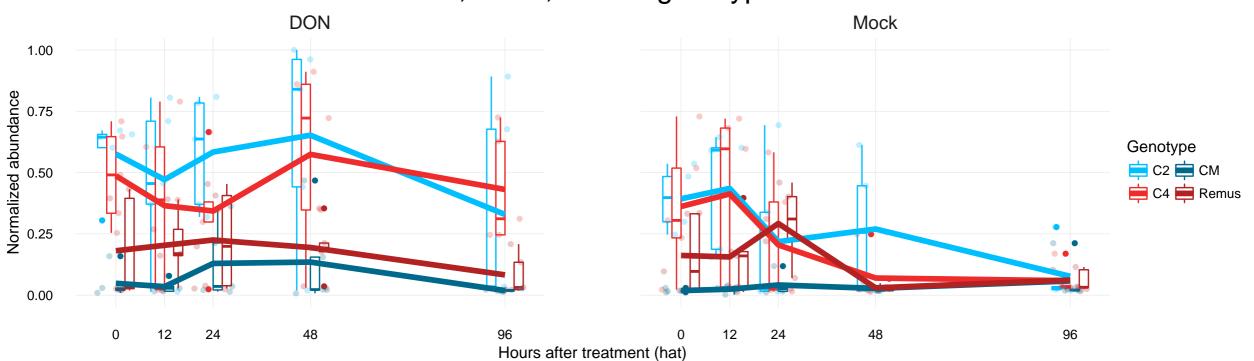
DON, Mock; all four genotypes

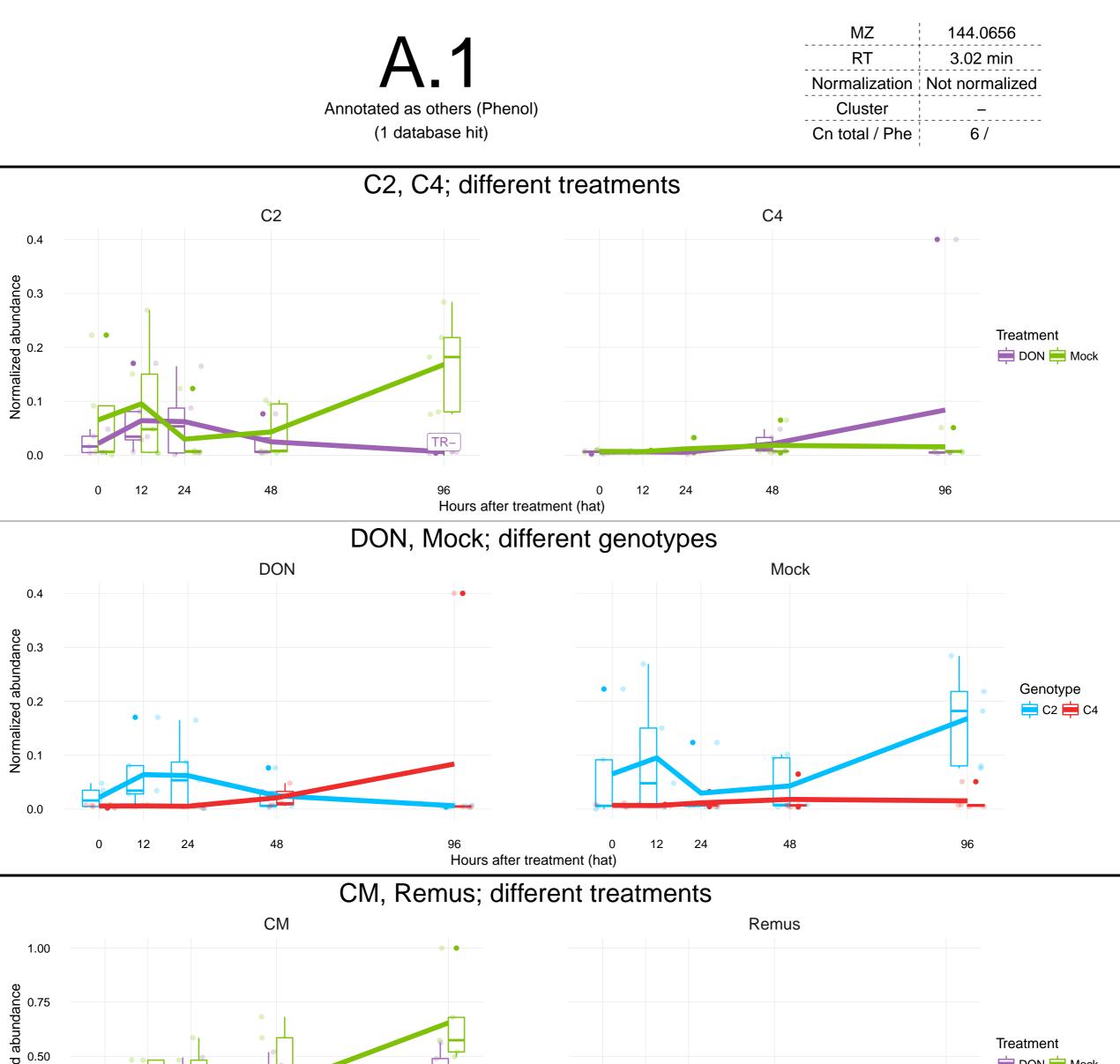


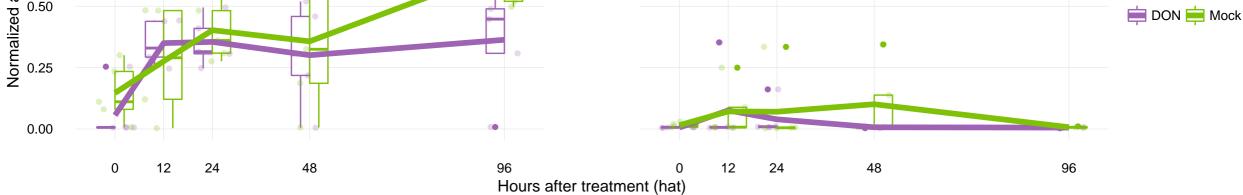




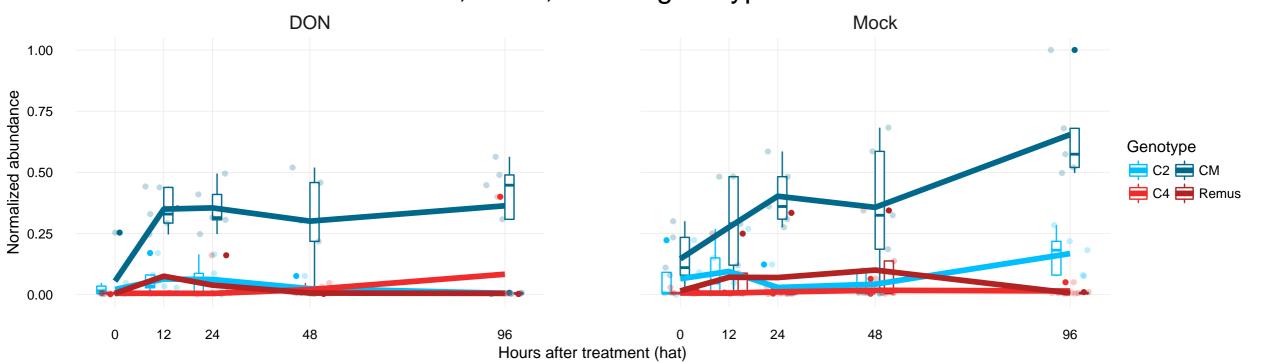
DON, Mock; all four genotypes







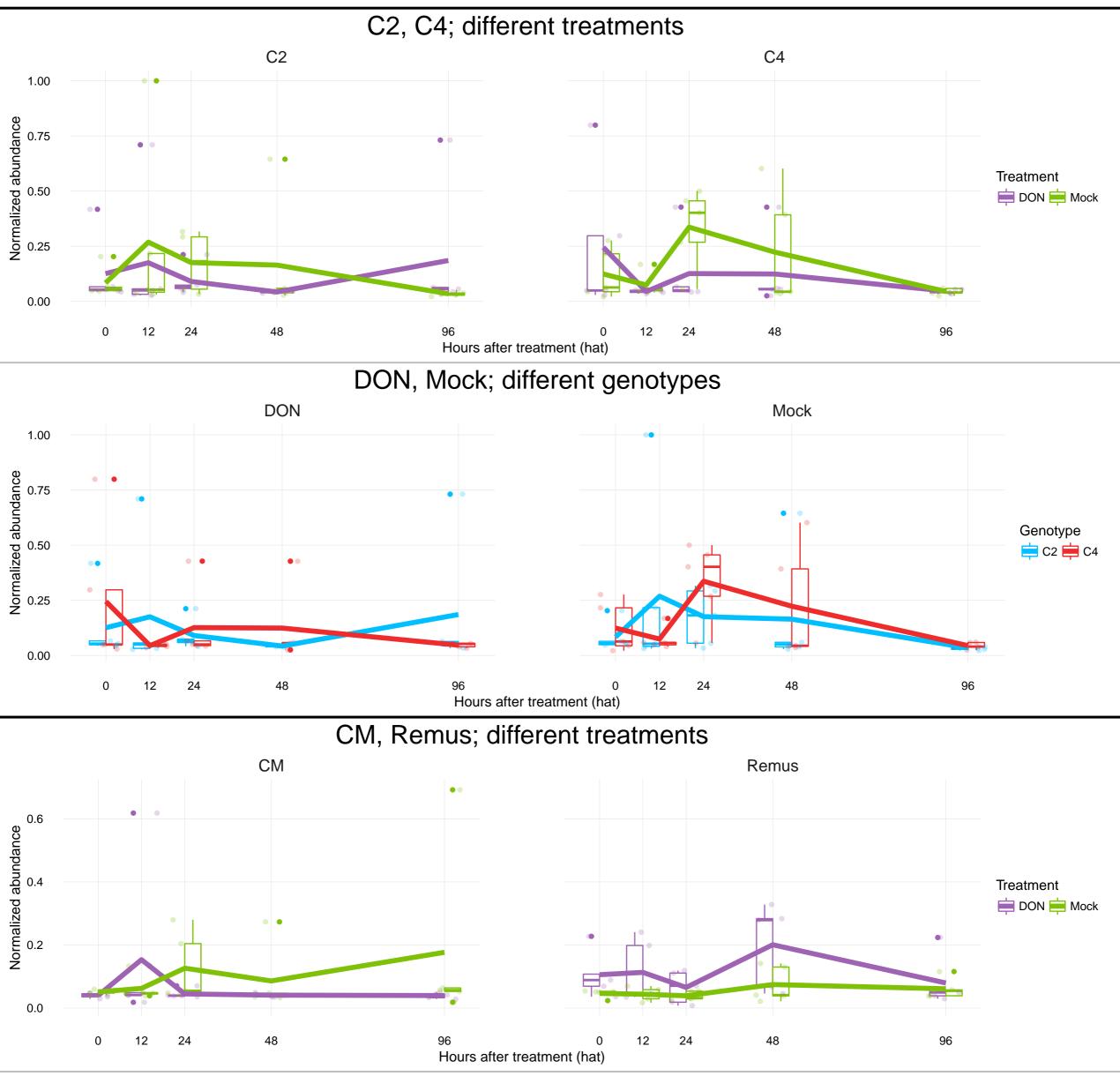
DON, Mock; all four genotypes



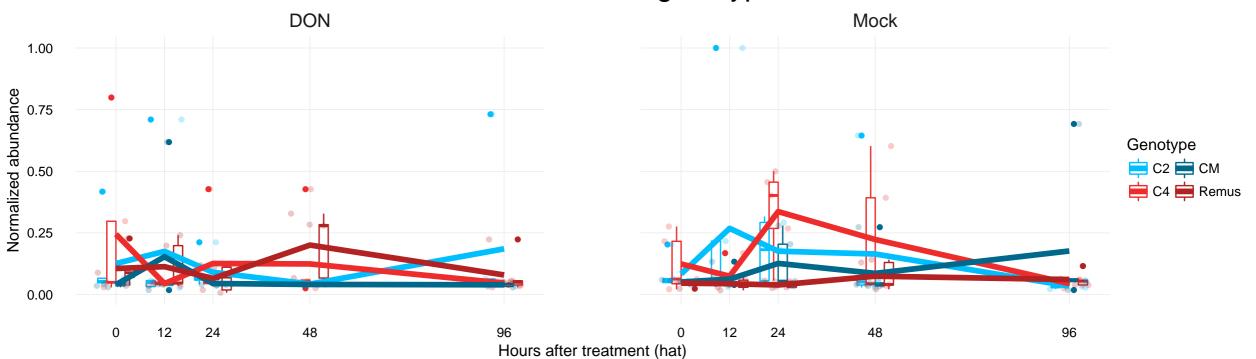
p-coumaric acid

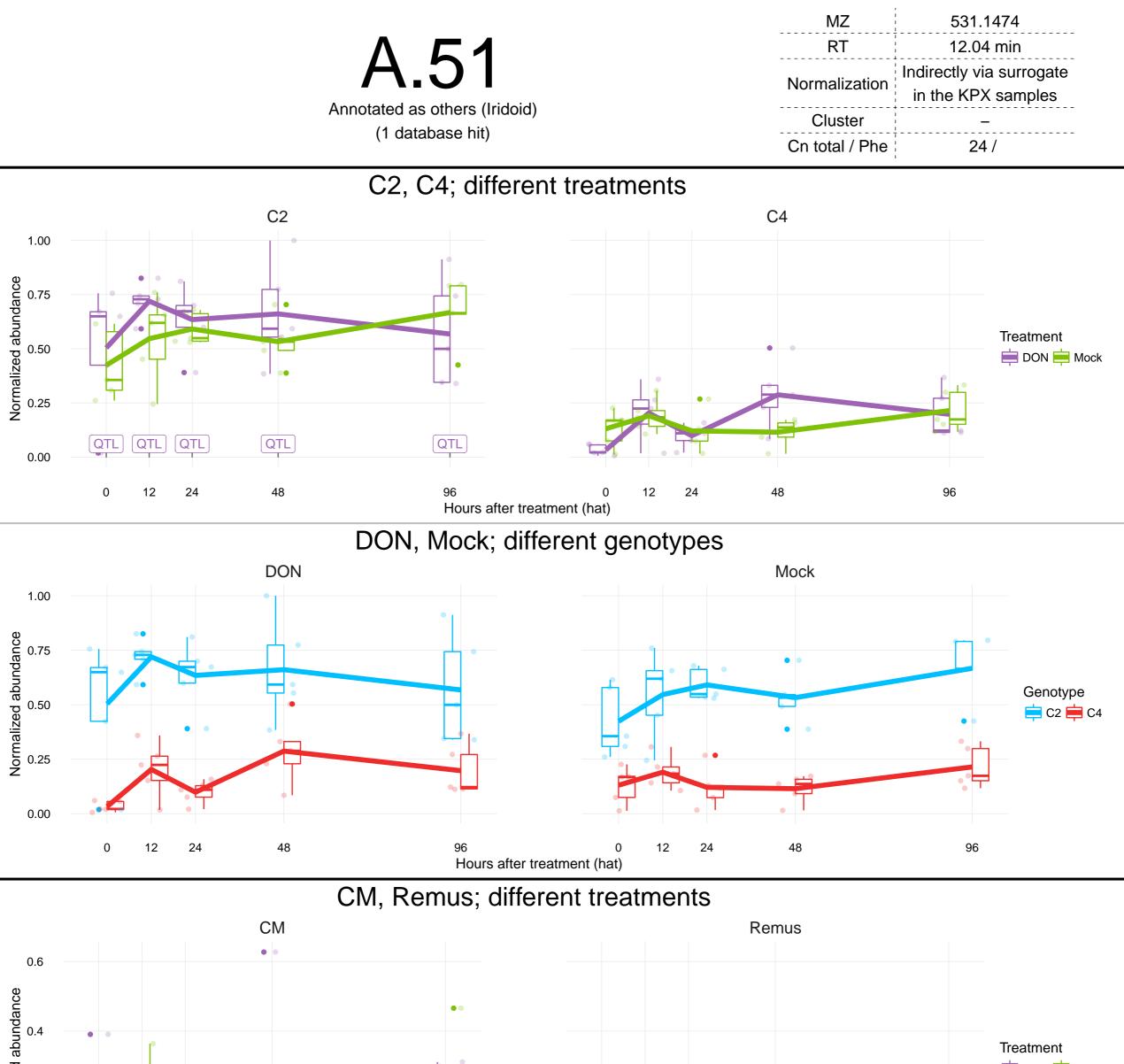
Identified metabolite (level 1)

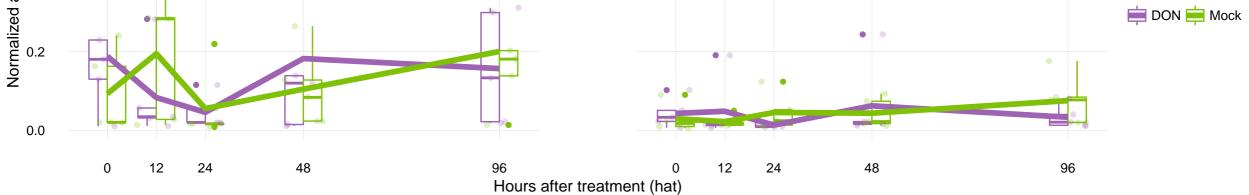
MZ	165.0546
RT	13.41 min
Normalization	Indirectly via surrogate in the KPX samples
Cluster	_
Cn total / Phe	9/



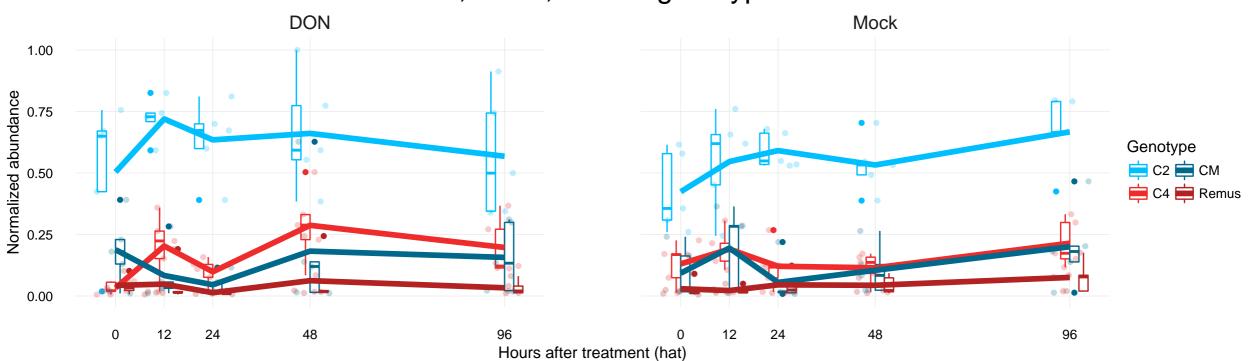
DON, Mock; all four genotypes

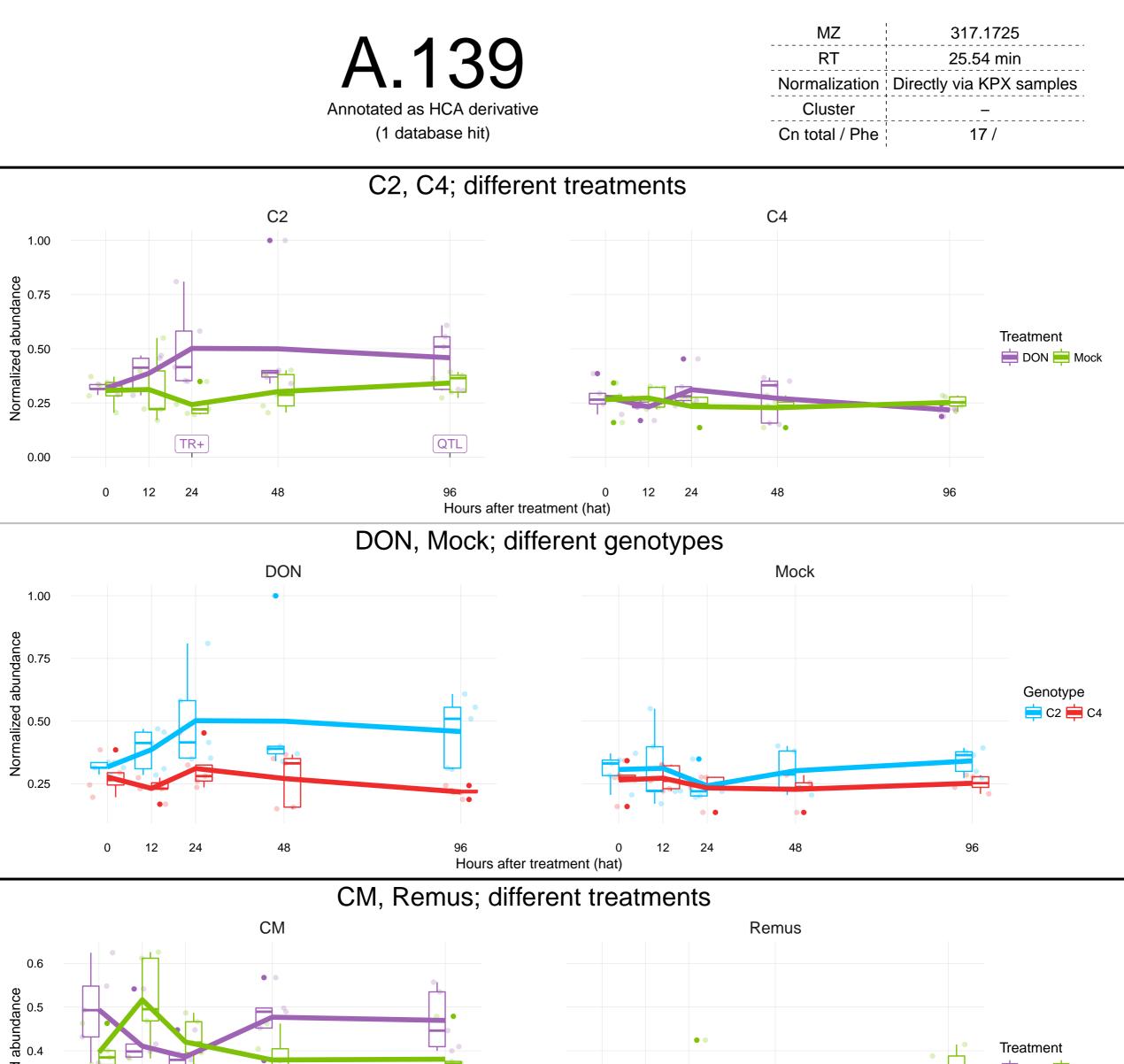


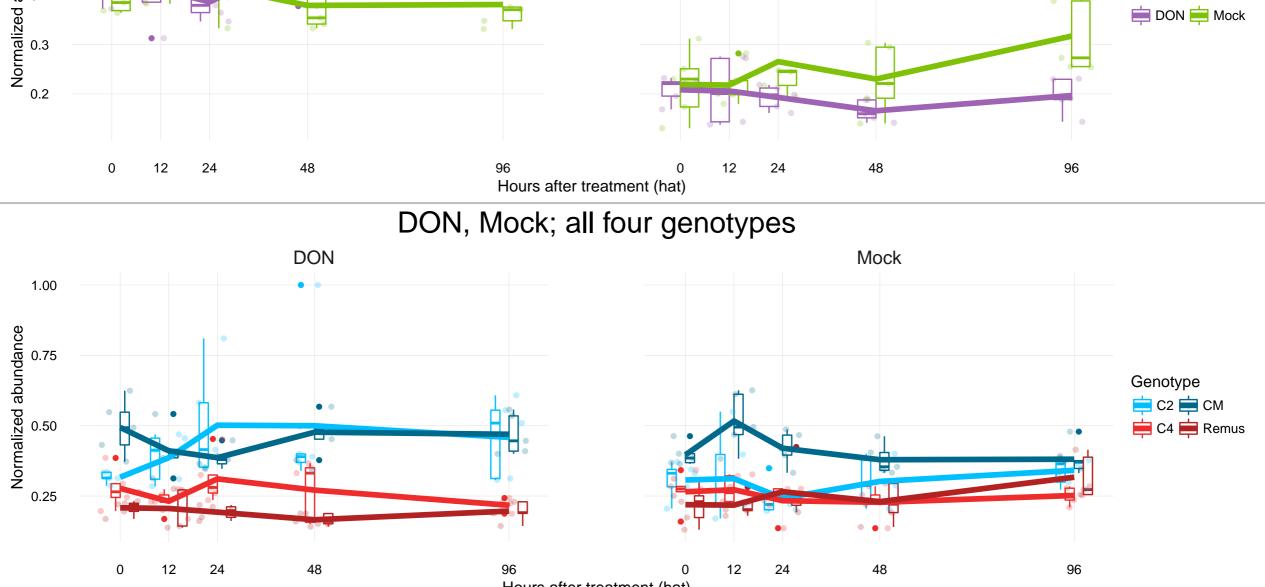




DON, Mock; all four genotypes

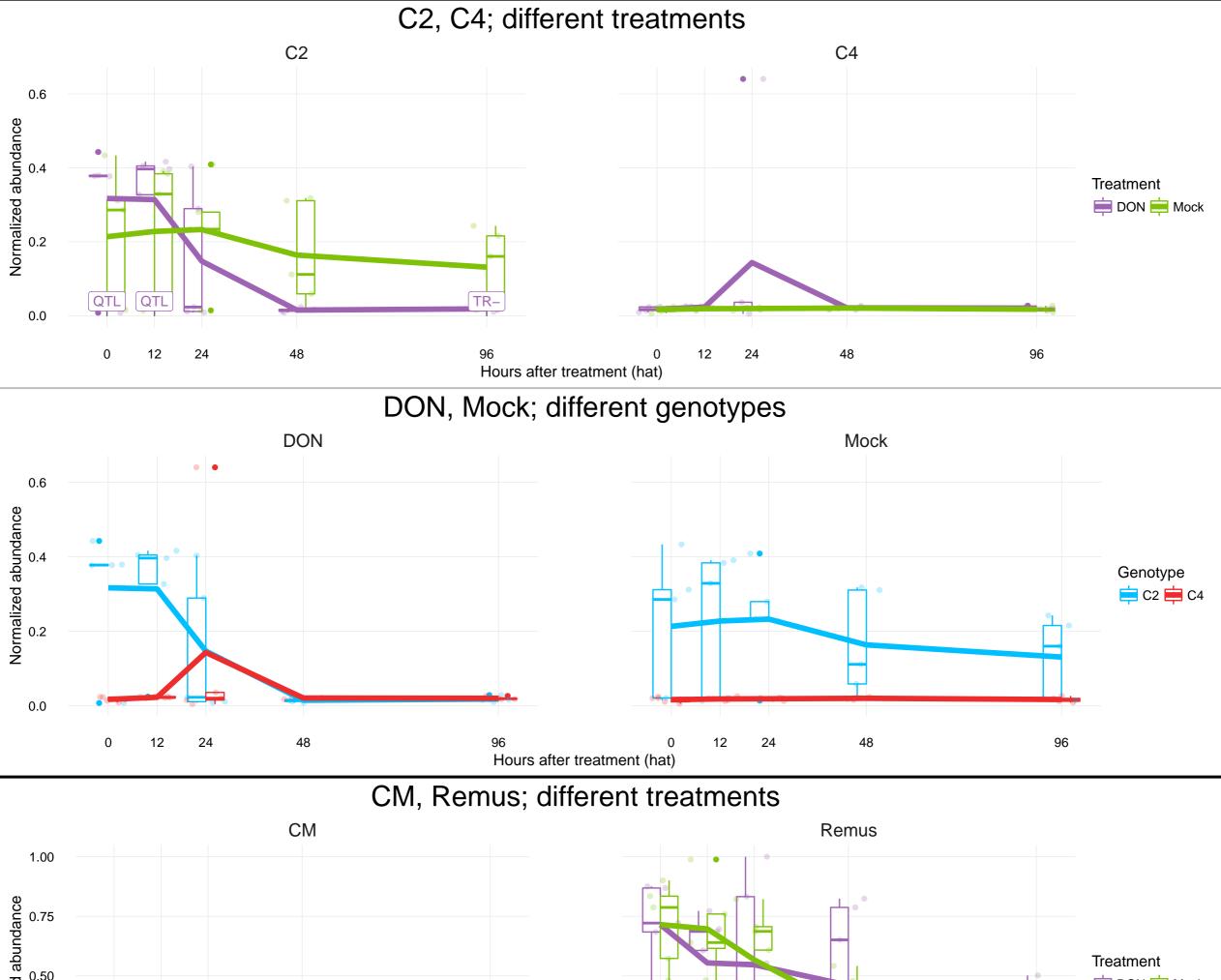


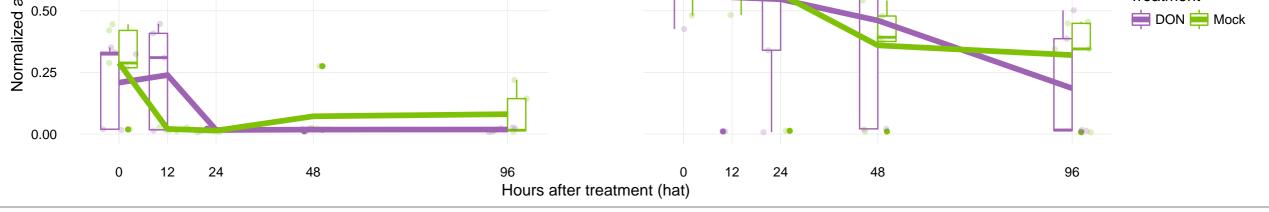




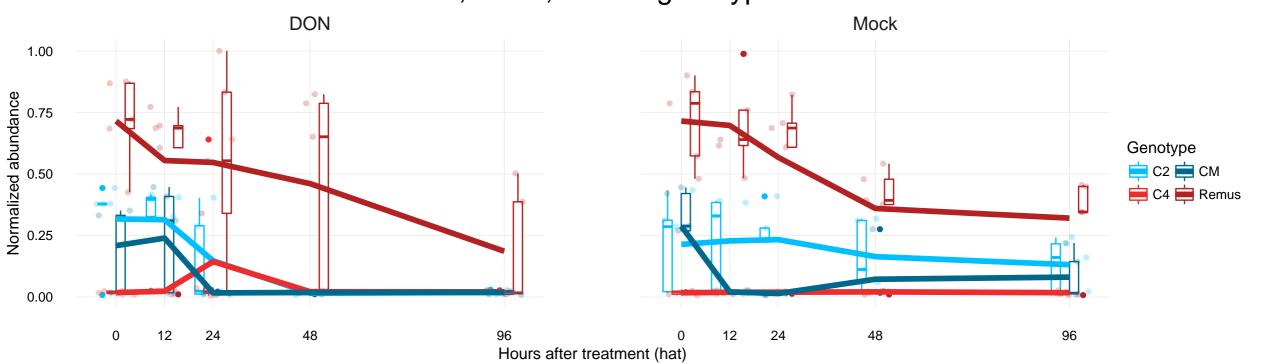
Hours after treatment (hat)

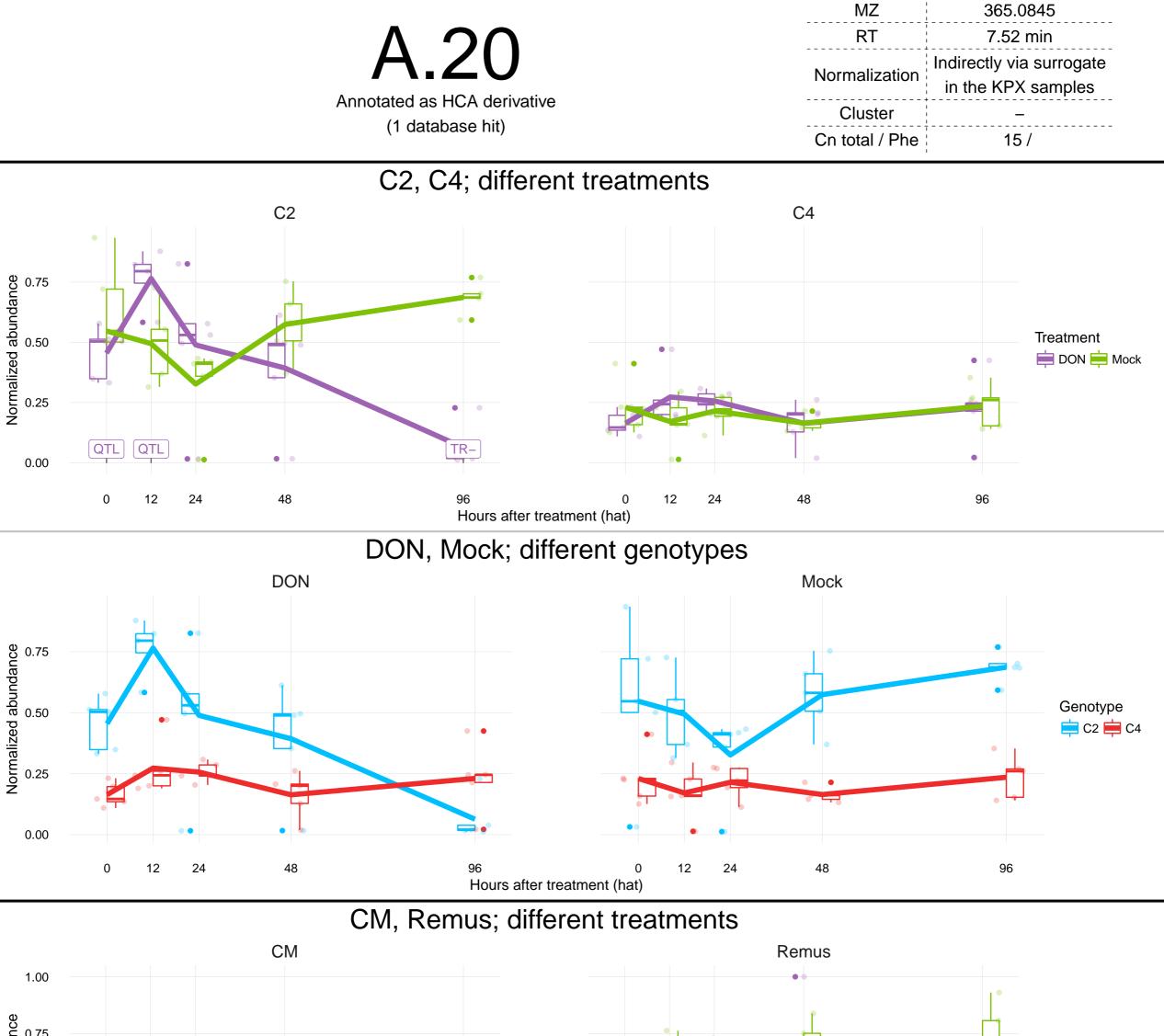


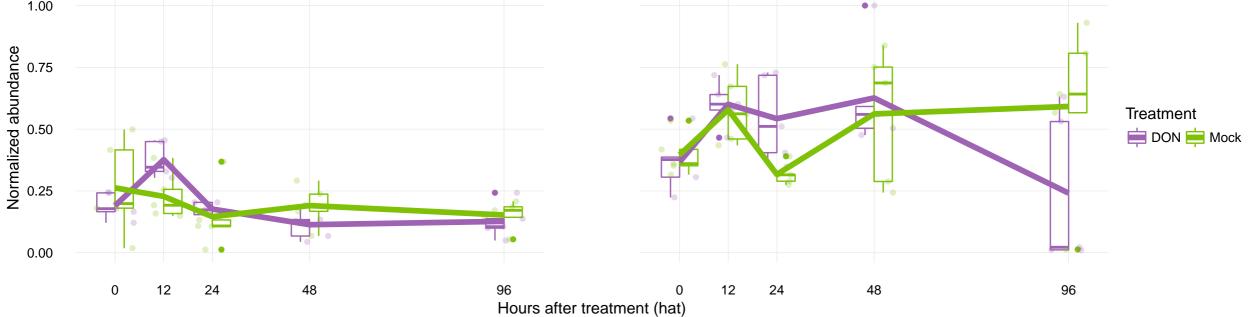




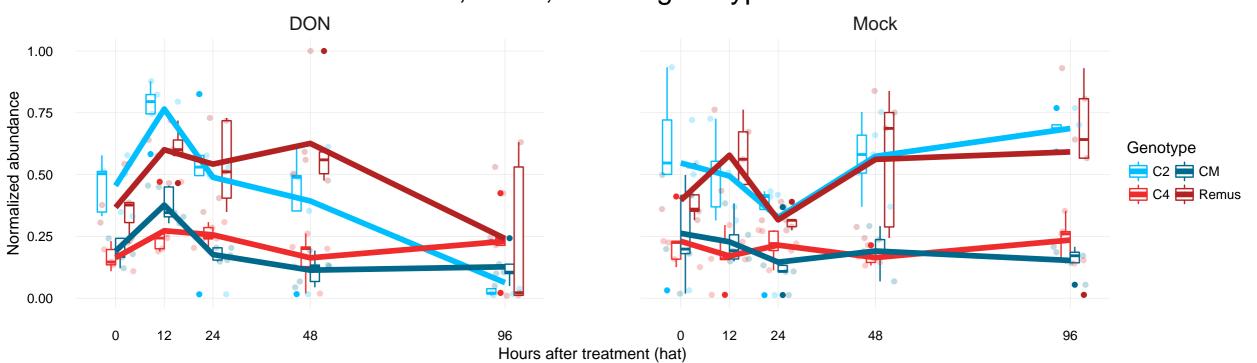
DON, Mock; all four genotypes

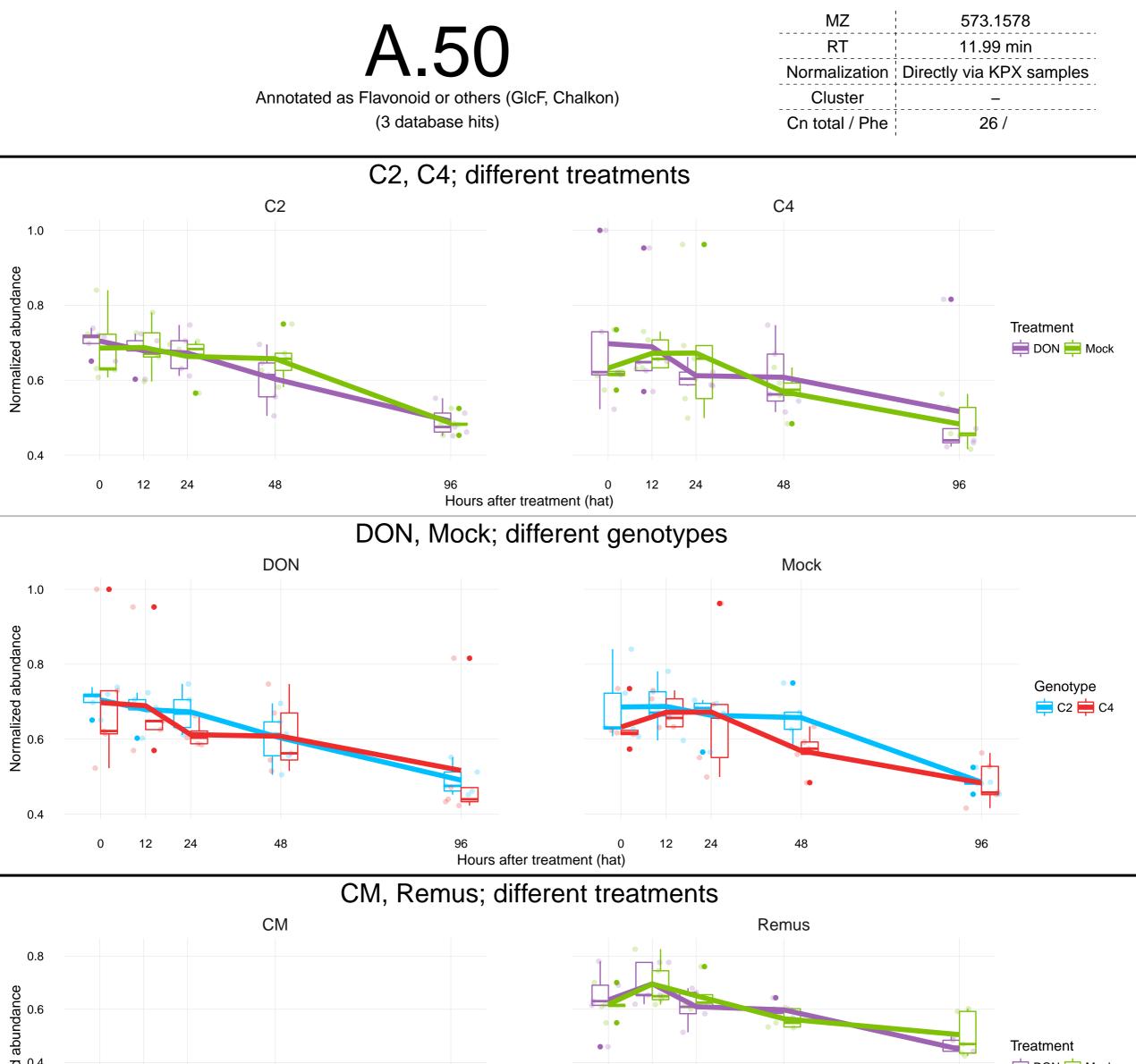


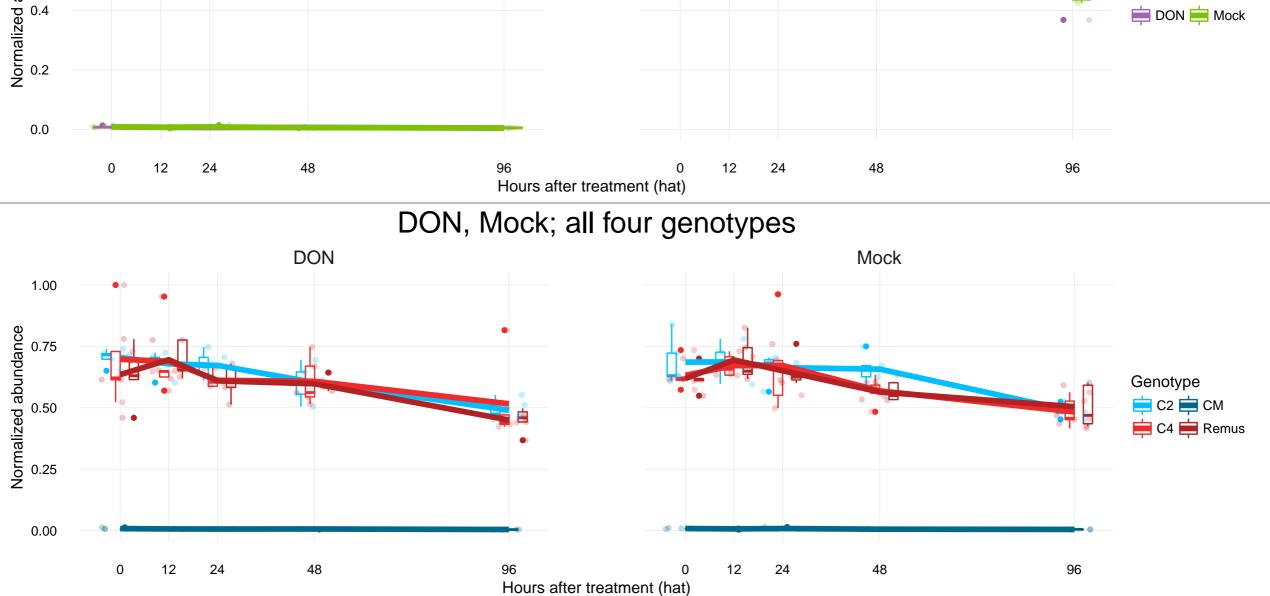


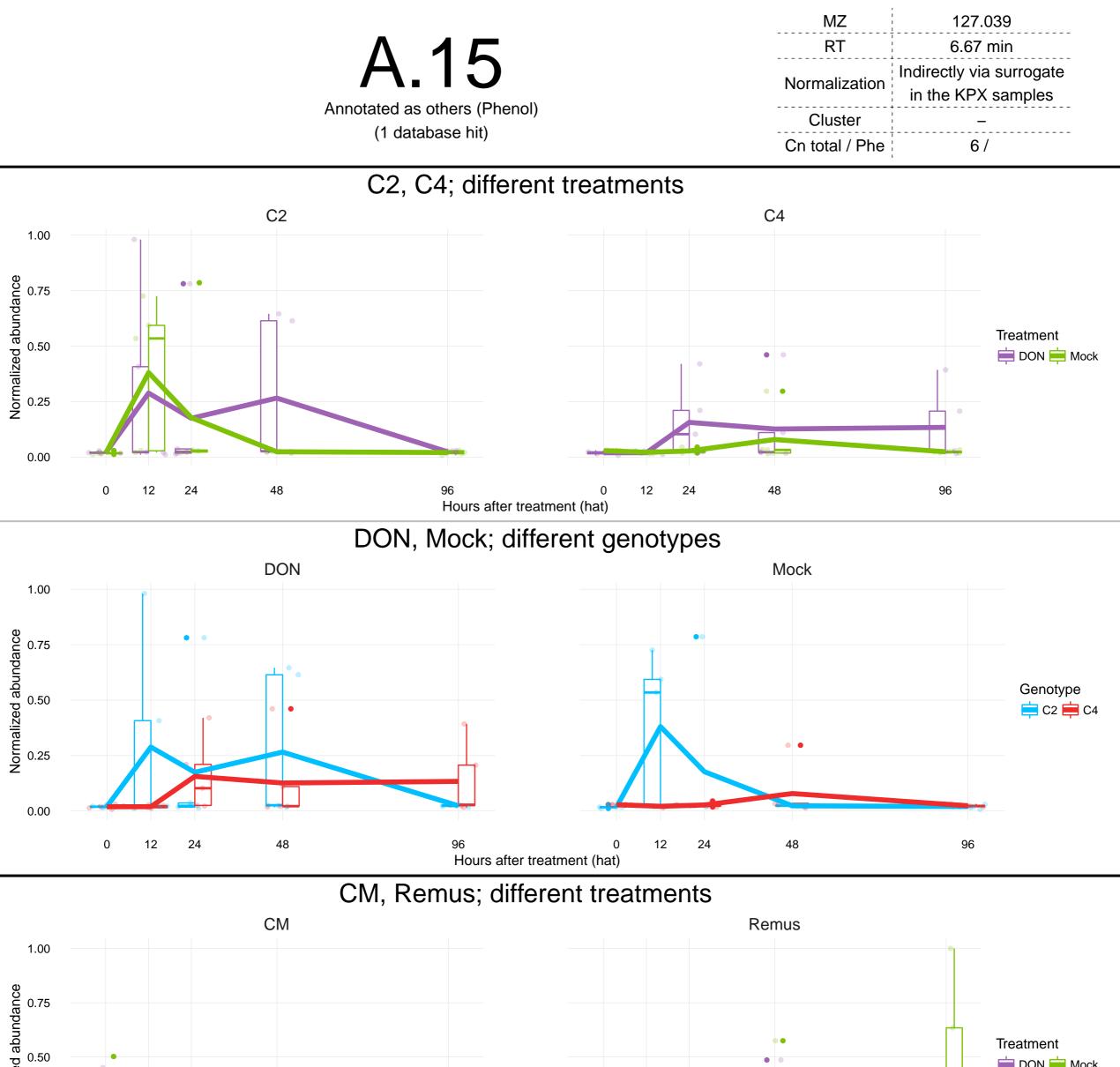


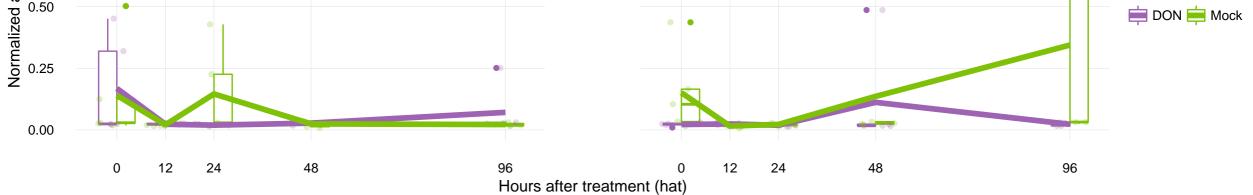
DON, Mock; all four genotypes



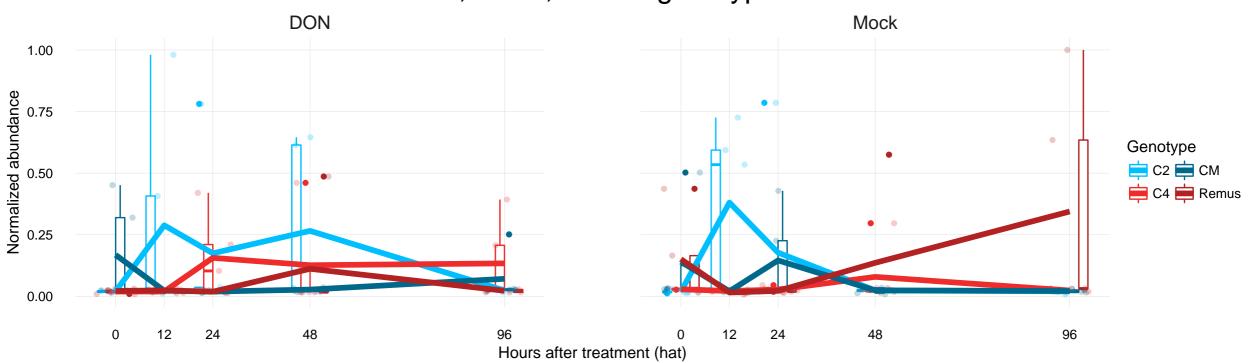


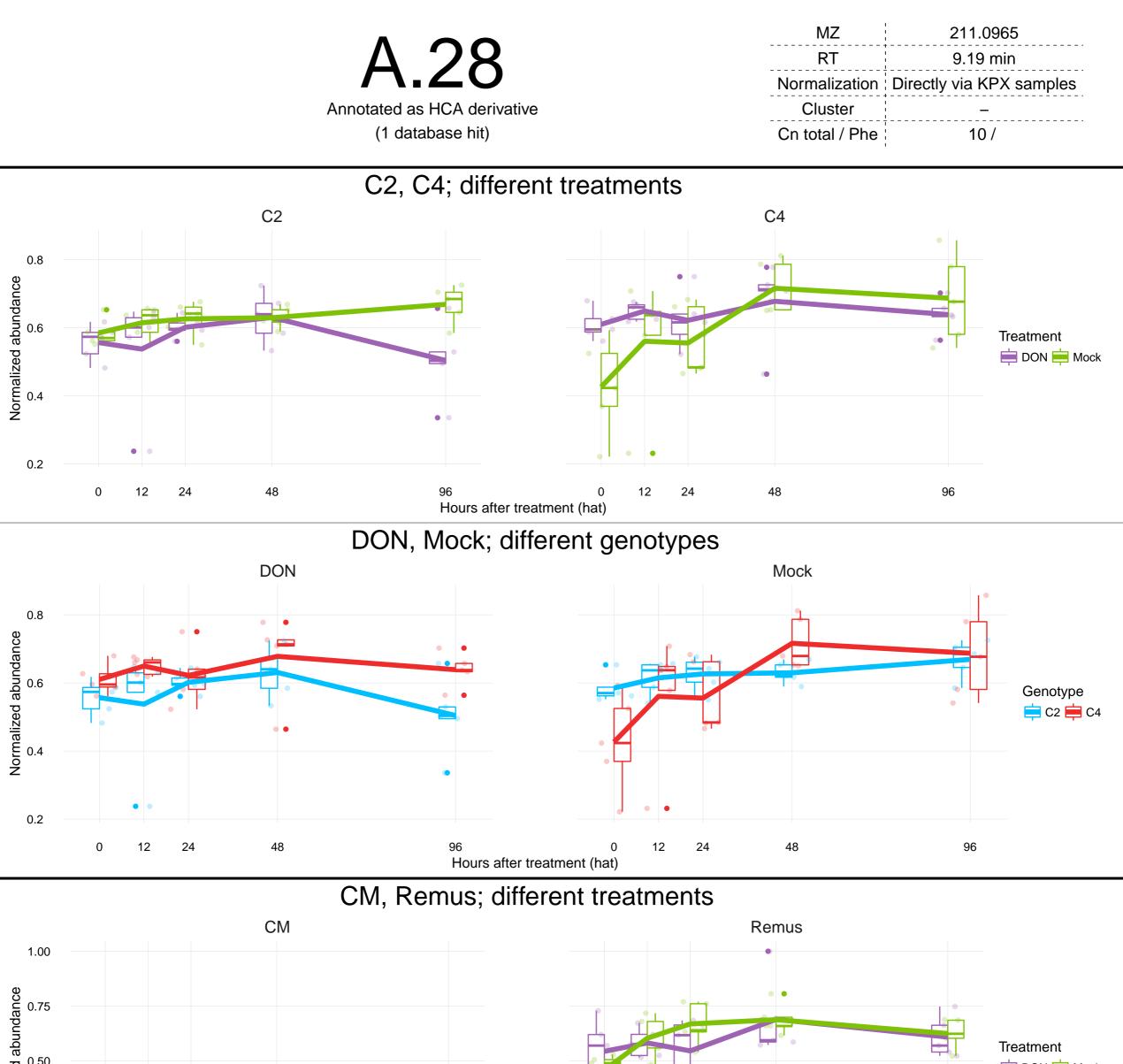


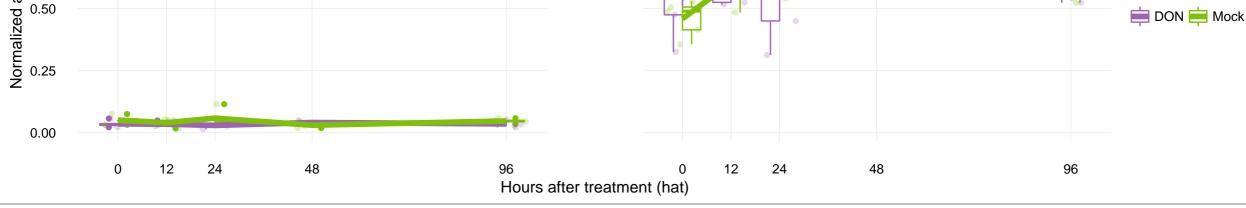




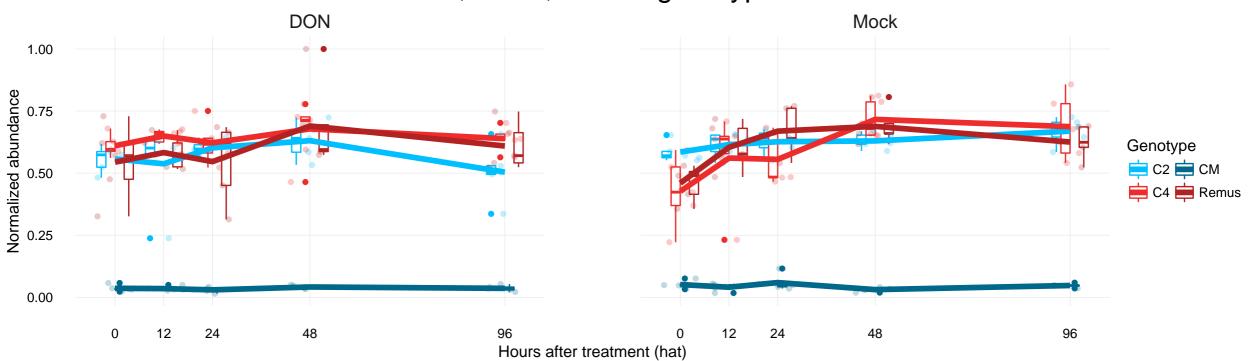
DON, Mock; all four genotypes

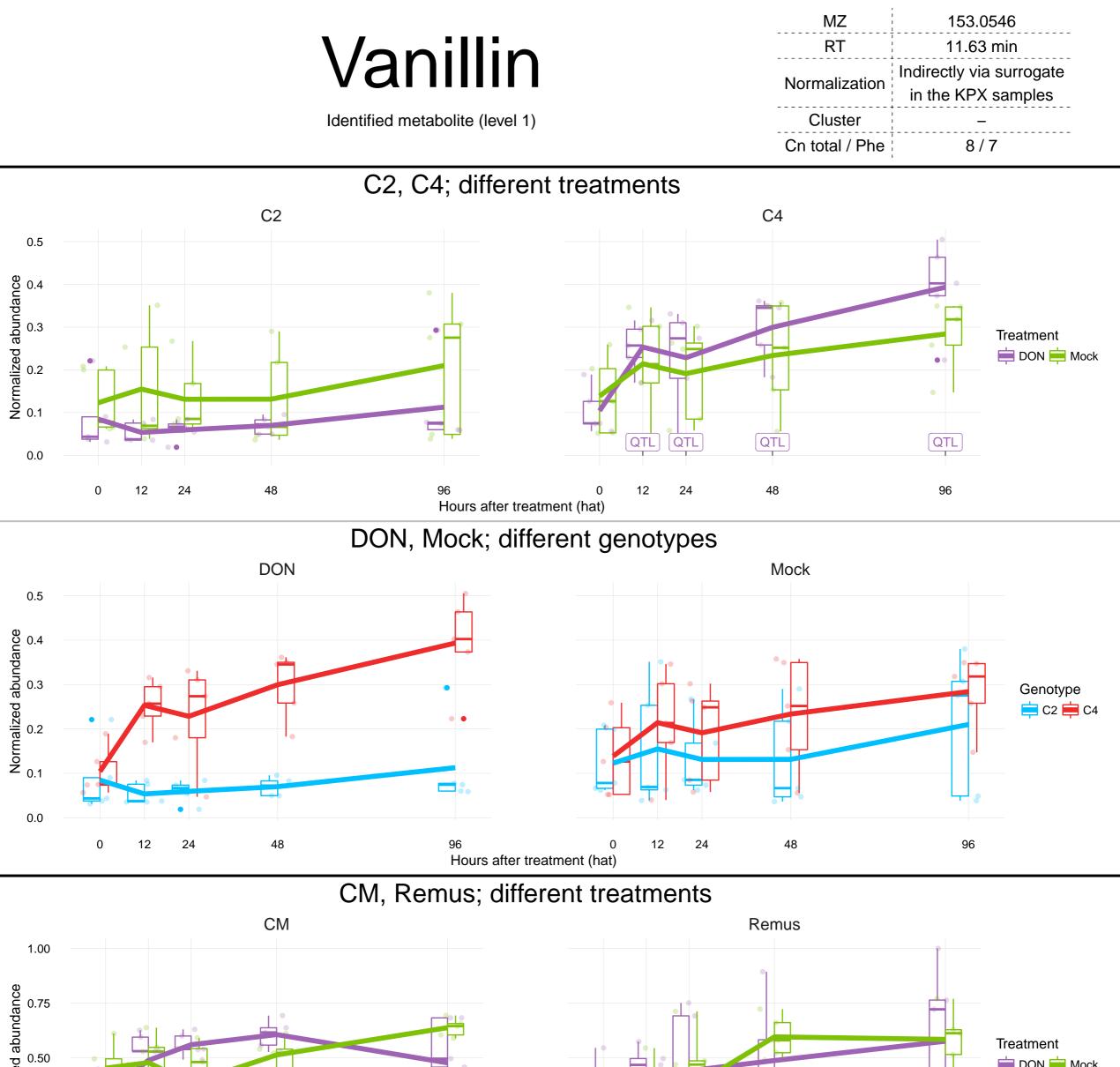


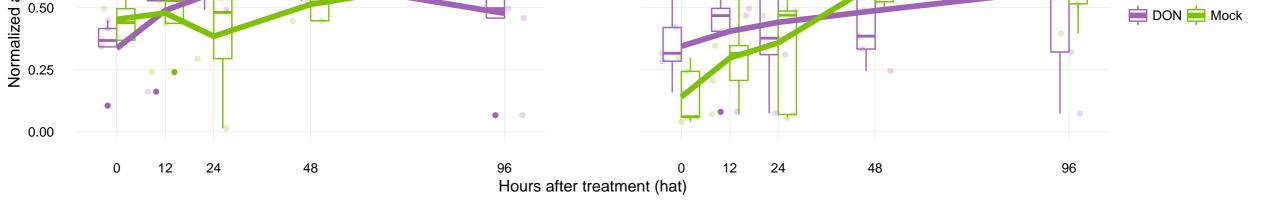




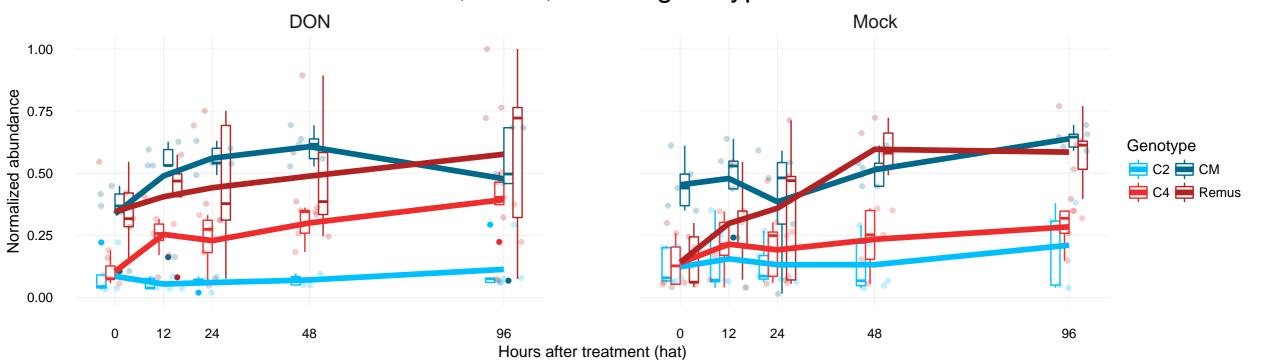
DON, Mock; all four genotypes

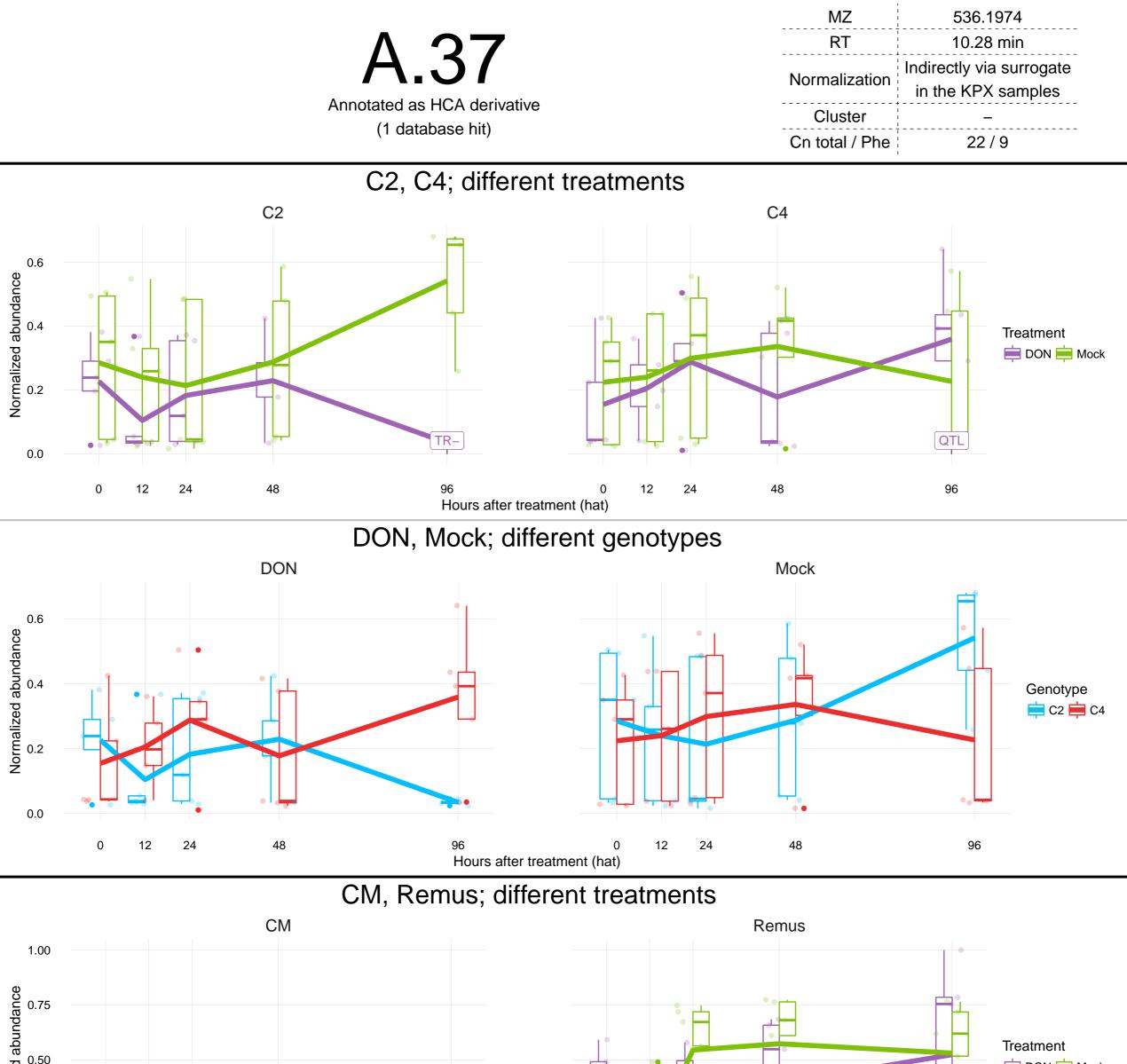


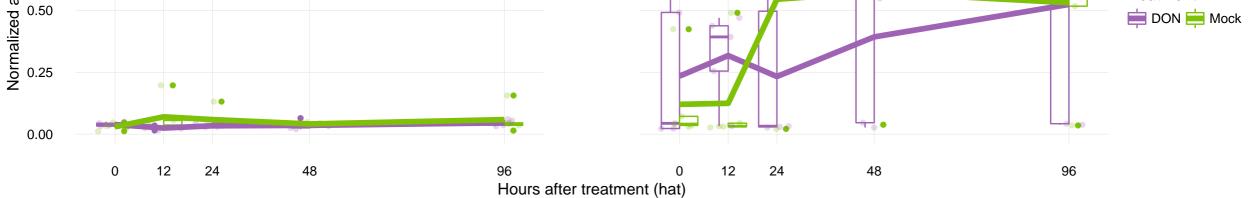




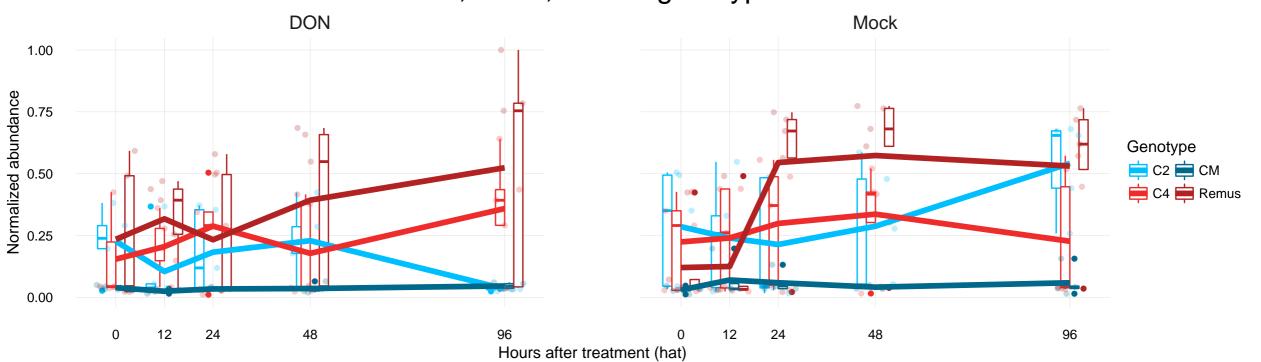
DON, Mock; all four genotypes

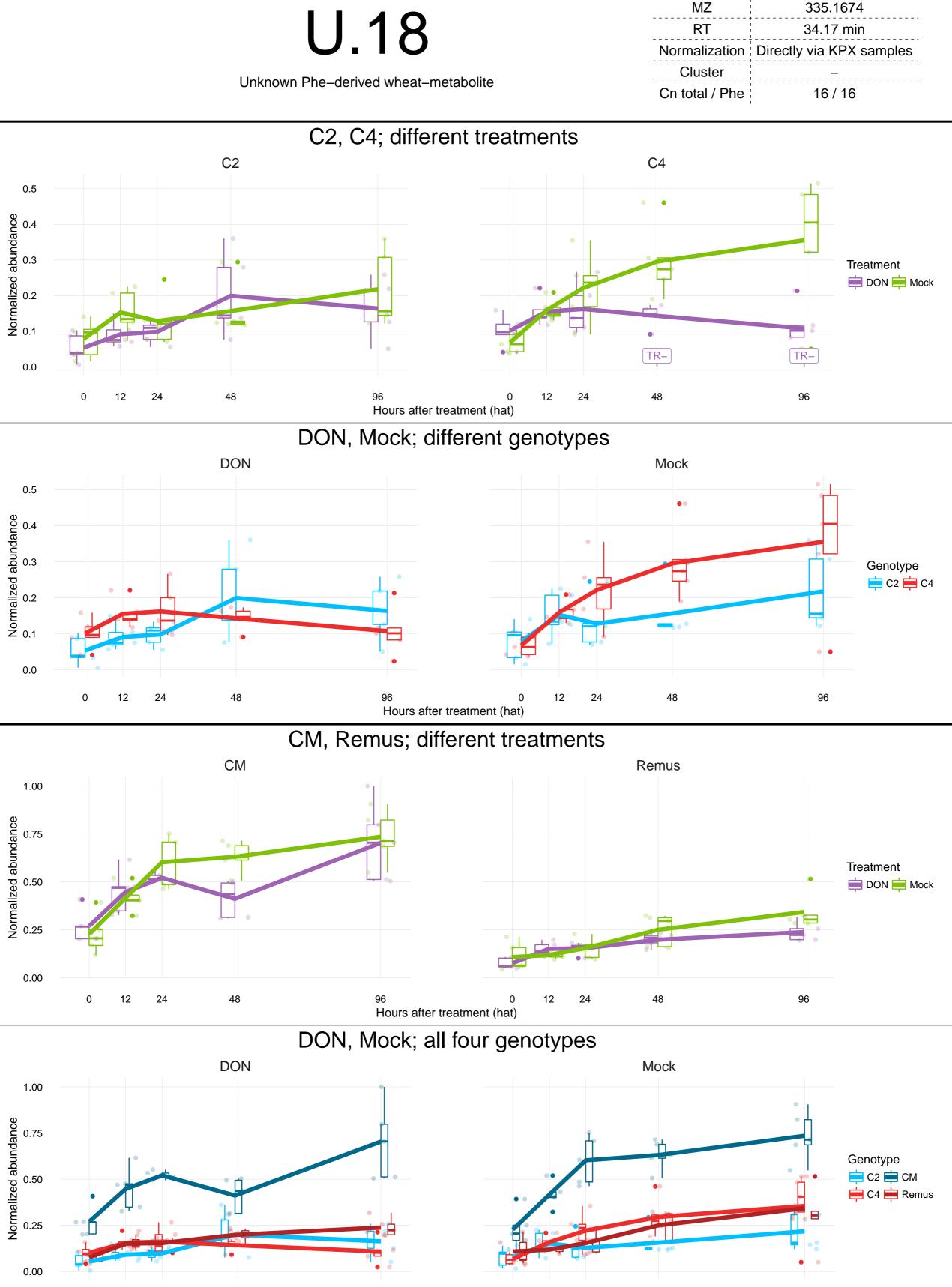




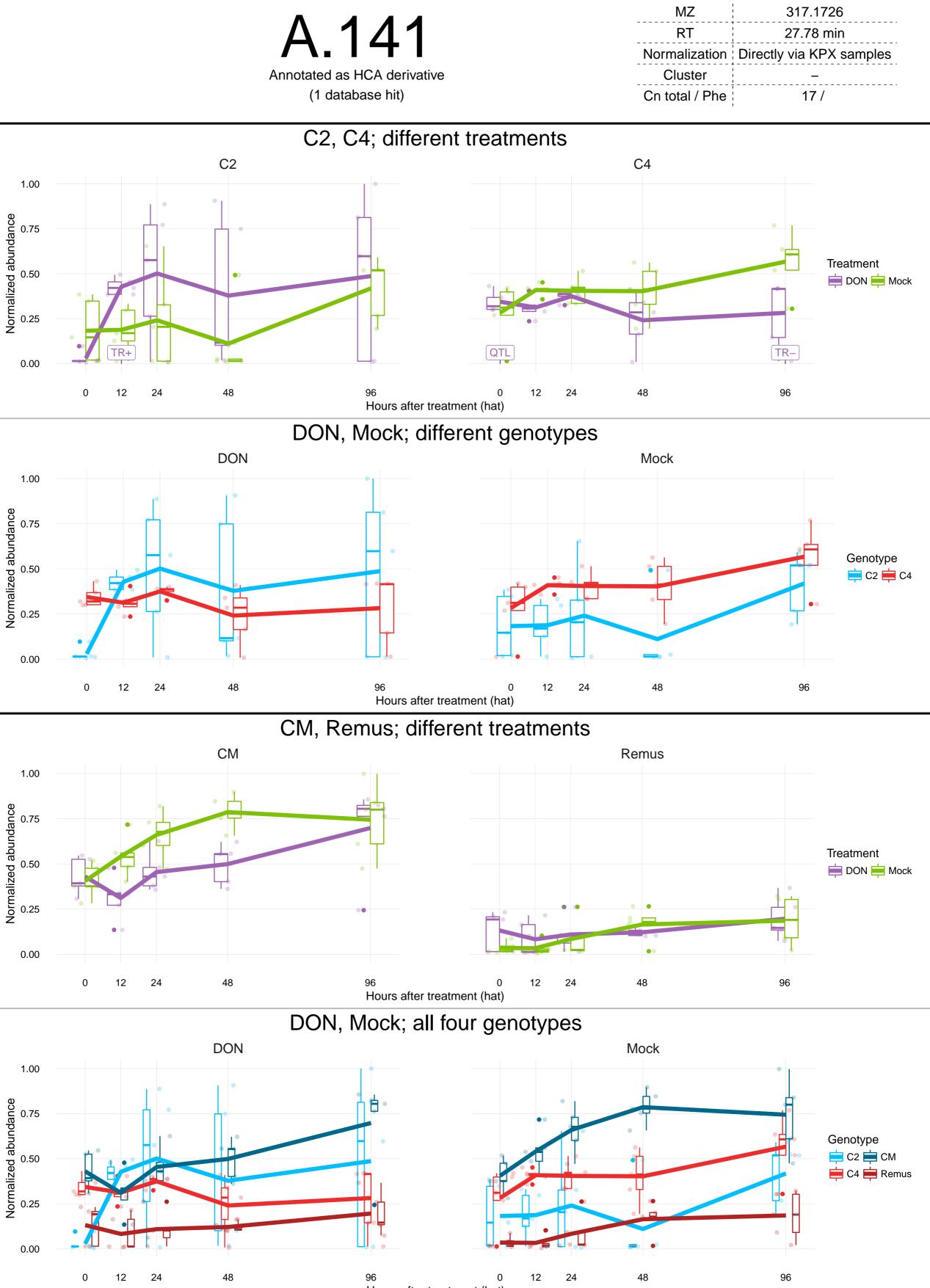


DON, Mock; all four genotypes

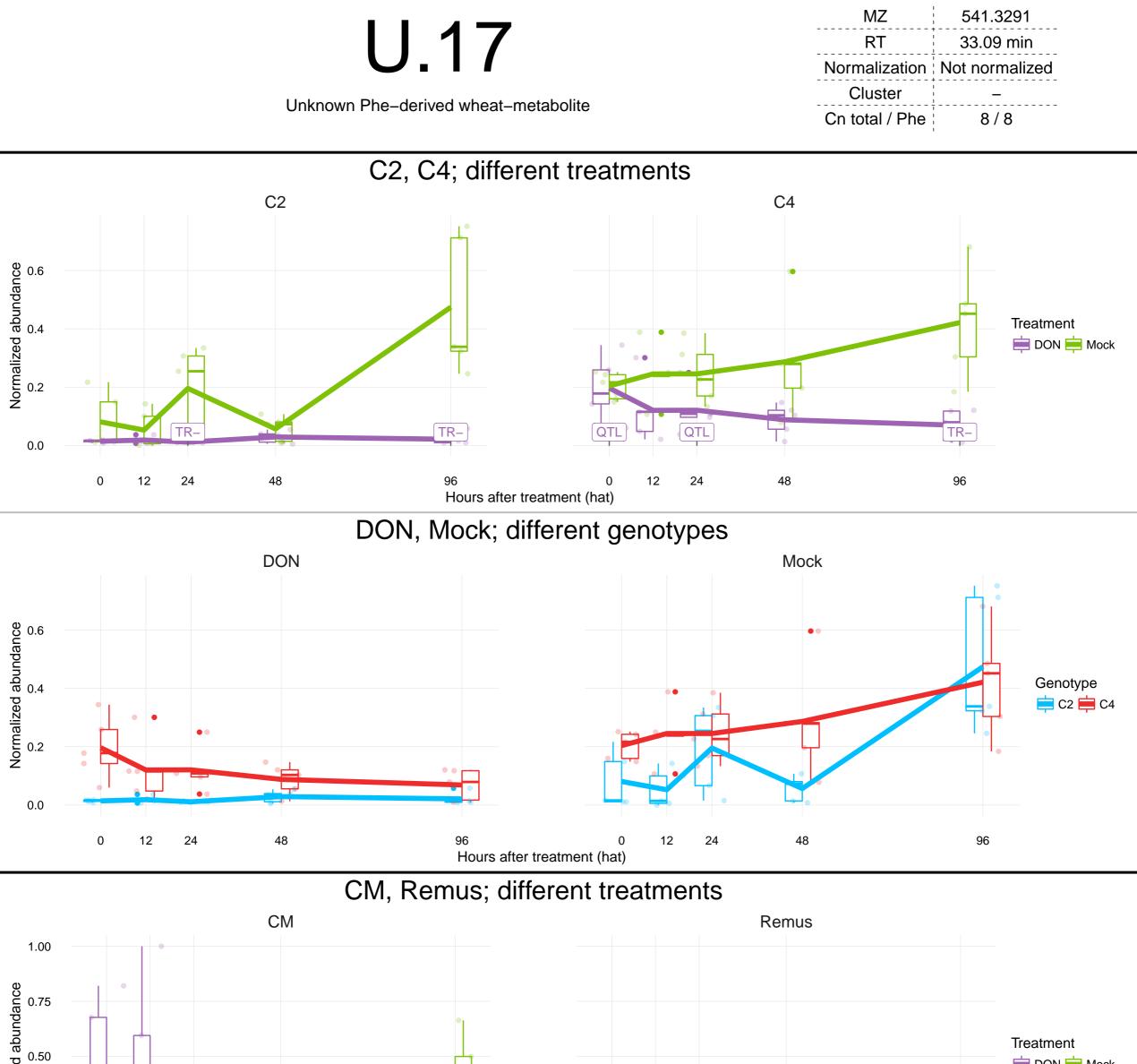


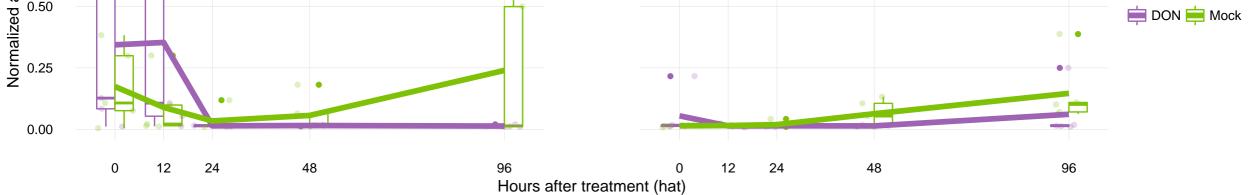


96 0 12 24 Hours after treatment (hat)

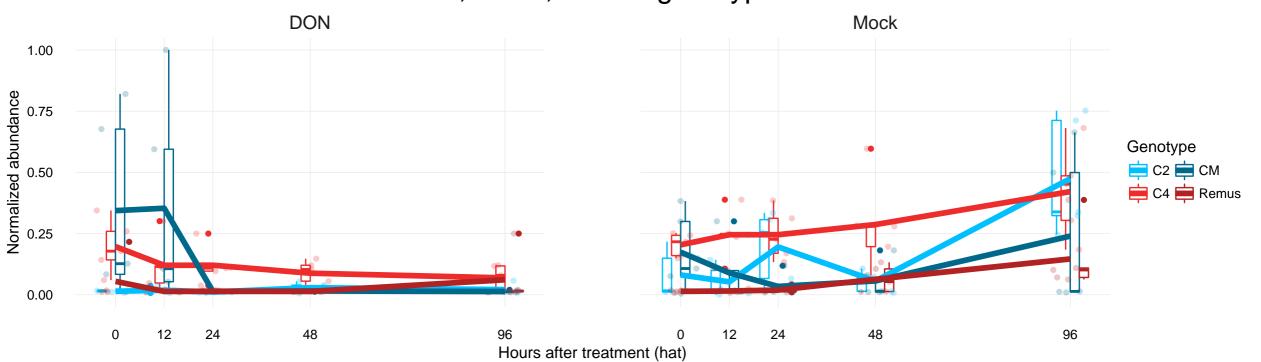


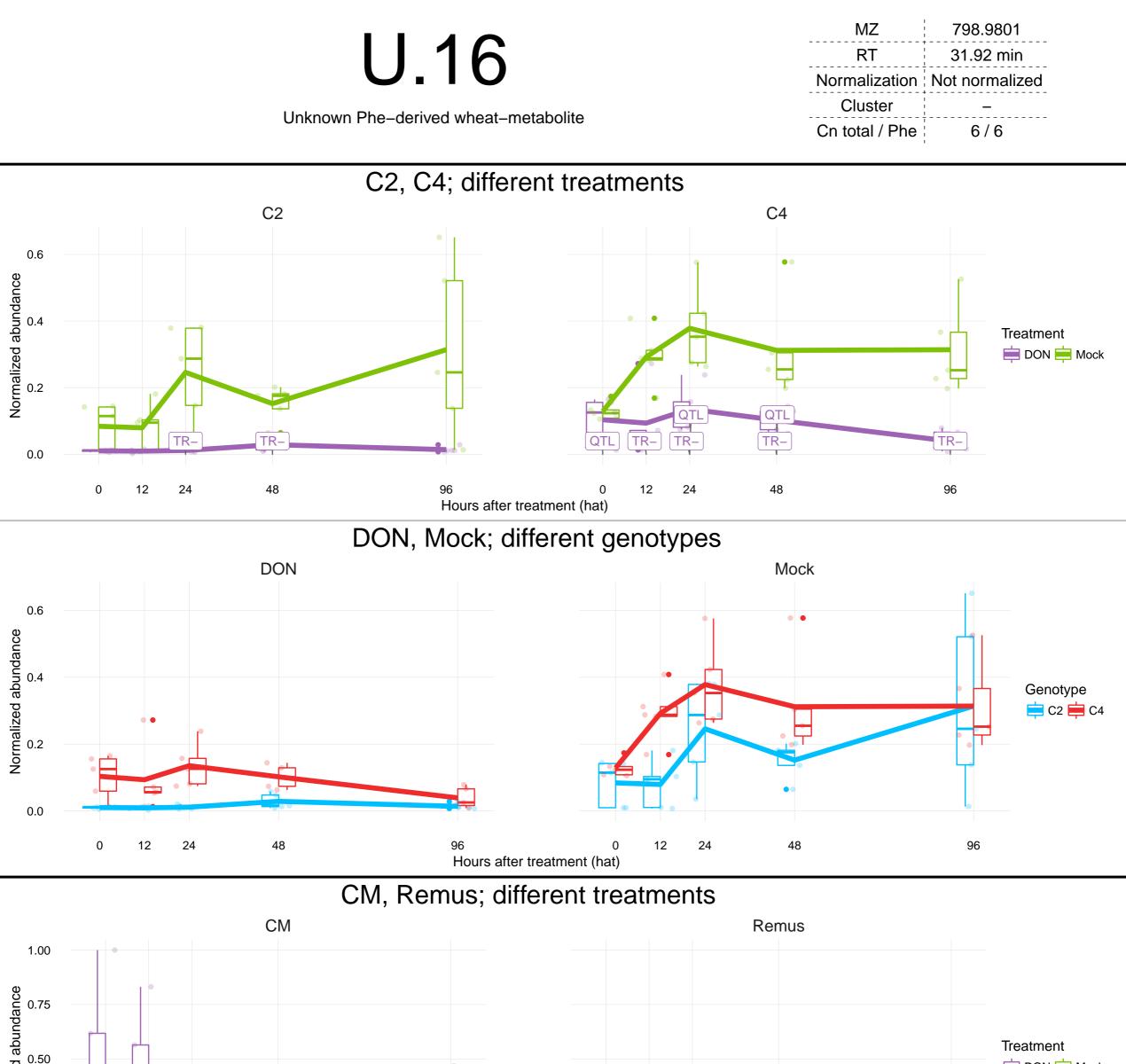
Hours after treatment (hat)

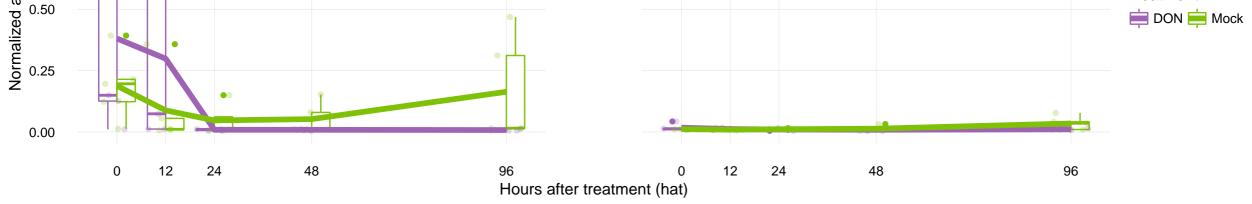




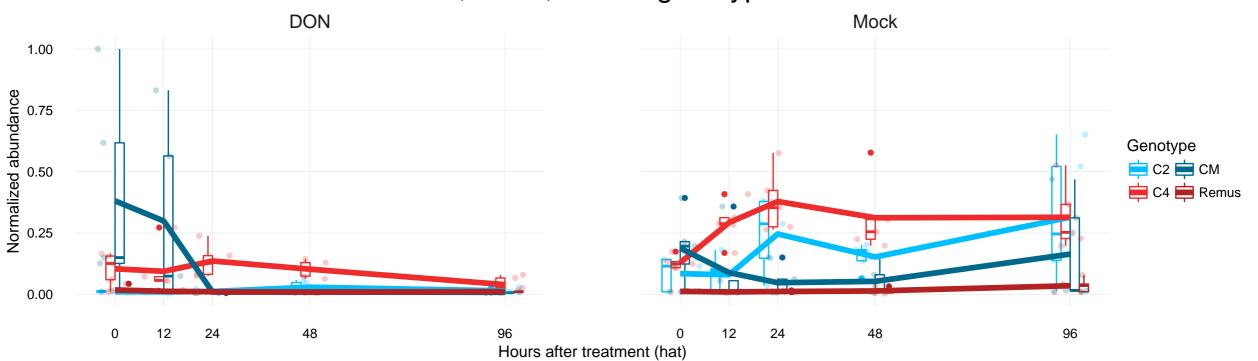
DON, Mock; all four genotypes

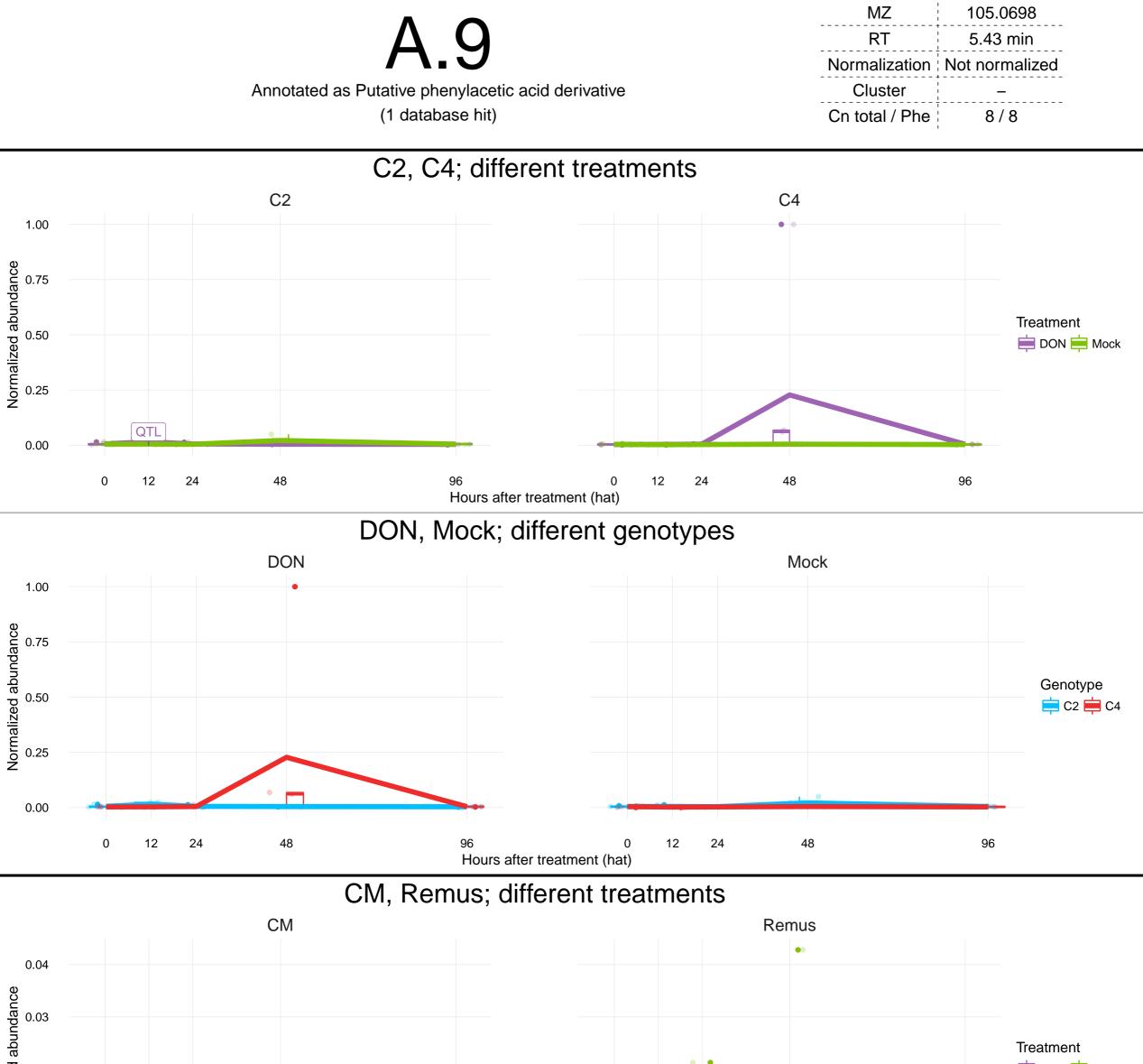


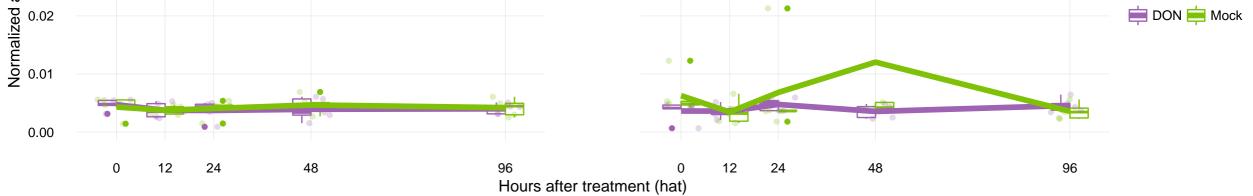




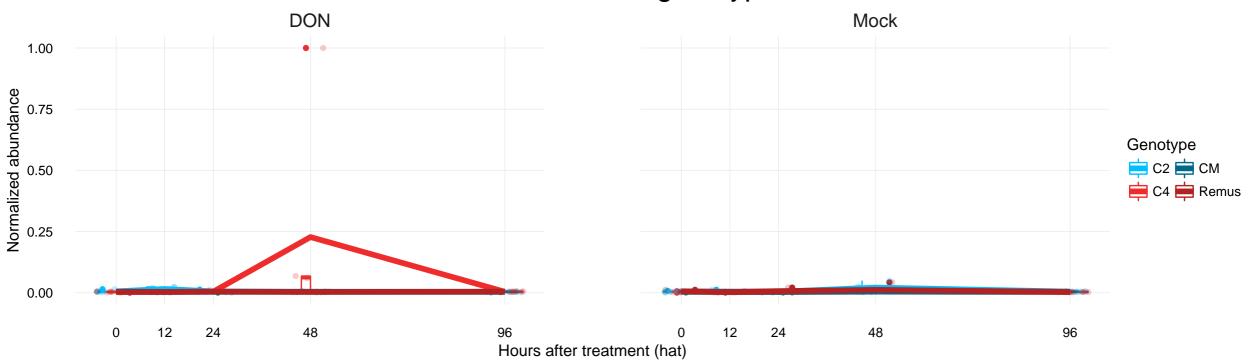
DON, Mock; all four genotypes



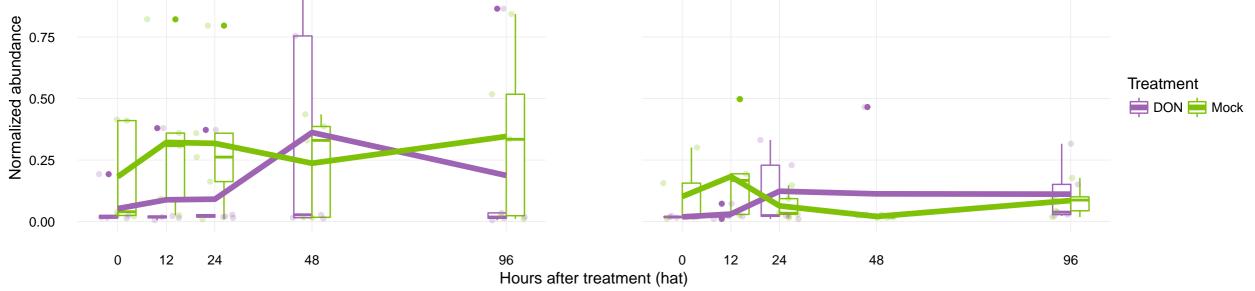




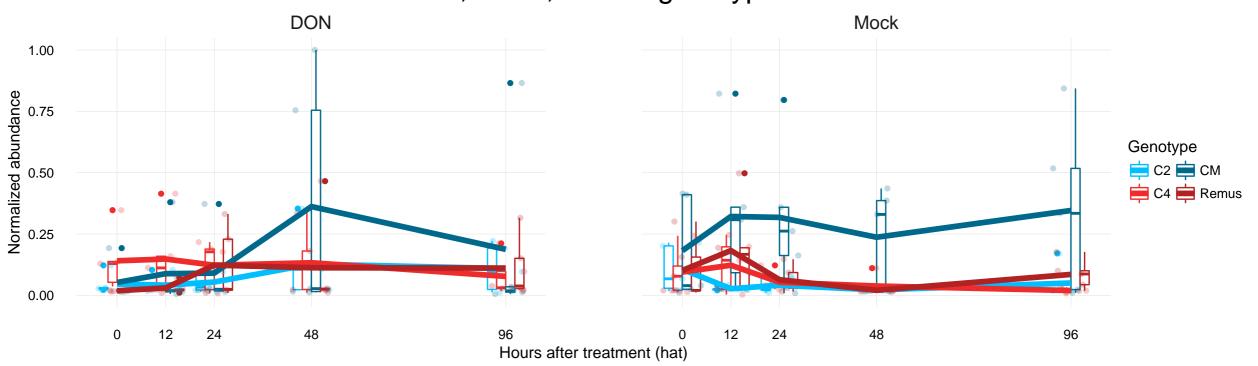
DON, Mock; all four genotypes



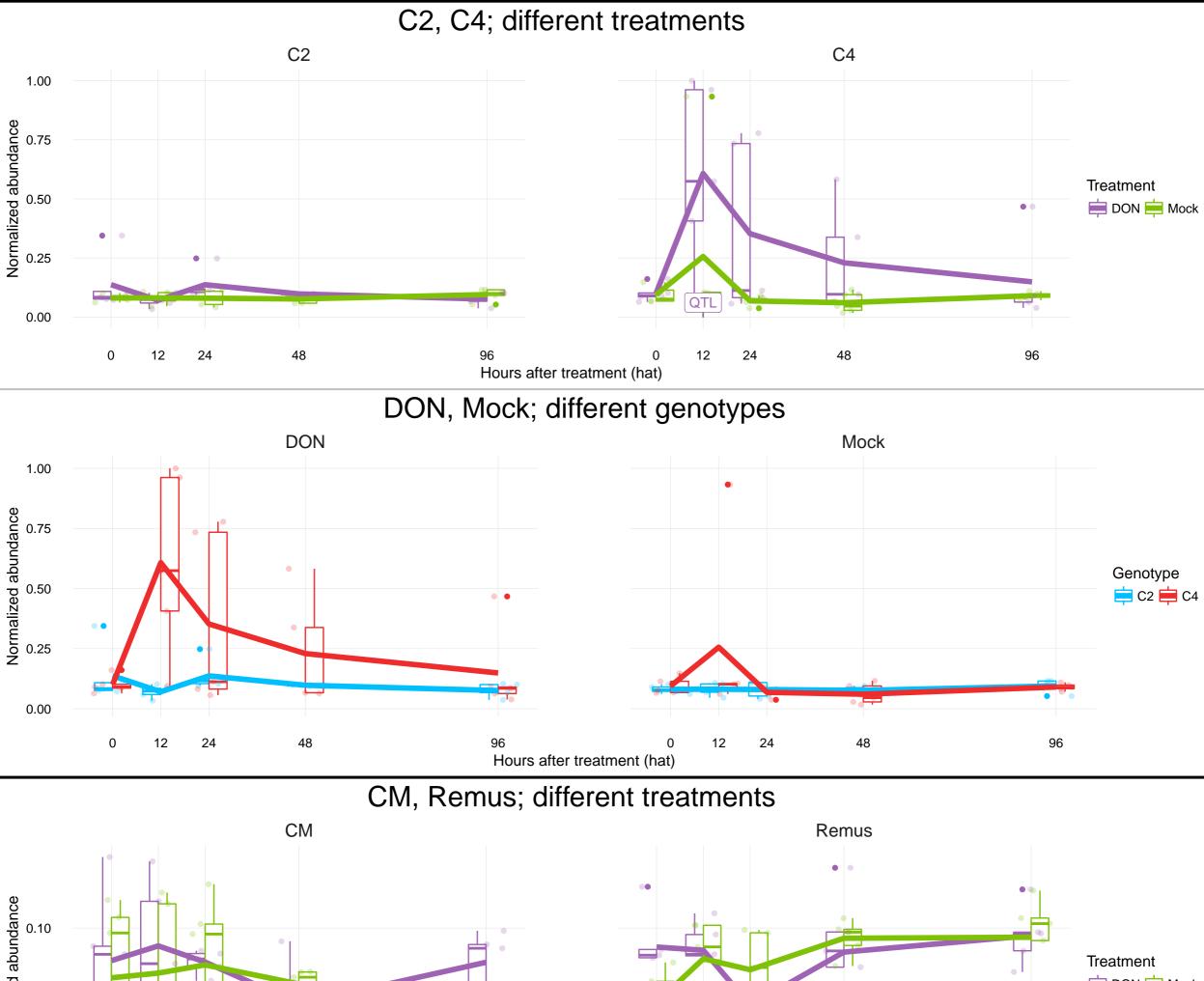
	A.106 Annotated as Flavonoid	MZ RT Normalization Cluster	373.1281 17.44 min Indirectly via surrogate in the KPX samples –			
	(30 database hits)	Cn total / Phe	20/9			
	C2, C4; different treatments	S				
	C2	C4				
0.4 -		 •				
Normalized abundance Normalized abundance Normalized abundance Normalized abundance Normalized abundance Normalized abundance			Treatment			
	0 12 24 48 96 0 12 Hours after treatment (hat)	24 48	96			
	DON, Mock; different genoty	vpes				
	DON	Mock				
- 4.0 ence 0.3 -						
Normalized abundance 7.0 abundance 7.0 abundance		•	Genotype C2 텆 C4			
0.0						
	0 12 24 48 96 0 12 Hours after treatment (hat)	24 48	96			
CM, Remus; different treatments						
1.00	CM	Remus				
1.00						

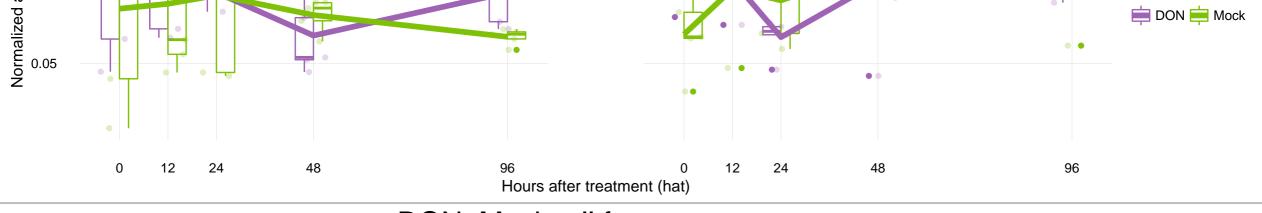


DON, Mock; all four genotypes

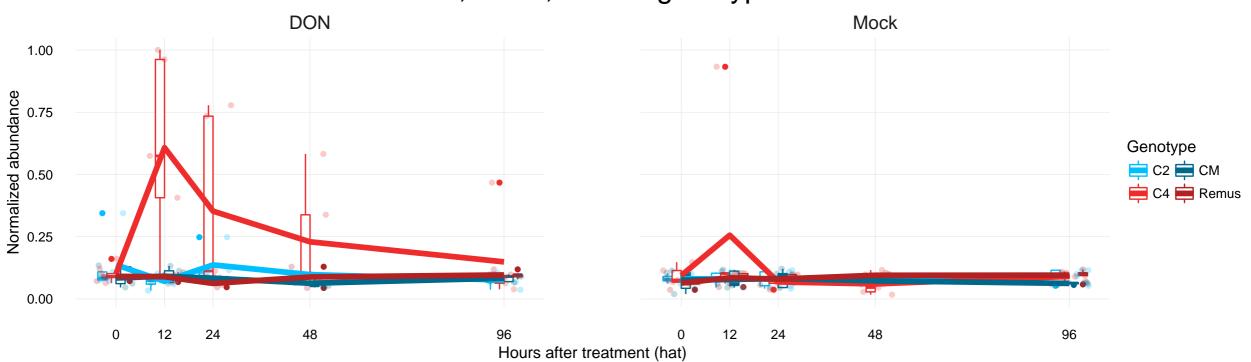




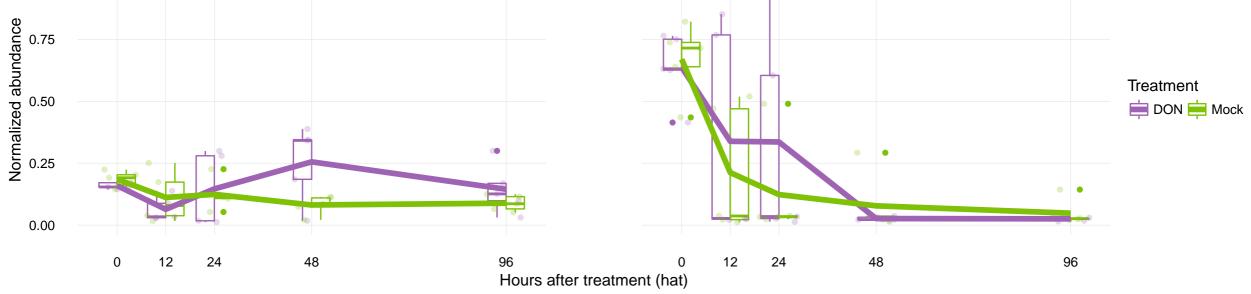




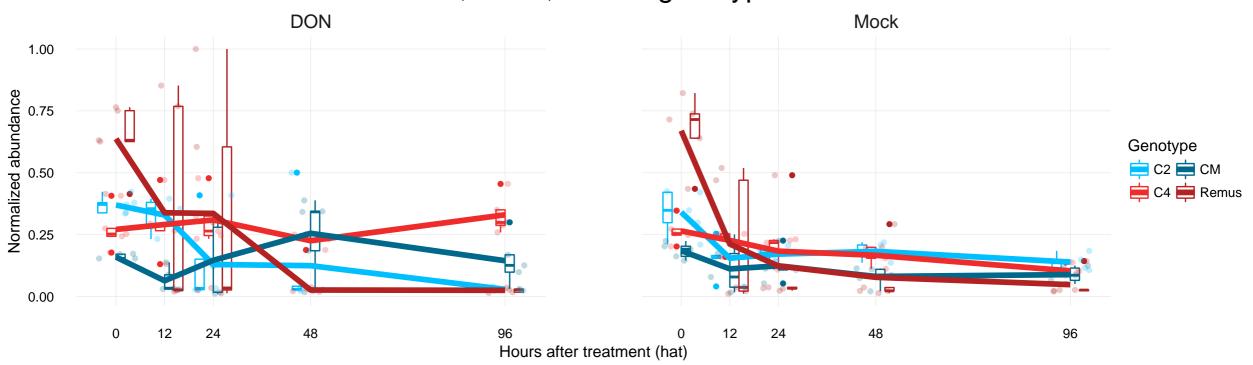
DON, Mock; all four genotypes

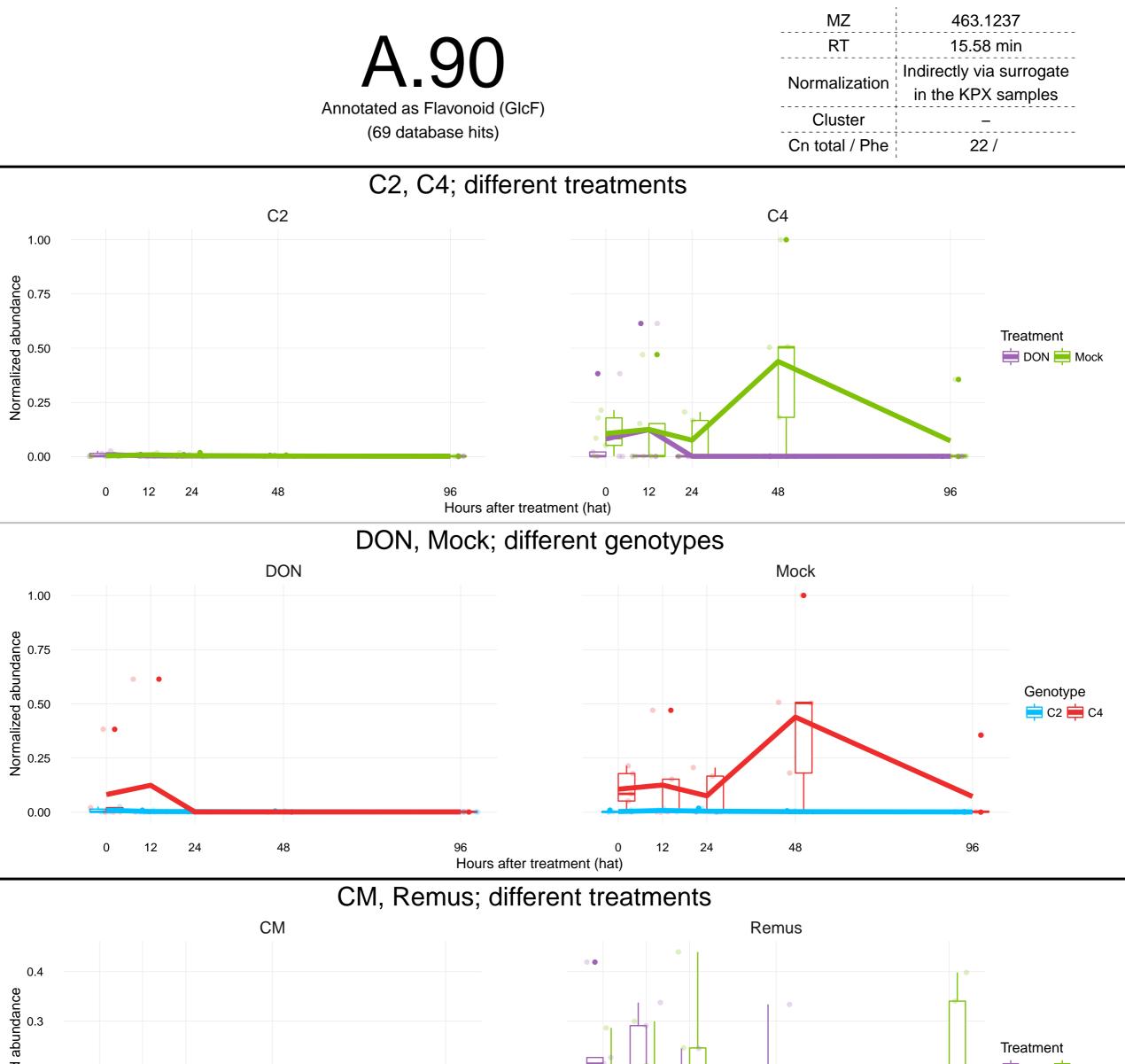


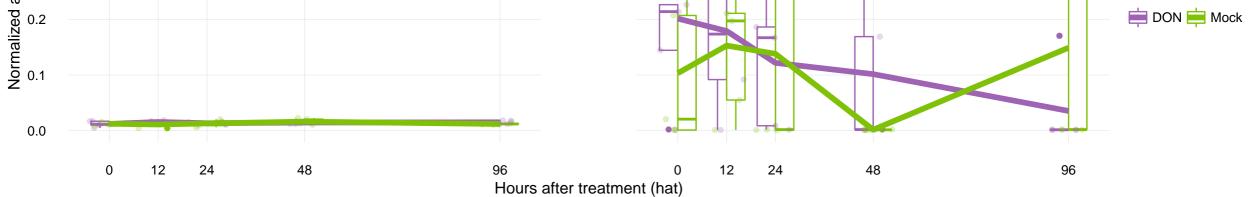
	MZ	395.1313			
A.33	RT	9.66 min Indirectly via surrogate			
	Normalization	in the KPX samples			
Annotated as HCA derivative	Cluster	—			
(1 database hit)	Cn total / Phe	17 /			
C2, C4; different treatment	ts				
C2	C4				
0.5	• •	•			
0.4 Output appropriate appropr					
		Treatment			
		🚔 DON 🚔 Mock			
E 0.1					
0.0 TR+		TR+			
0 12 24 48 96 0 12	24 48	96			
Hours after treatment (hat) DON, Mock; different genot	VDes				
DON	Mock				
0.5					
0.4 0.3 0.2 0.1					
		Genotype 텆 C2 븢 C4			
≥ _{0.1}					
0.0					
0 12 24 48 96 0 12 Hours after treatment (hat)	2 24 48	96			
CM, Remus; different treatments					
CM	Remus				
1.00					



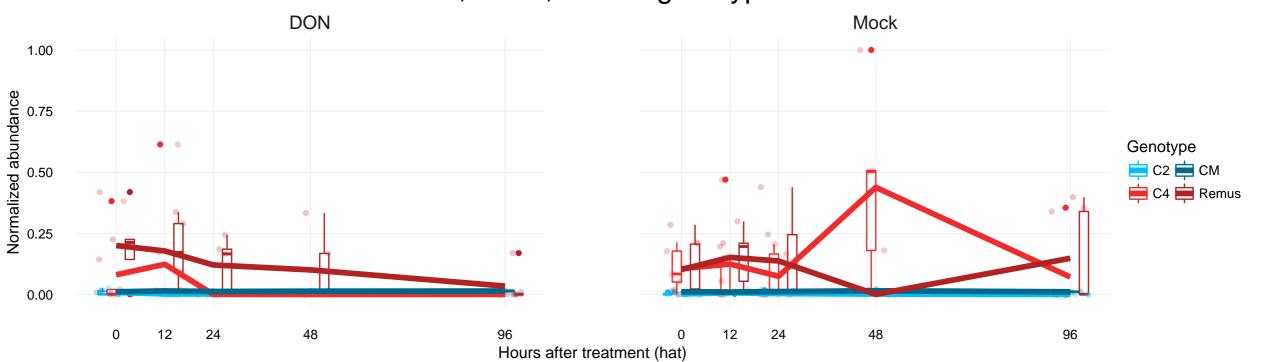
DON, Mock; all four genotypes

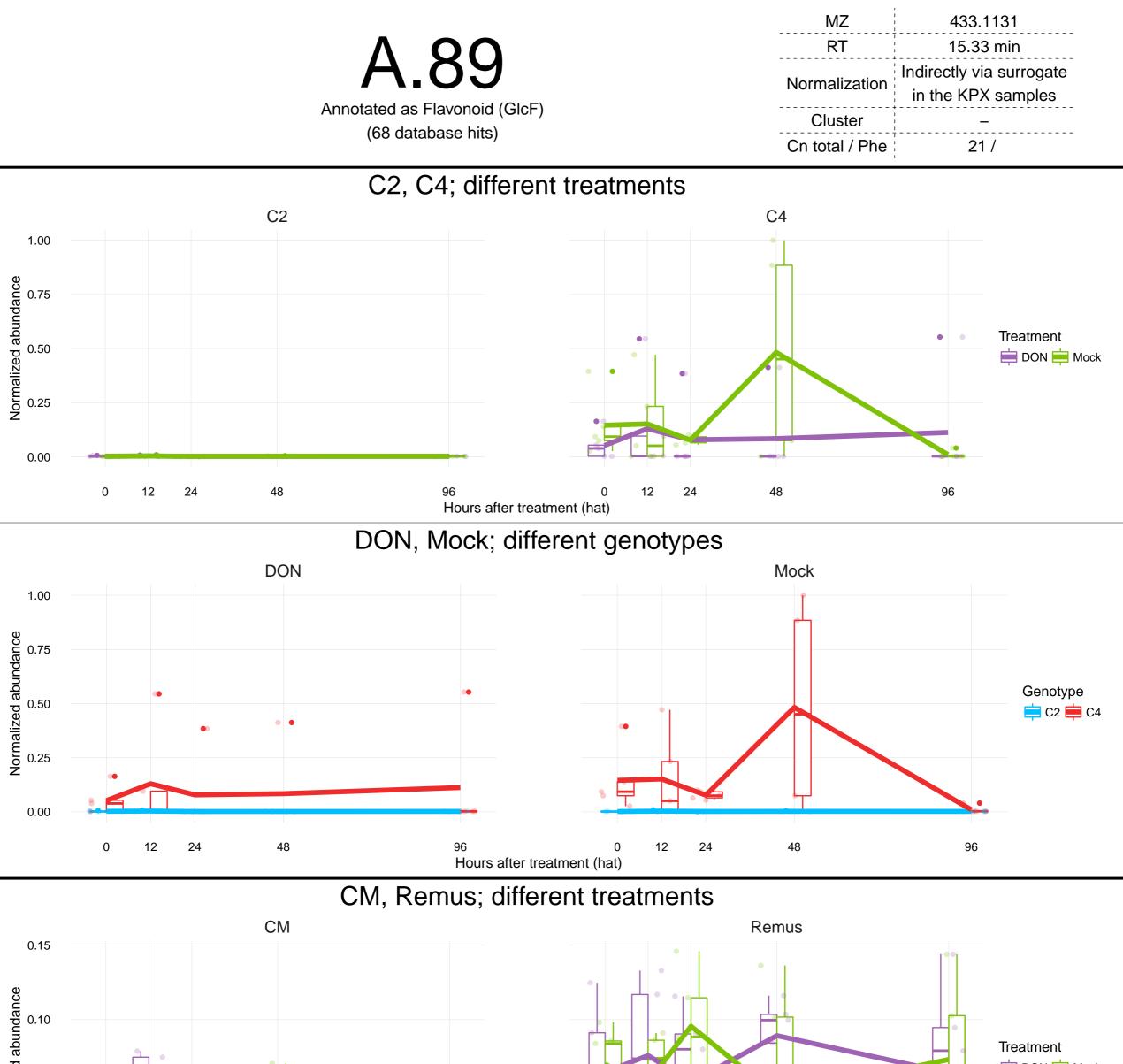


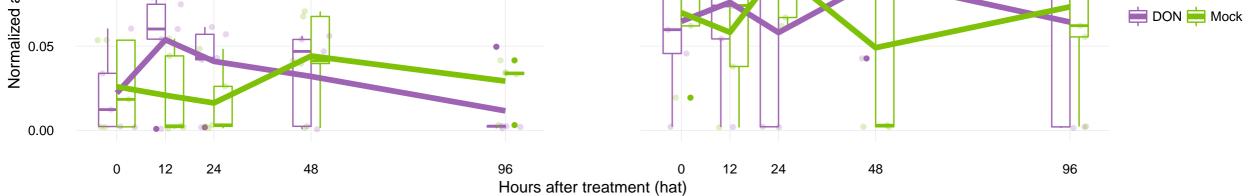




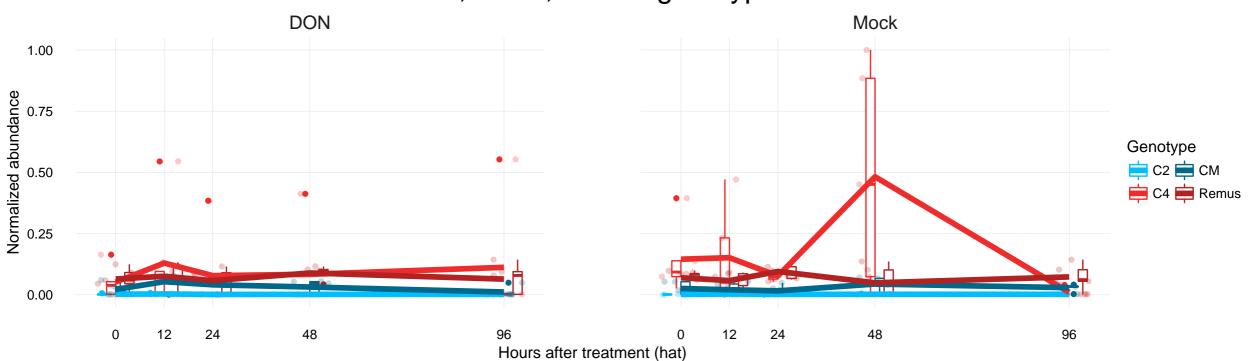
DON, Mock; all four genotypes

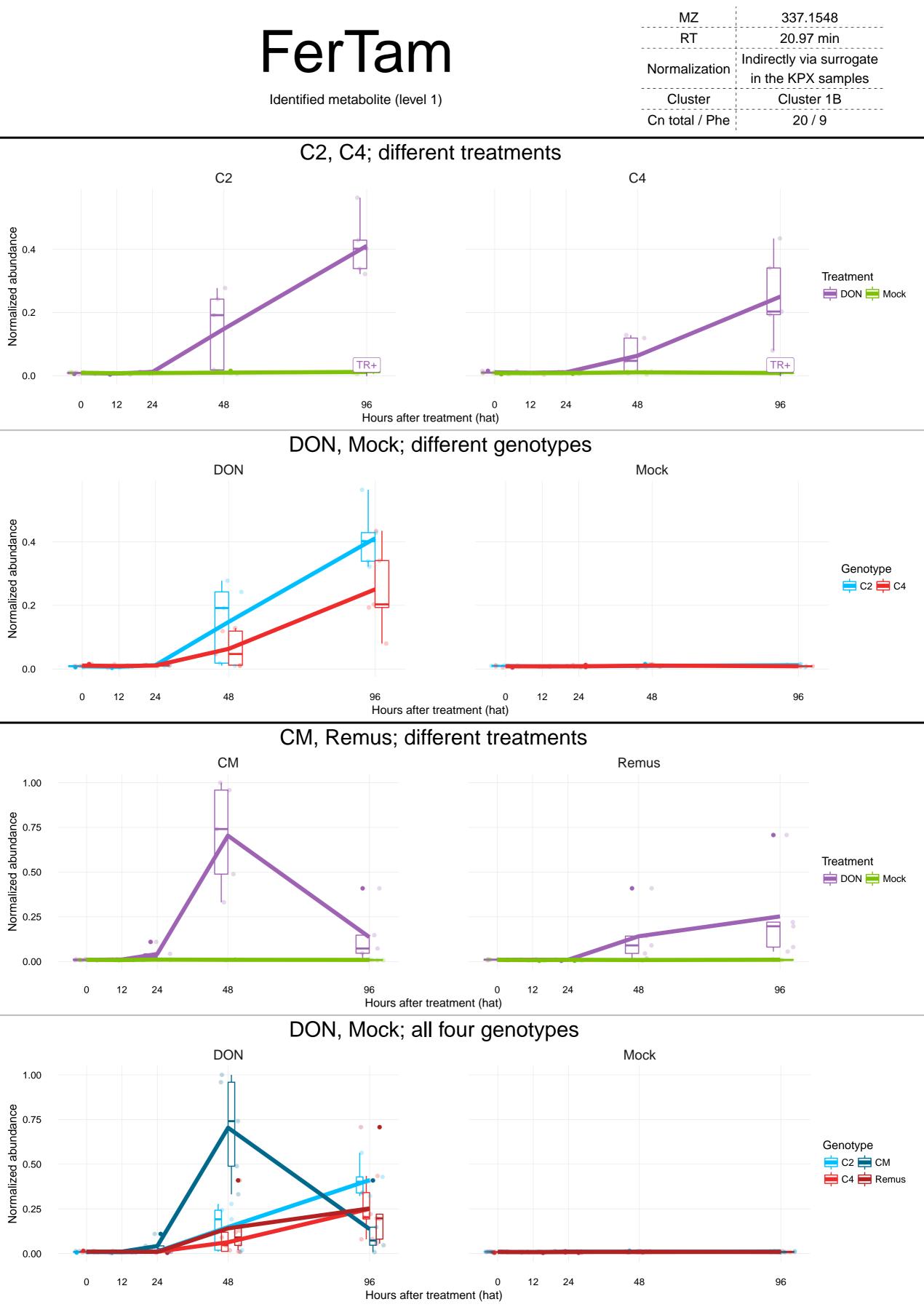


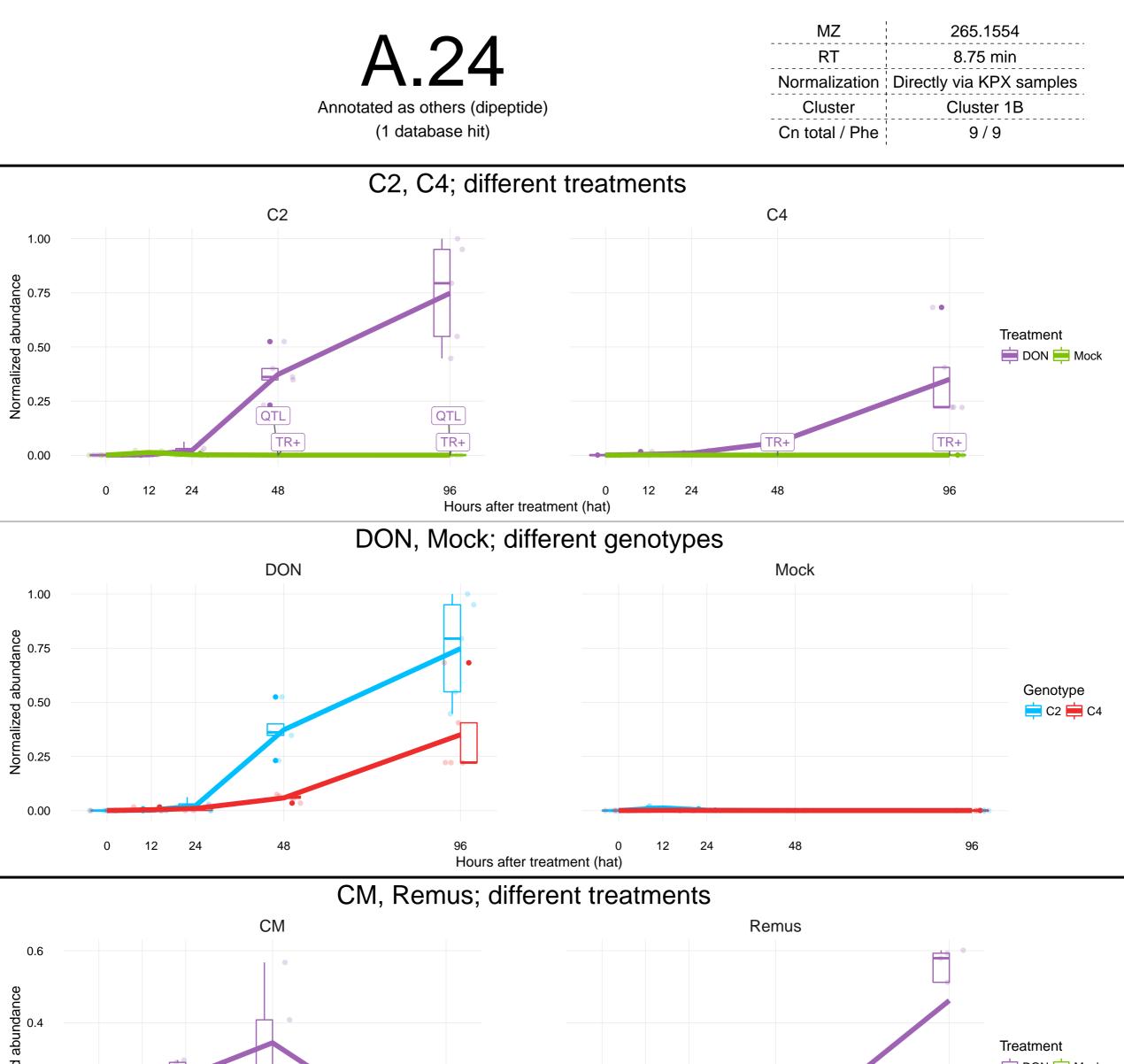


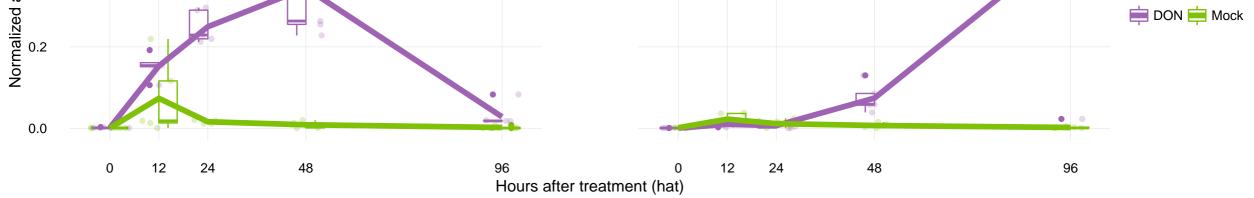


DON, Mock; all four genotypes

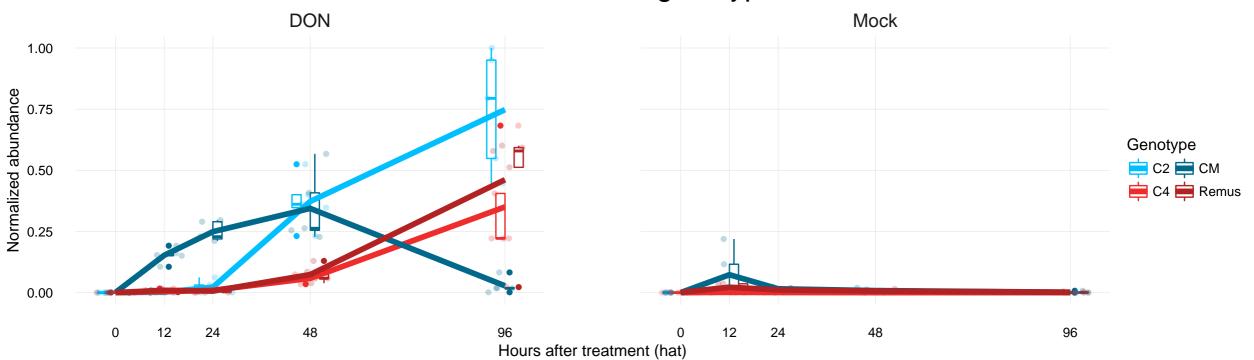


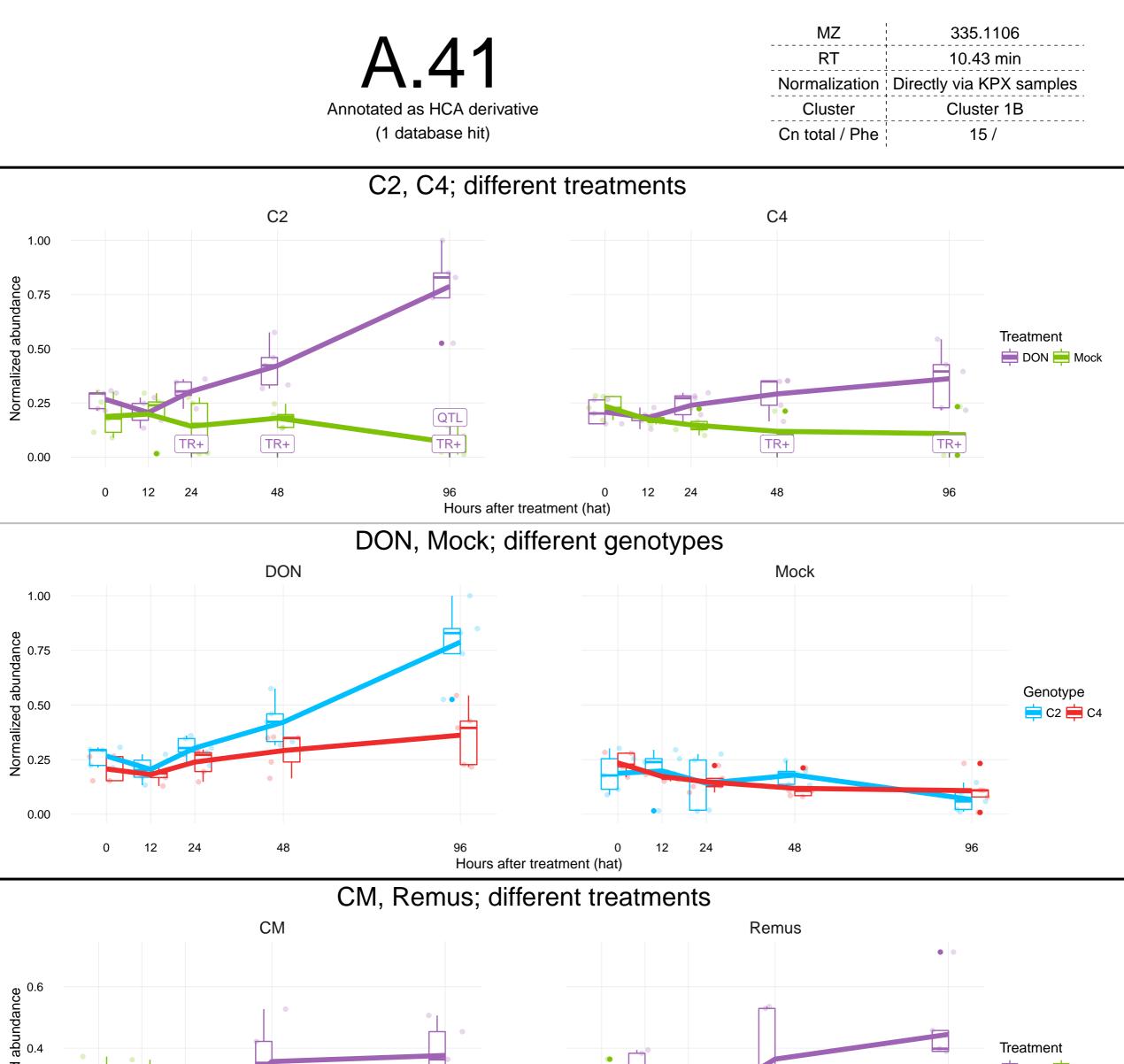


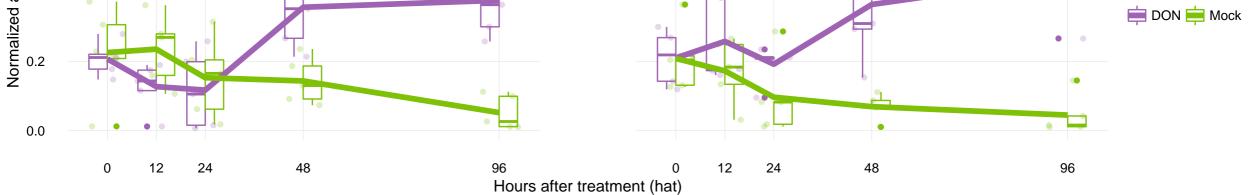




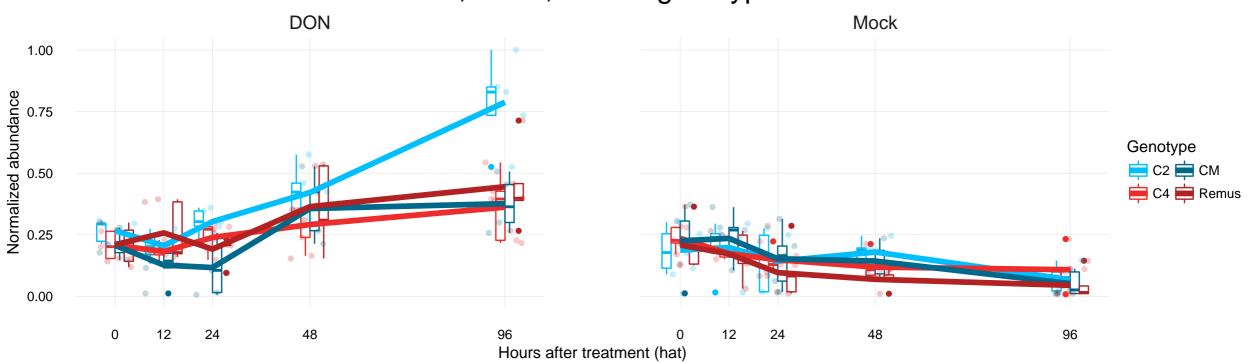
DON, Mock; all four genotypes

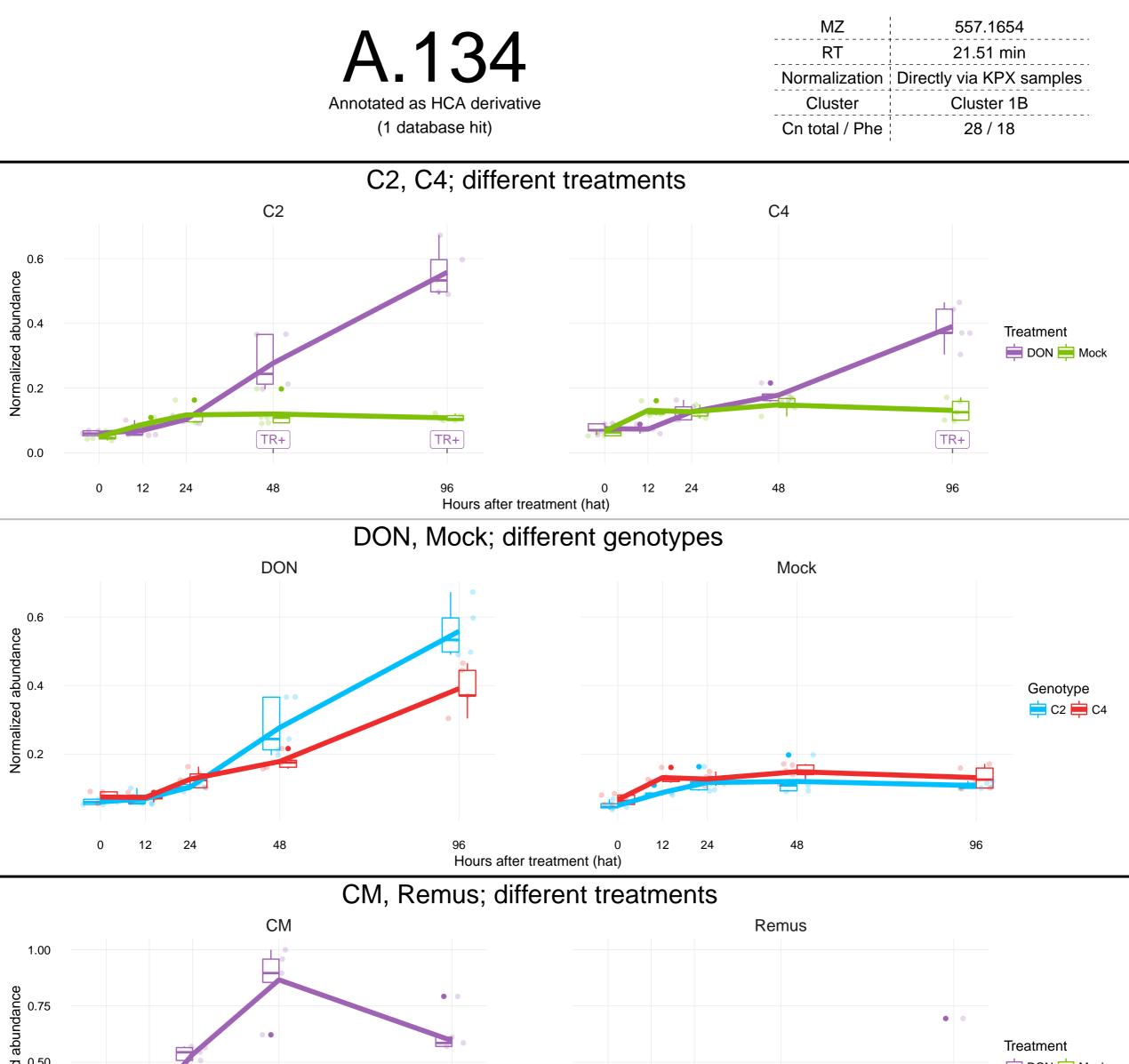


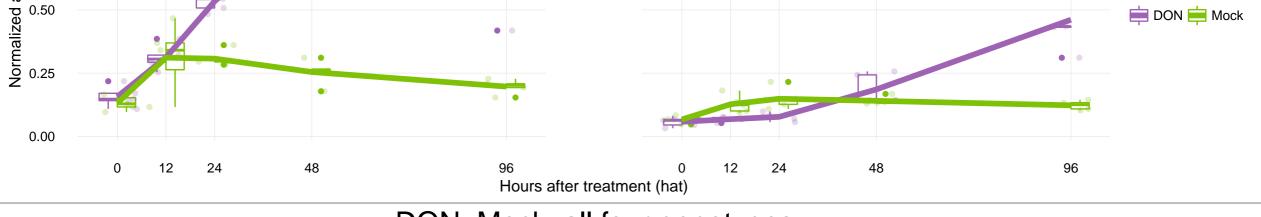




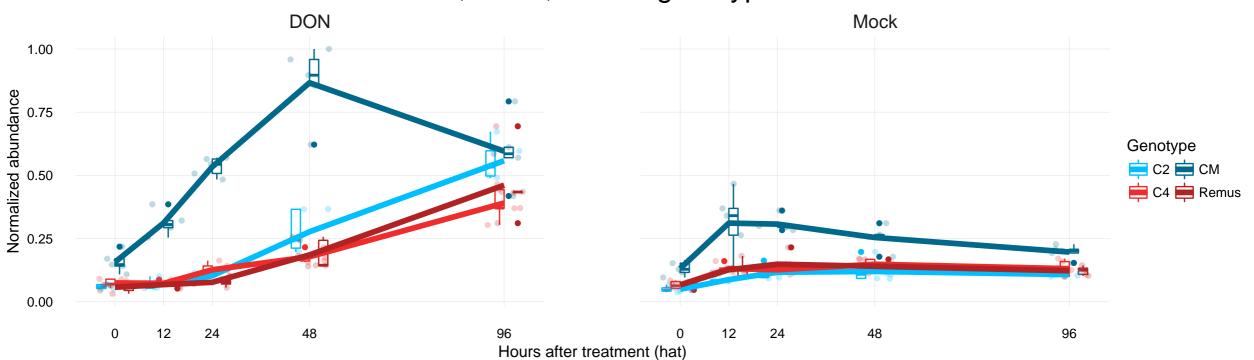
DON, Mock; all four genotypes

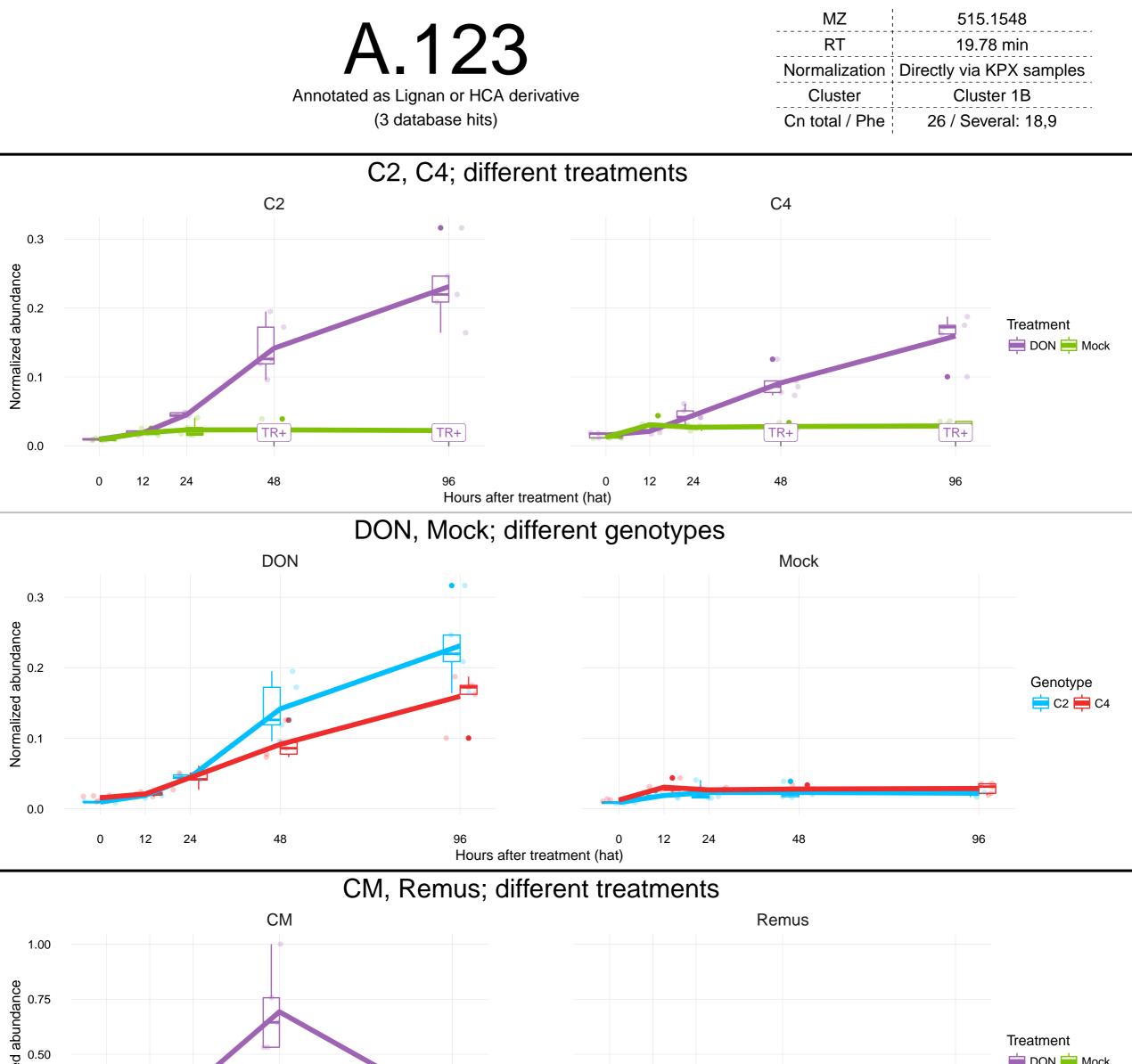


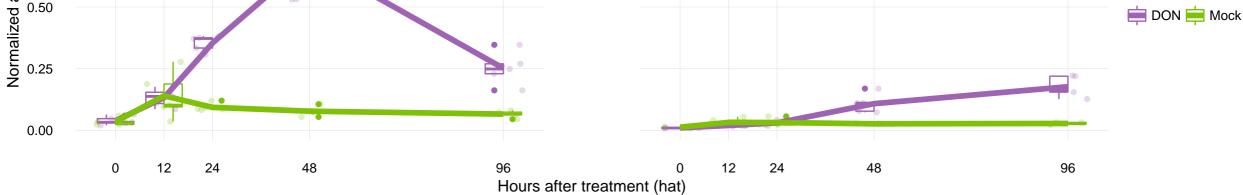




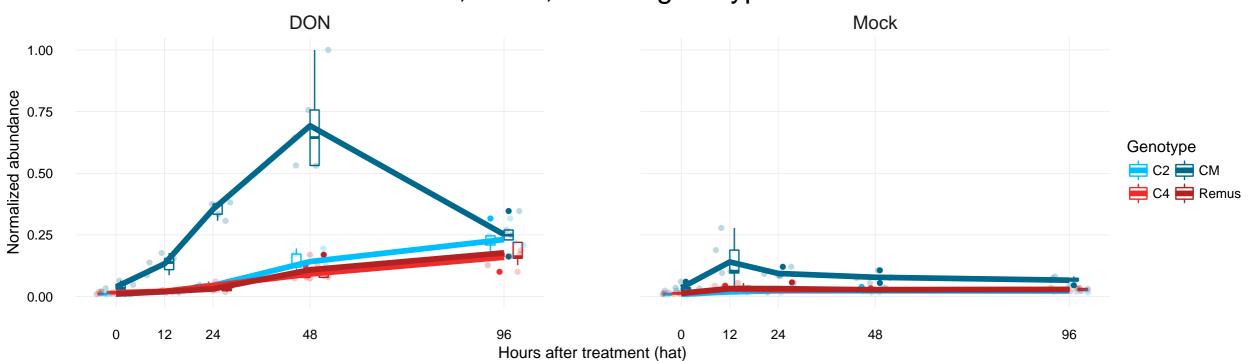
DON, Mock; all four genotypes

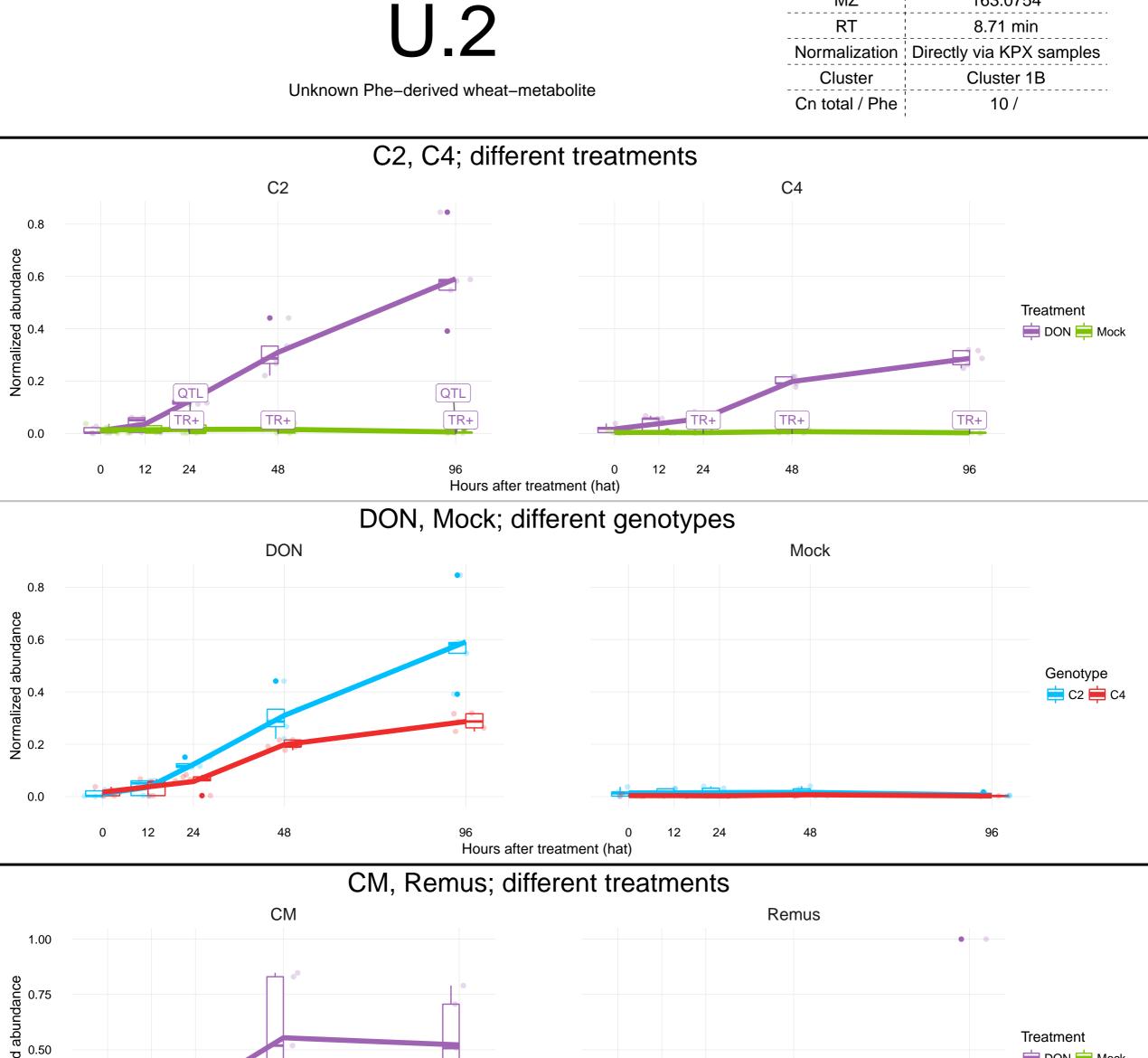






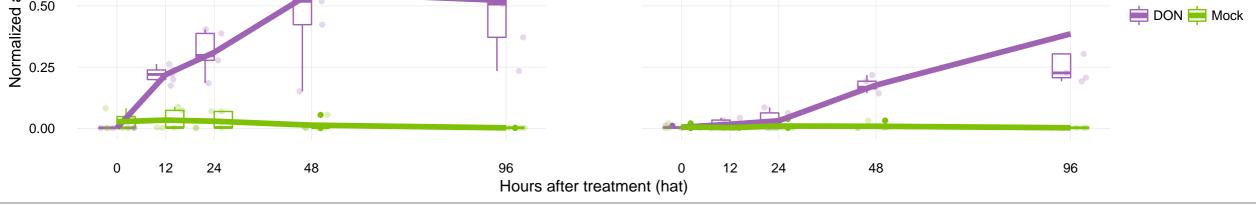
DON, Mock; all four genotypes



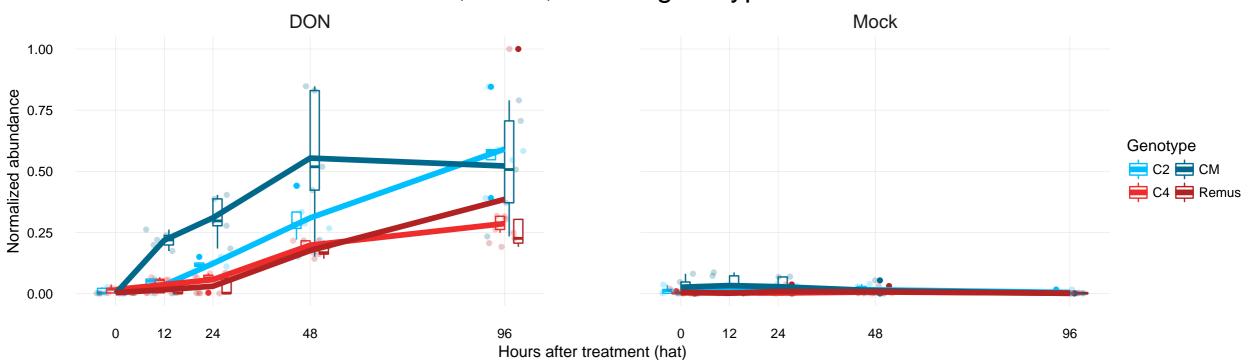


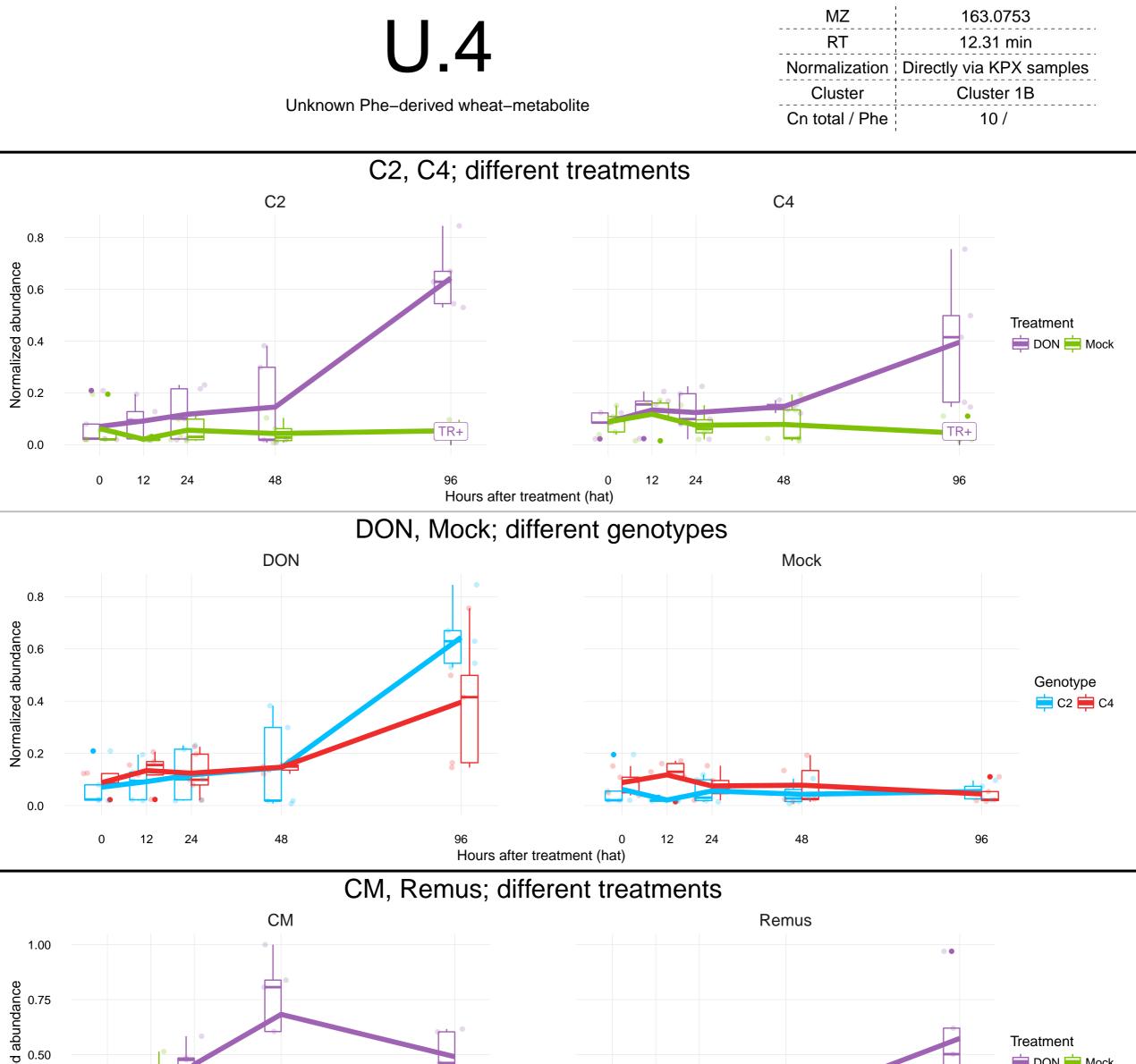
ΜZ

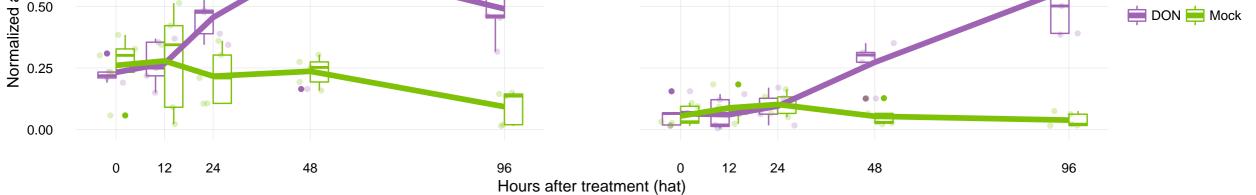
163.0754



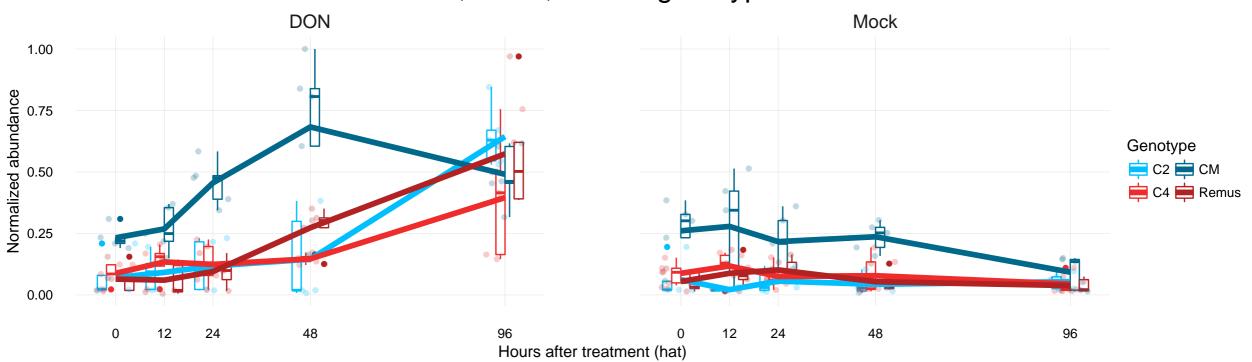
DON, Mock; all four genotypes

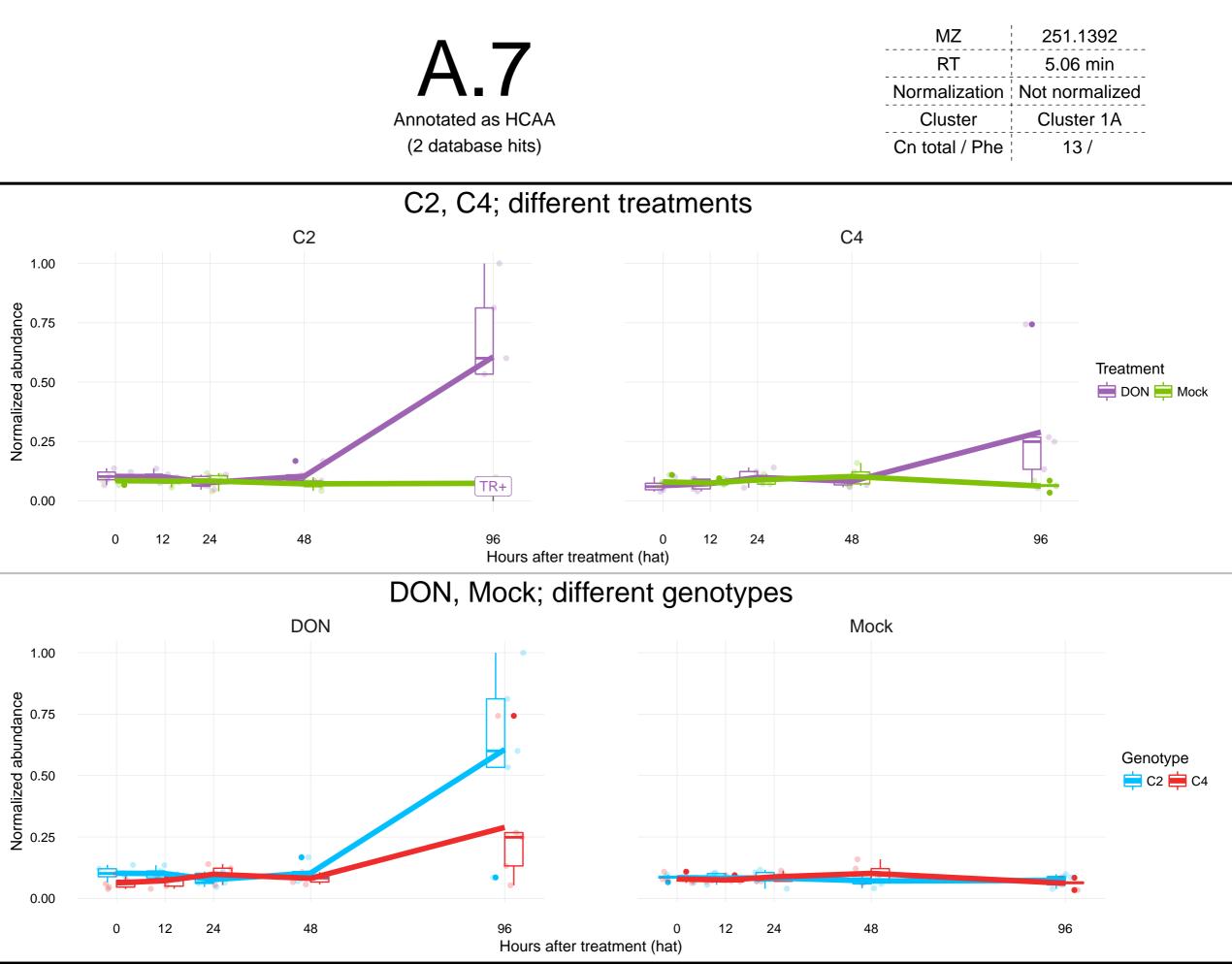




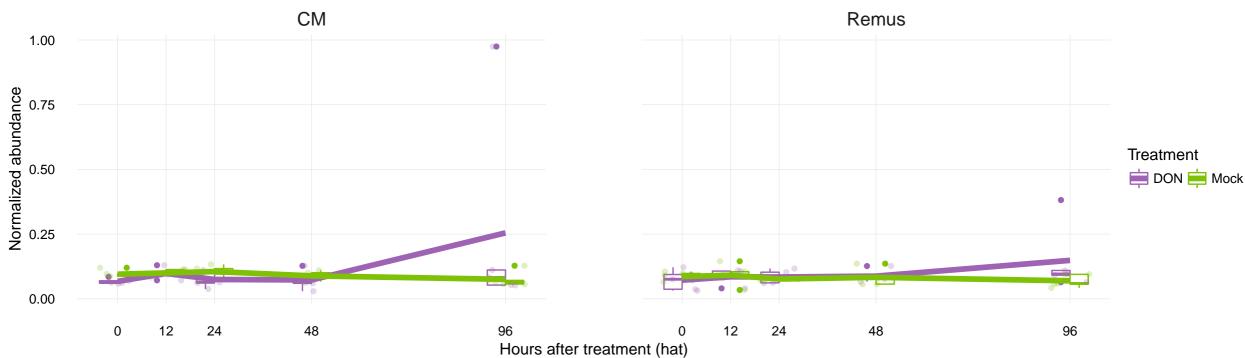


DON, Mock; all four genotypes

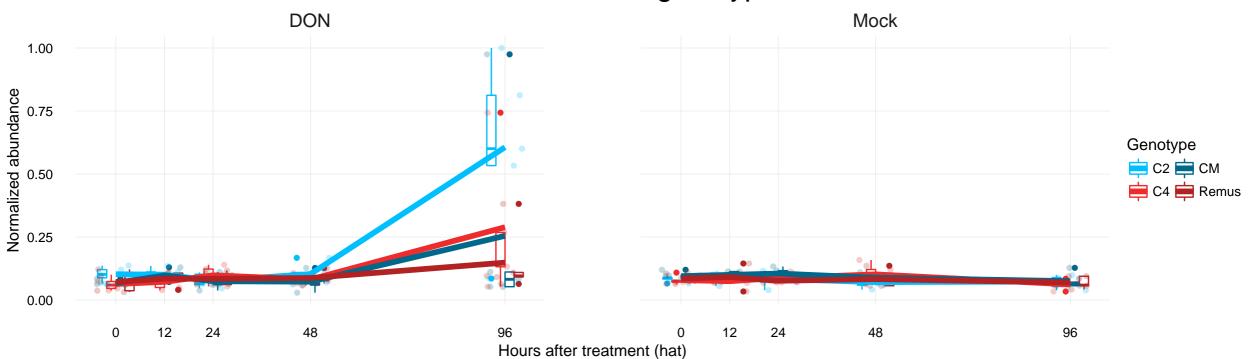


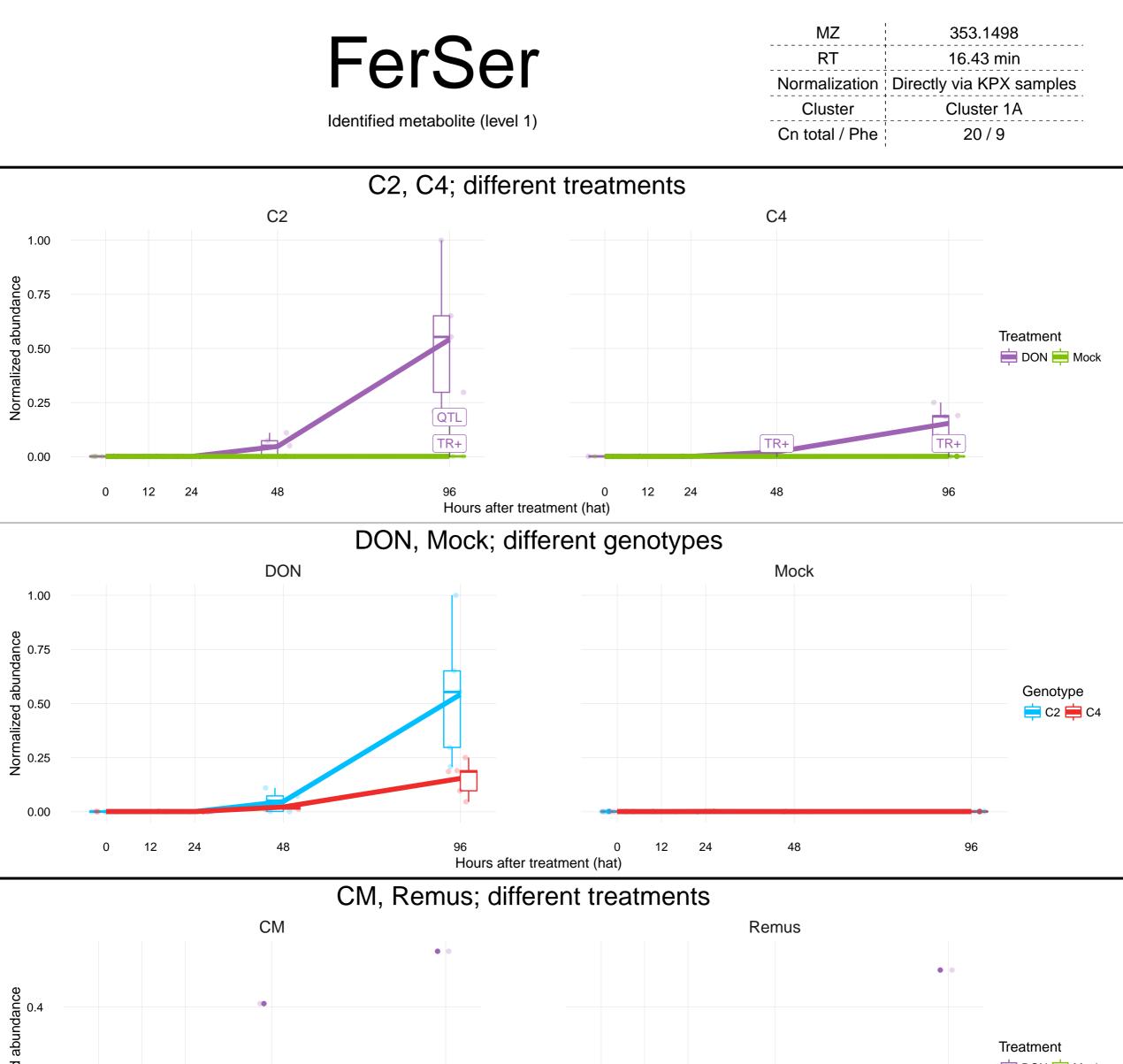


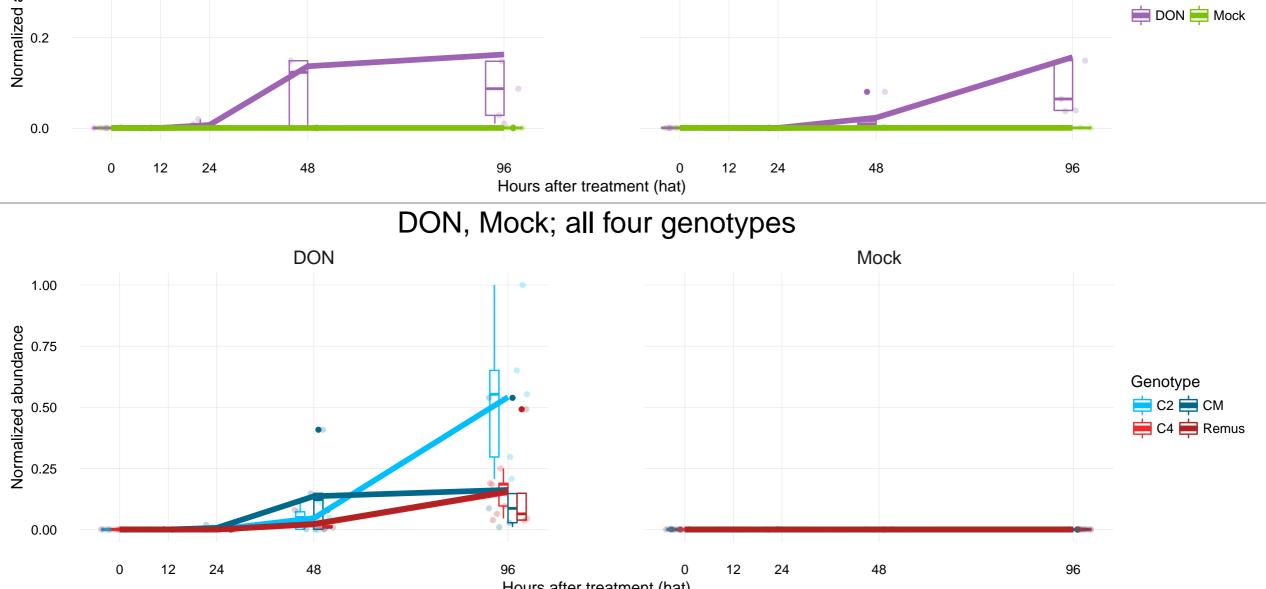
CM, Remus; different treatments



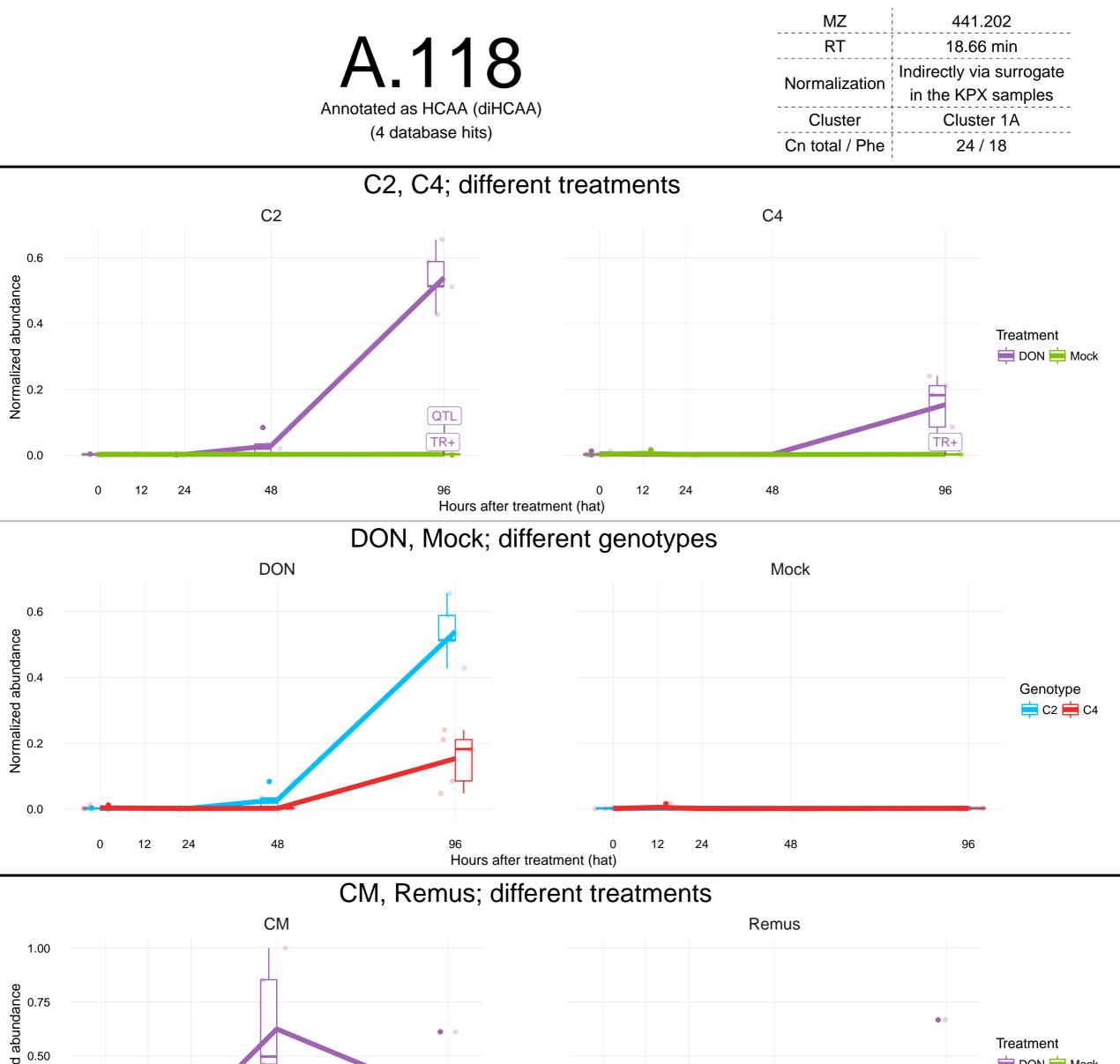
DON, Mock; all four genotypes

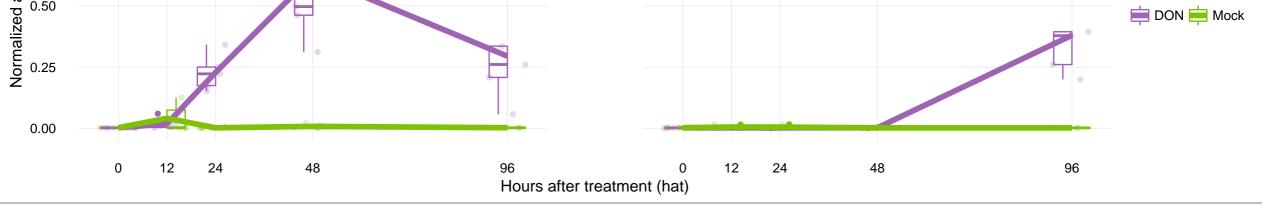




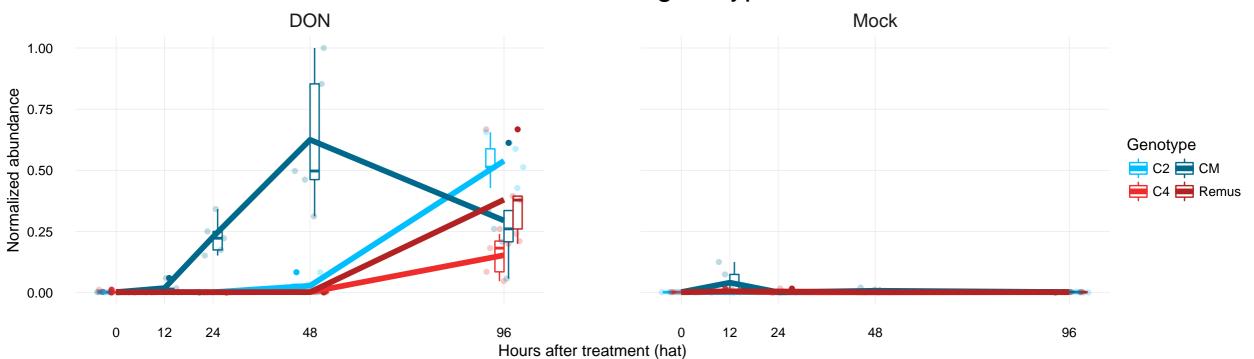


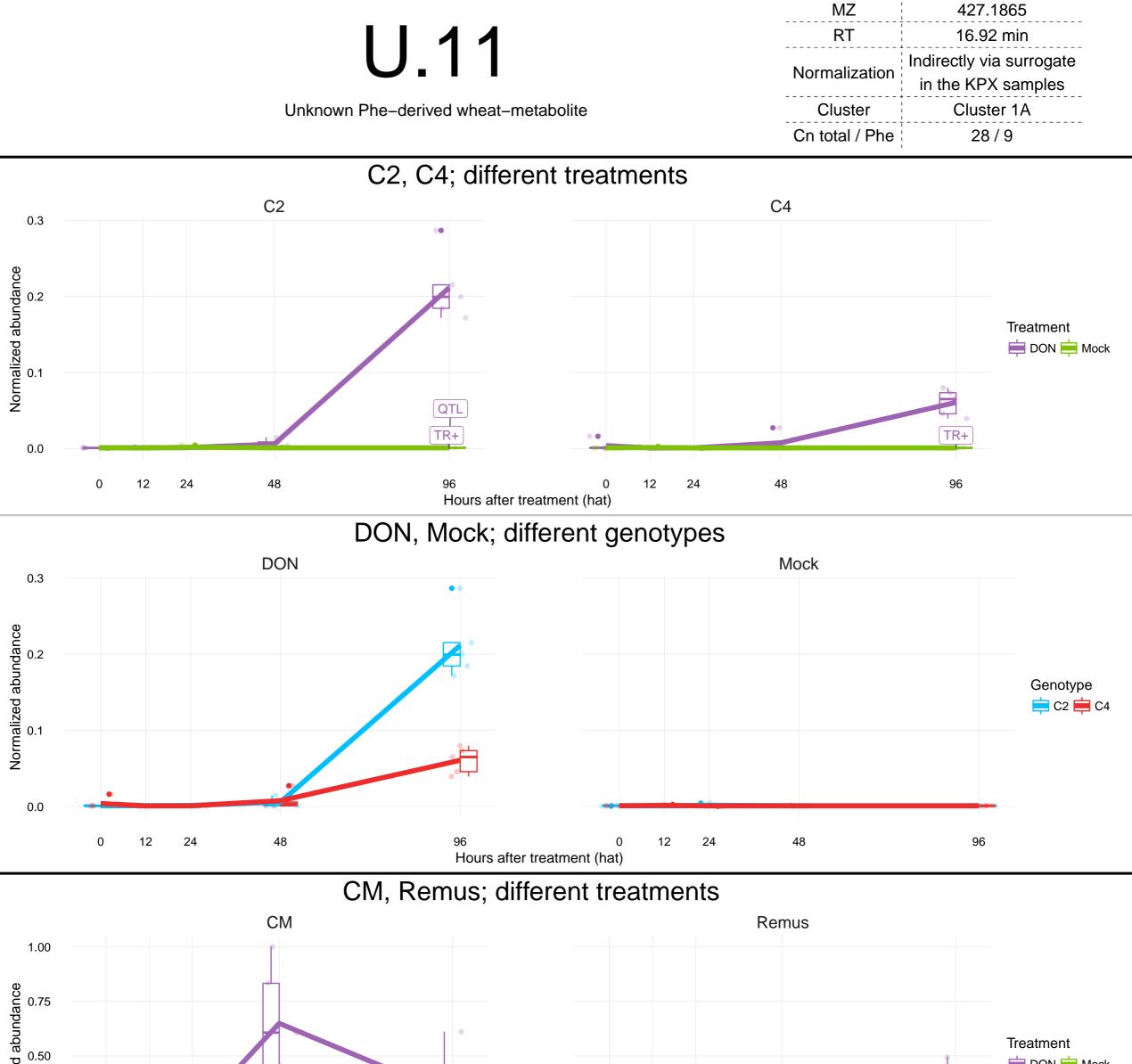
Hours after treatment (hat)

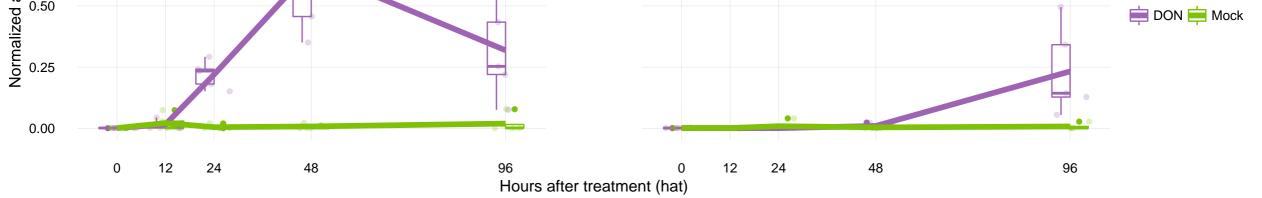




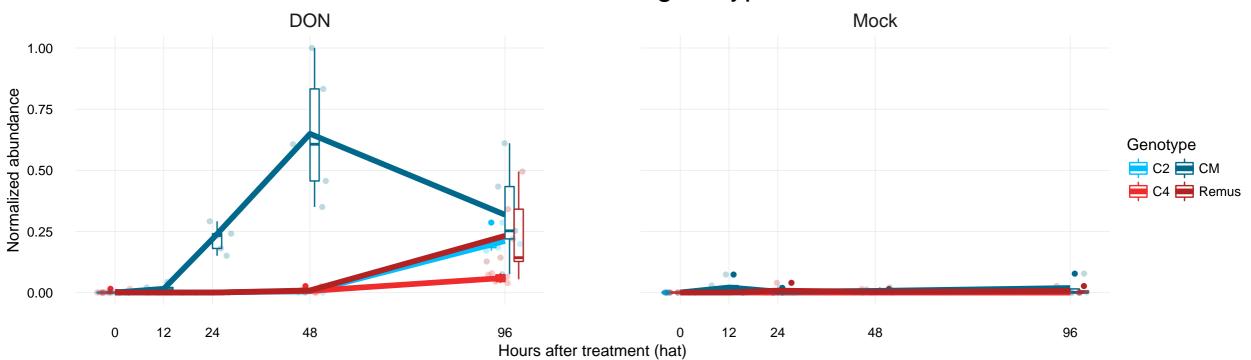
DON, Mock; all four genotypes

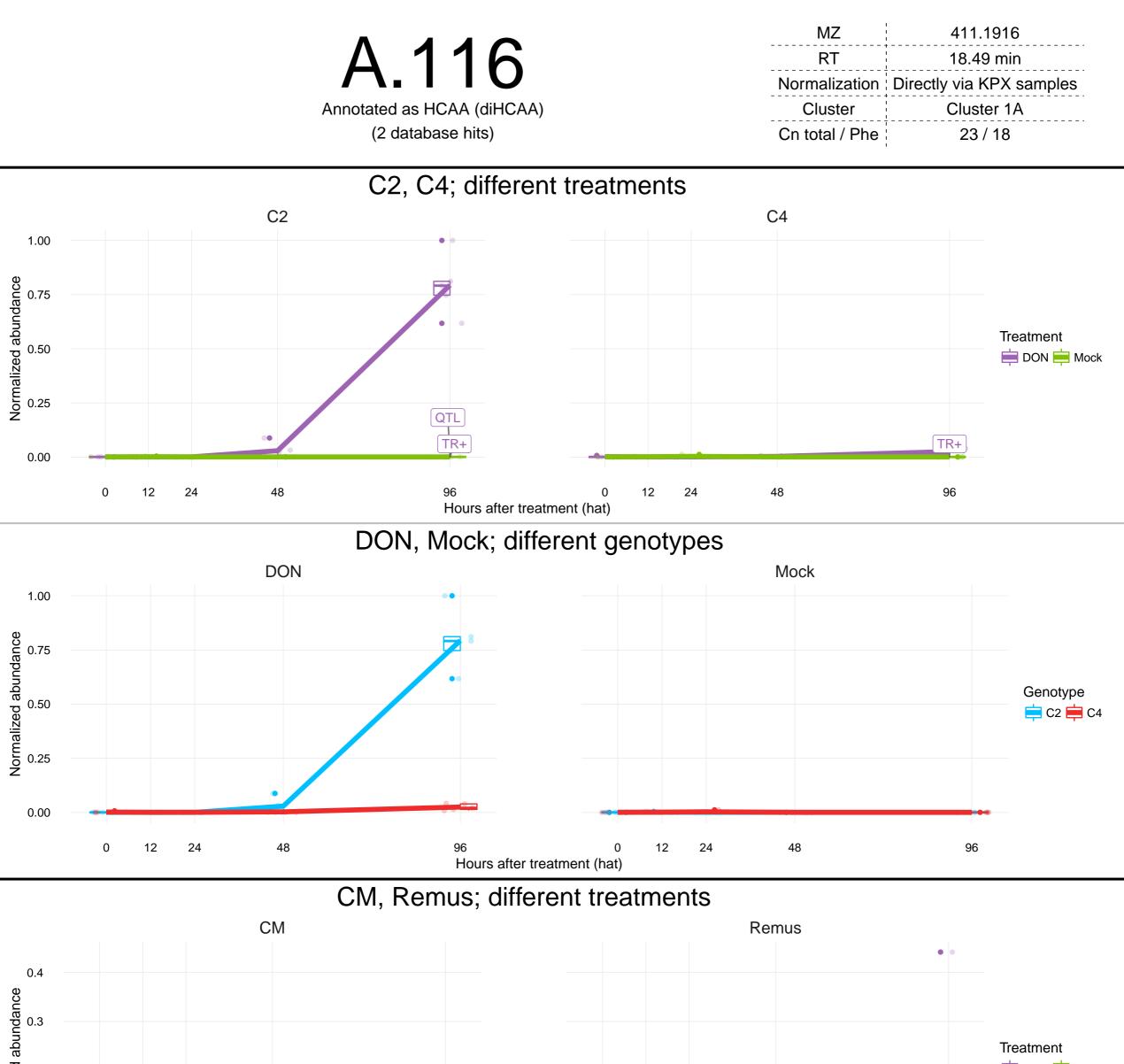


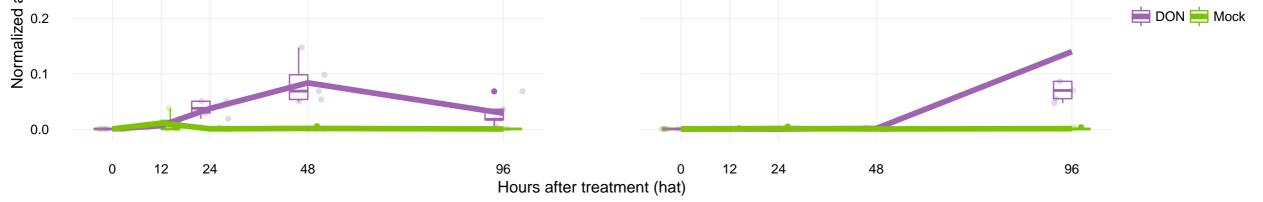




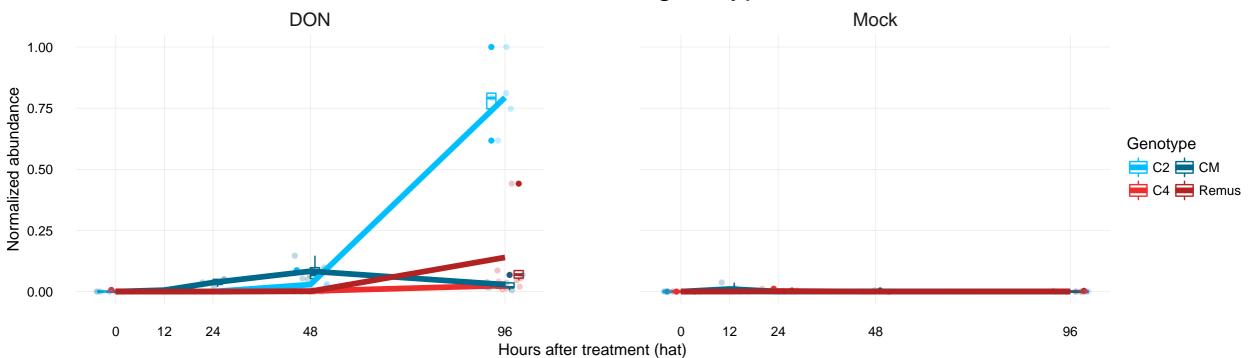
DON, Mock; all four genotypes

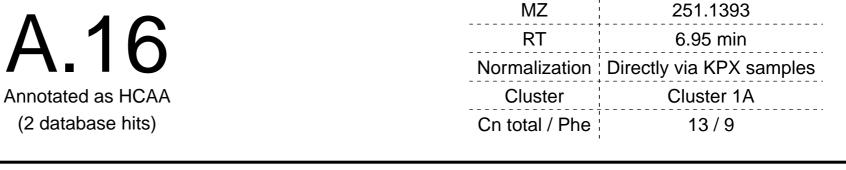


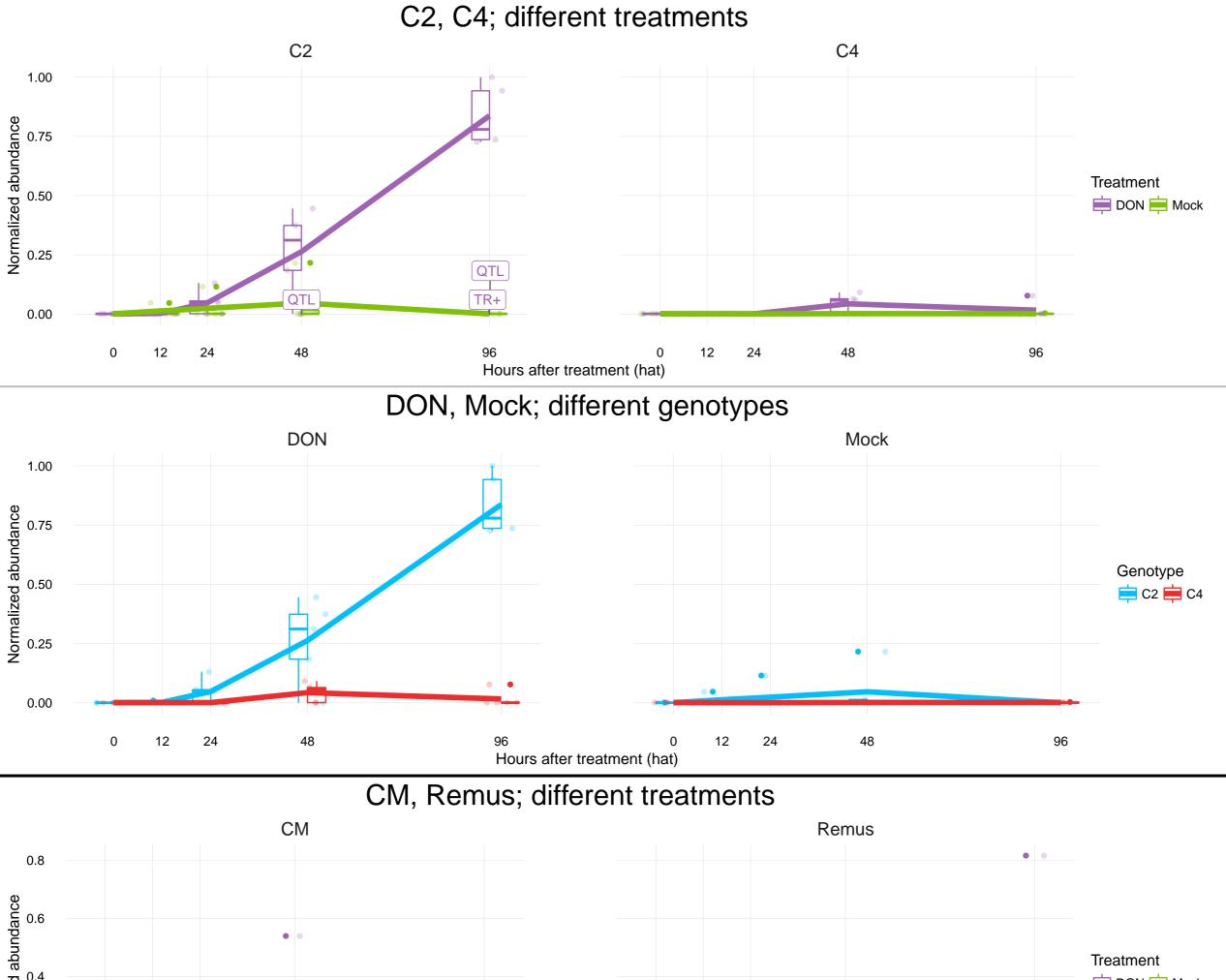


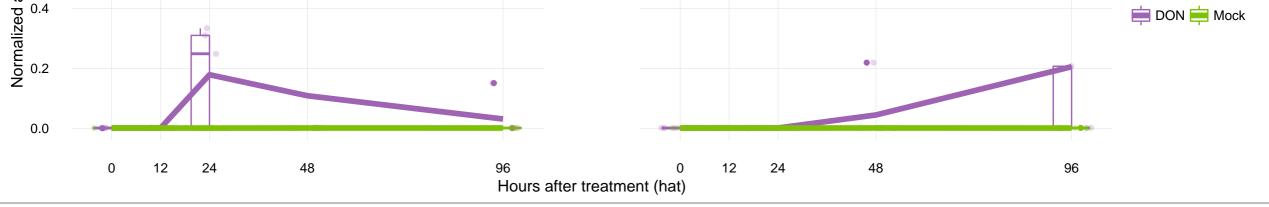


DON, Mock; all four genotypes

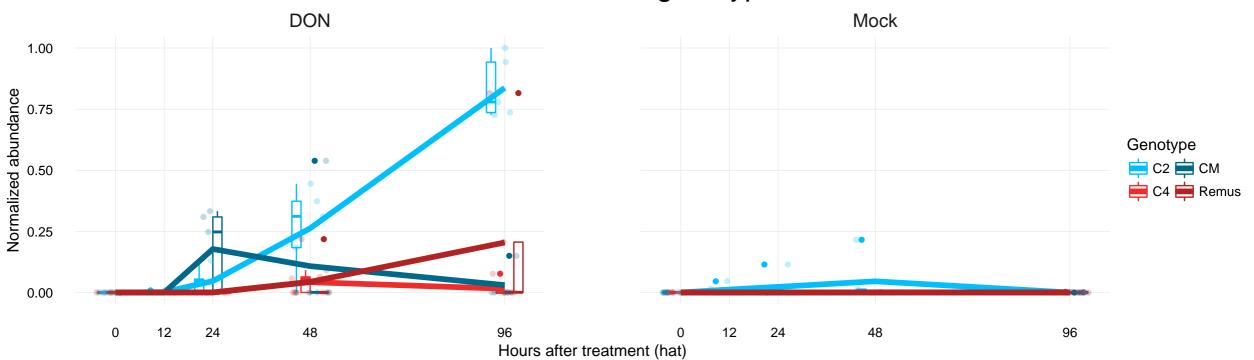


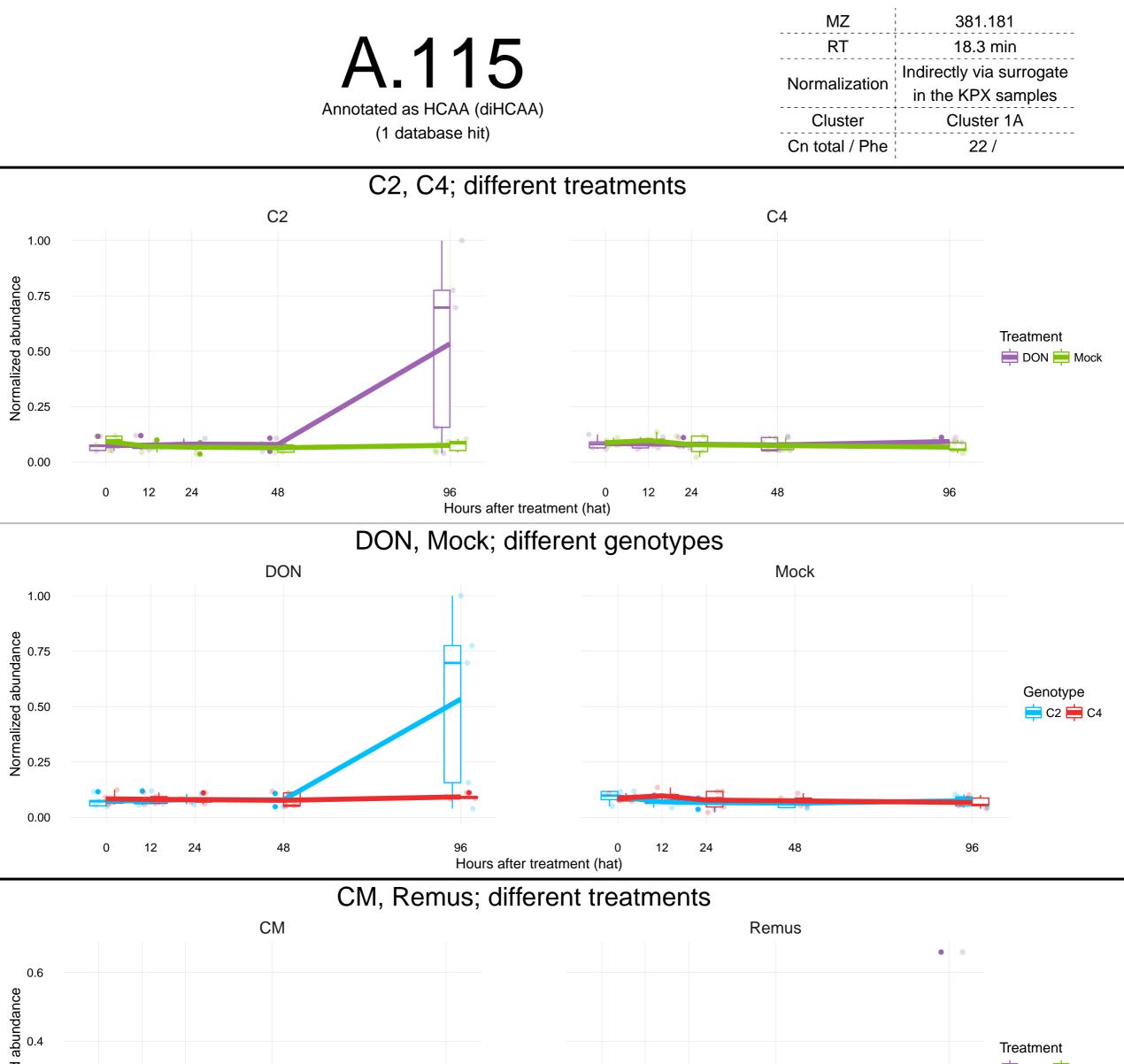


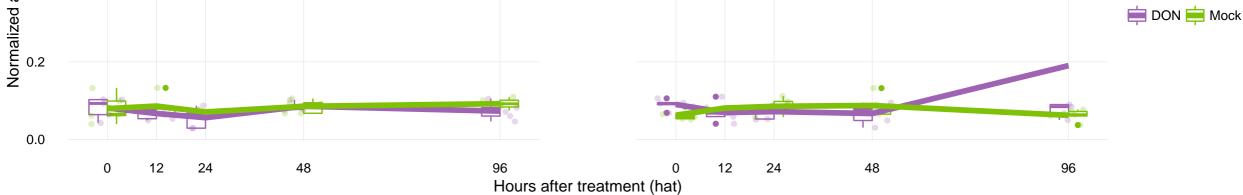




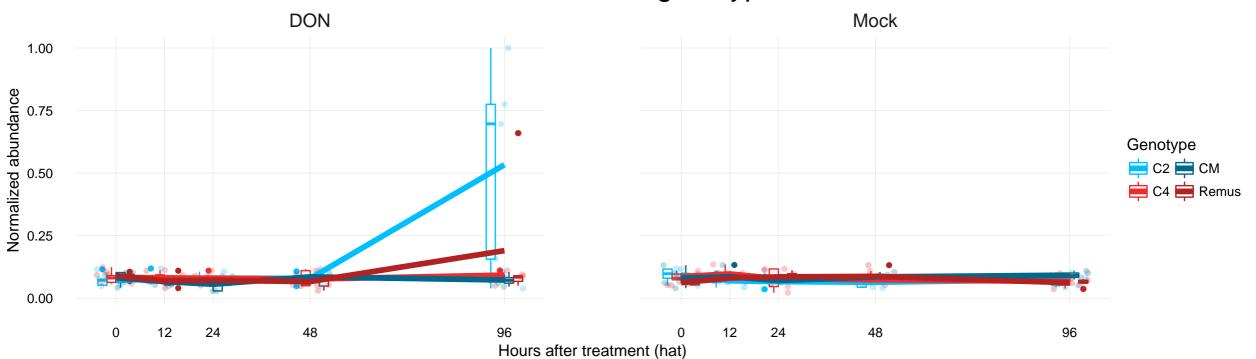
DON, Mock; all four genotypes

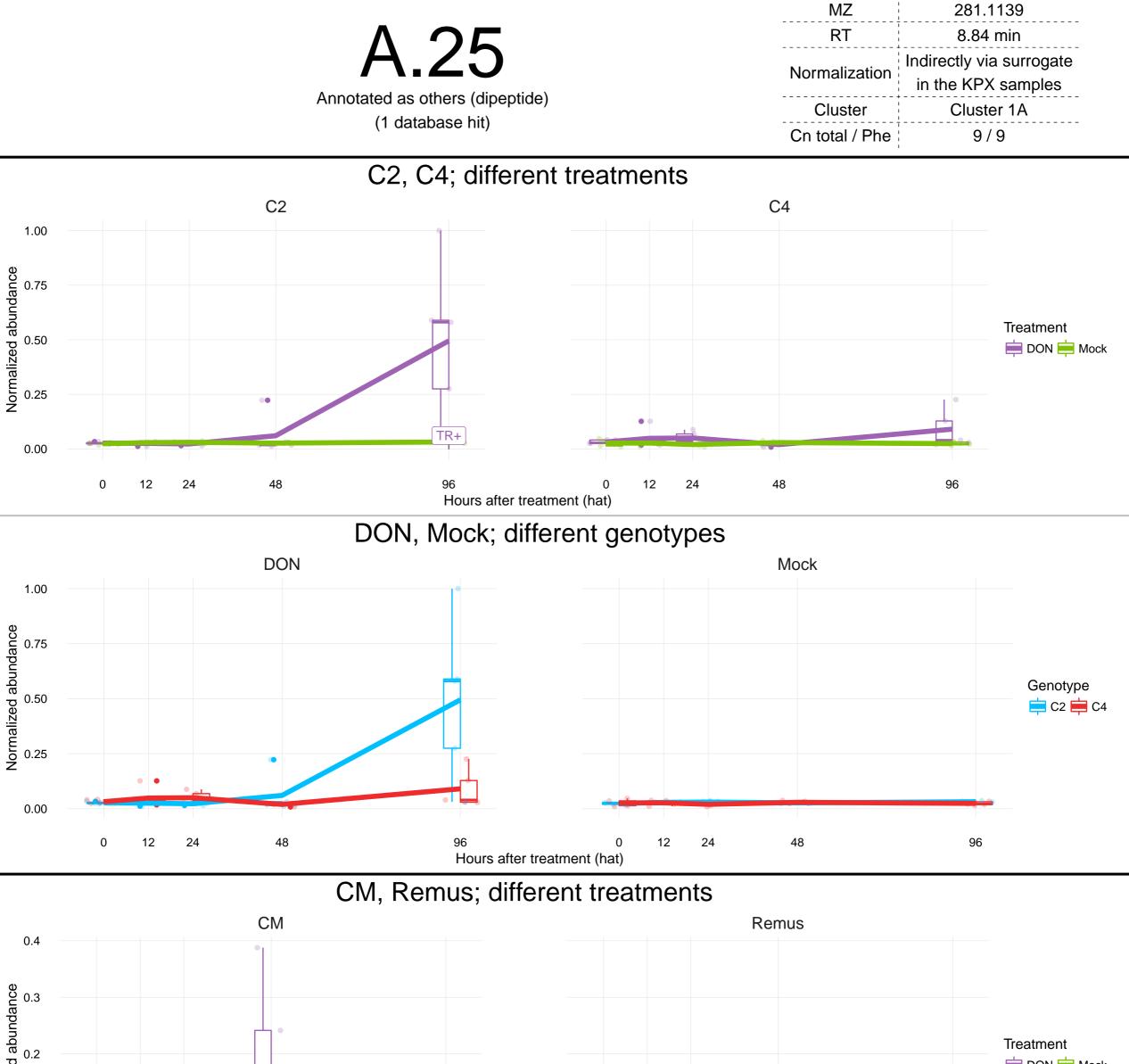


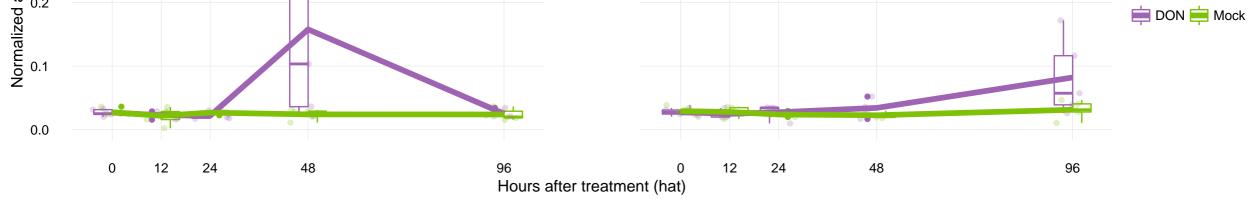




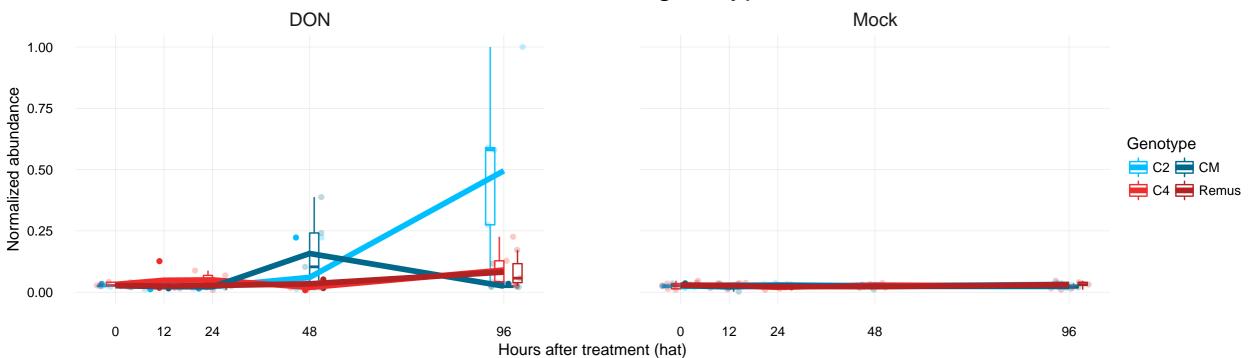
DON, Mock; all four genotypes

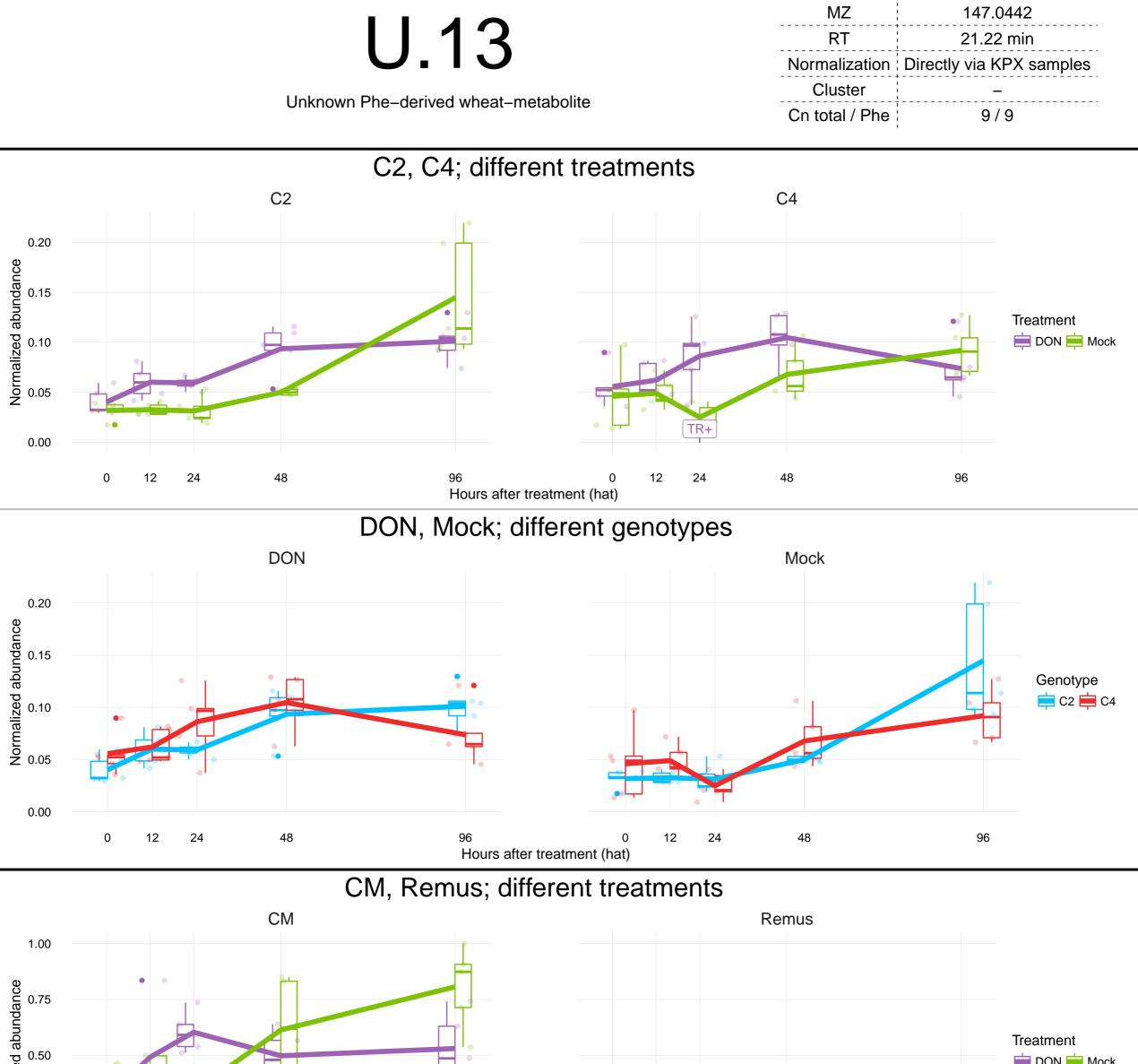


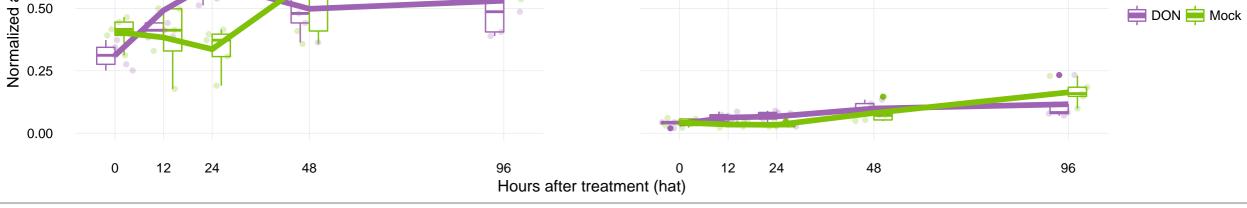




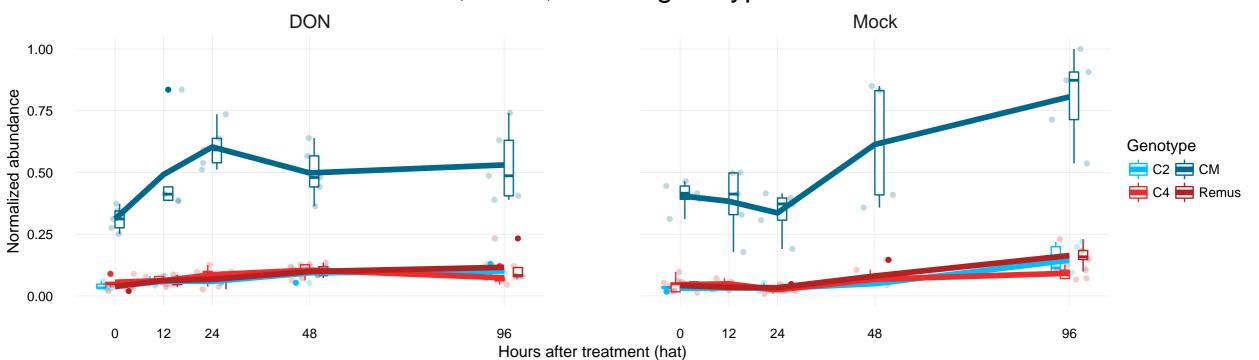
DON, Mock; all four genotypes

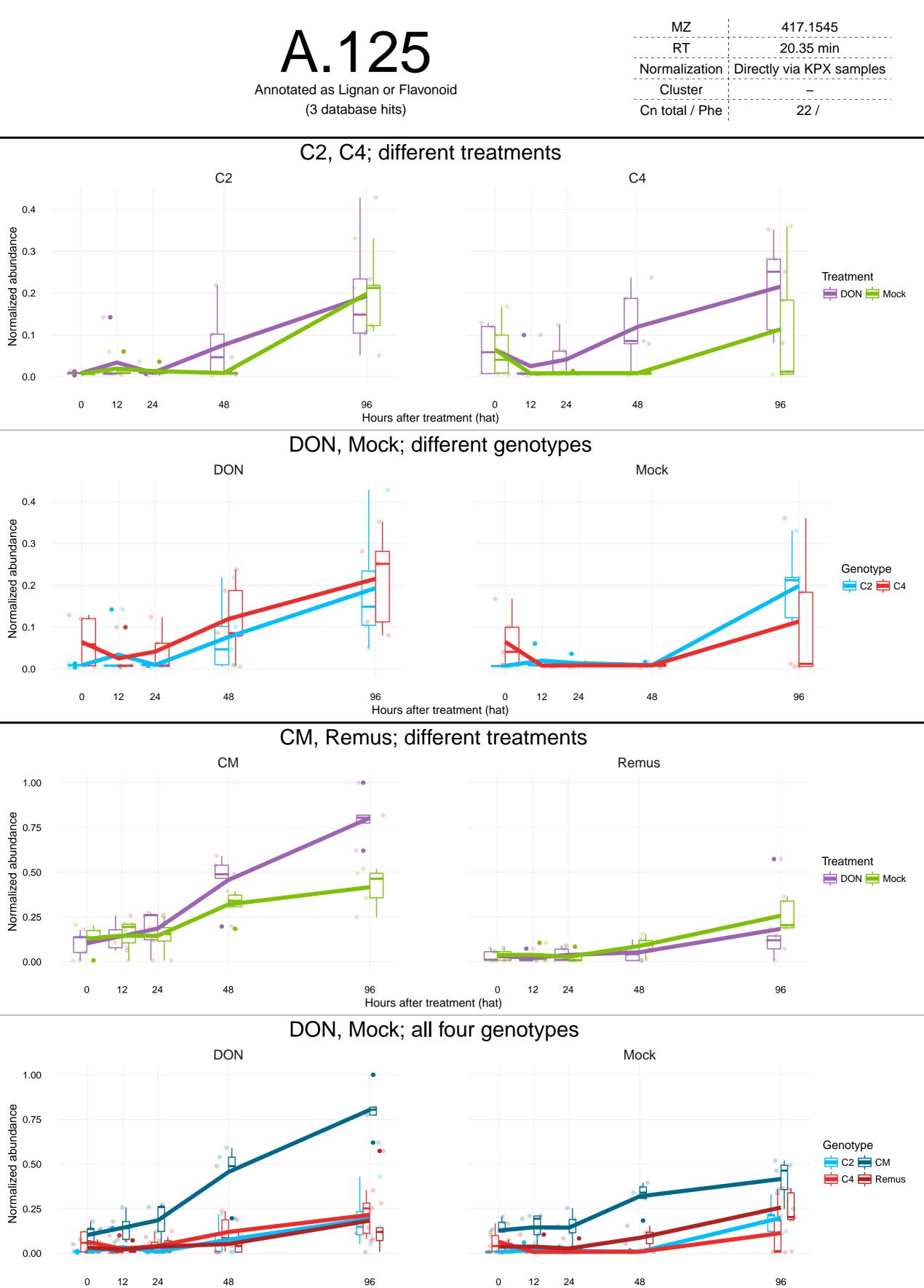




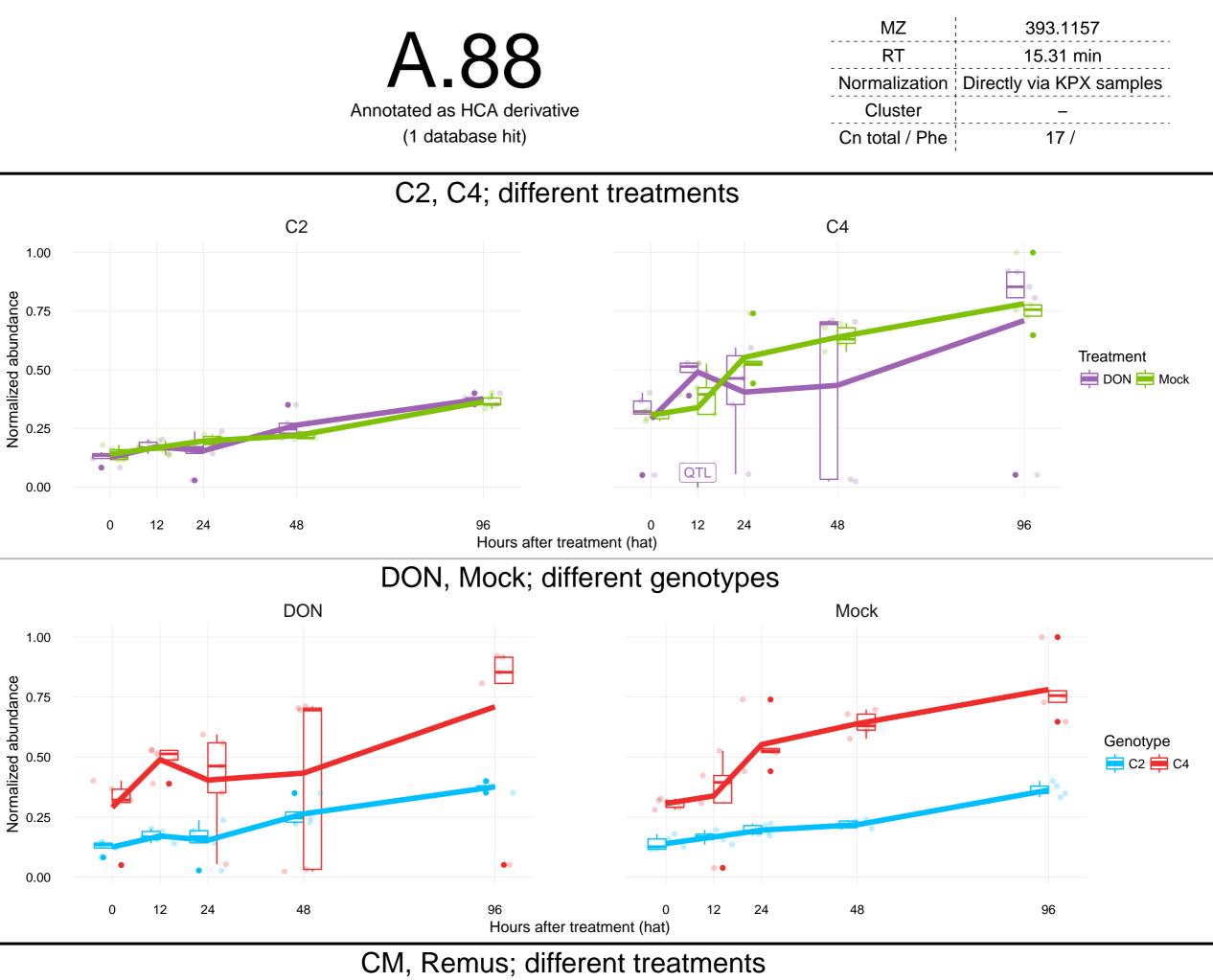


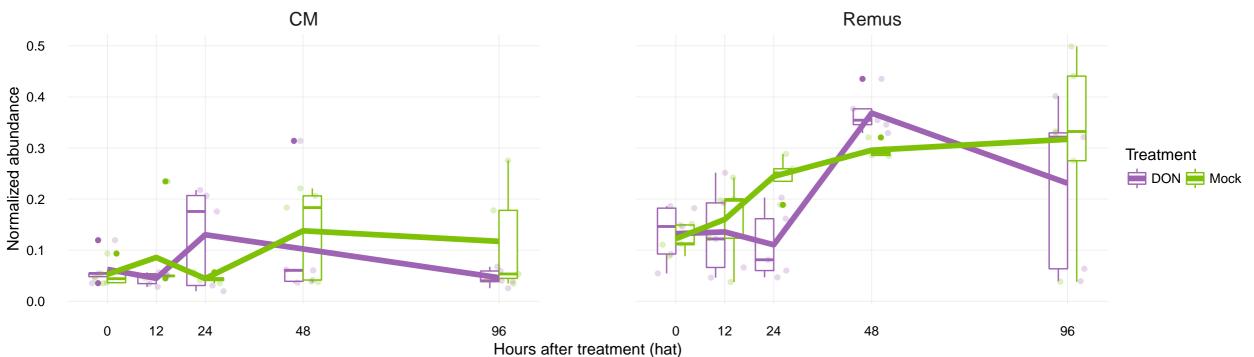
DON, Mock; all four genotypes



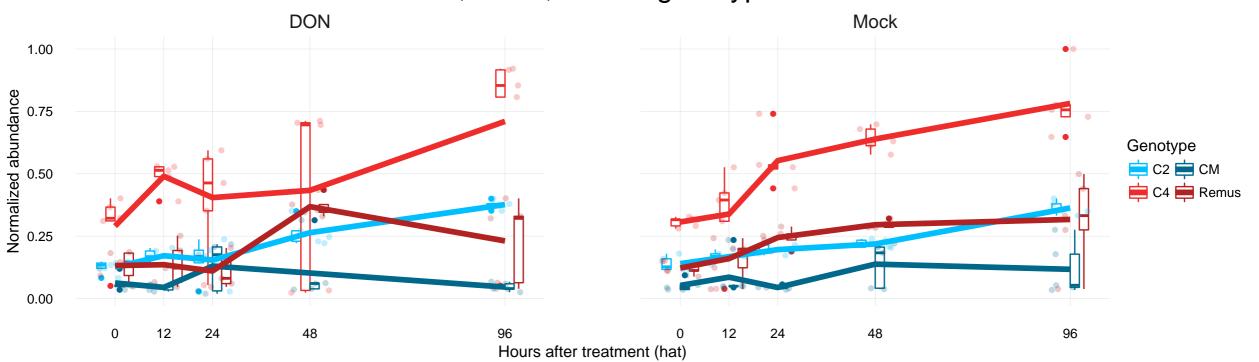


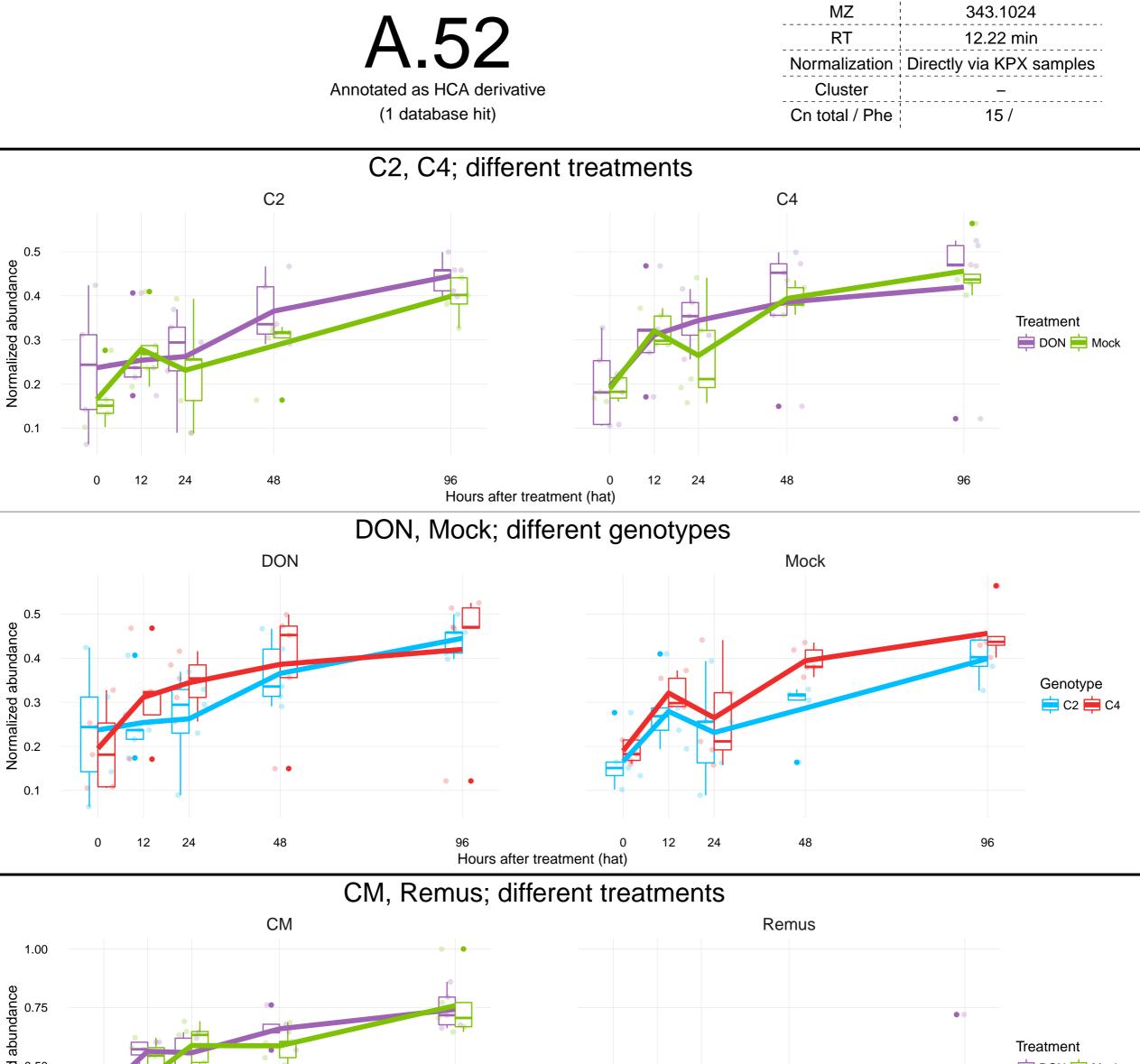
Hours after treatment (hat)

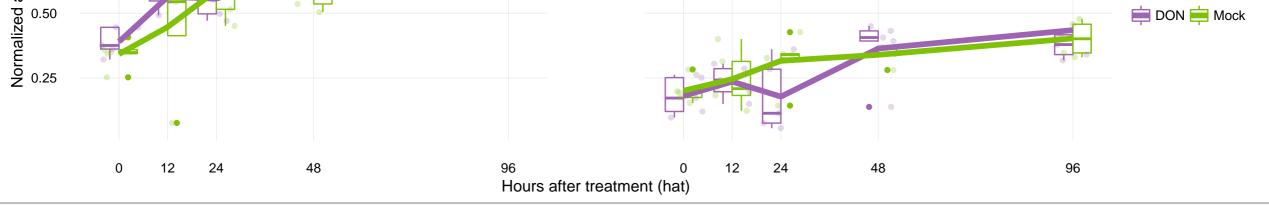




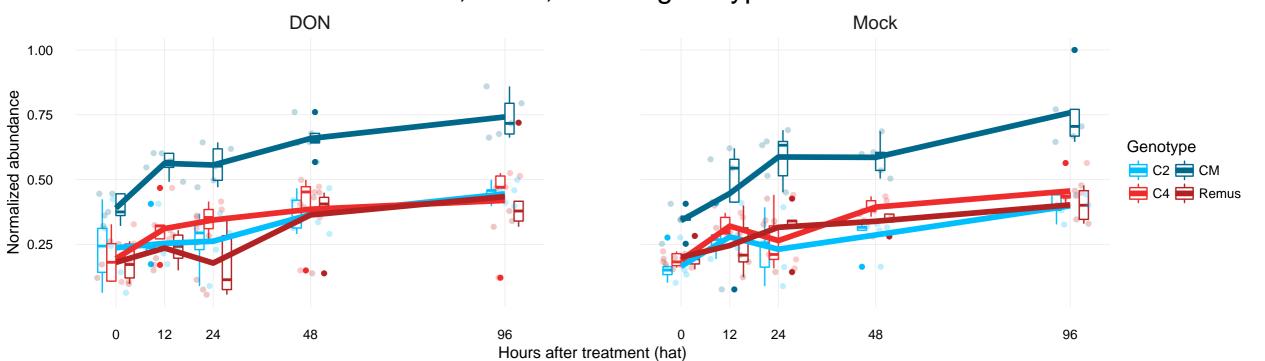
DON, Mock; all four genotypes

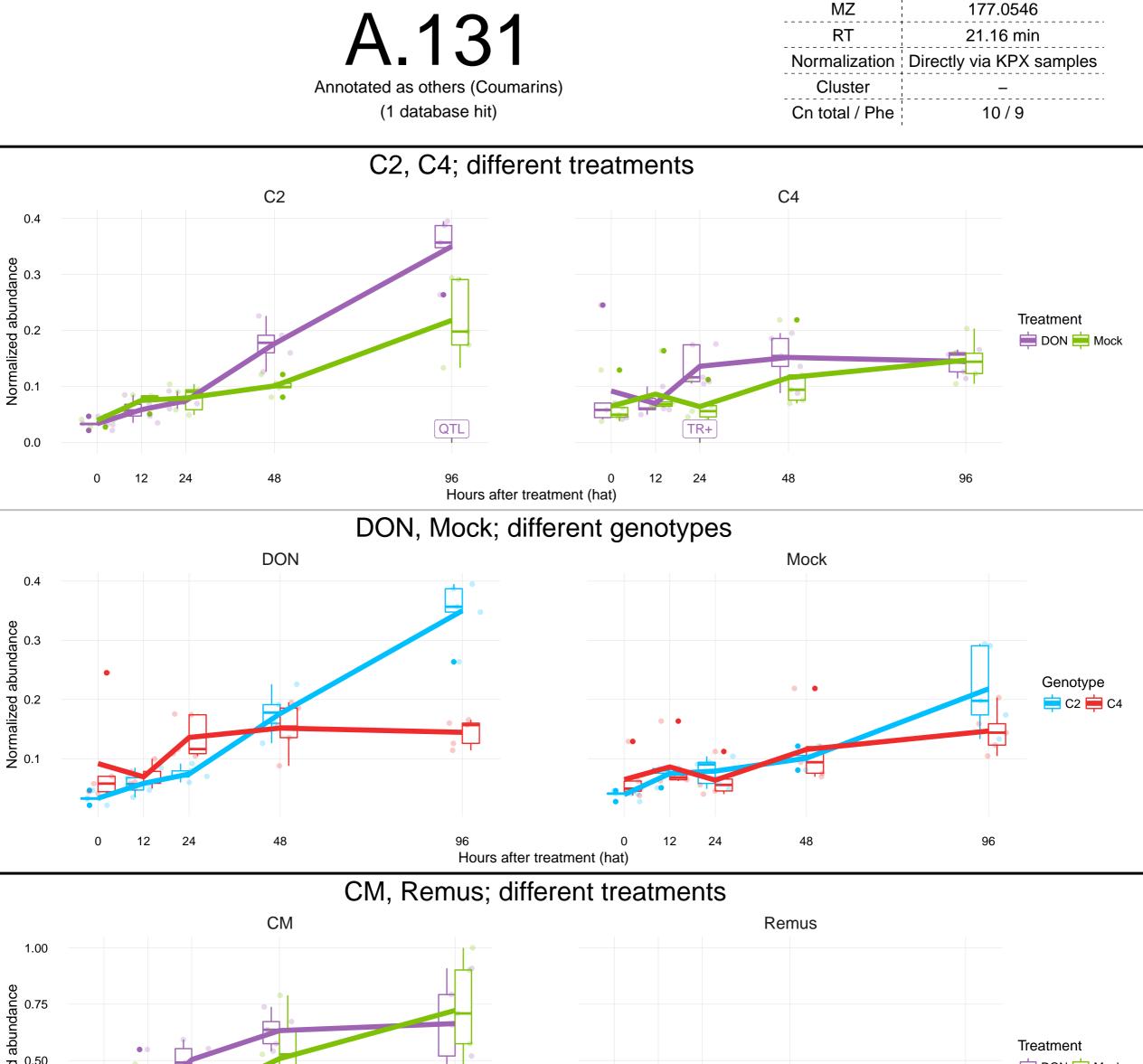


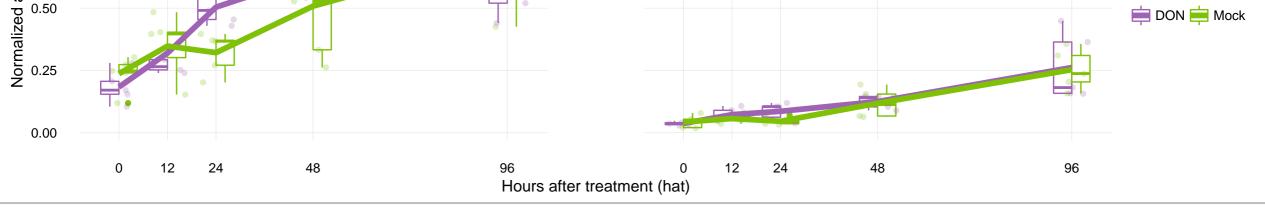




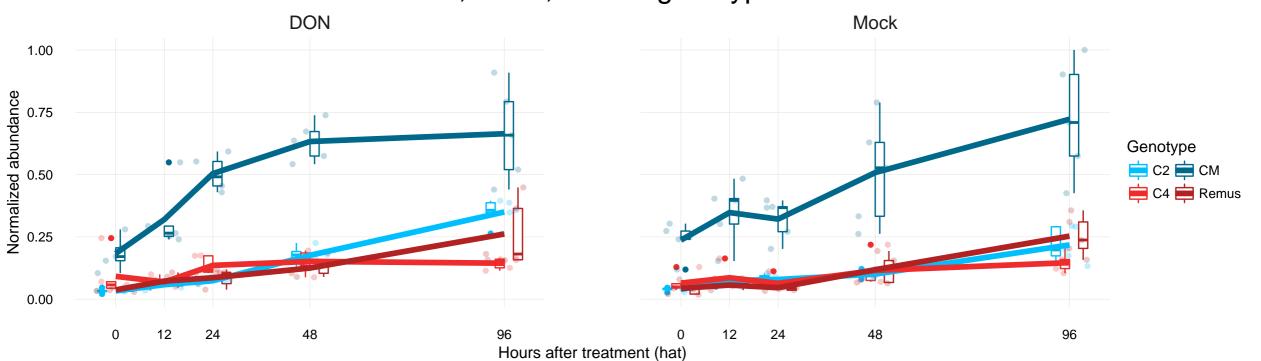
DON, Mock; all four genotypes



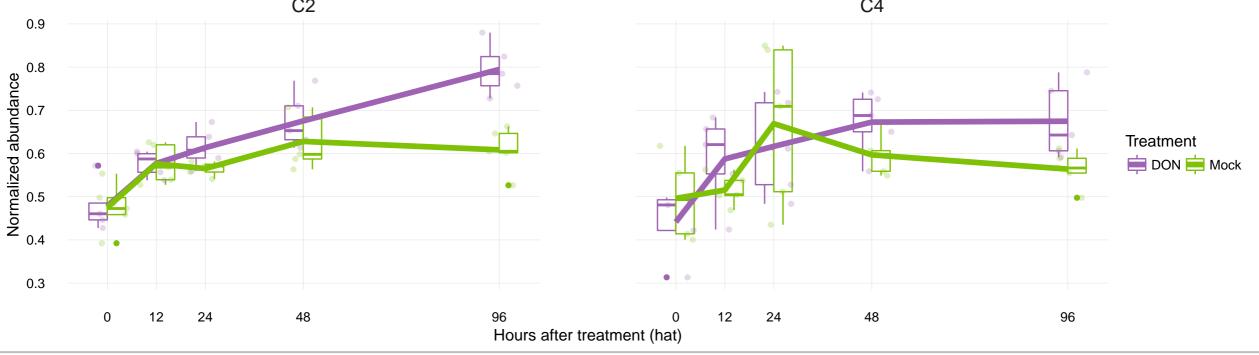




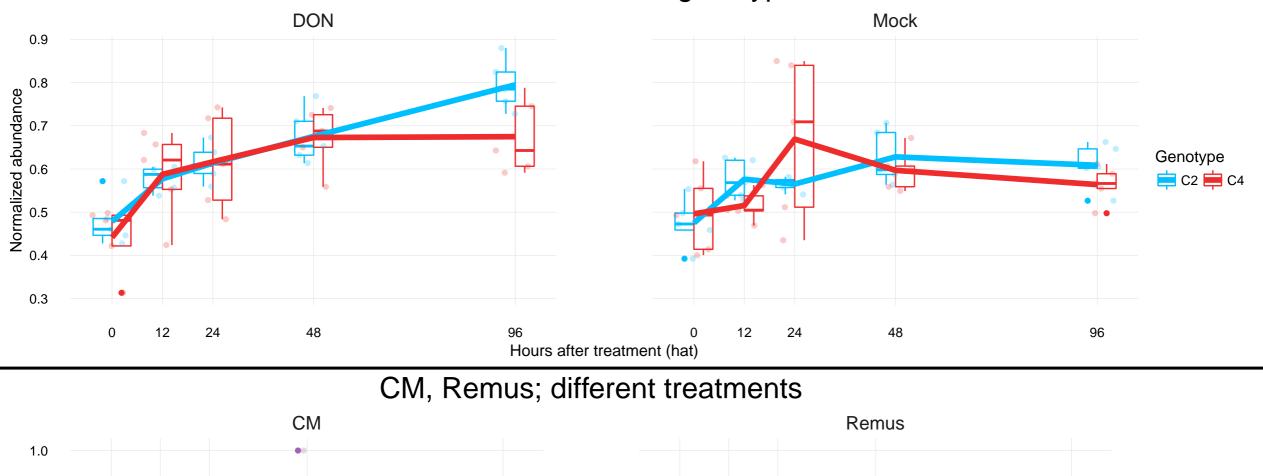
DON, Mock; all four genotypes

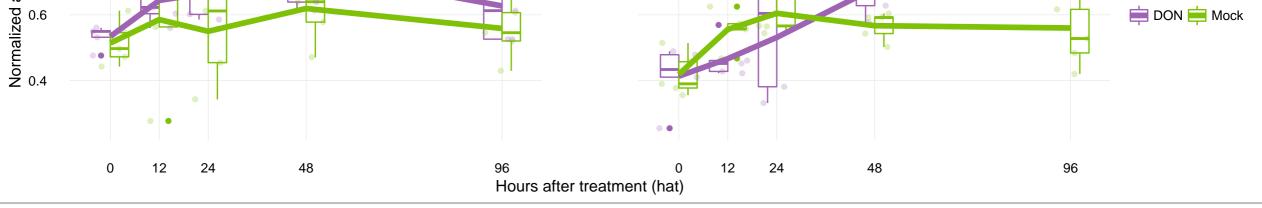


	MZ	405.1181
A.128	RT	20.88 min
A.IZU	Normalization	Directly via KPX samples
Annotated as Flavonoid	Cluster	_
(25 database hits)	Cn total / Phe	20 /
C2, C4; different treatments		
C2	C4	



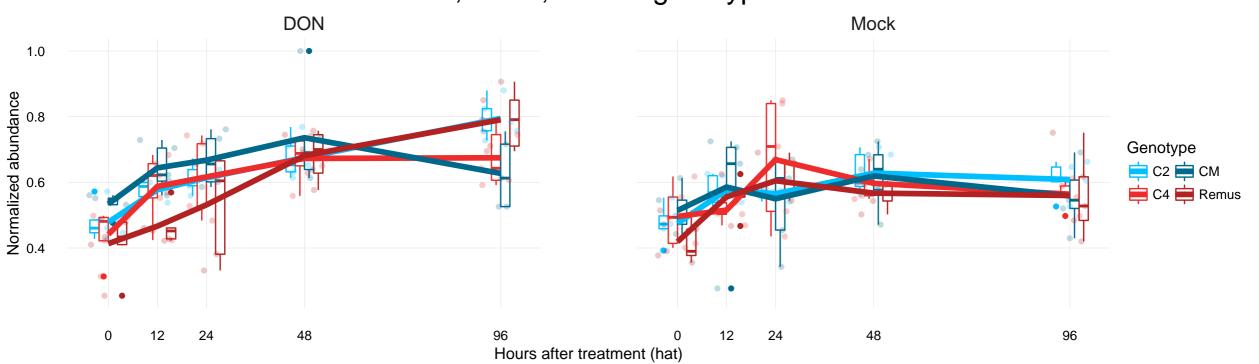
DON, Mock; different genotypes

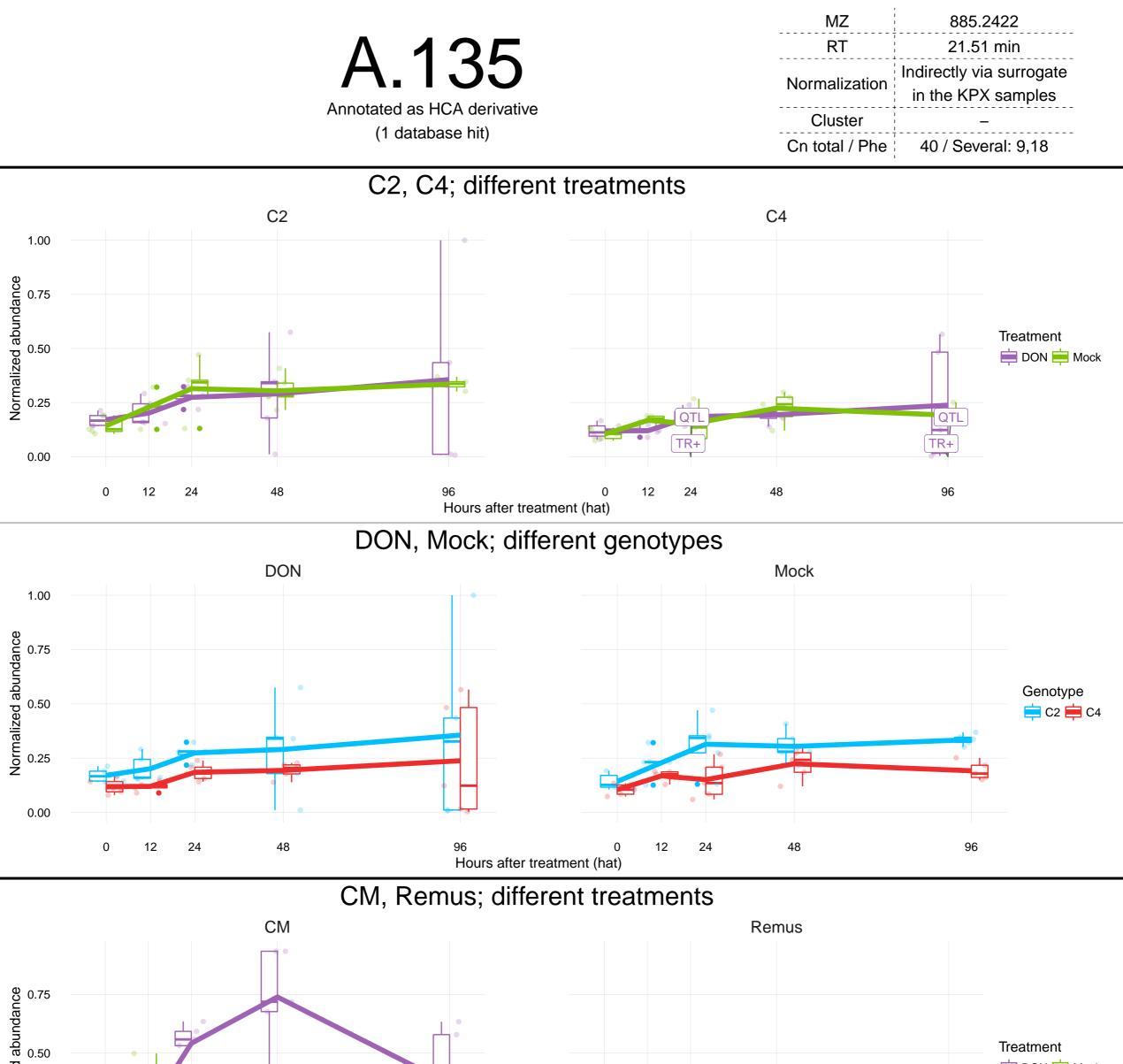


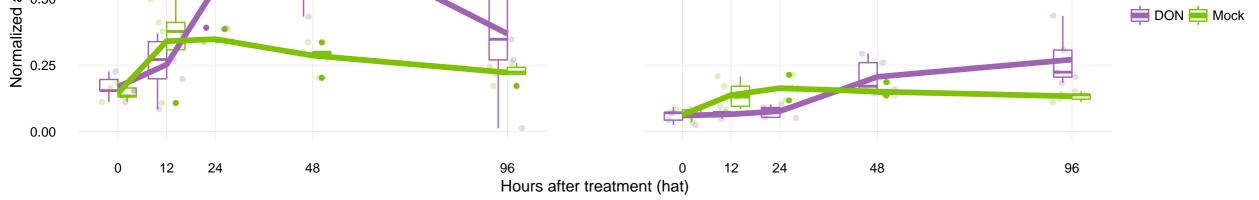


DON, Mock; all four genotypes

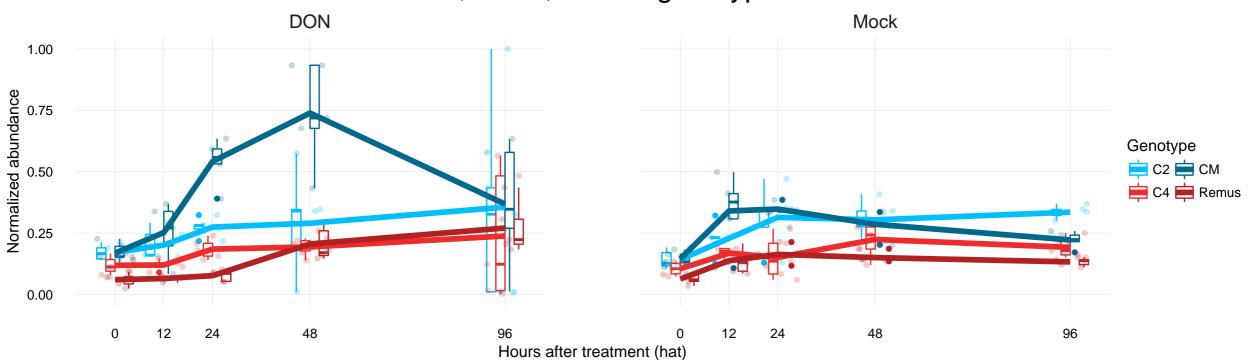
abundance 8.0

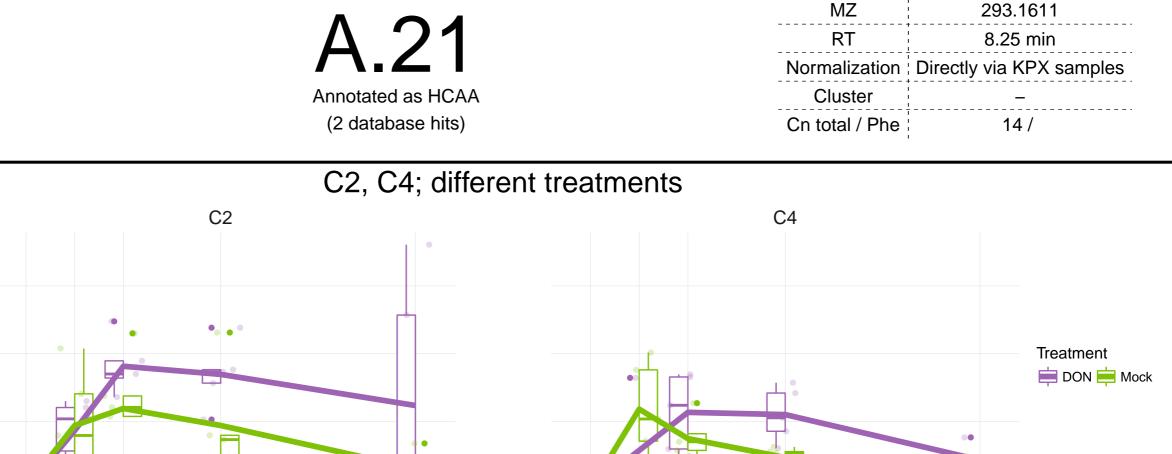






DON, Mock; all four genotypes





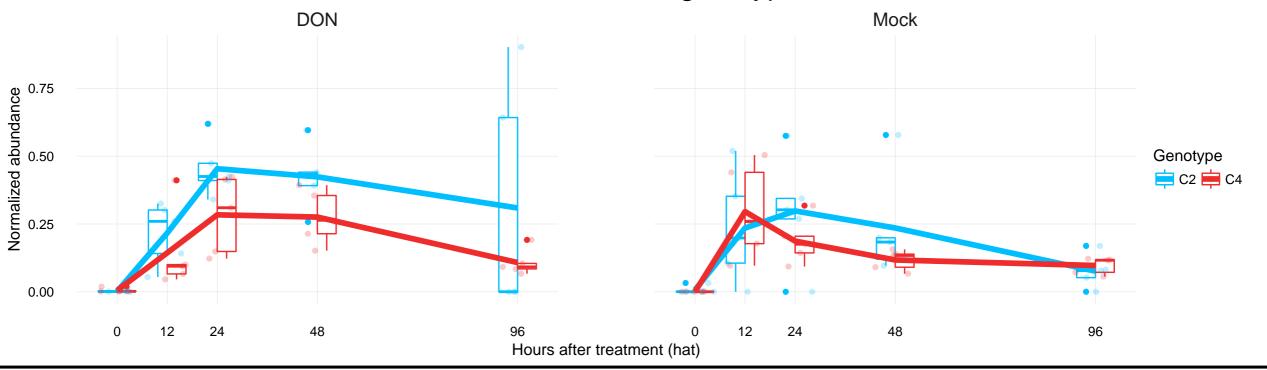
96



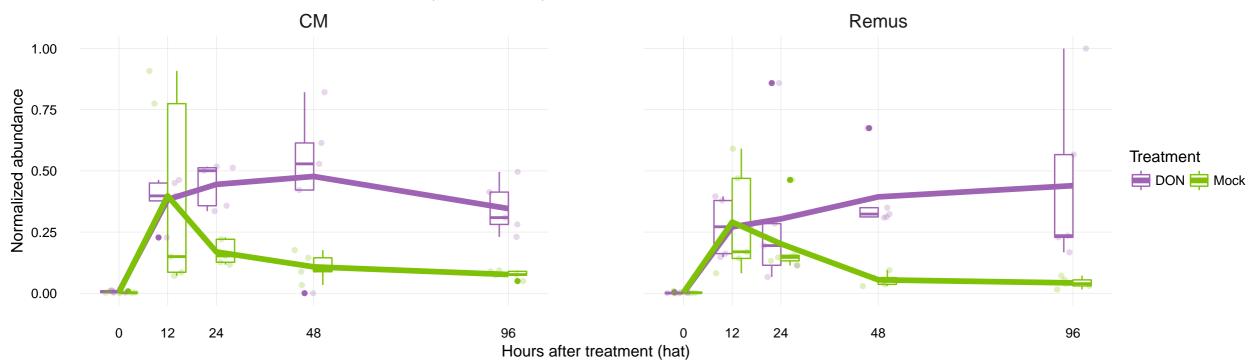
Normalized abundance 0.50 0.25

0.00

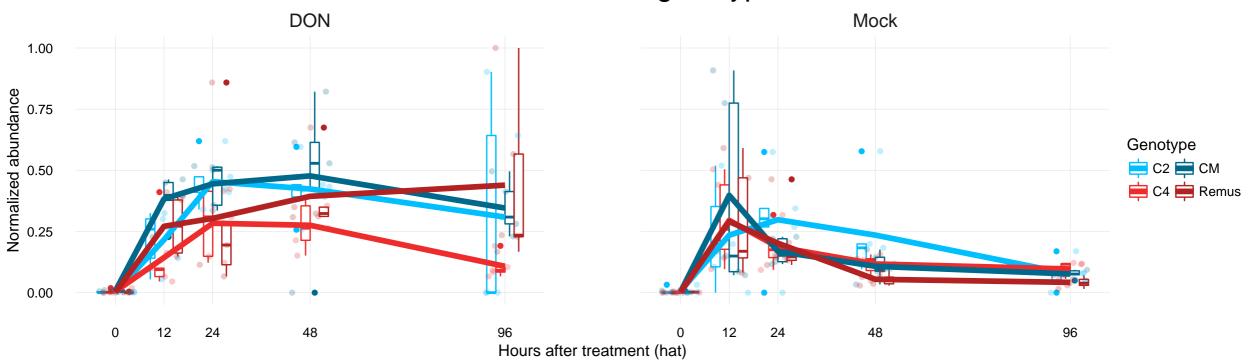
DON, Mock; different genotypes



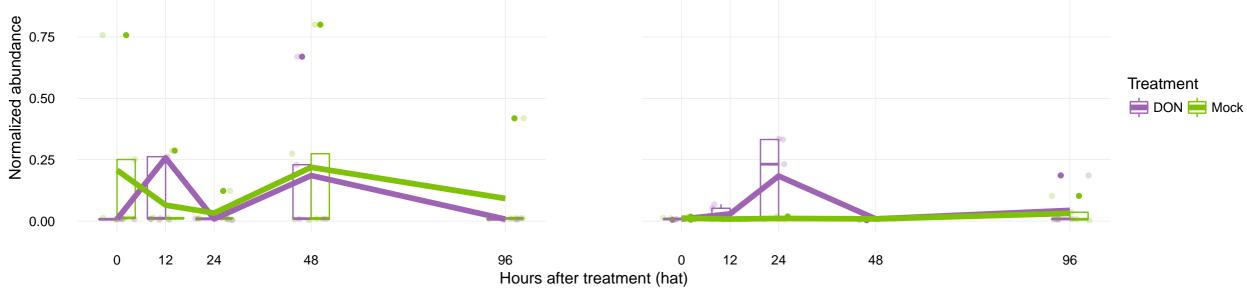
CM, Remus; different treatments



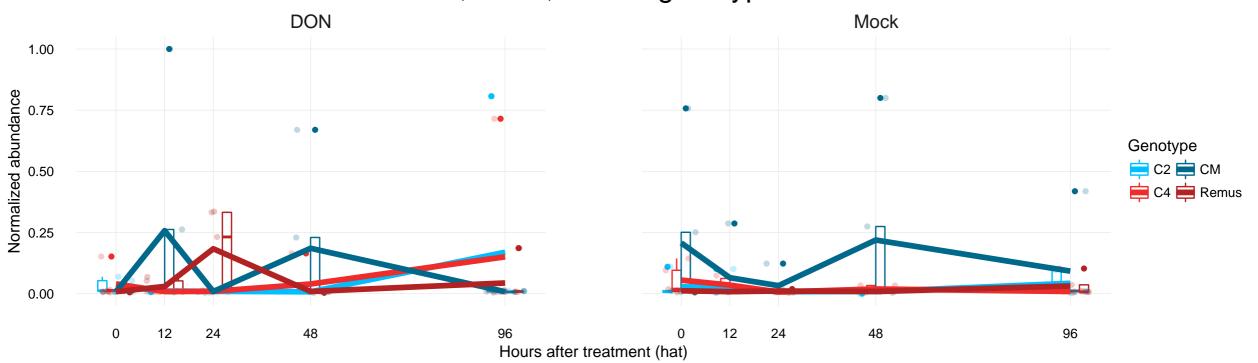
DON, Mock; all four genotypes



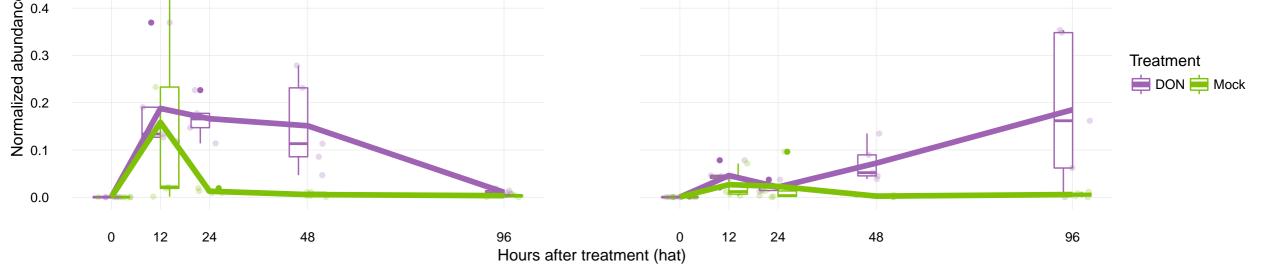
			124 Anotated as Flavonoid		MZ RT Normalization Cluster	20.2 Indirectly v	.1385 25 min via surrogate X samples
			(30 database hits)		Cn total / Phe	2	0 /
			C2, C4; differer	nt treatments			
		C2			C4		
0.8			• •			••	_
ance							
Normalized abundance							Treatment
alized							🚔 DON 🚔 Mock
E 0.2 N				•	• •		_
0.0							
	0 12 24	48	96	0 12 24	48	96	
		L DON		erent genotypes	Mock		
0.8			••				
e			• •				
Normalized abundance							
qe qa 0.4							Genotype C2 🚔 C4
rmaliz							
0 ^{0.2} Z	• •	٠		• 4		(° -1	•
0.0			-				-
	0 12 24	48	96 Hours after tre	0 12 24 eatment (hat)	48	96	
	CM, Remus; different treatments						
		СМ			Remus		
1.00	•						-



DON, Mock; all four genotypes

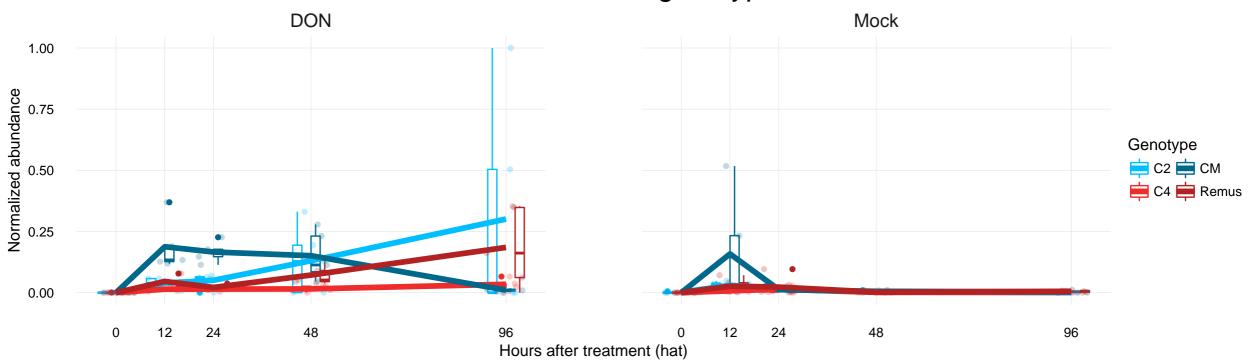


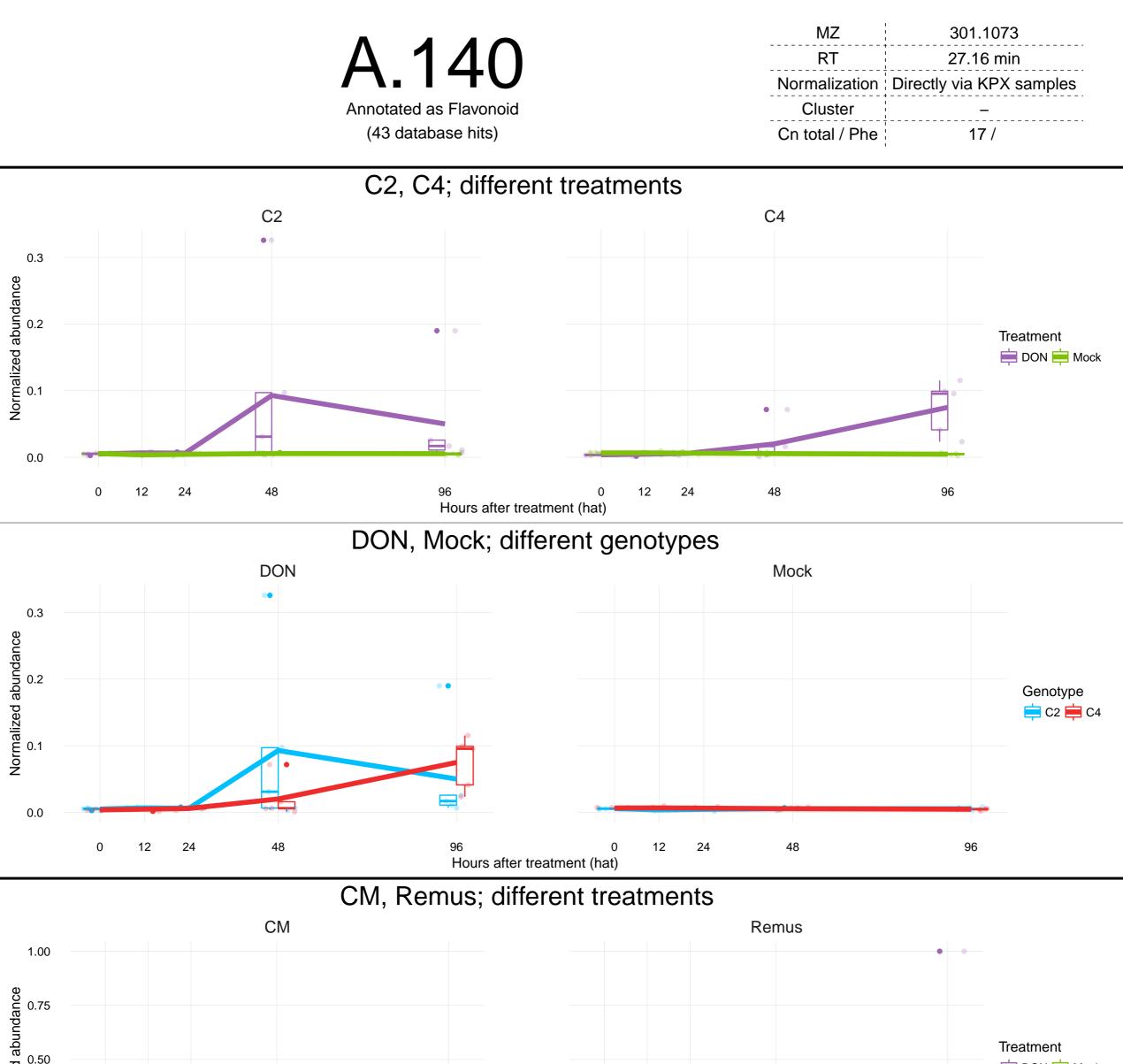
		MZ	235.1	447
		RT	7.48	min
	A.19	Normalization	Indirectly via in the KPX	
	Annotated as HCAA	Cluster		
	(1 database hit)	Cn total / Phe	9/	9
	C2, C4; different treatments			
	C2	C4		
1.00				
ance 0.75				
bund				Treatment
0.50 izeq 0.50				DON 🚔 Mock
Normalized abundance 0.50 0.25				
Z			TR+	
0.00				
	0 12 24 48 96 0 12 24 Hours after treatment (hat)	48	96	
	DON, Mock; different genotype	S		
	DON	Mock		
1.00				
0.75				
Normalized abundance 0.50 0.25				Genotype
о о.50 хера				C2 🚔 C4
0.25				
Ž				
0.00				
	0 12 24 48 96 0 12 24 Hours after treatment (hat)	48	96	
	CM, Remus; different treatments			
	CM	Remus		
0.5				
0.4				

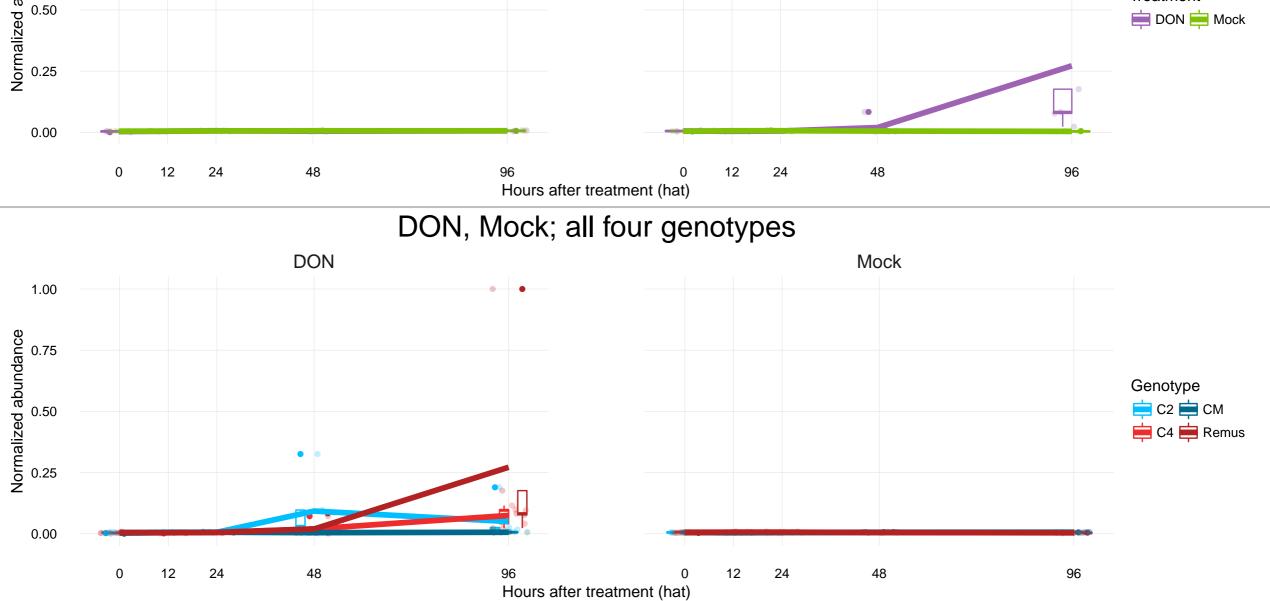


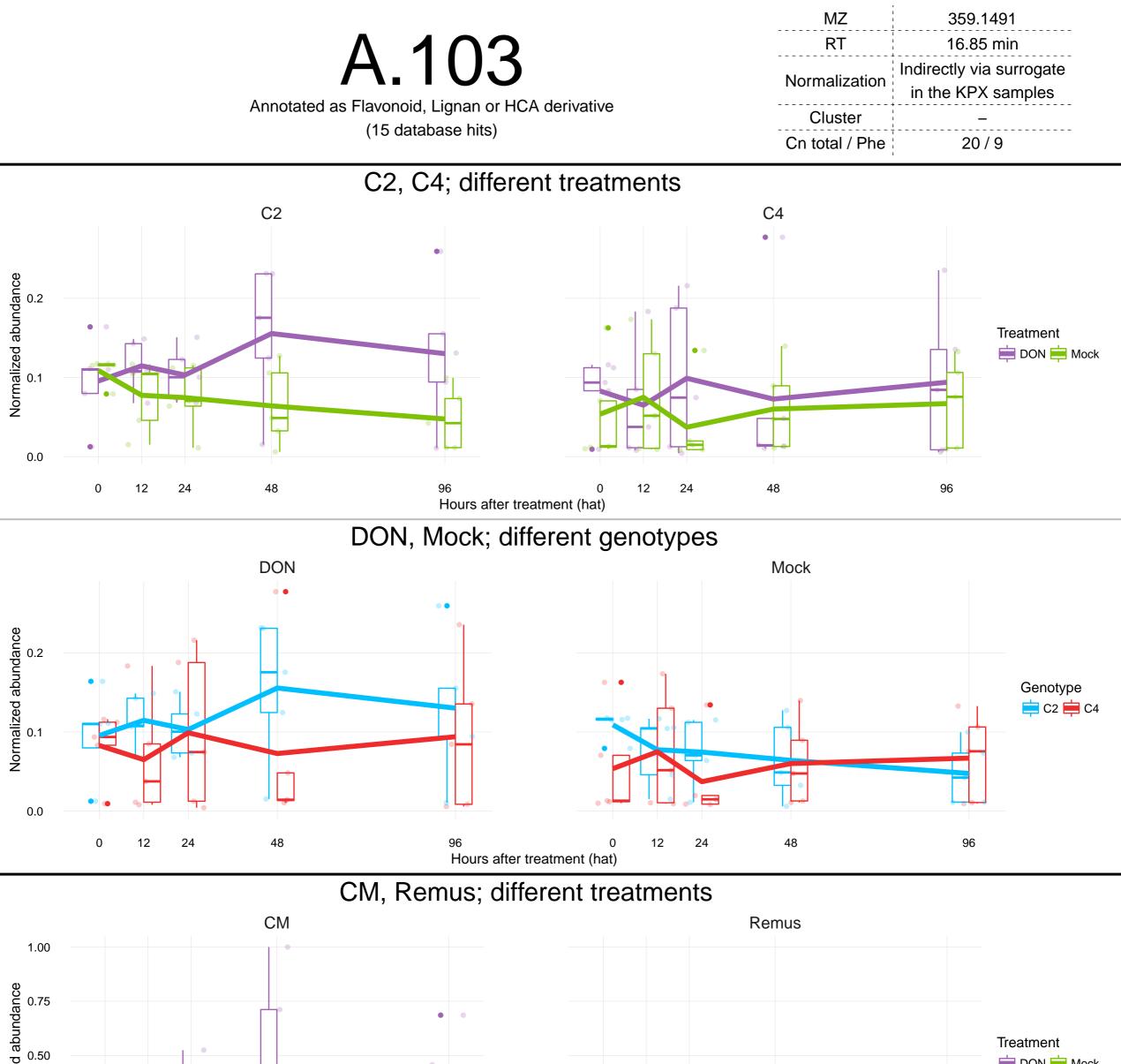
DON, Mock; all four genotypes

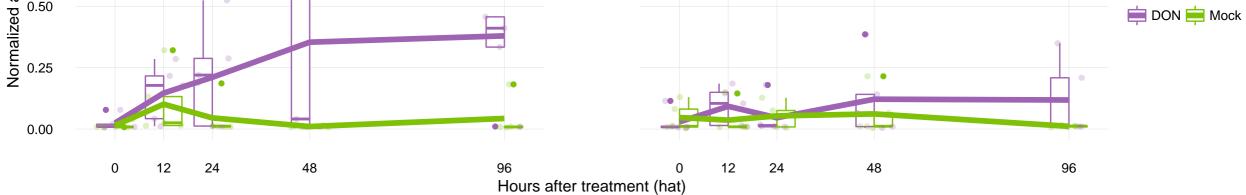
•



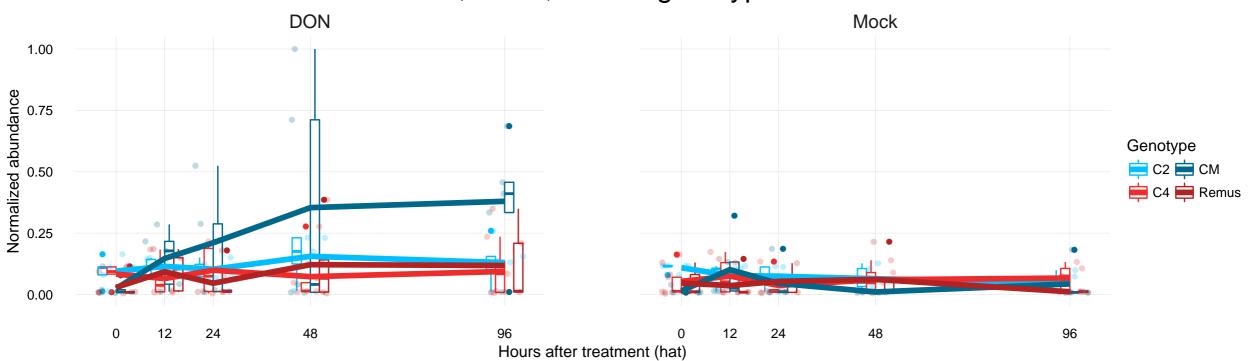








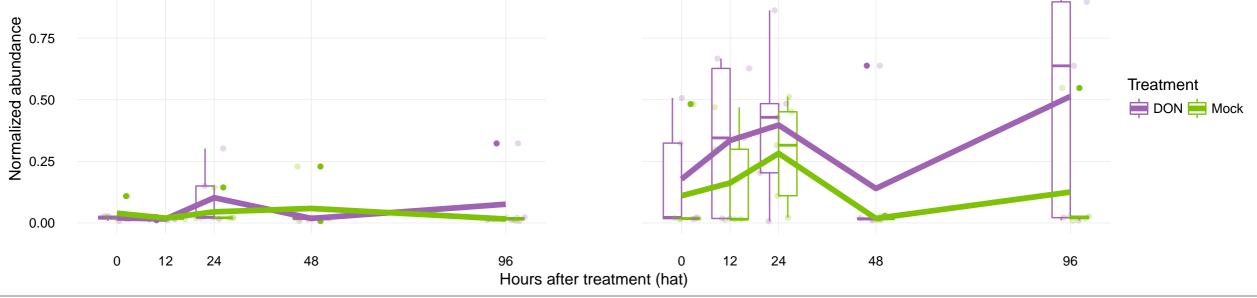
DON, Mock; all four genotypes



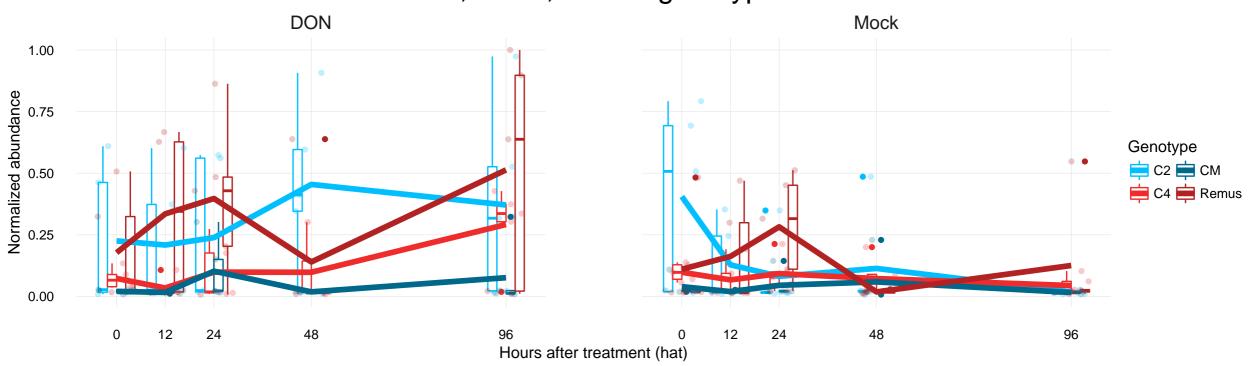
	A.18 Annotated as others (1 database hit)	MZ RT Normalization Cluster Cn total / Phe	153.0545 7.3 min Indirectly via surrogate in the KPX samples – 8 /
	C2, C4; different treatments		
1.00 Normalized aprindance 0.50 0.00	C2 0 12 24 48 96 0 12 24 Hours after treatment (hat)	C4 48	Treatment DON € Mock
	DON, Mock; different genotypes	6	
1.00	DON	Mock	
1.00 0.75 0.50 0.25 0.00			Genotype C2 C4
	0 12 24 48 96 0 12 24 Hours after treatment (hat)	48	96
	CM, Remus; different treatments		
1.00	CM	Remus	•

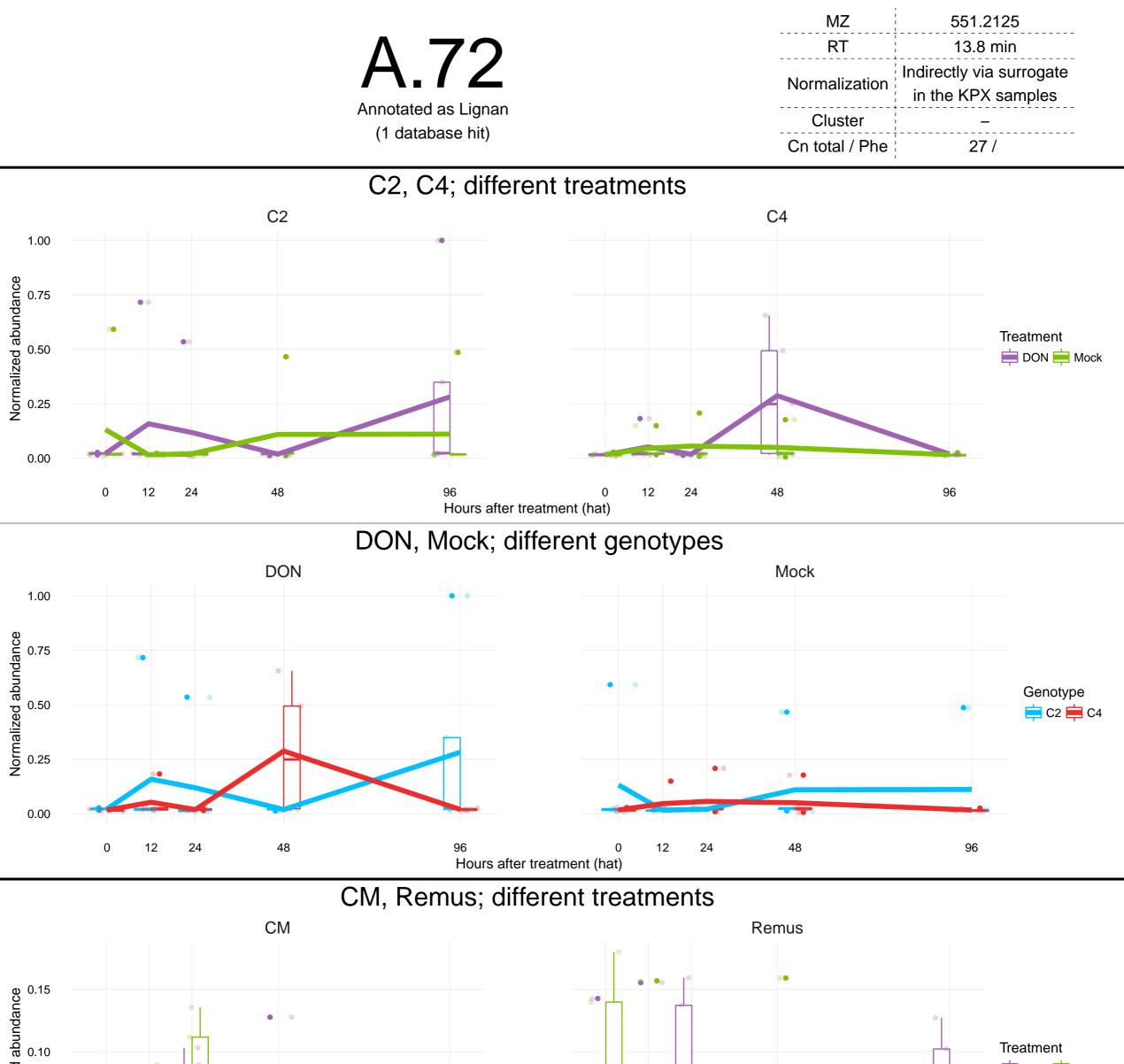
┸

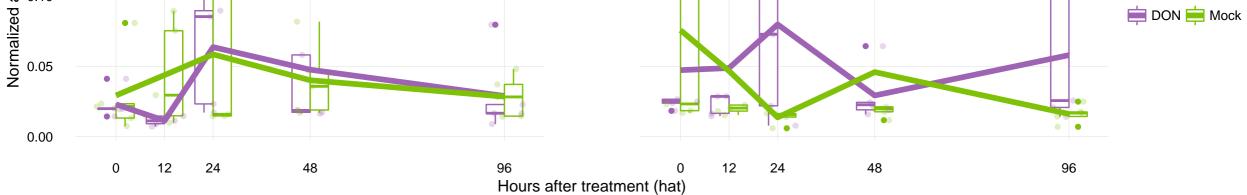




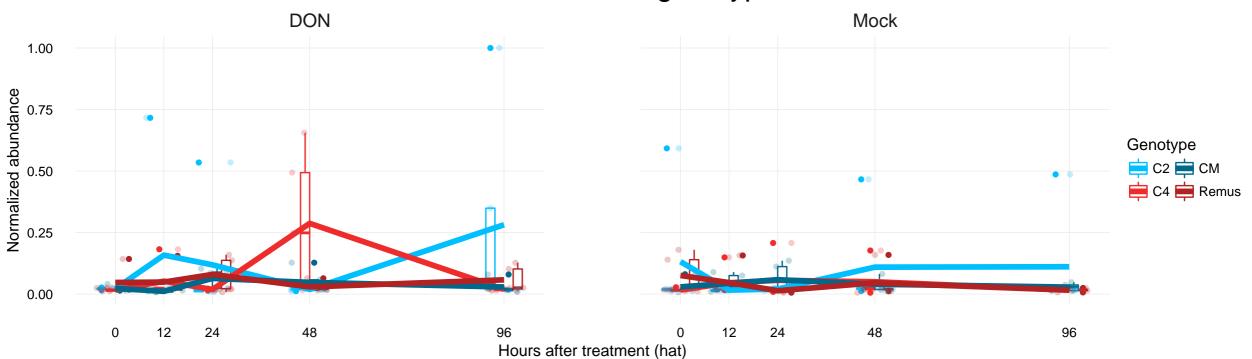
DON, Mock; all four genotypes

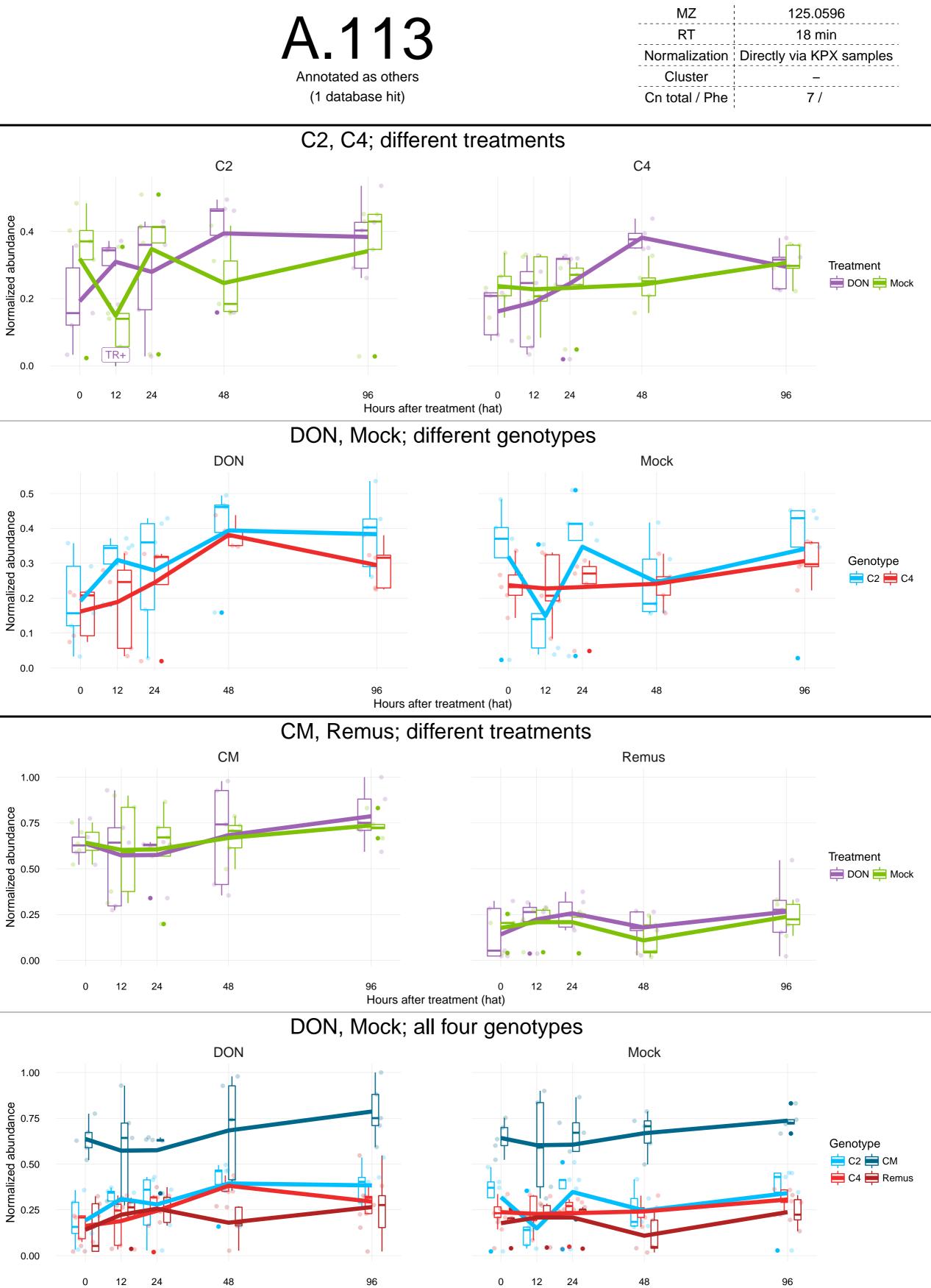




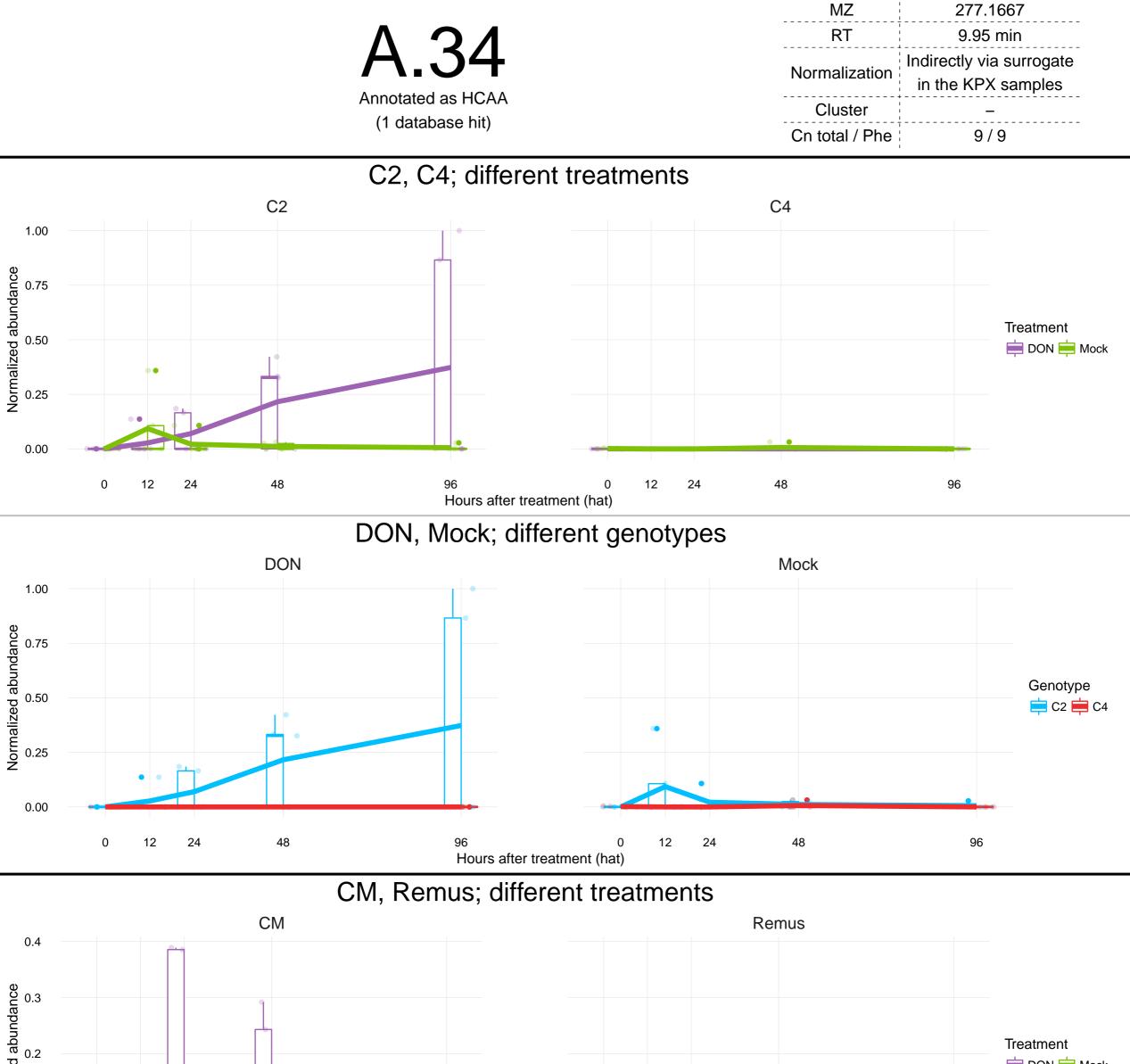


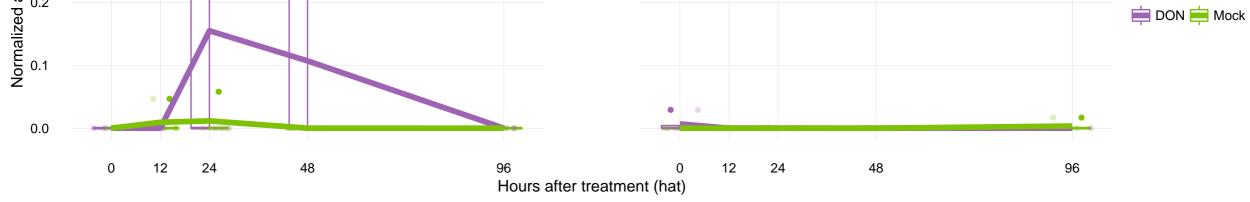
DON, Mock; all four genotypes



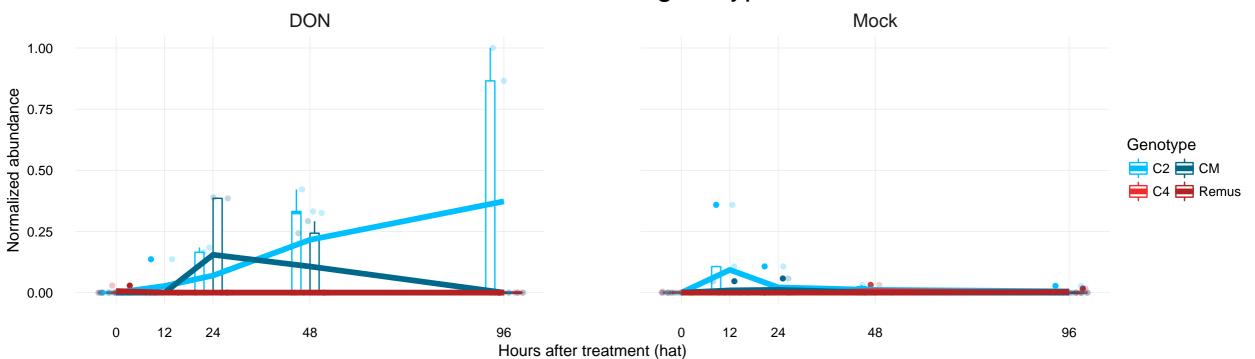


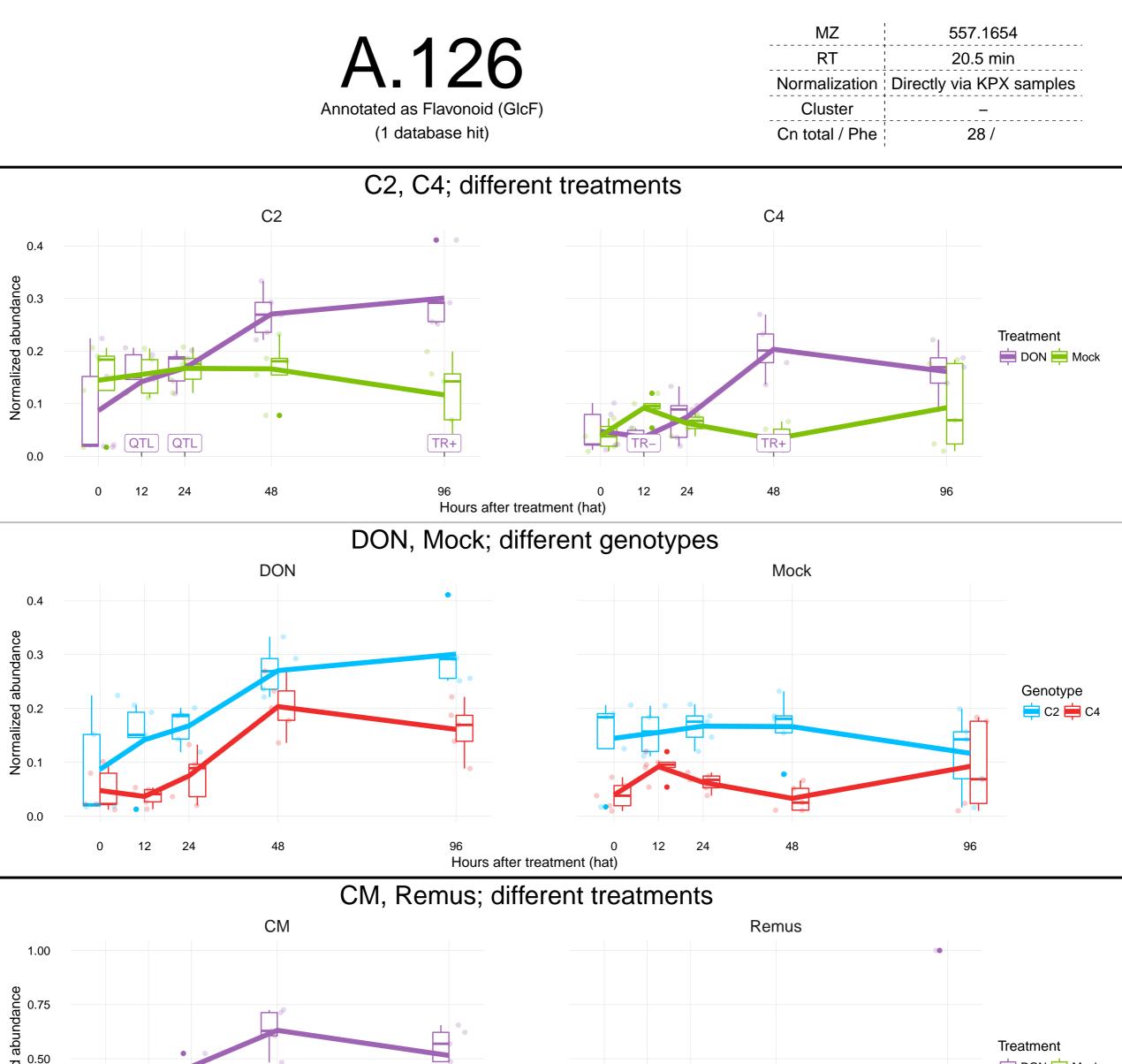
Hours after treatment (hat)

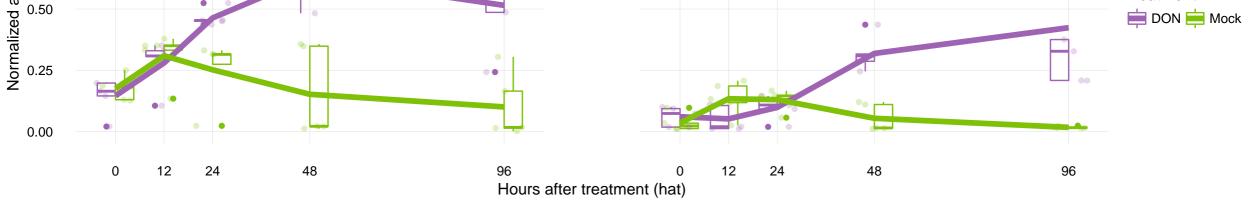




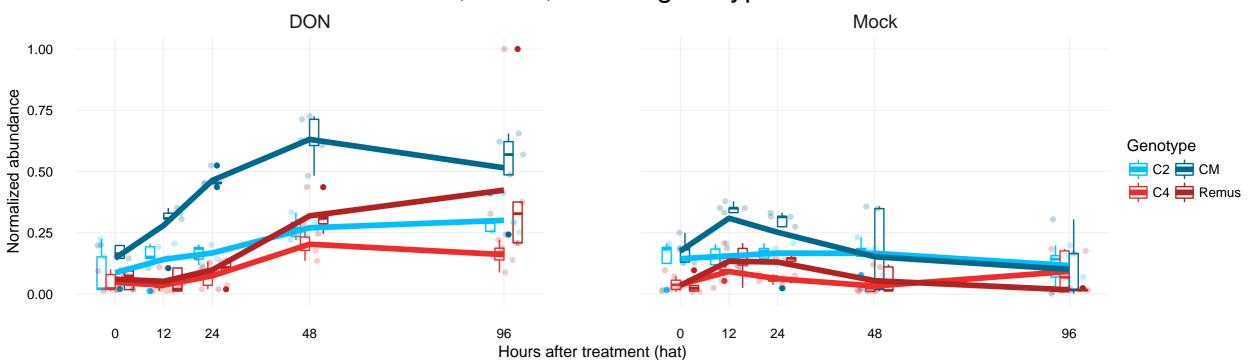
DON, Mock; all four genotypes

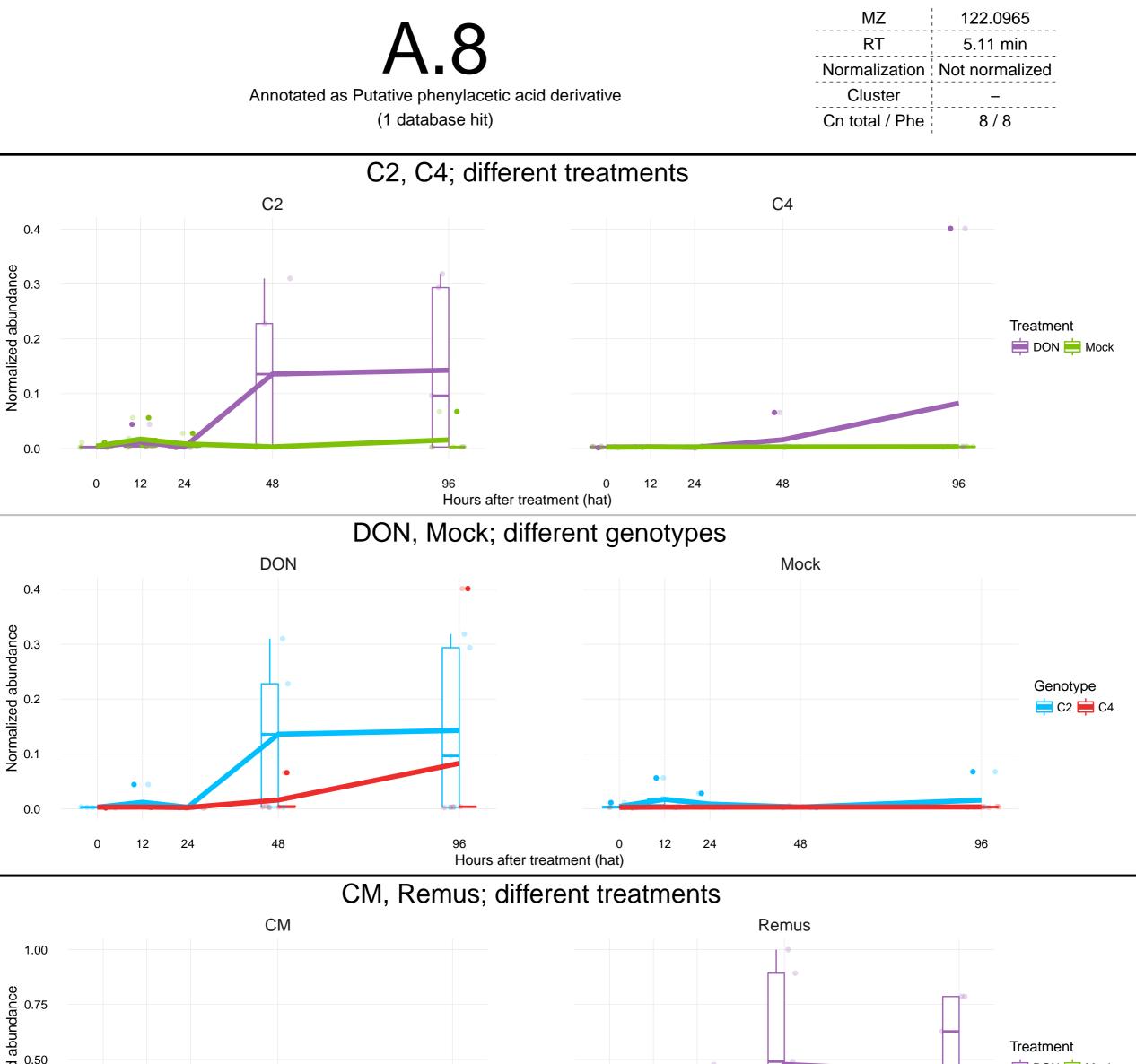




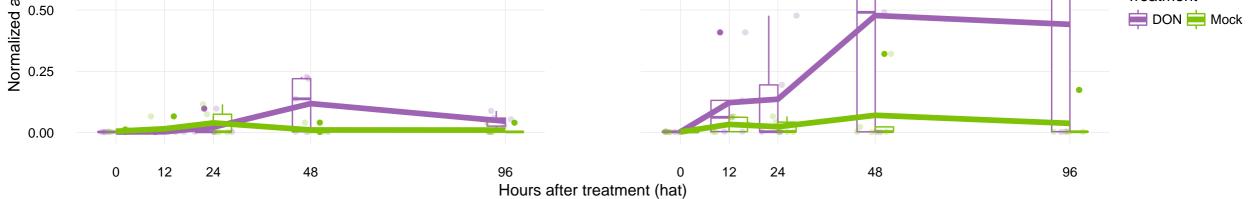


DON, Mock; all four genotypes

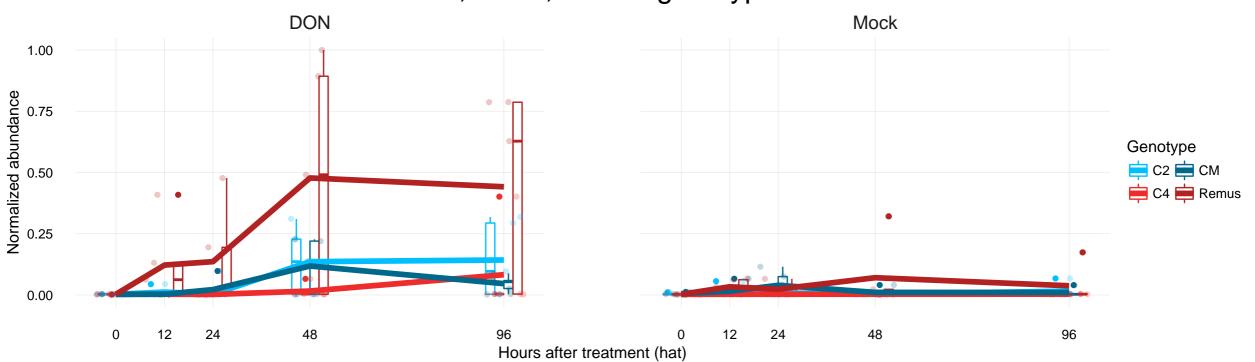


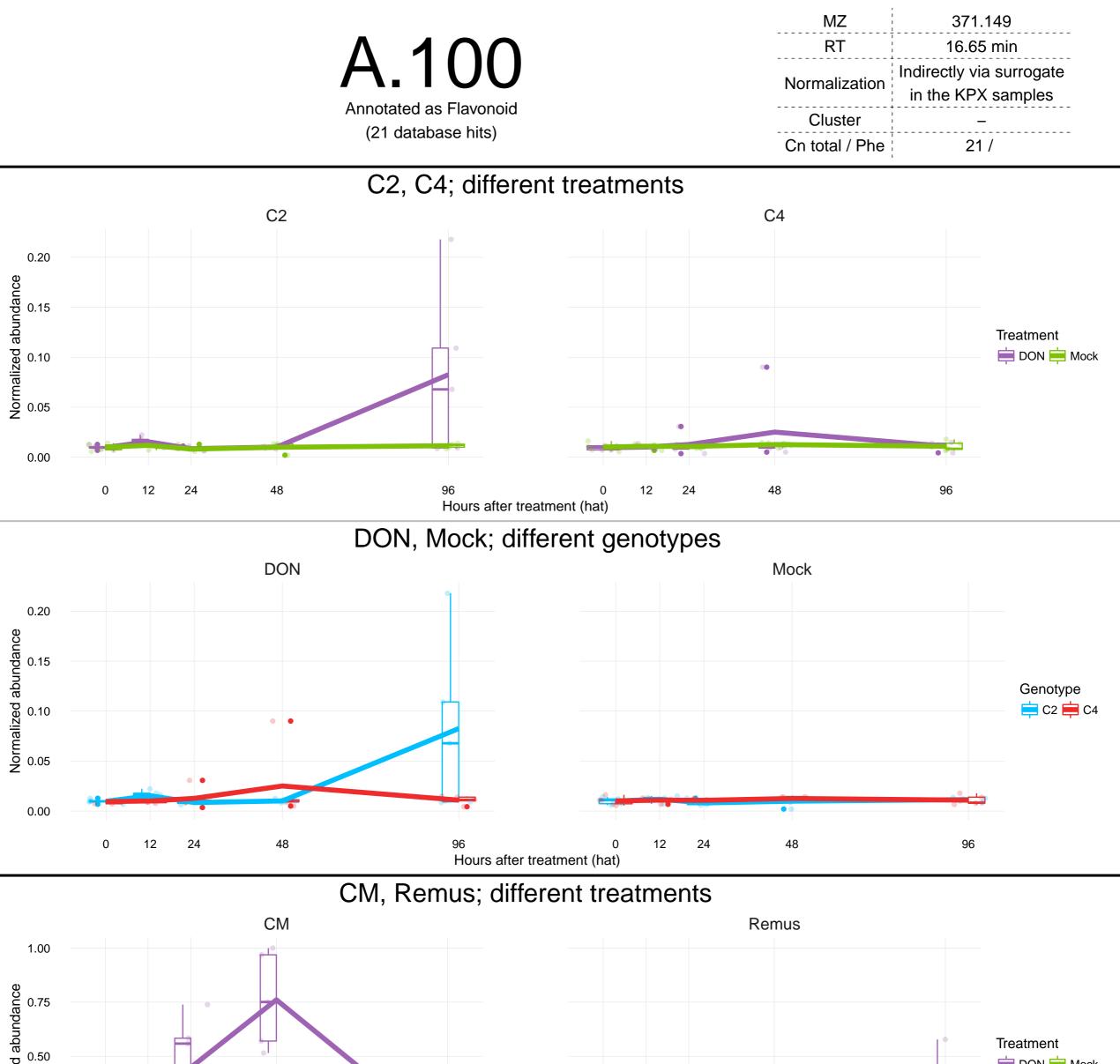


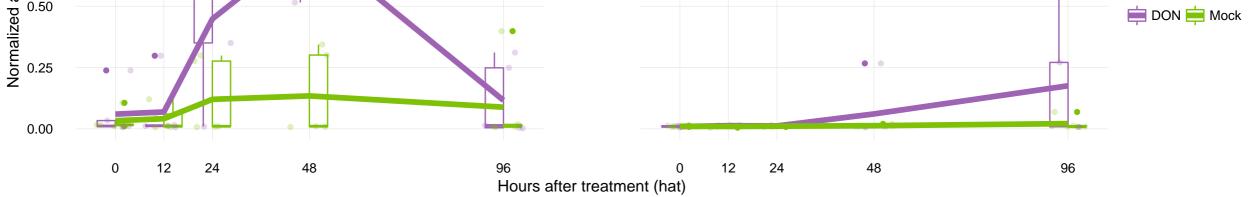
Treatment



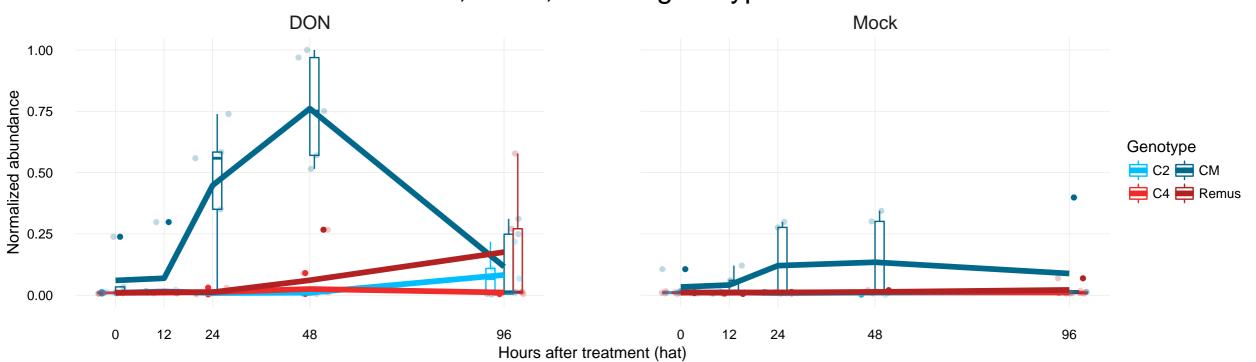
DON, Mock; all four genotypes

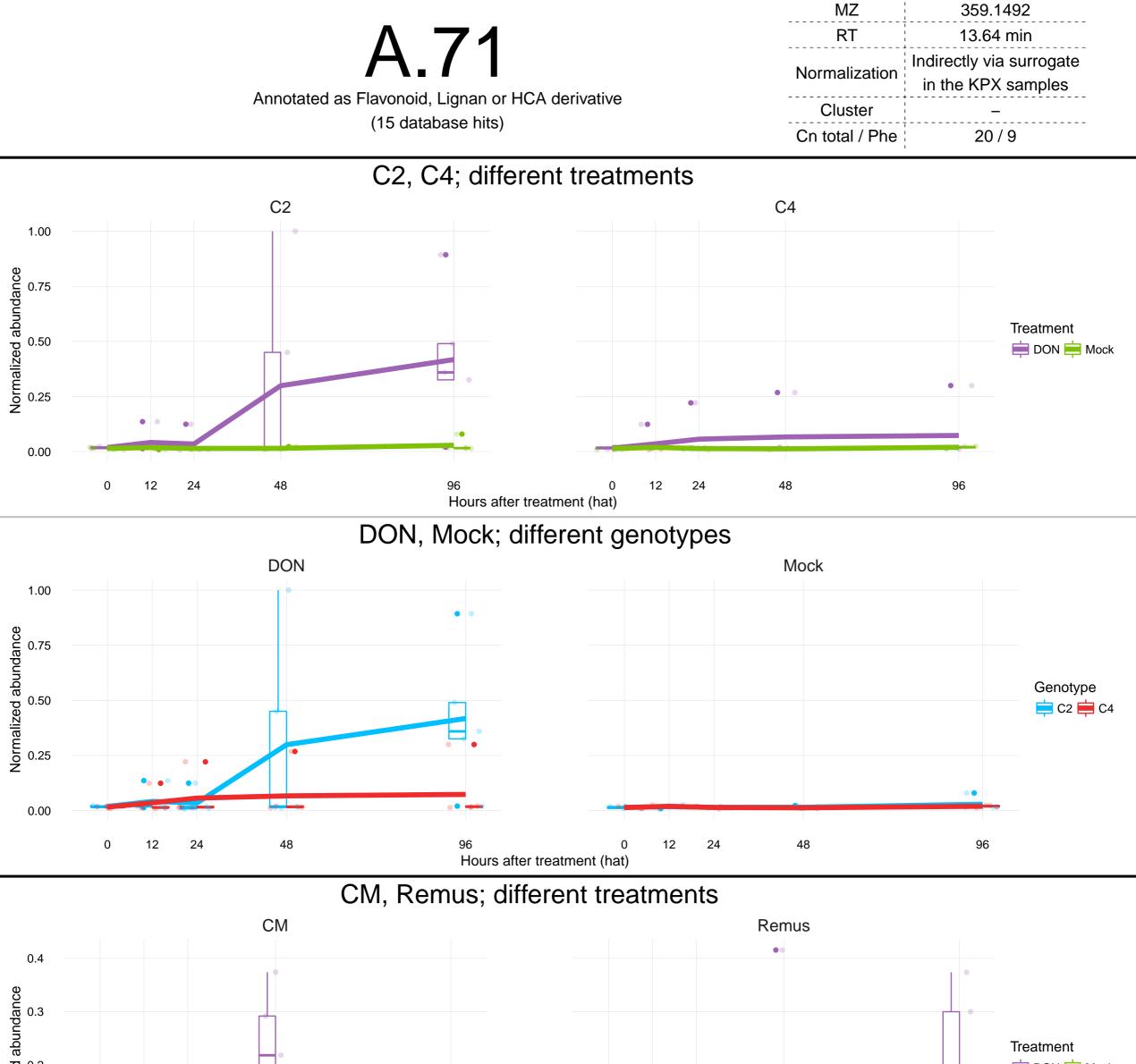


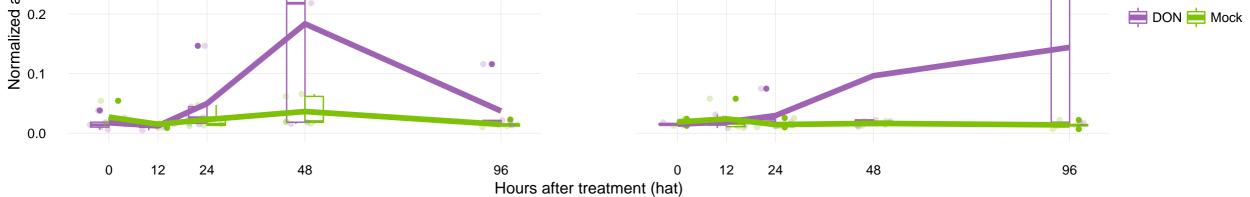




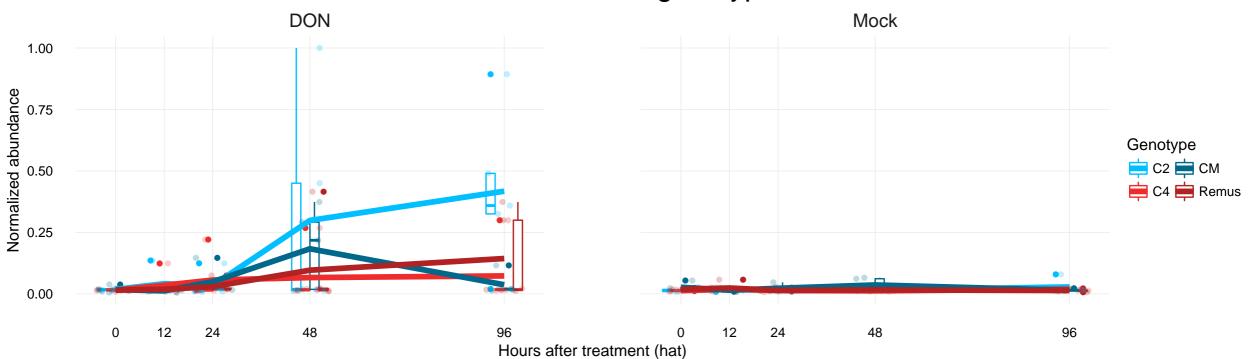
DON, Mock; all four genotypes

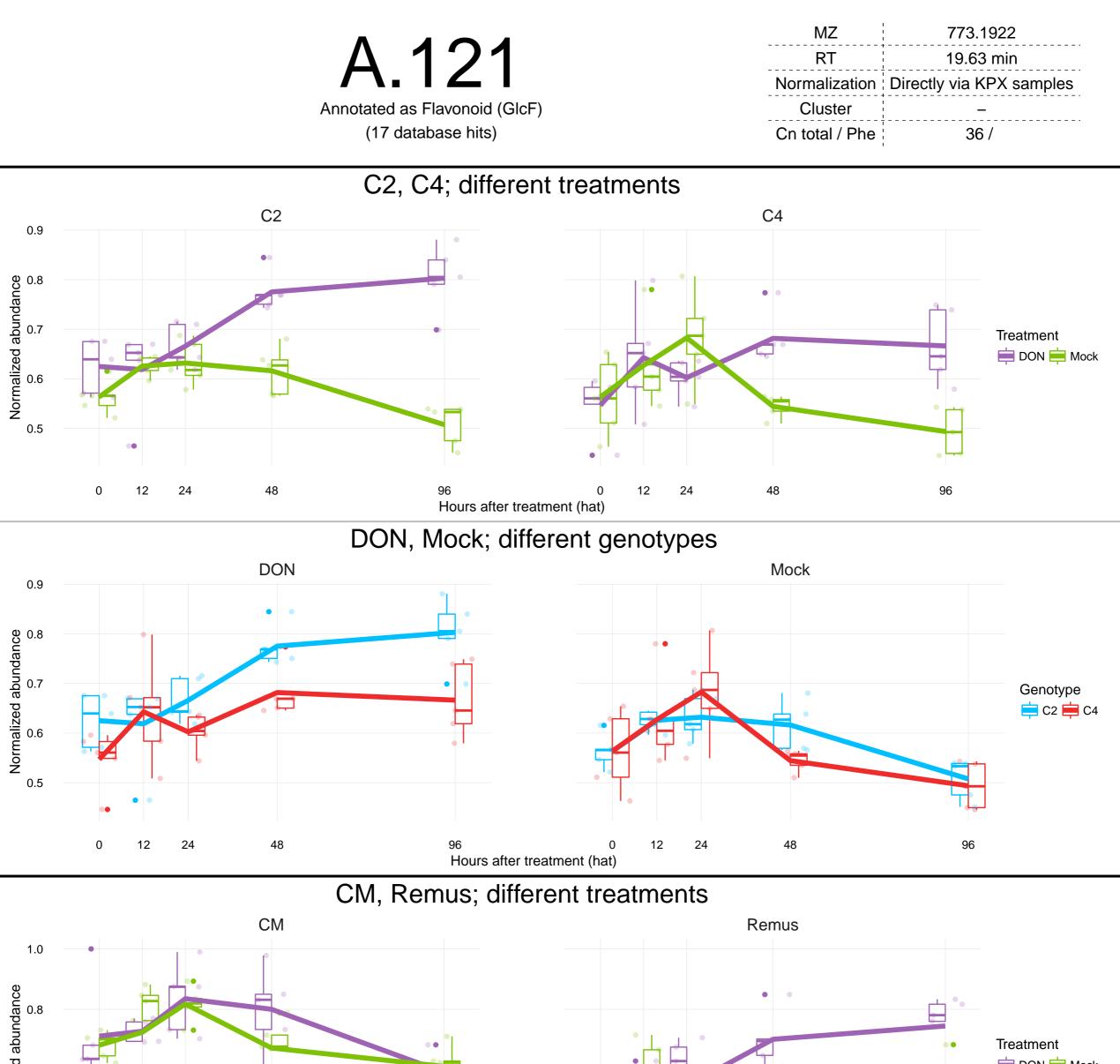


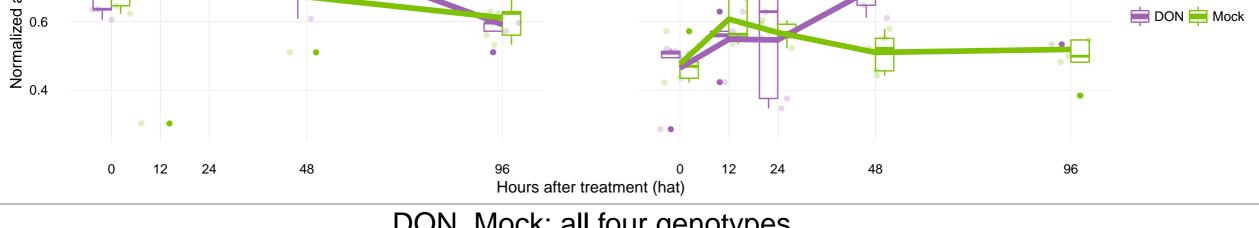


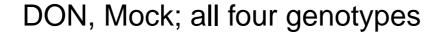


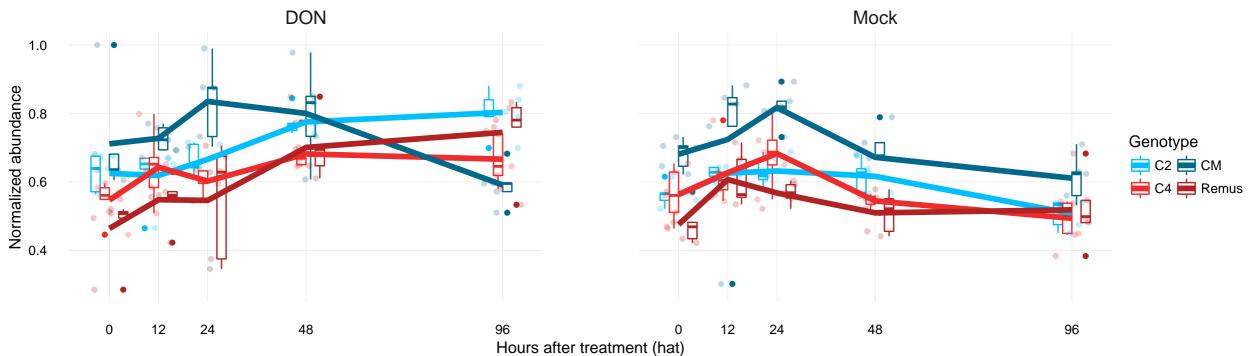
DON, Mock; all four genotypes

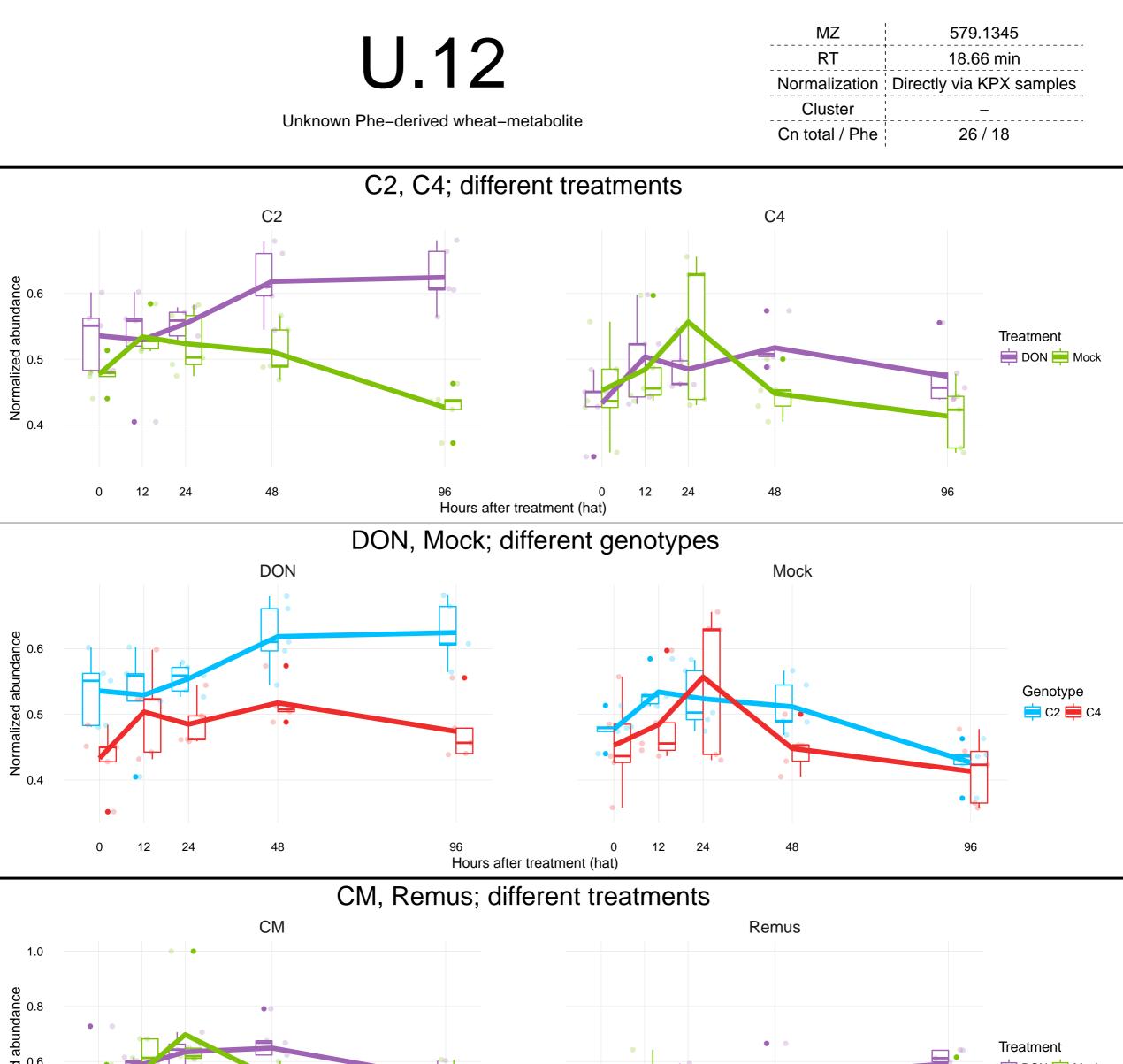


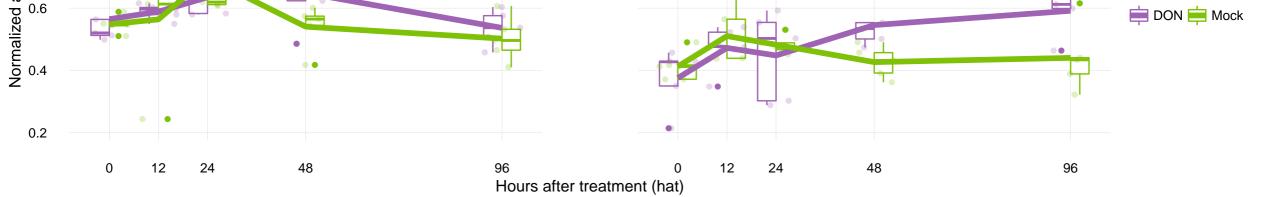




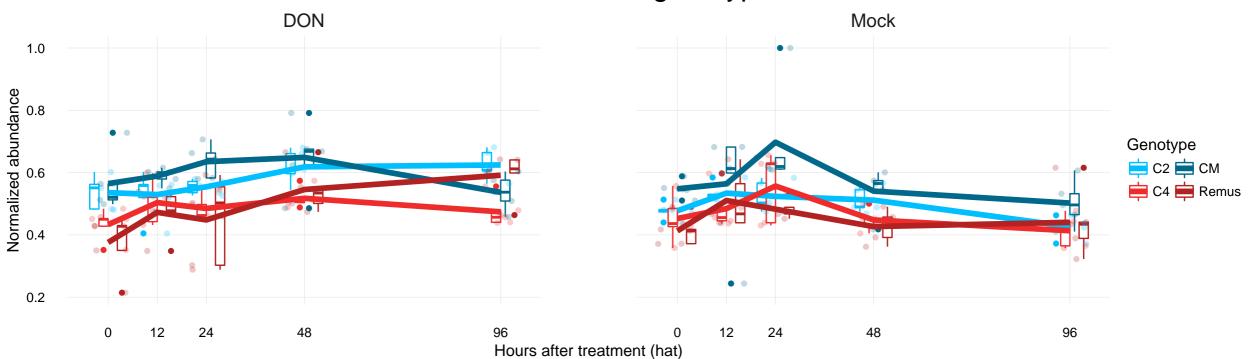


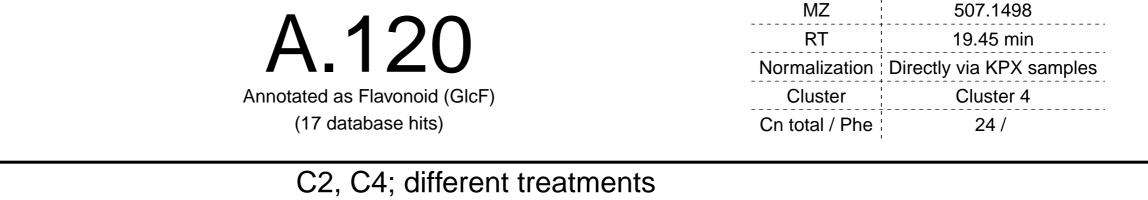


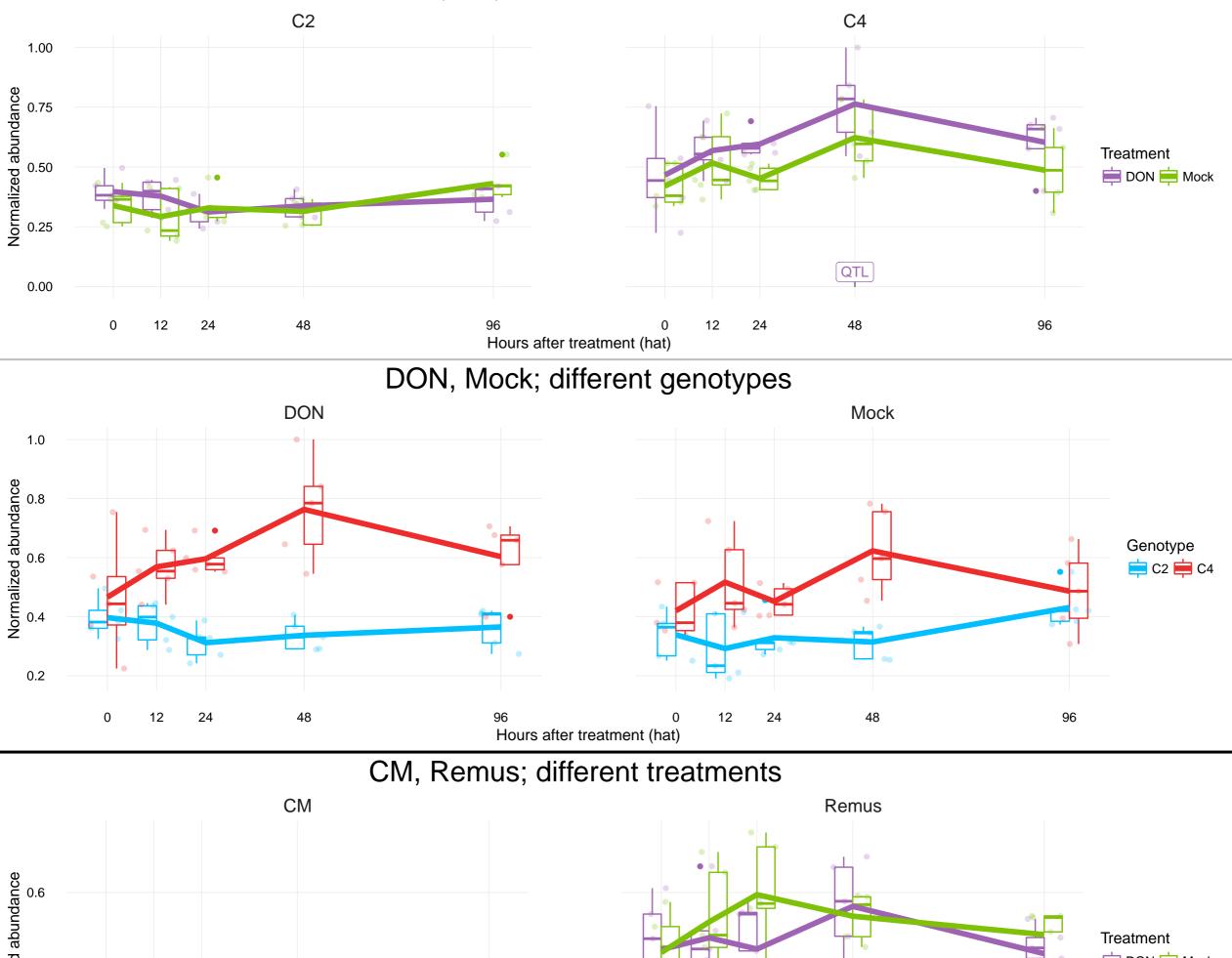


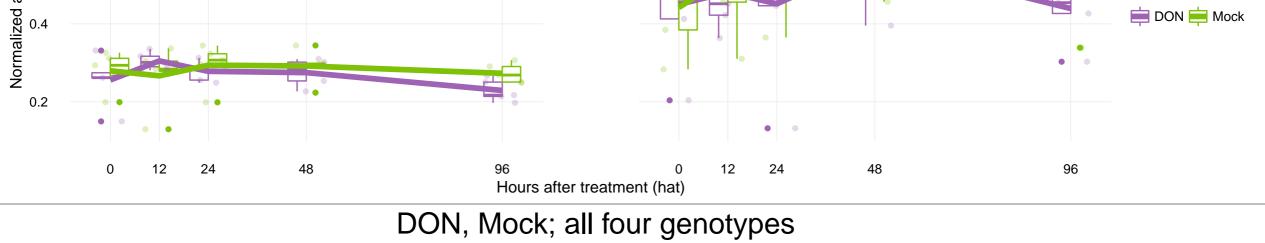


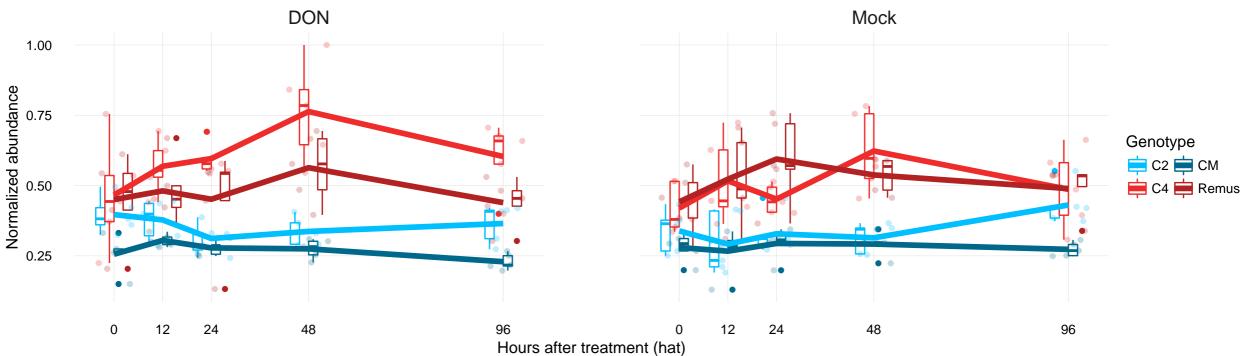
DON, Mock; all four genotypes

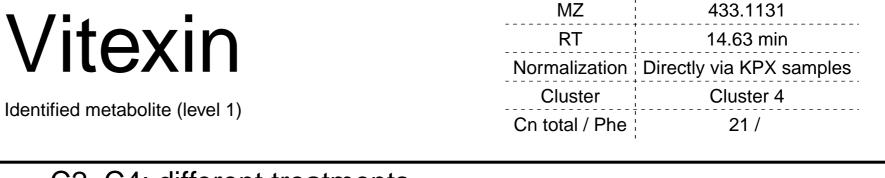


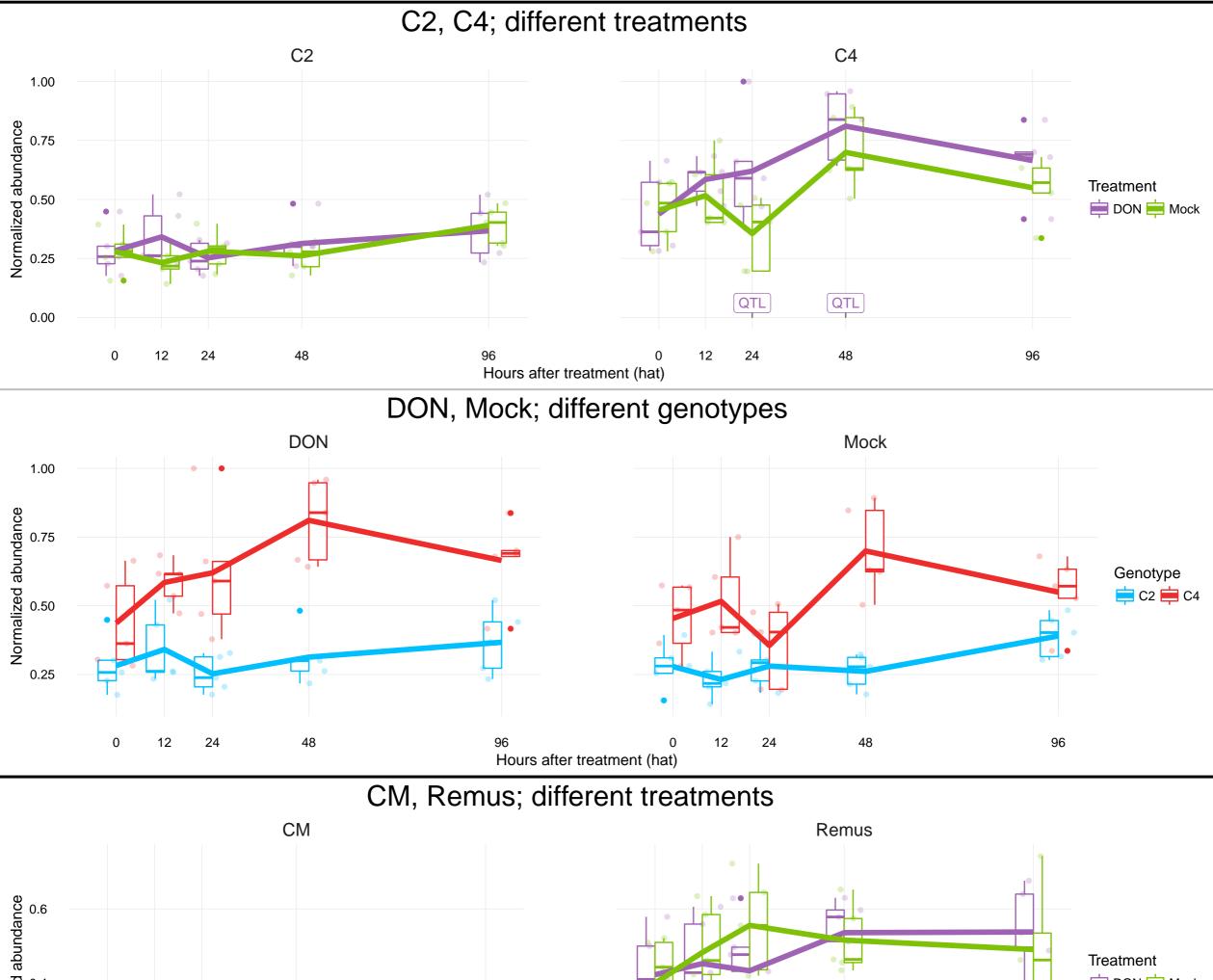


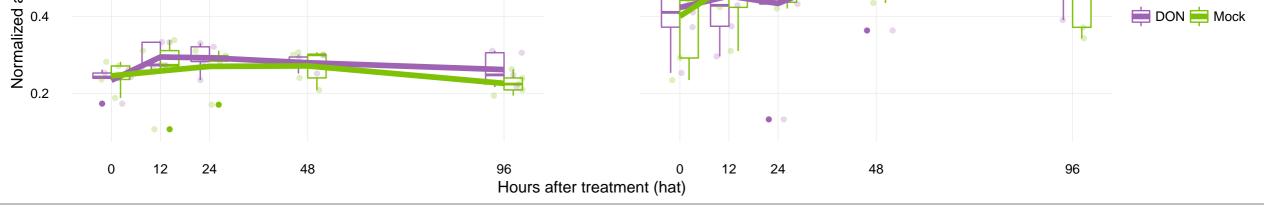




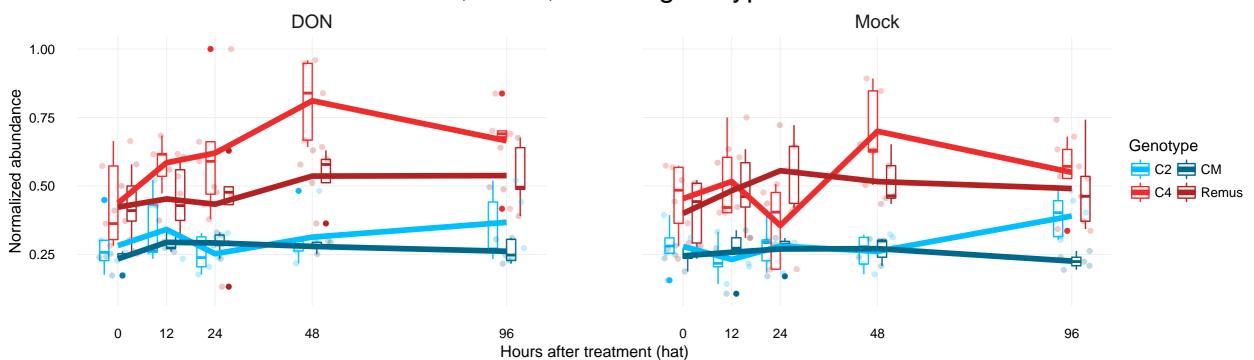


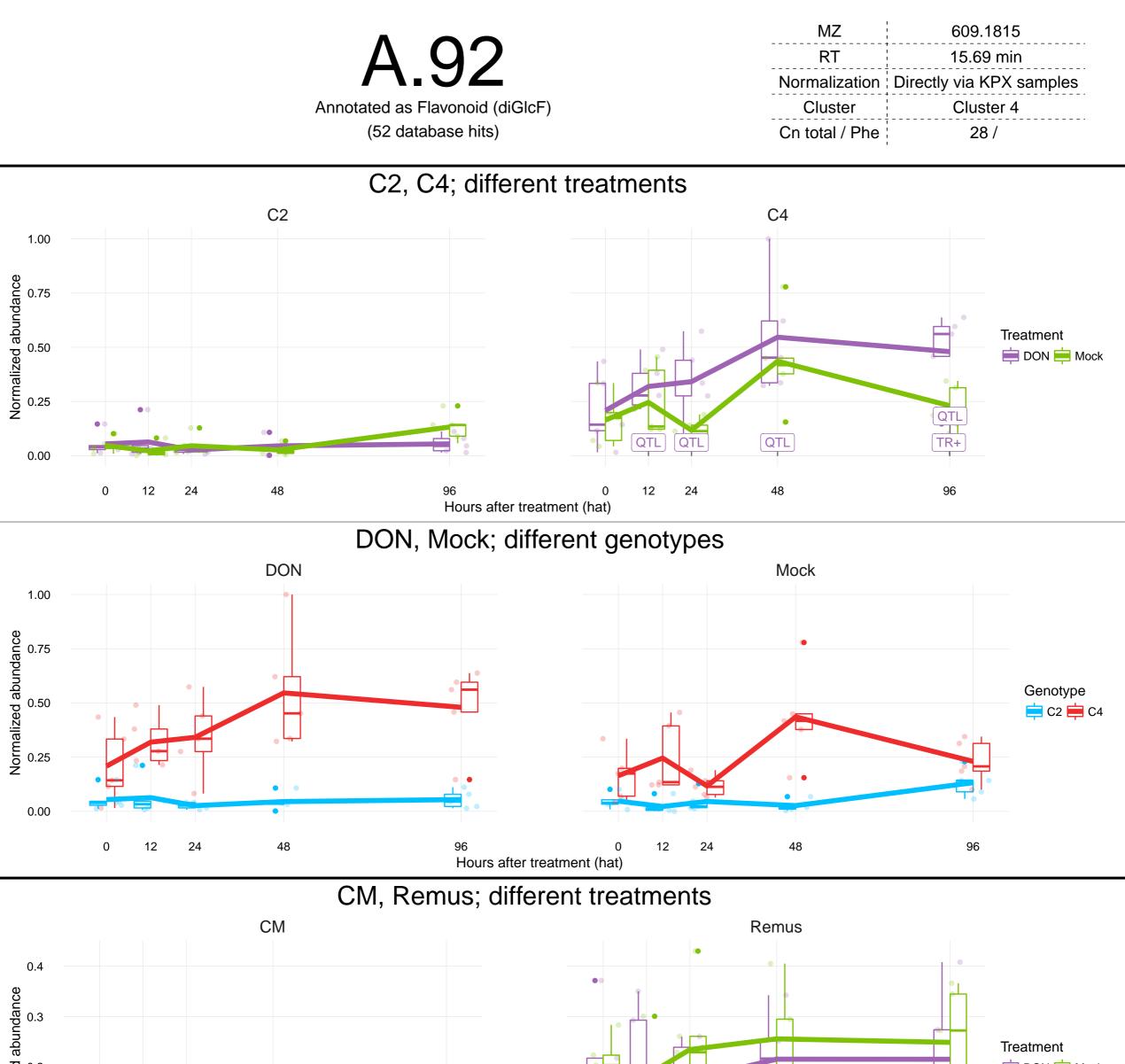


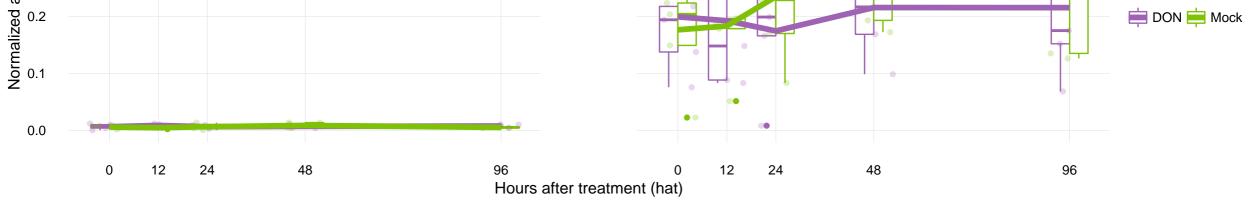




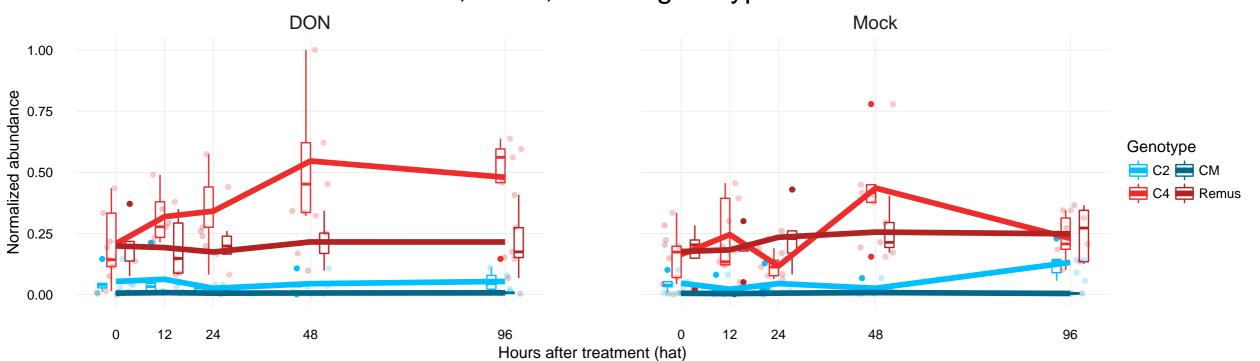
DON, Mock; all four genotypes







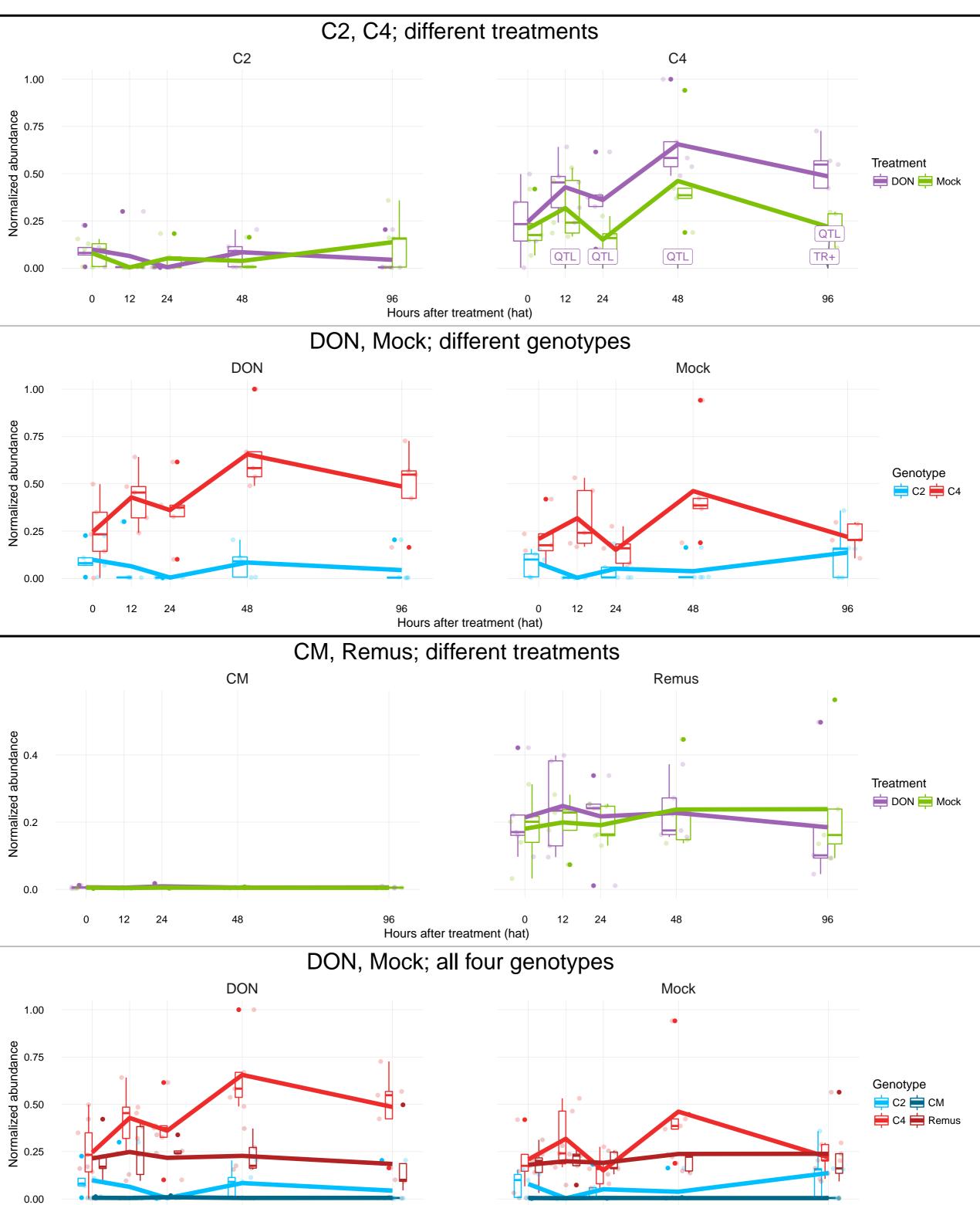
DON, Mock; all four genotypes



Homoorientin

Identified metabolite (level 1)

MZ	449.1081
RT	13.88 min
Normalization	Directly via KPX samples
Cluster	Cluster 4
Cn total / Phe	21 /



Hours after treatment (hat)

96

0

12

24

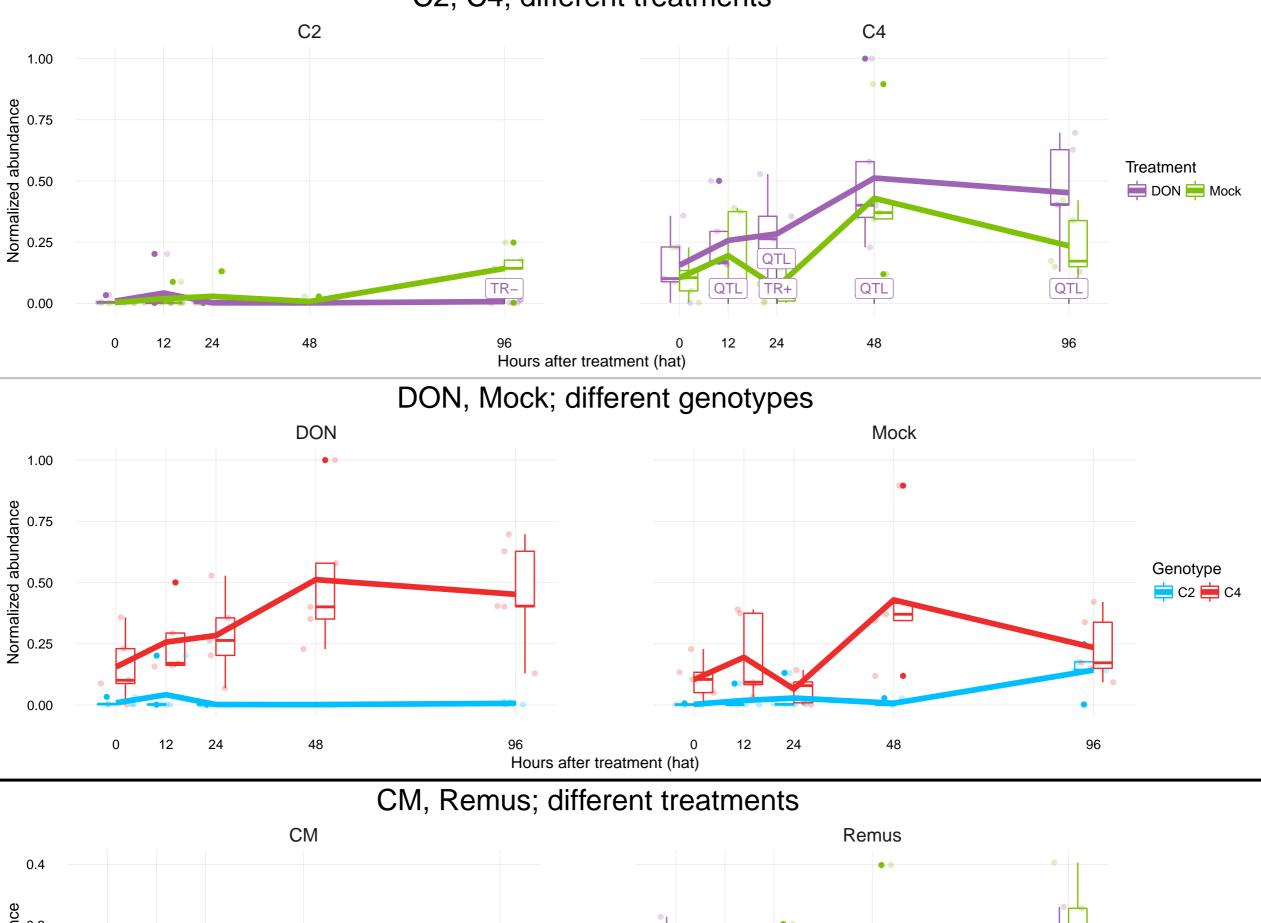
48

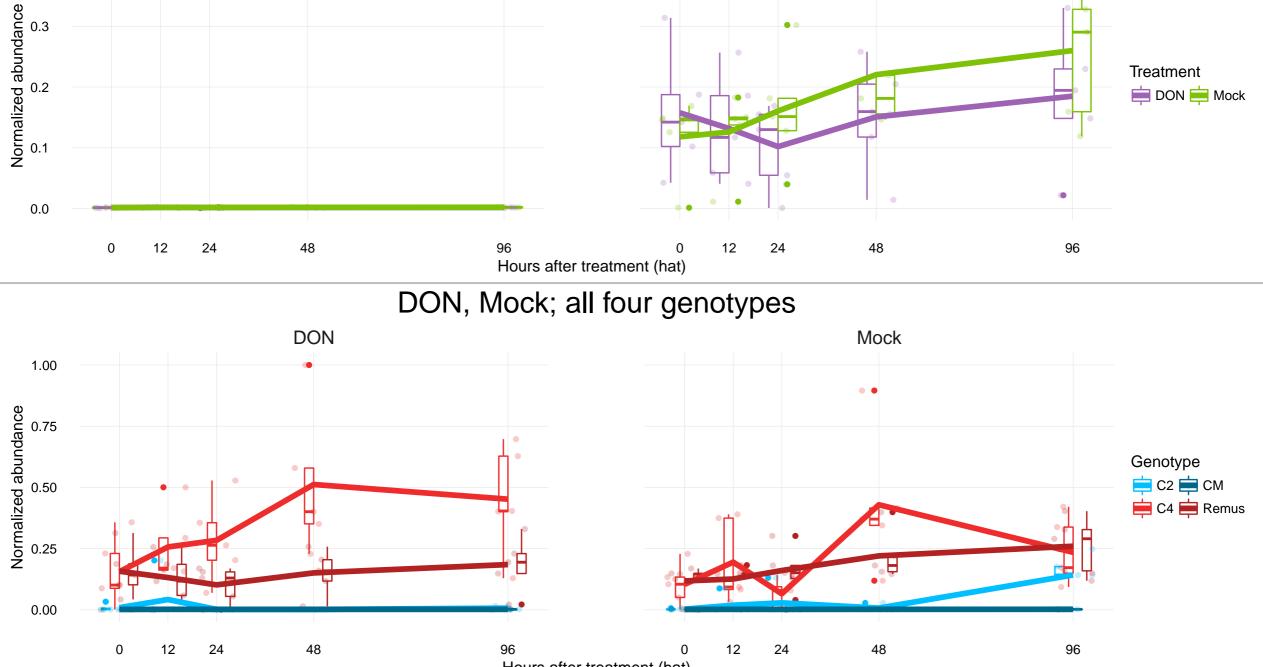
0 12 24 at) 48

96

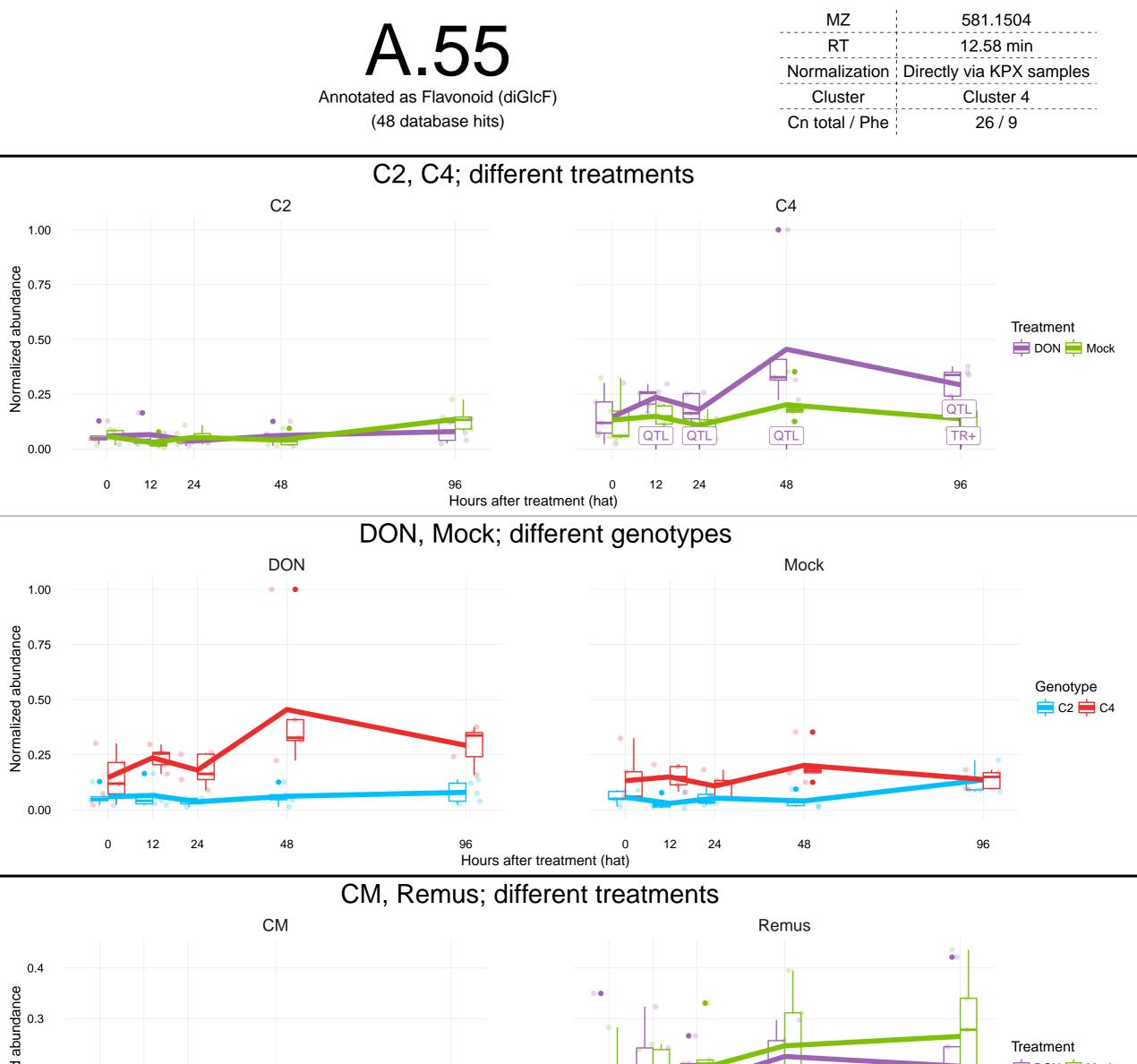
	MZ	625.1765
A.70	RT	13.46 min
$\Lambda I U$	Normalization	Directly via KPX samples
Annotated as Flavonoid (diGlcF)	Cluster	Cluster 4
(60 database hits)	Cn total / Phe	28 /

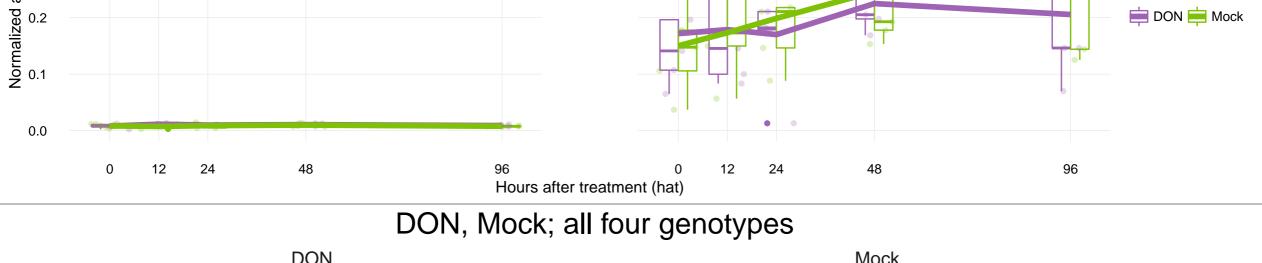


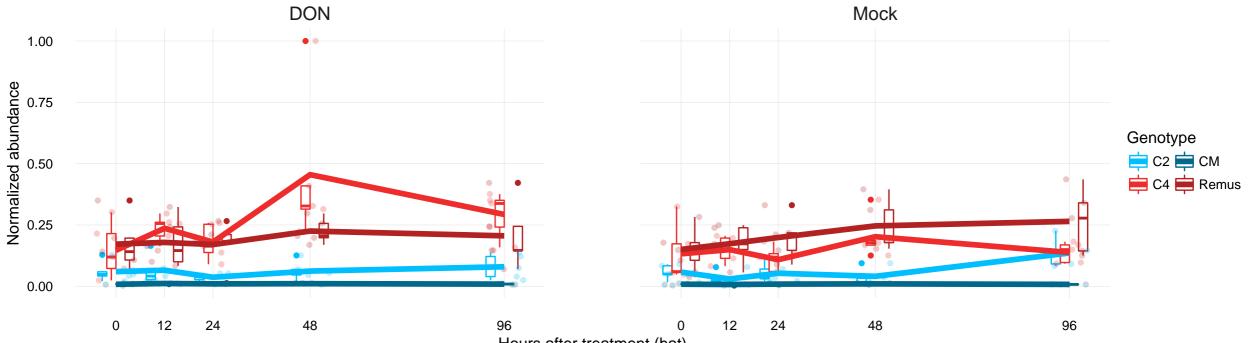




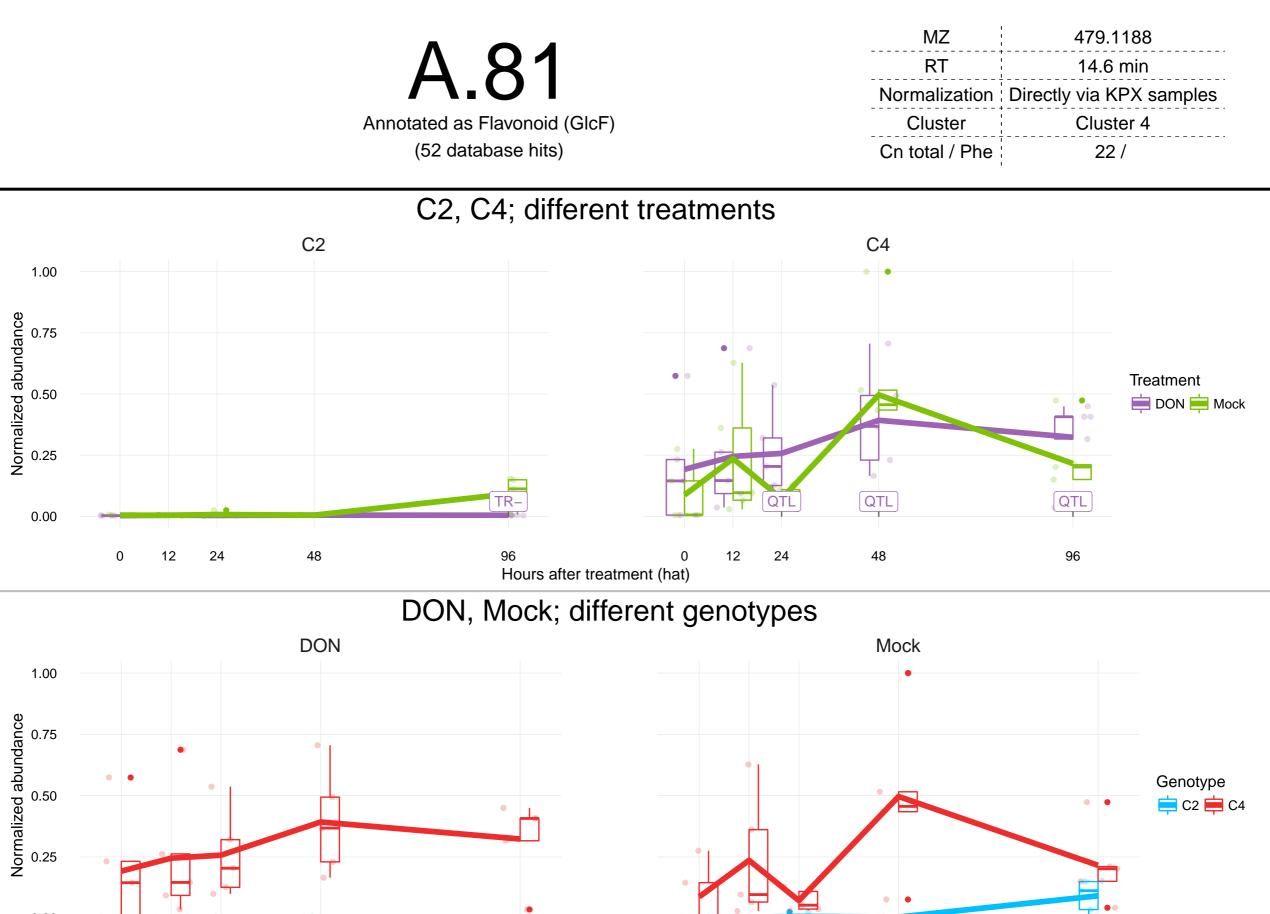
Hours after treatment (hat)

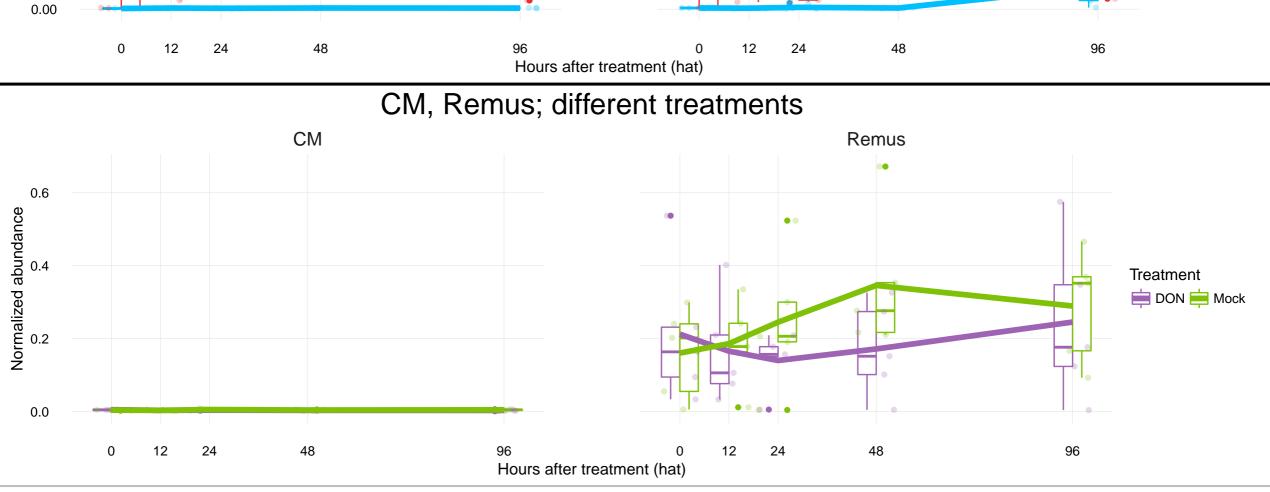




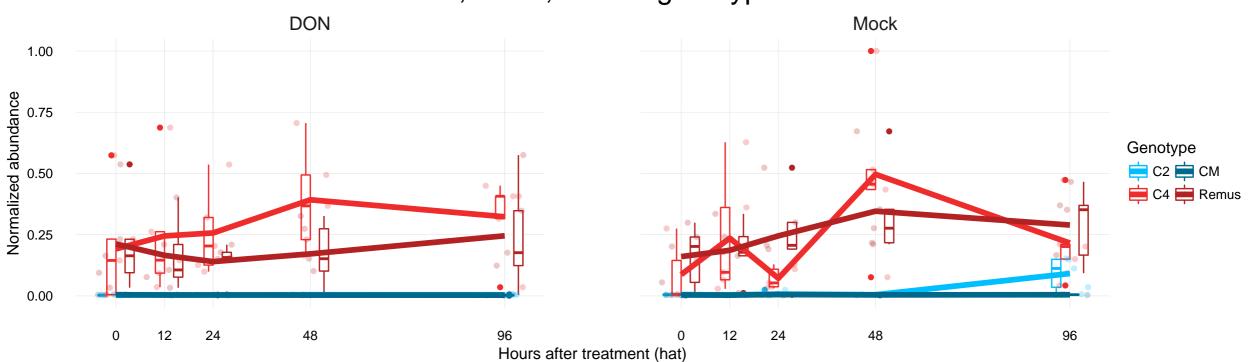


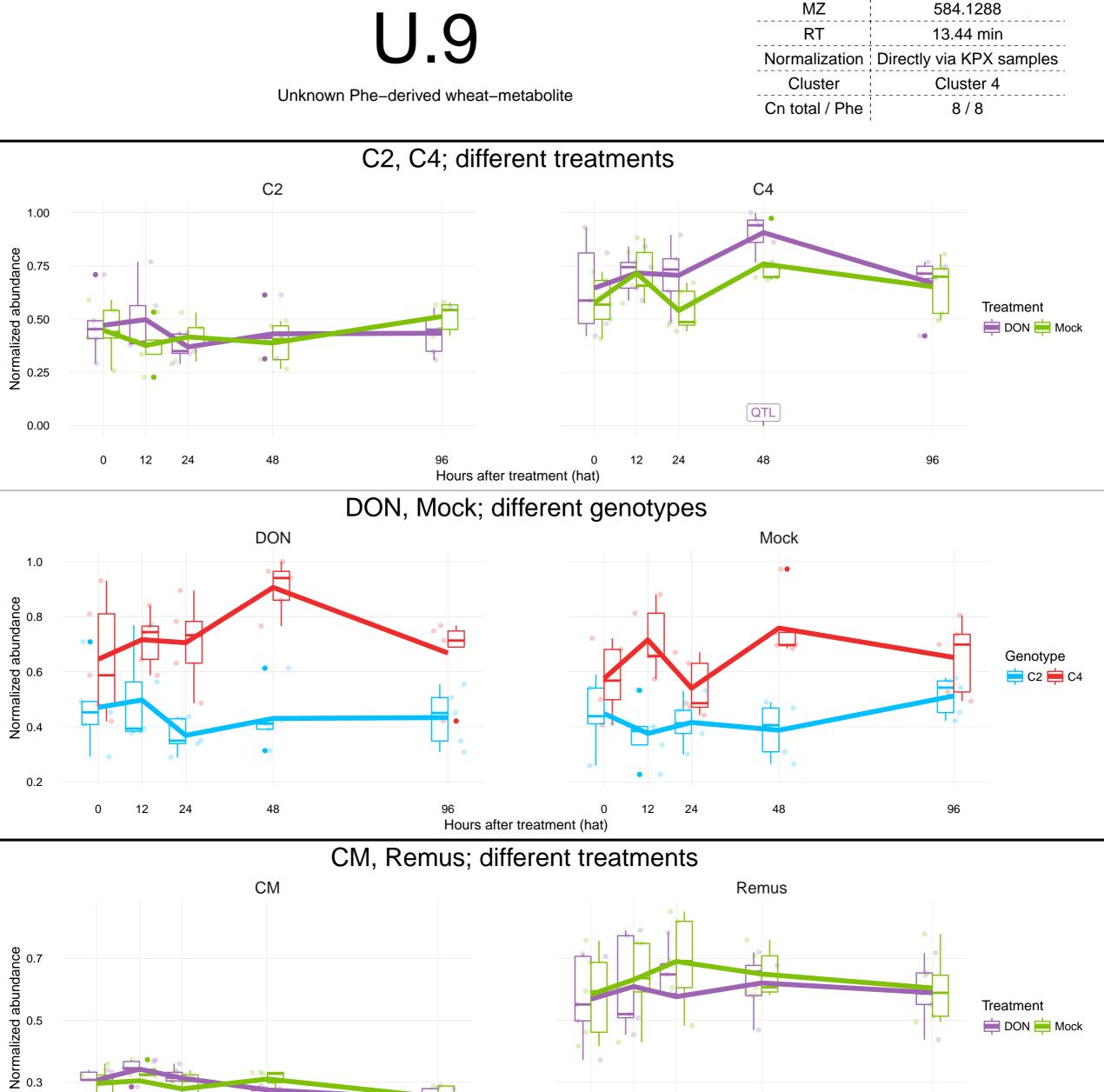
Hours after treatment (hat)

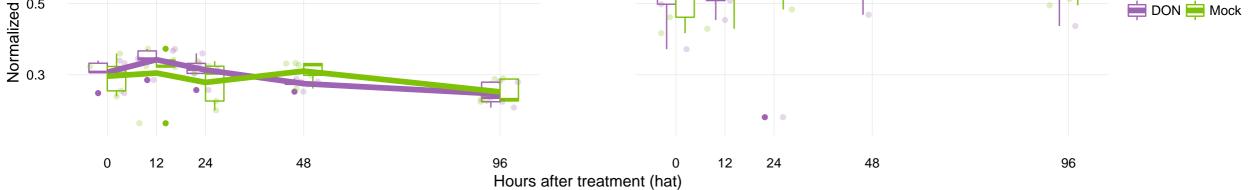




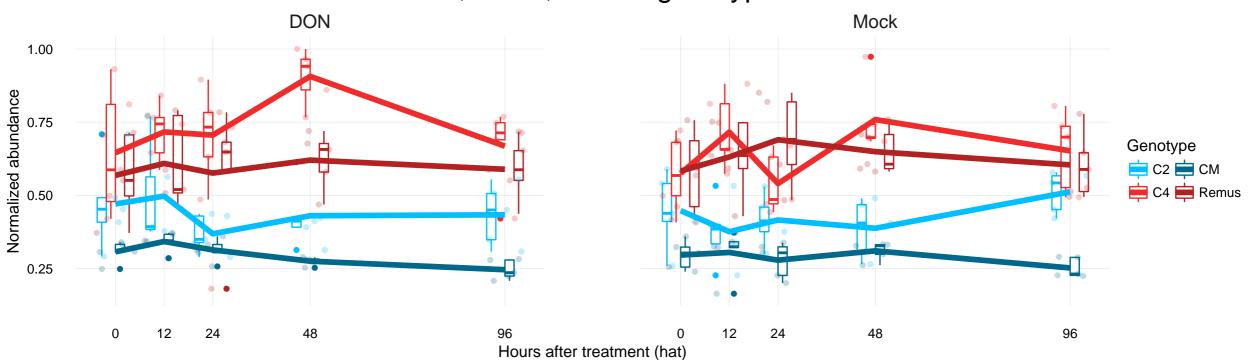
DON, Mock; all four genotypes

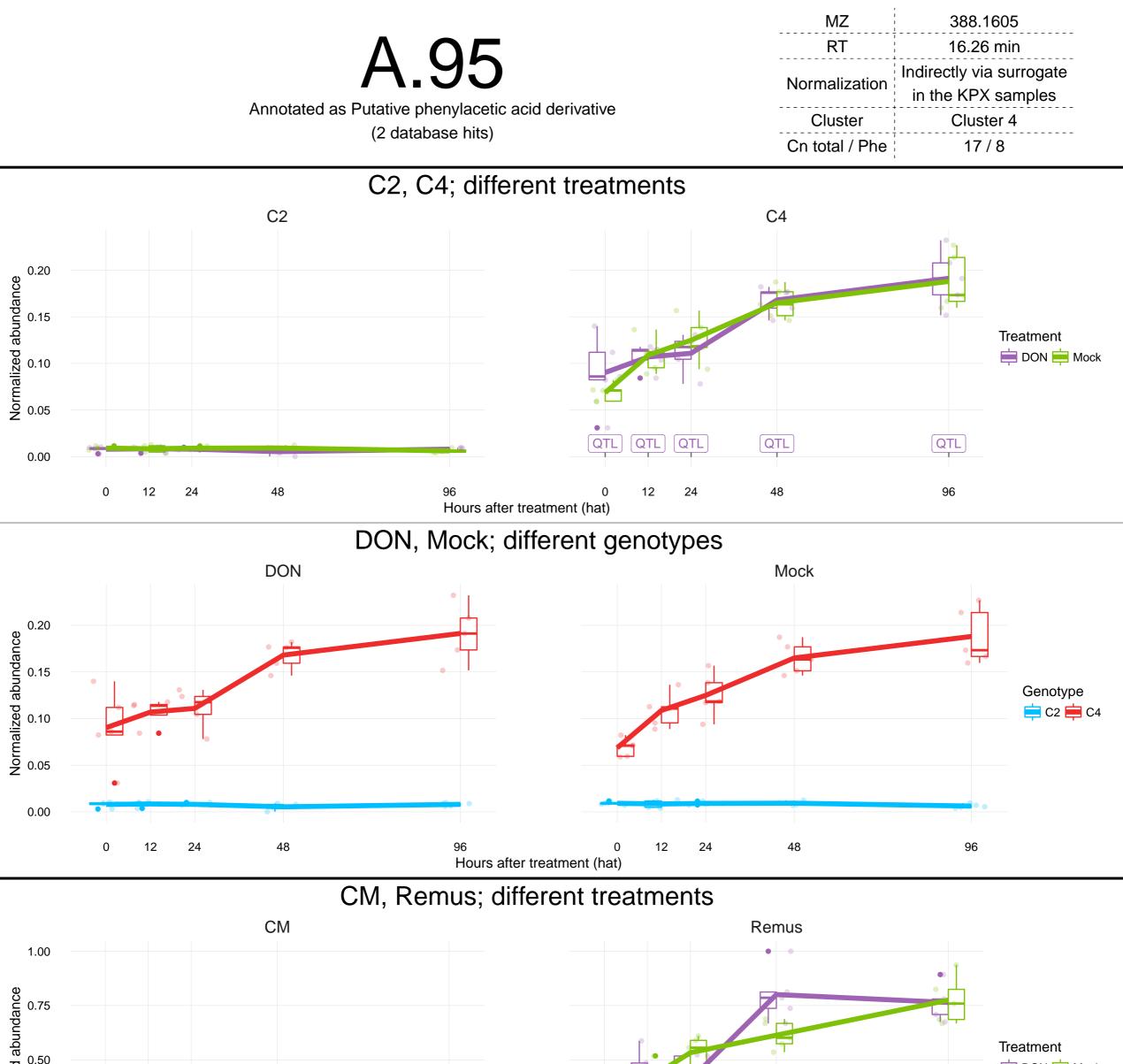


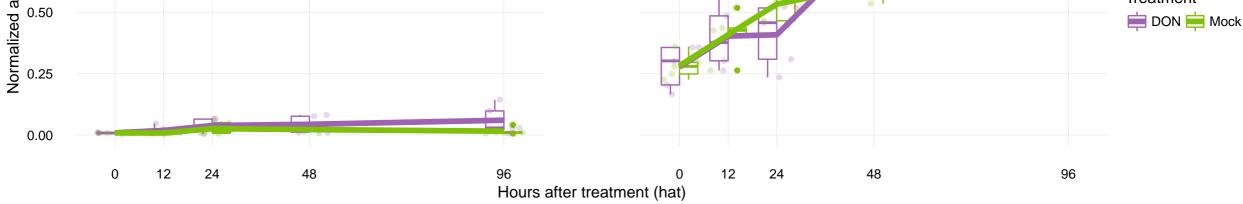




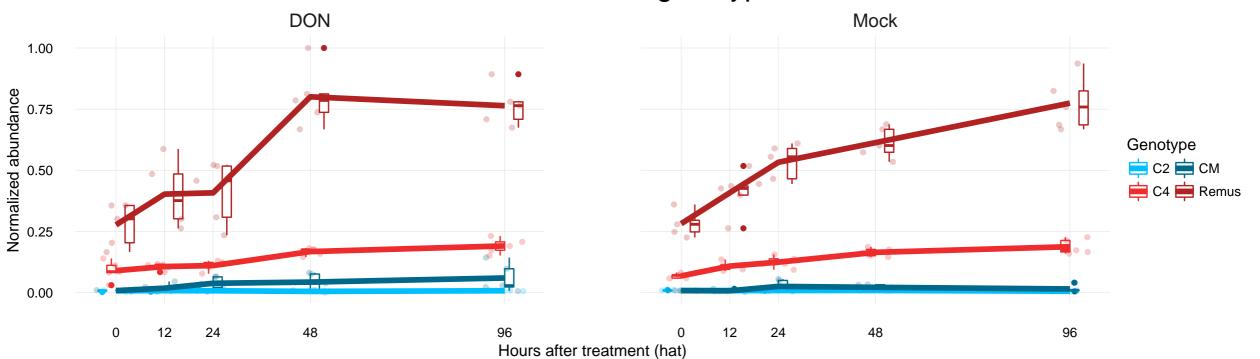
DON, Mock; all four genotypes

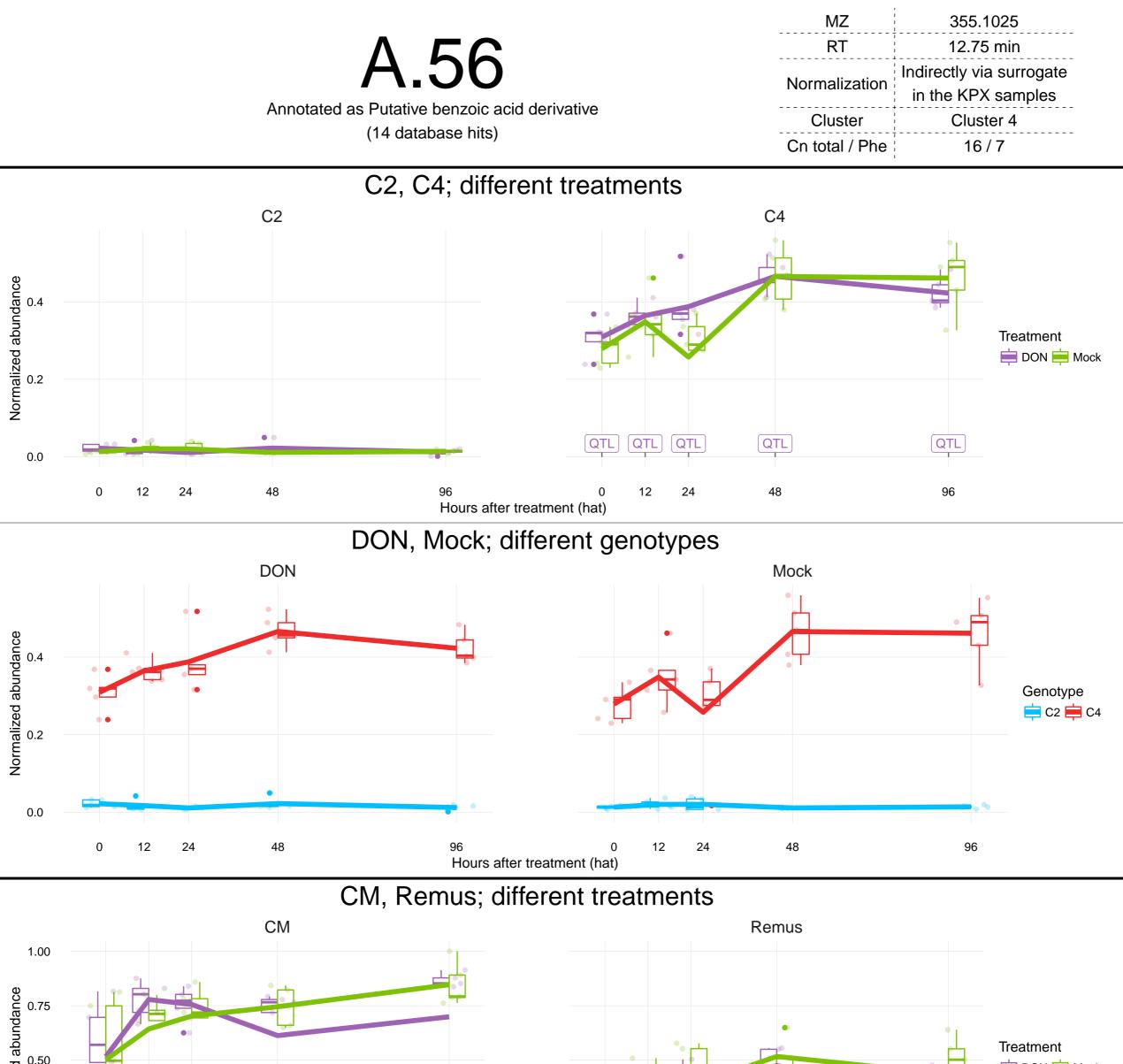


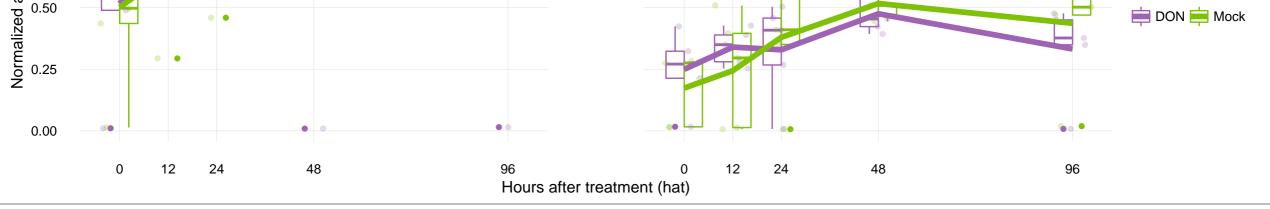




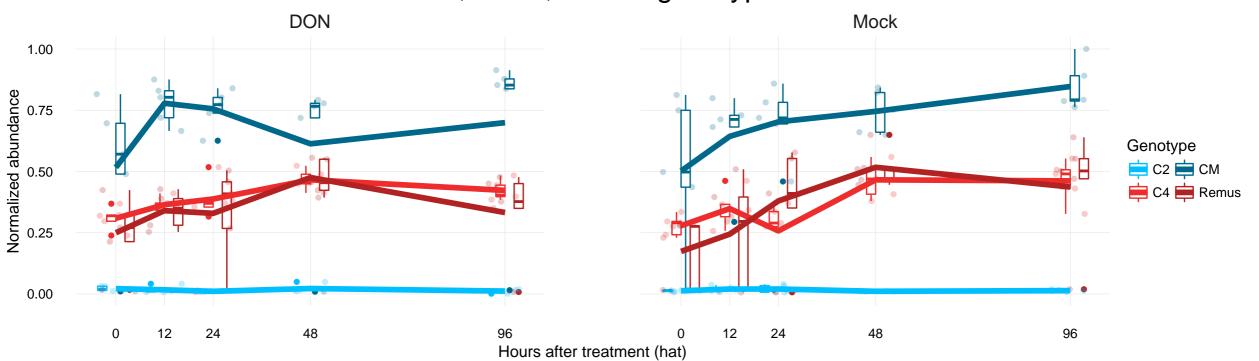
DON, Mock; all four genotypes







DON, Mock; all four genotypes



					MZ	584.234
			ΛΟΛ		RT	14.65 min
			A.82		Normalization	Indirectly via surrogate in the KPX samples
		Anno	otated as others (Iridoid))	Cluster	Cluster 4
			(1 database hit)		Cn total / Phe	
			C2, C4; differe	nt treatments		
		C2			C4	
0.4						••
0.3 □				•		
nuqa						
ар 90.2 —						Treatment
Normalized abundance					•	•
δ 0.1 Ζ	•	•	•	•		
0.0		•			QTL	
	0 12 24	48	⁹⁶ Hours after trea	0 12 24 atment (hat)	48	96
		C	DON, Mock; diff	erent genotypes		
		DON			Mock	
0.4			•			
0.3		•				
Normalized abundance	•		•	••	•	
eq at		•				Genotype C2 🖨 C4
maliz				••	•'	•
วั 0.1 X				•		
	••	•	•	•••		

 48
 96 Hours after treatment (hat)
 0 12
 12
 24
 48

 CM, Remus; different treatments

96

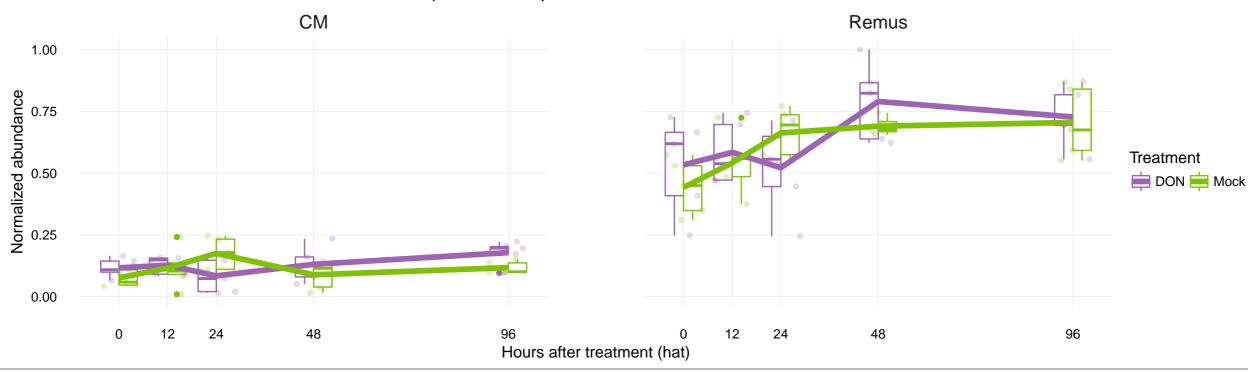
0.0

0

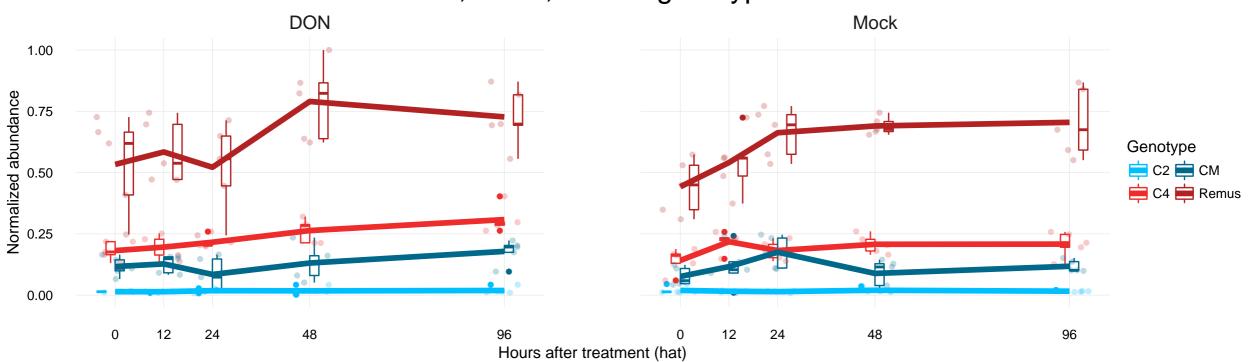
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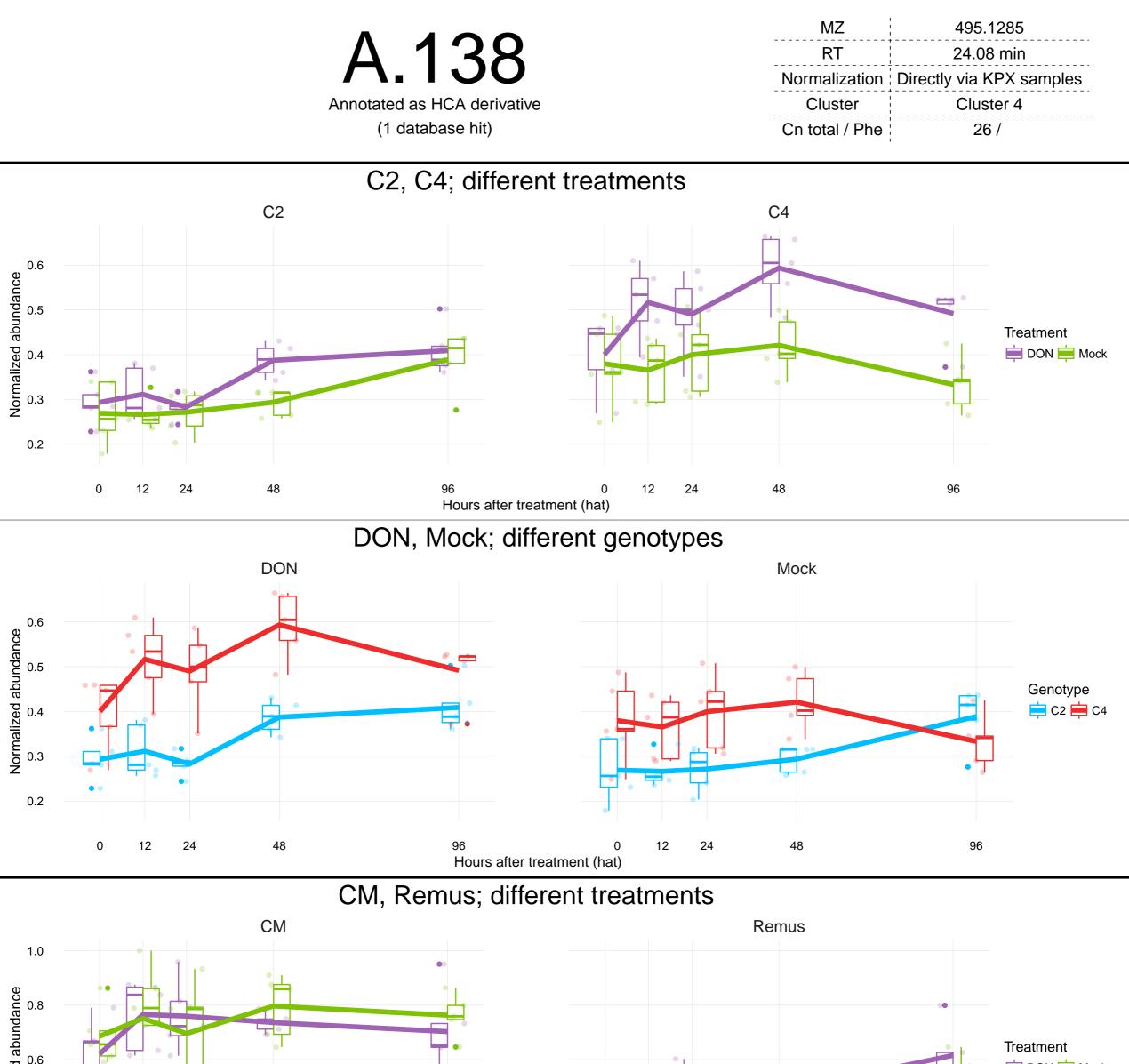
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•

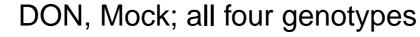


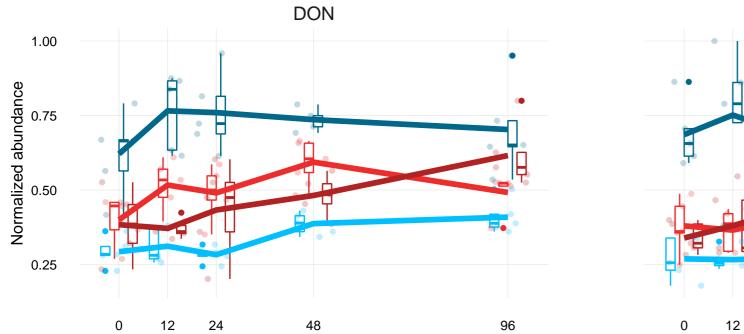
DON, Mock; all four genotypes

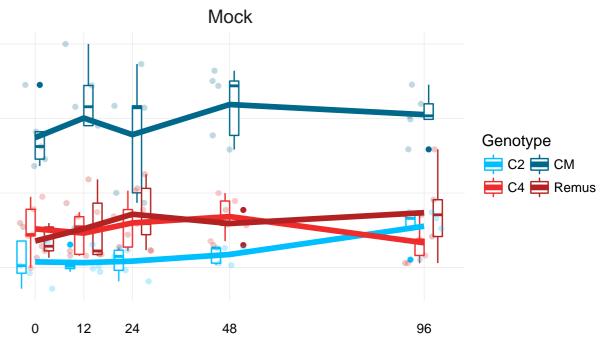


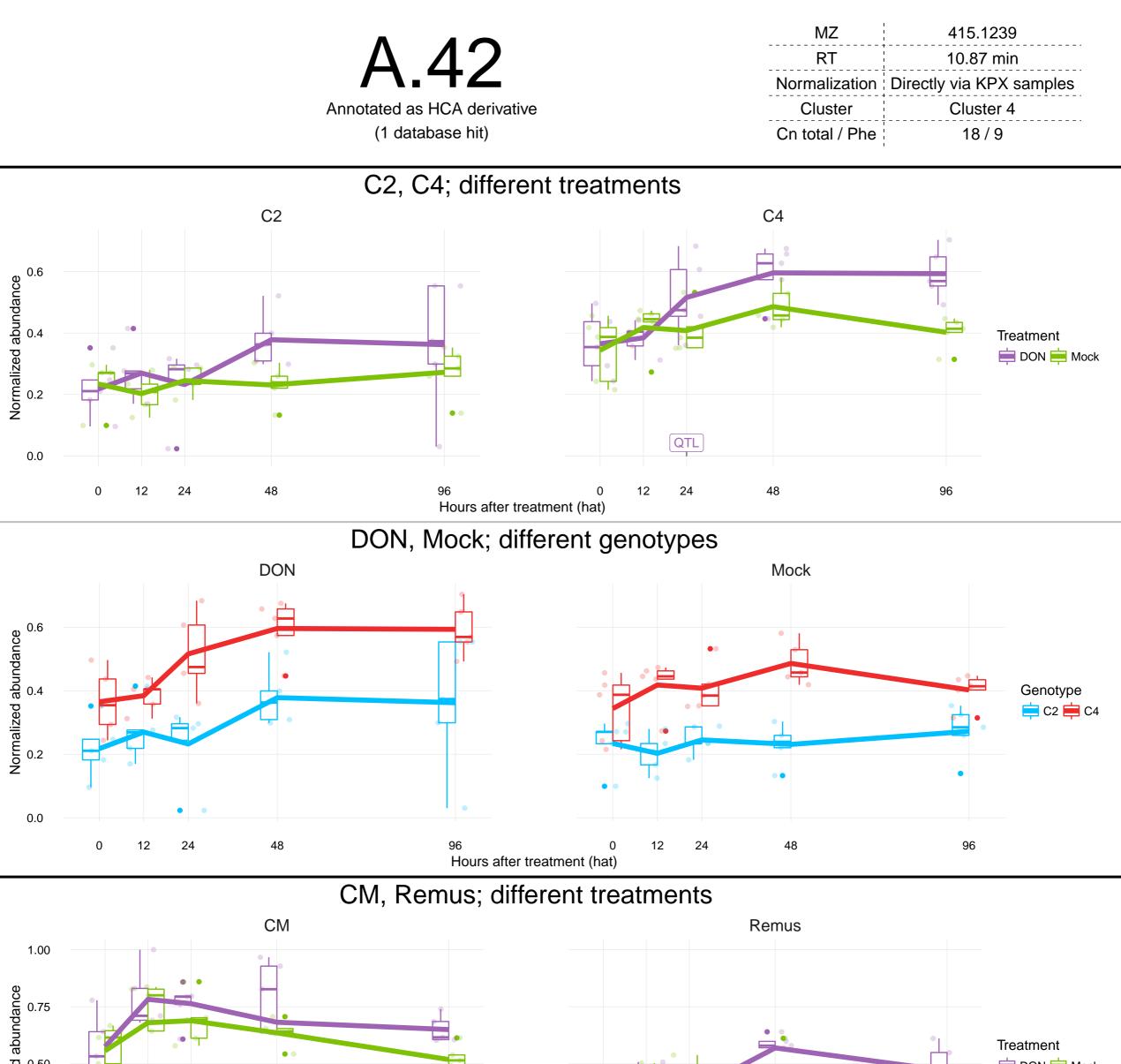


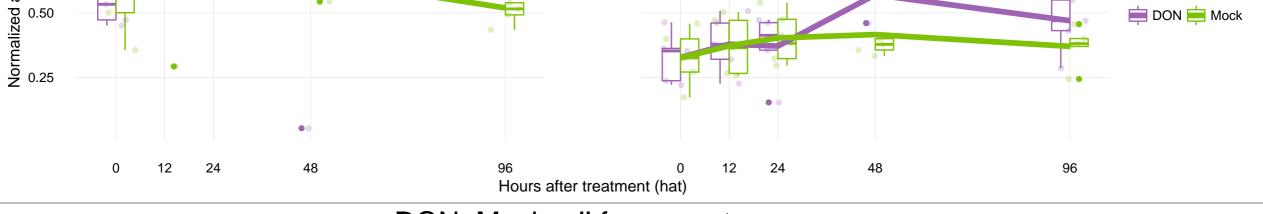




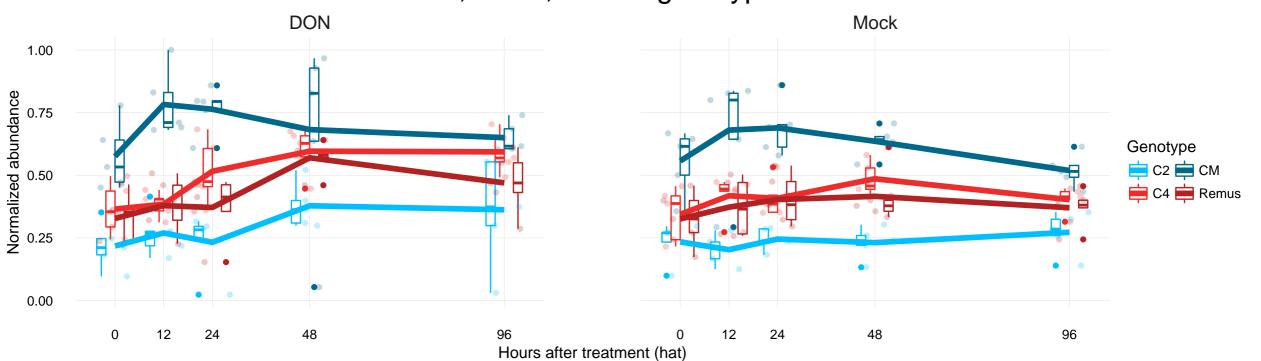


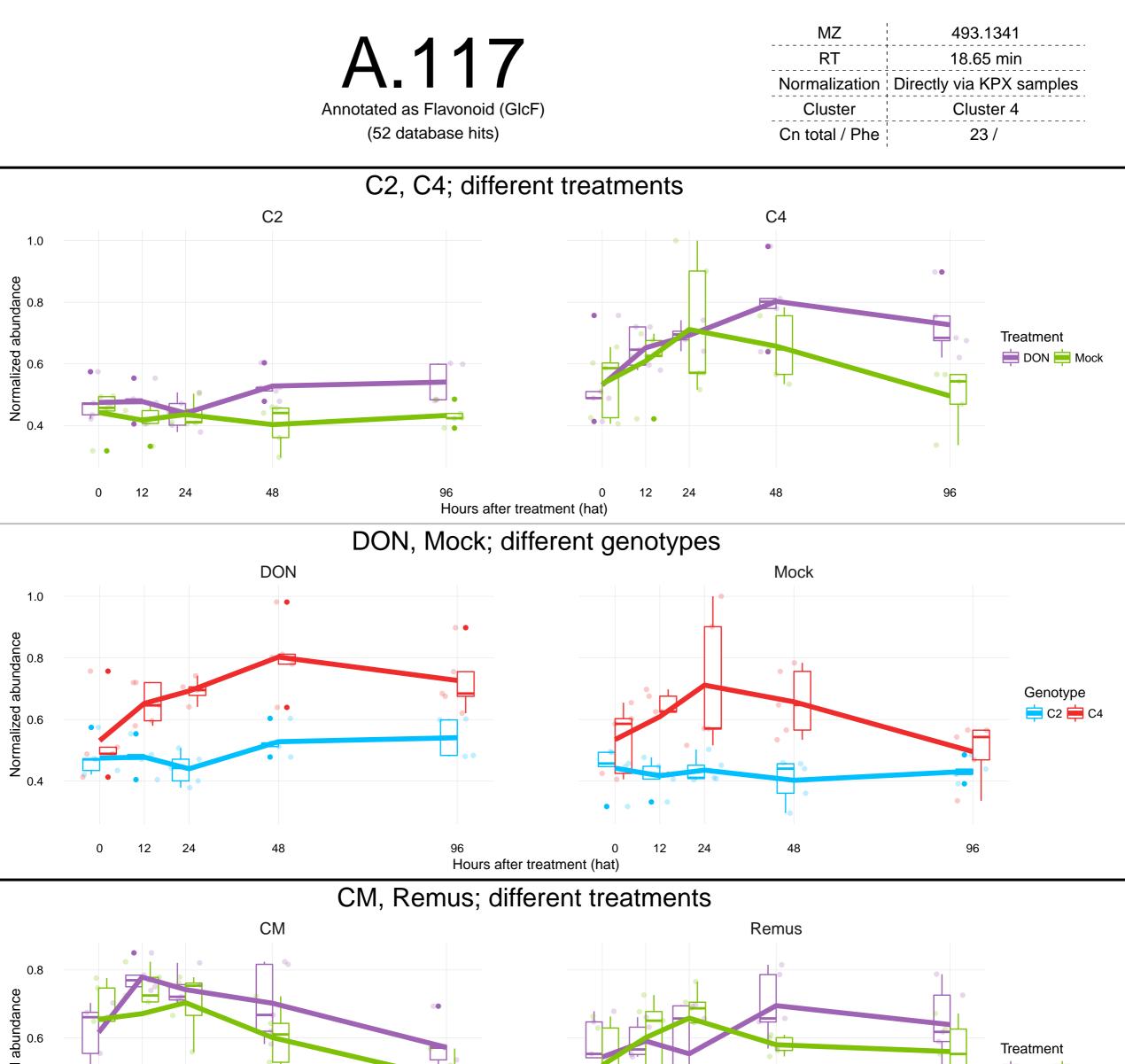


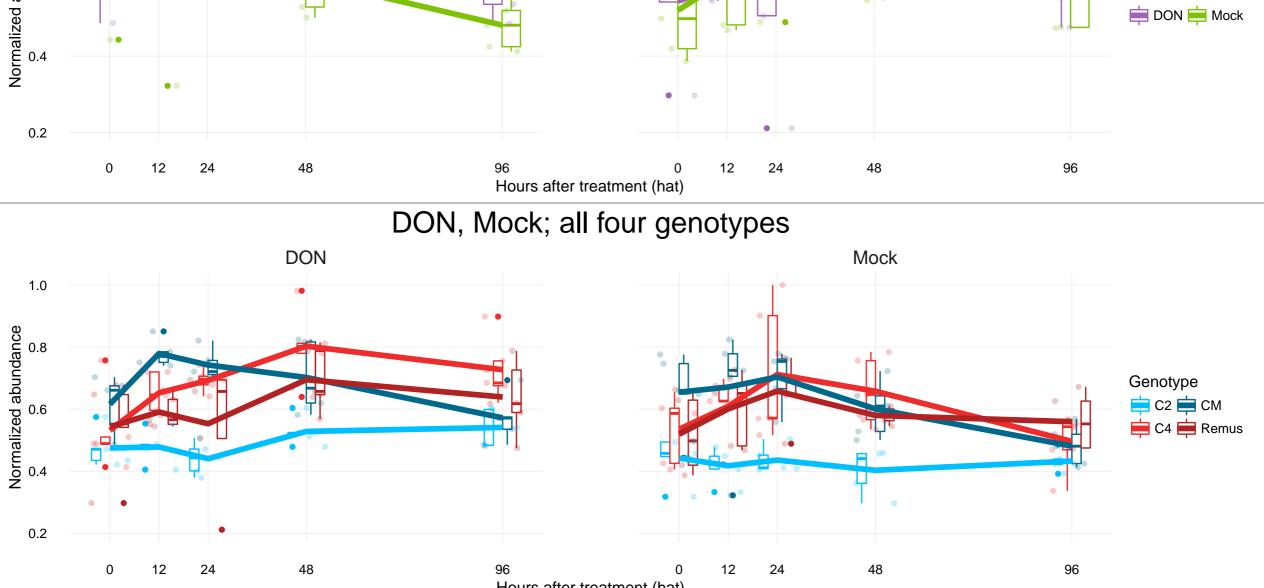


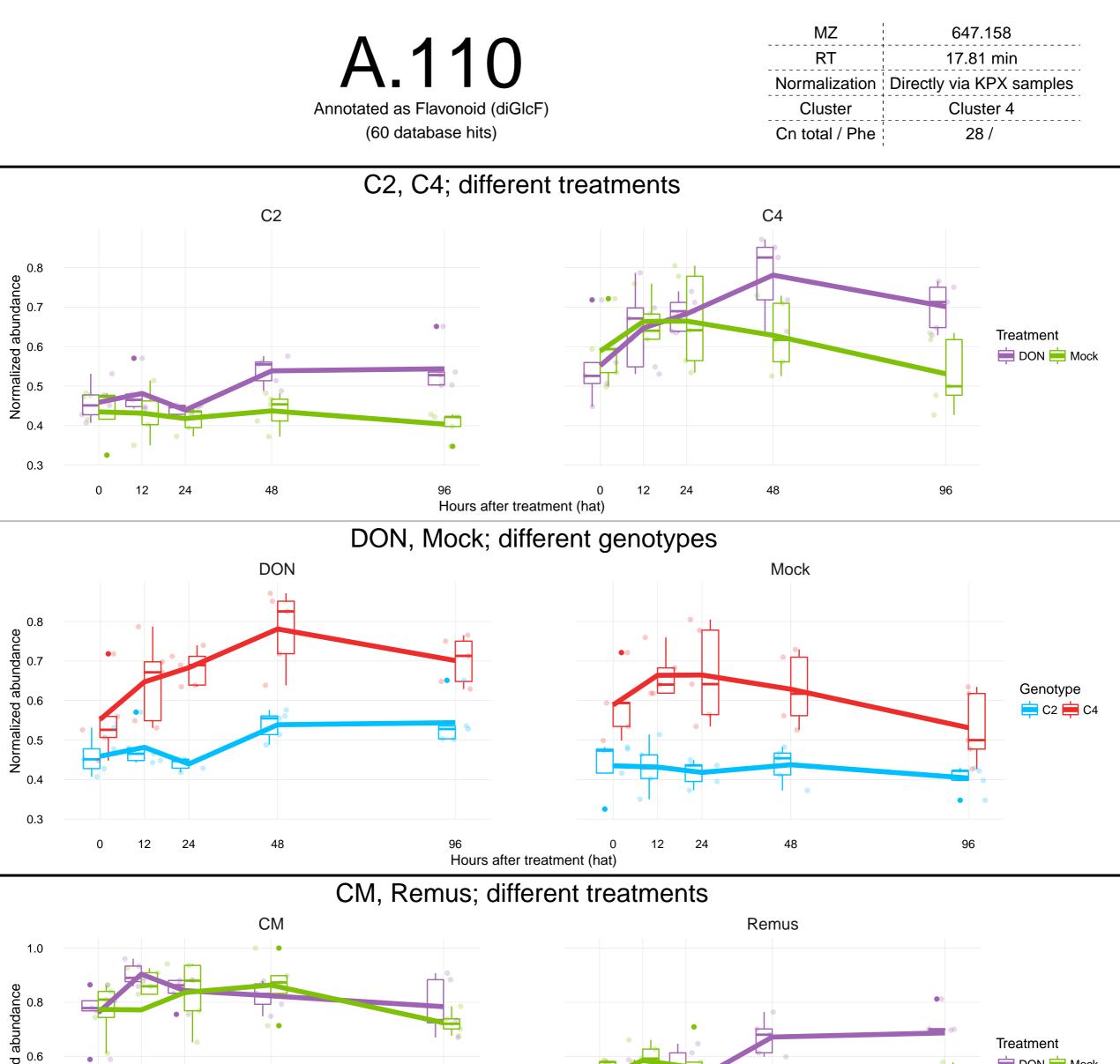


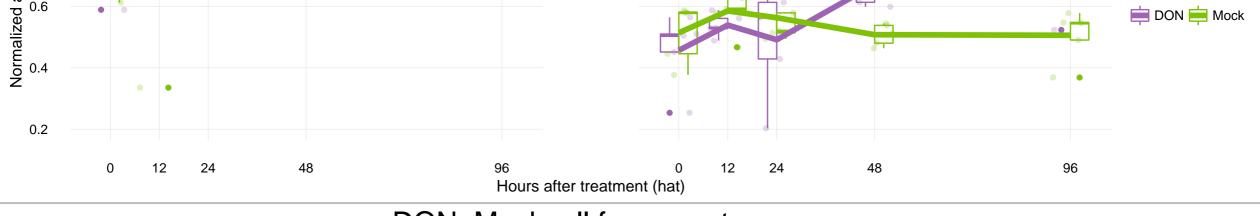
DON, Mock; all four genotypes



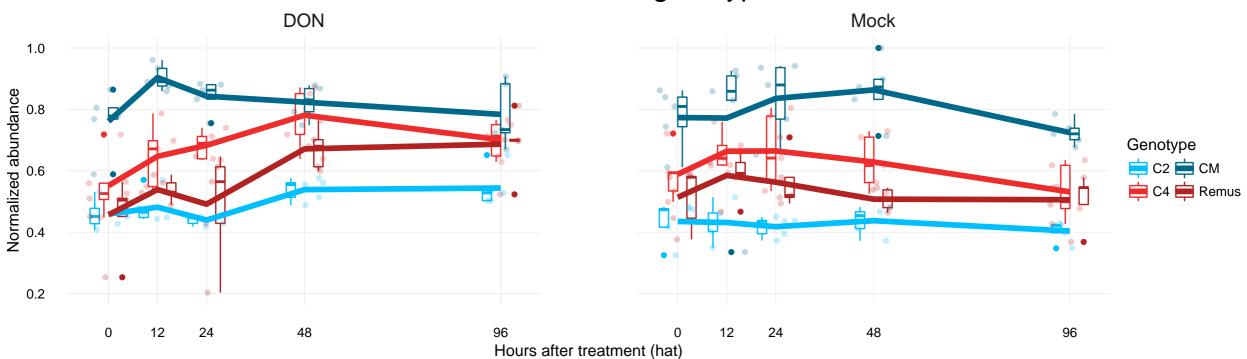


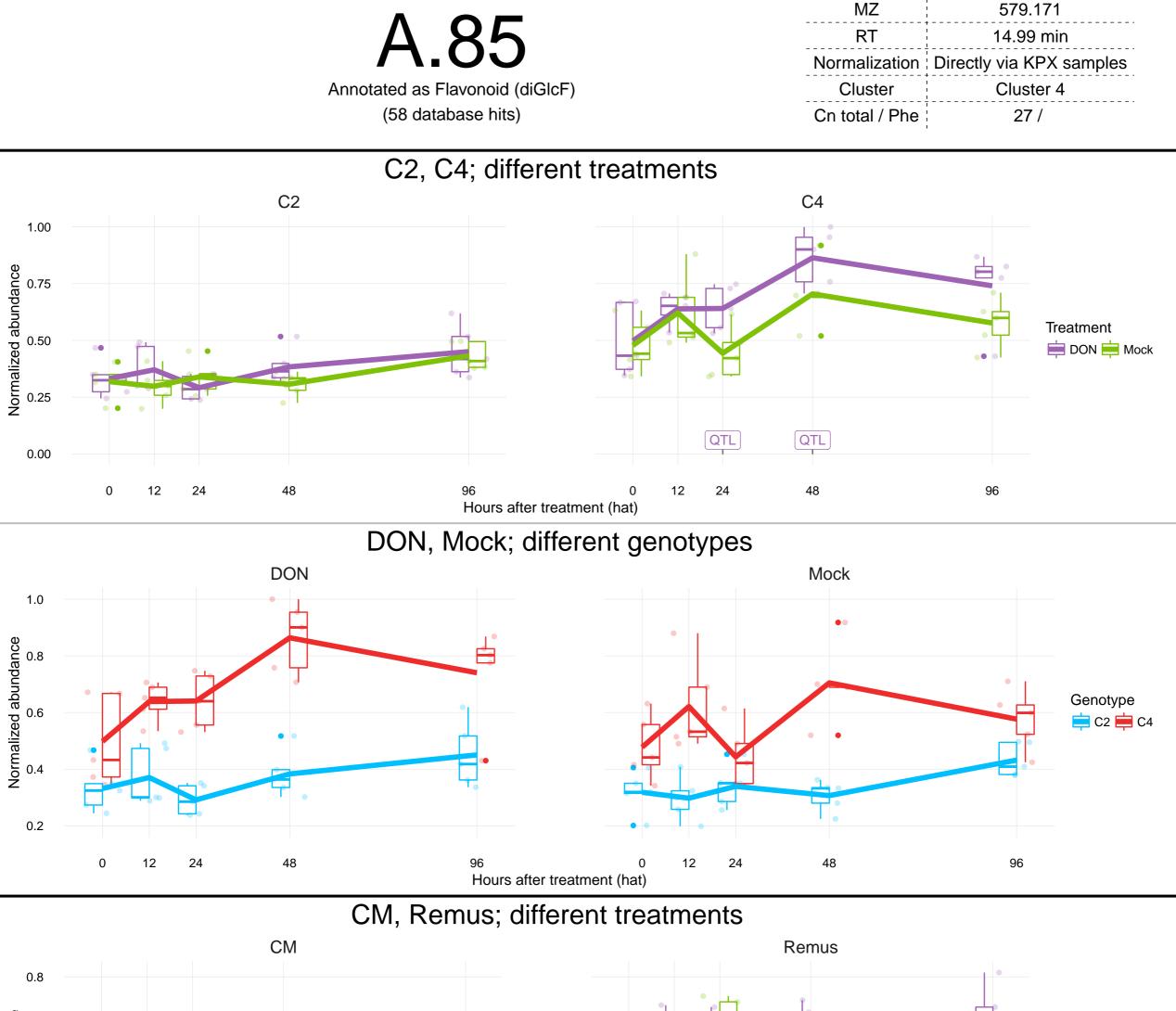




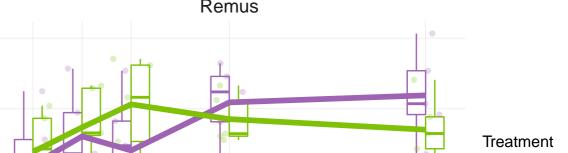


DON, Mock; all four genotypes

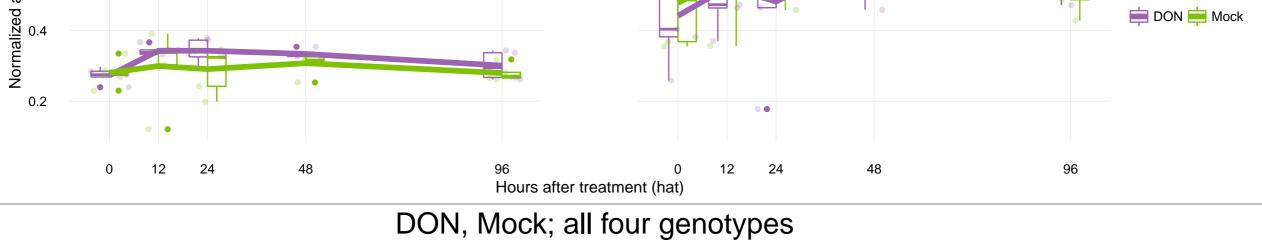


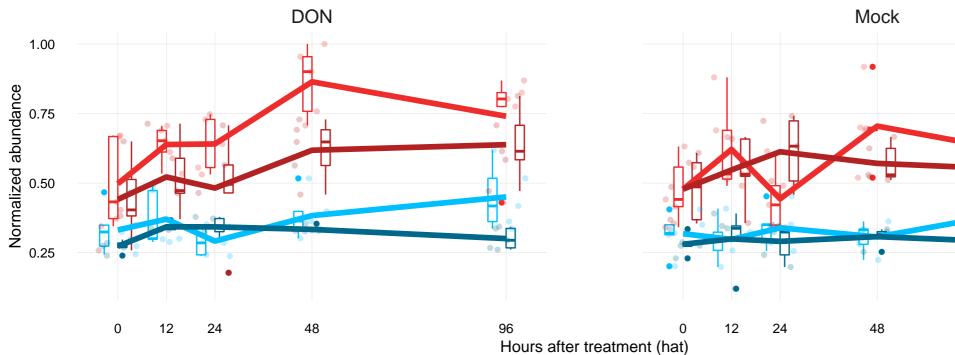


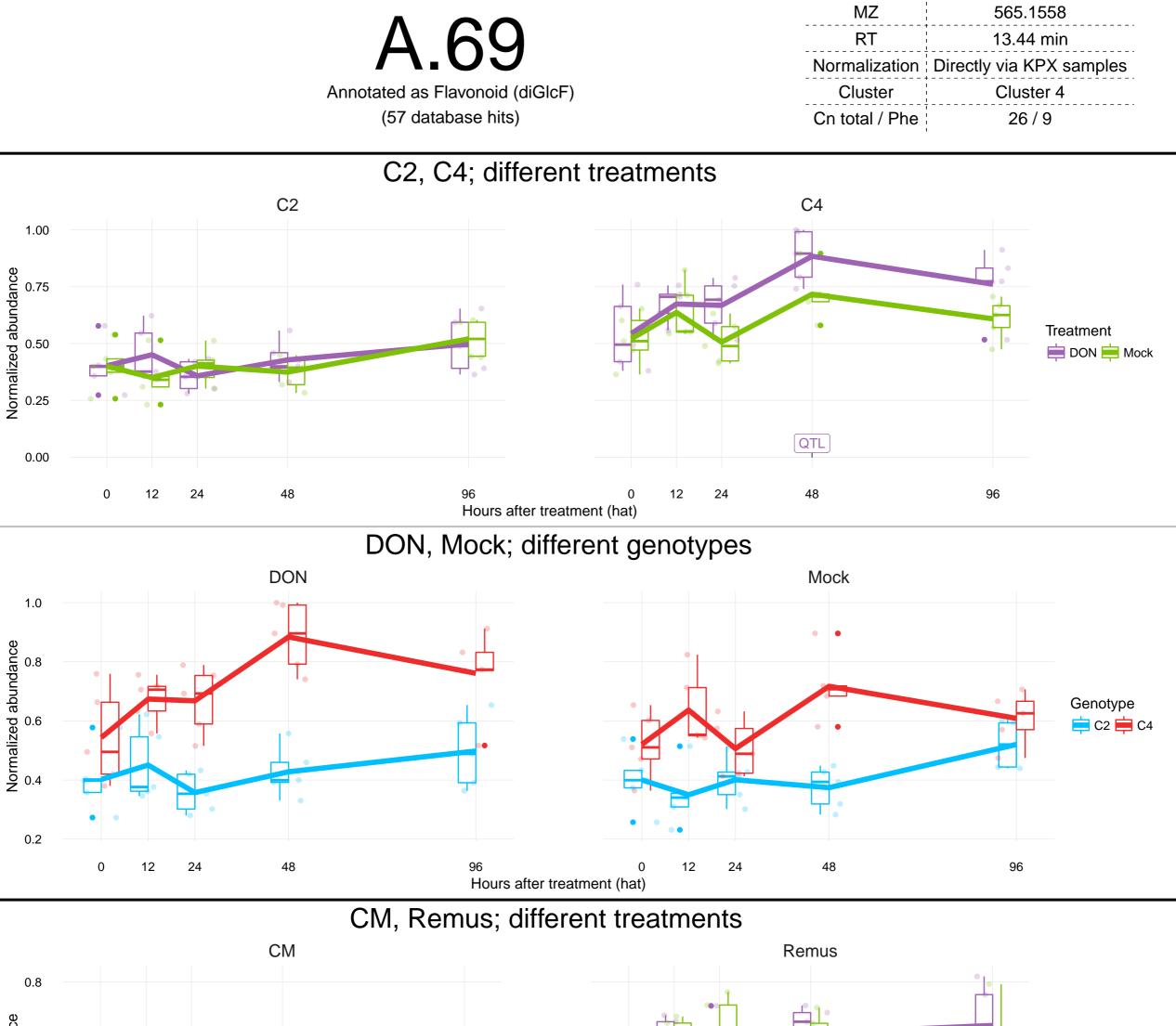
aprindance

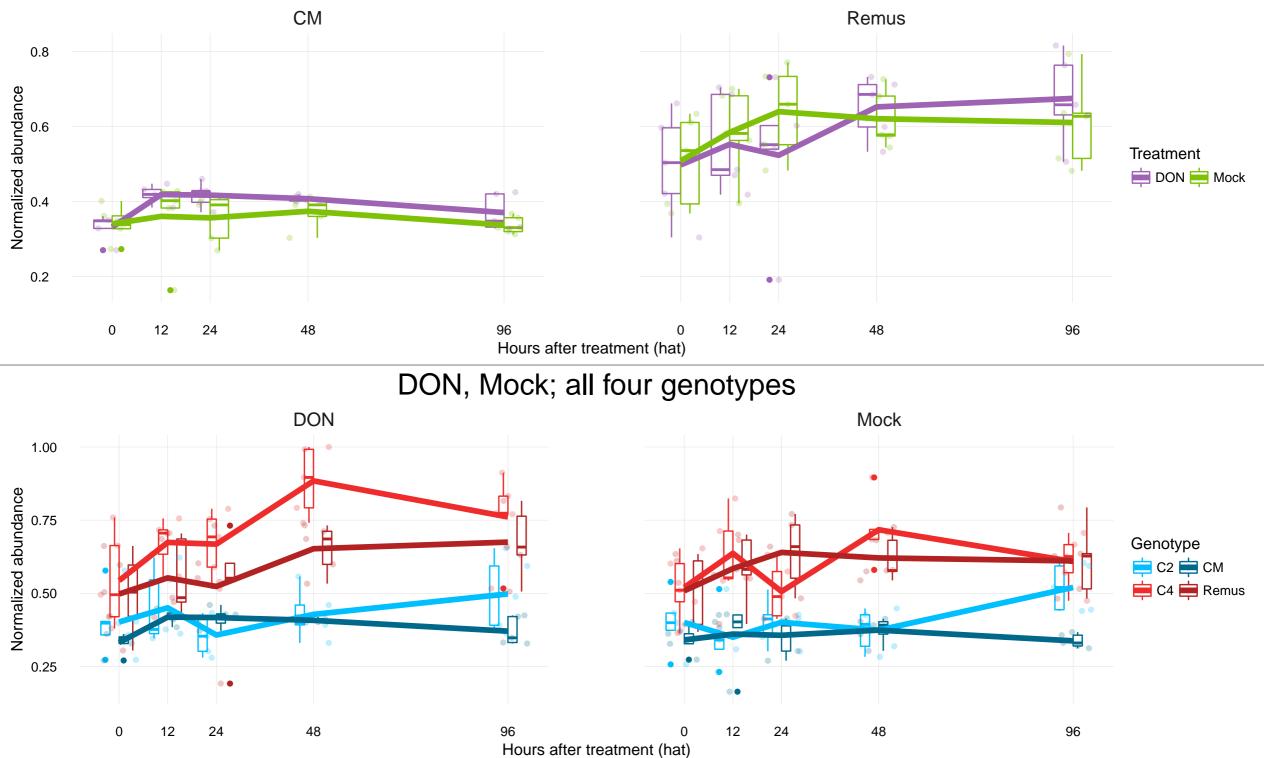


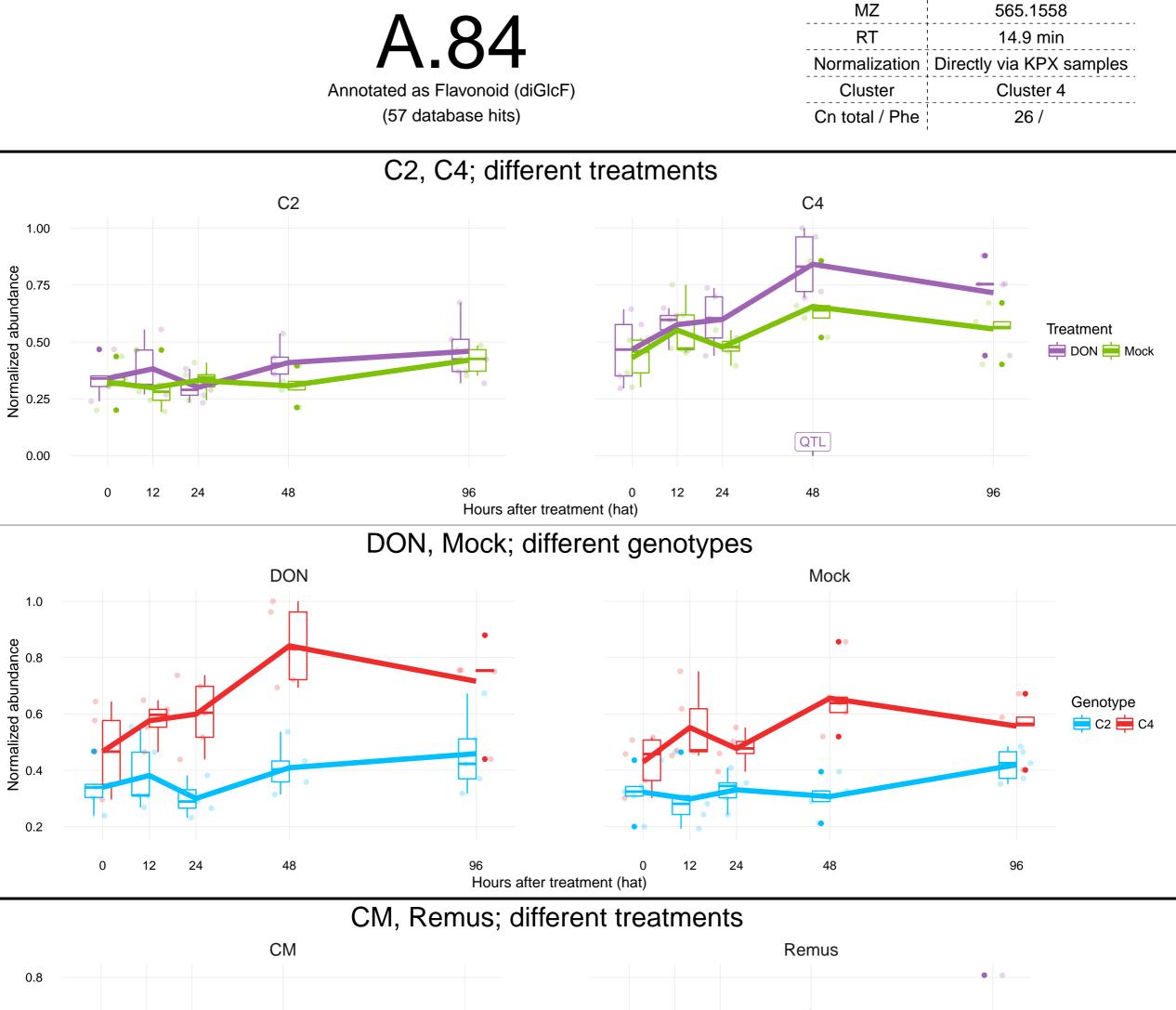
Genotype C2 CM C4 Remus

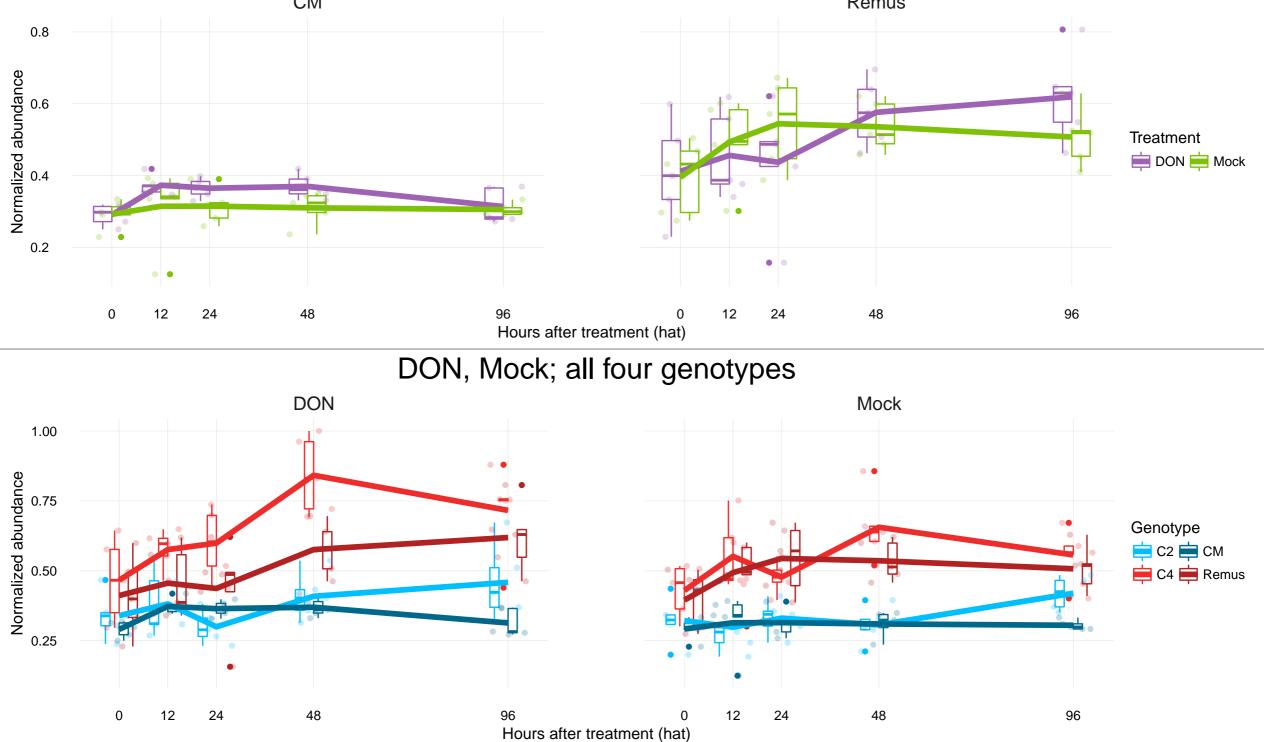


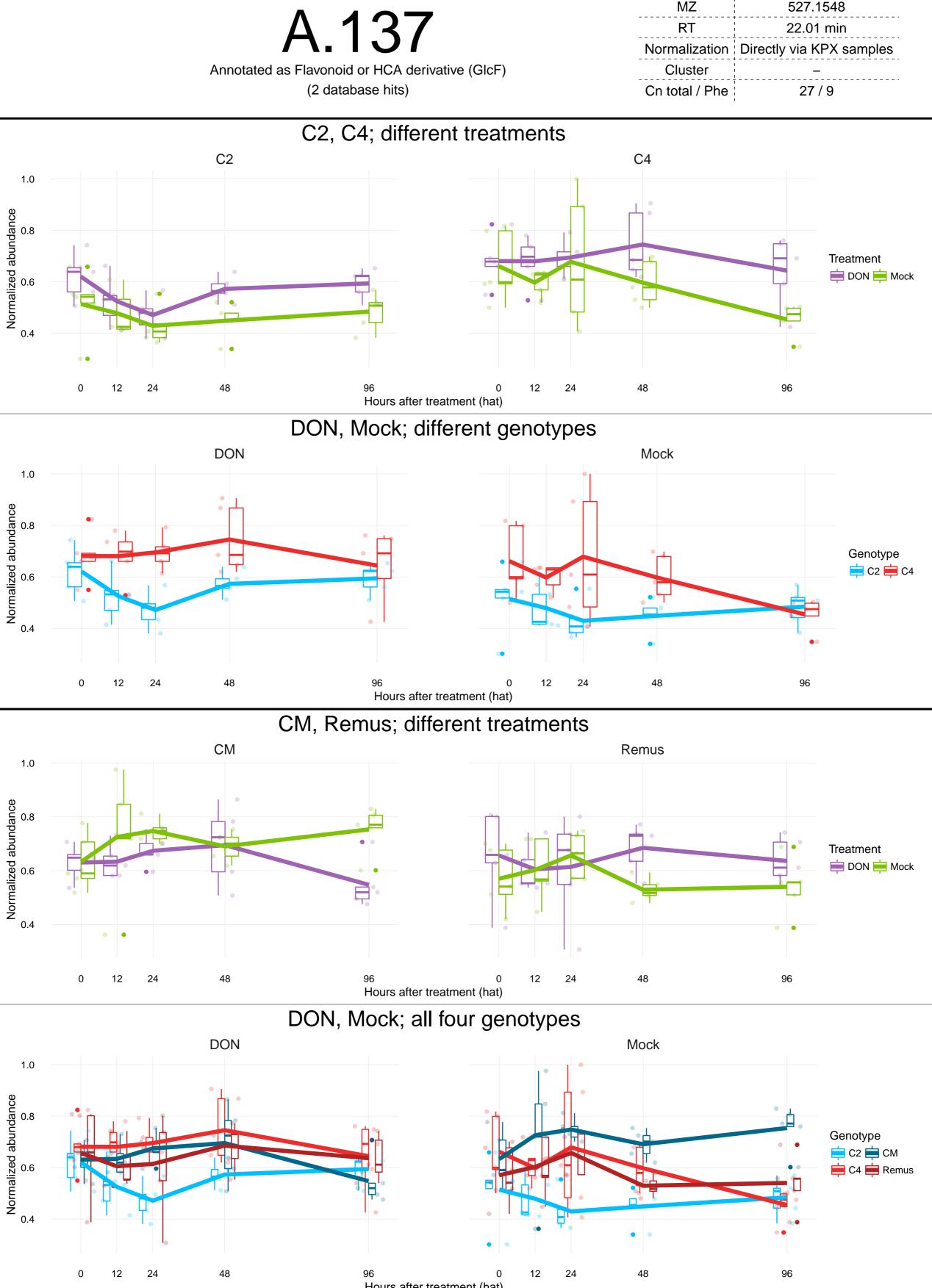


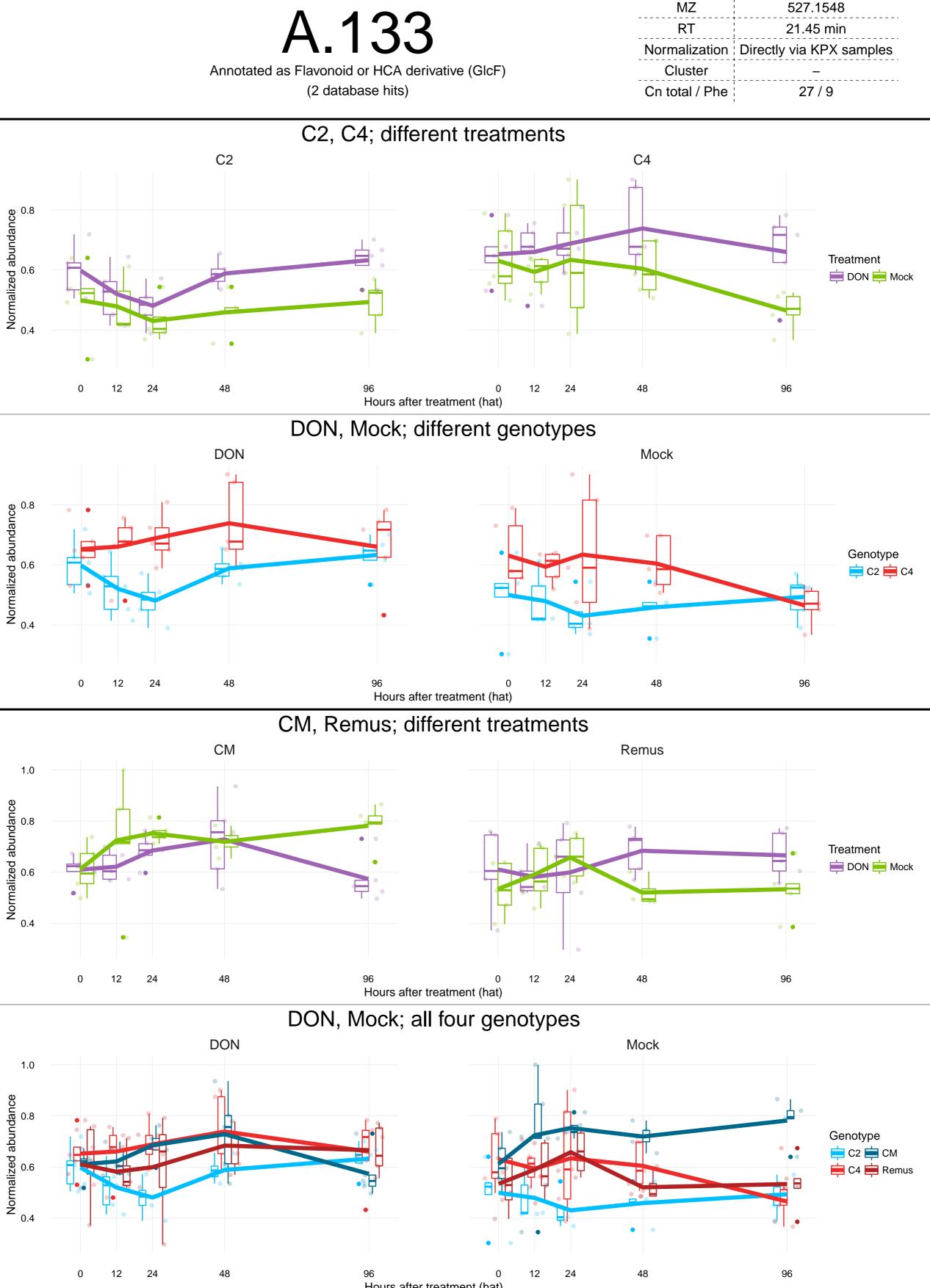












		Annotated as Flavonoid (diF) (1 database hit)		MZ RT Normalization Cluster Cn total / Phe	675.2072 20.99 min Directly via KPX samples – 36 /
		C2, C4; different	treatments		
	C2			C4	
Normalized abundance 0.0 0.4 0.2		96 Hours after treatme	0 12 24 ent (hat)	48	Treatment DON <a>Mock
		DON, Mock; differ	ent genotypes		
0.8	DON	,,,		Mock	
Normalized abundance 9.0 9.0					Genotype C2 C4

96

CM, Remus; different treatments

Hours after treatment (hat)

12

0

24

48

96

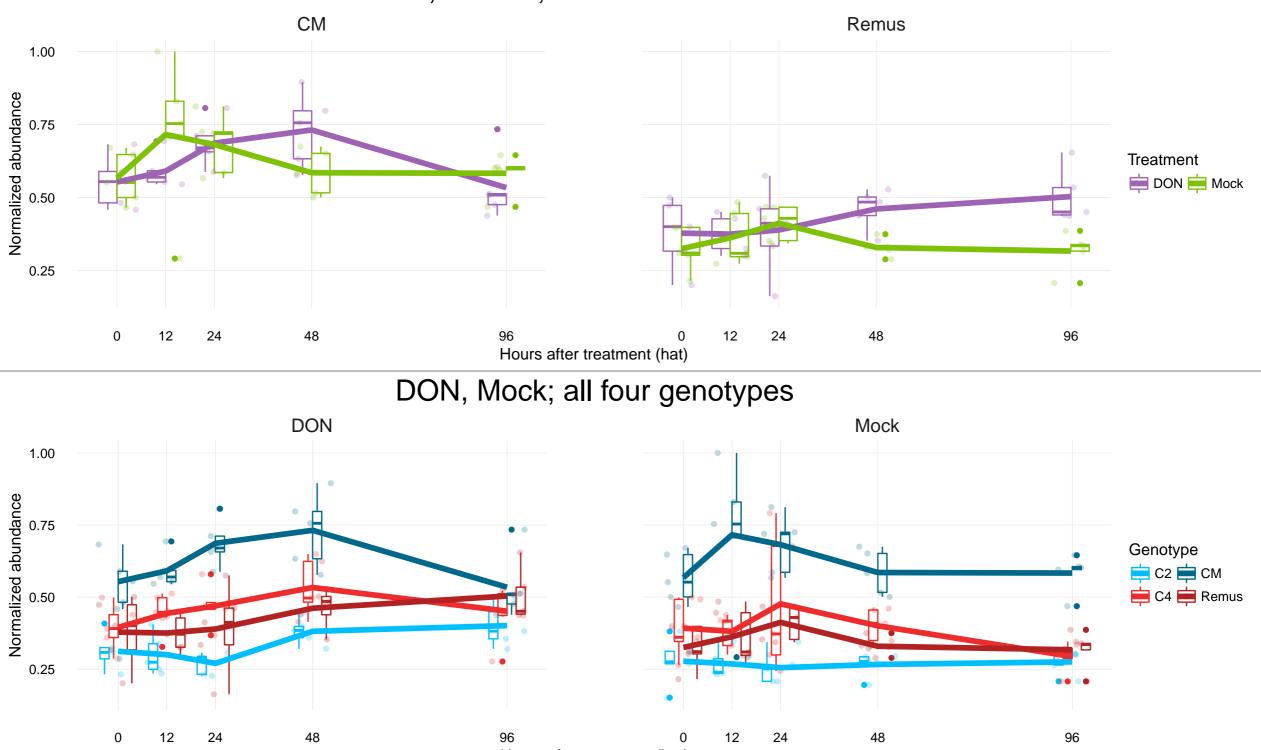
0.2

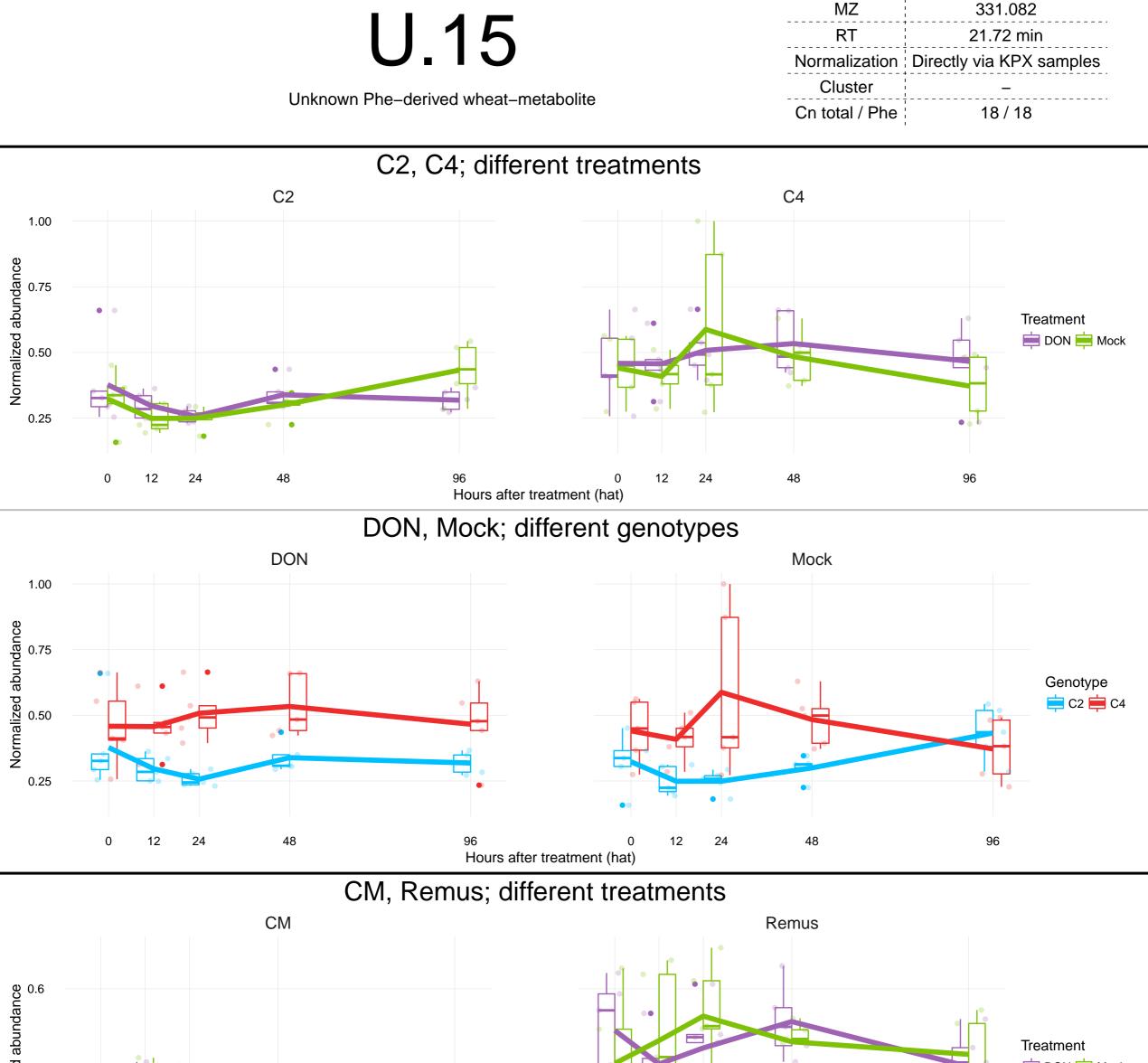
0

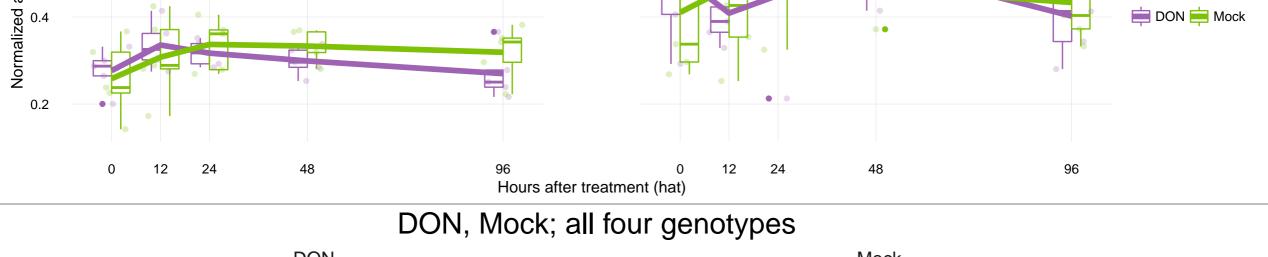
12

24

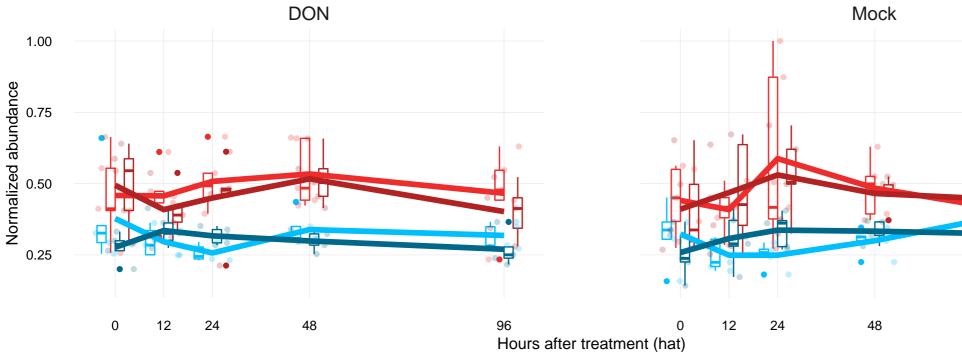
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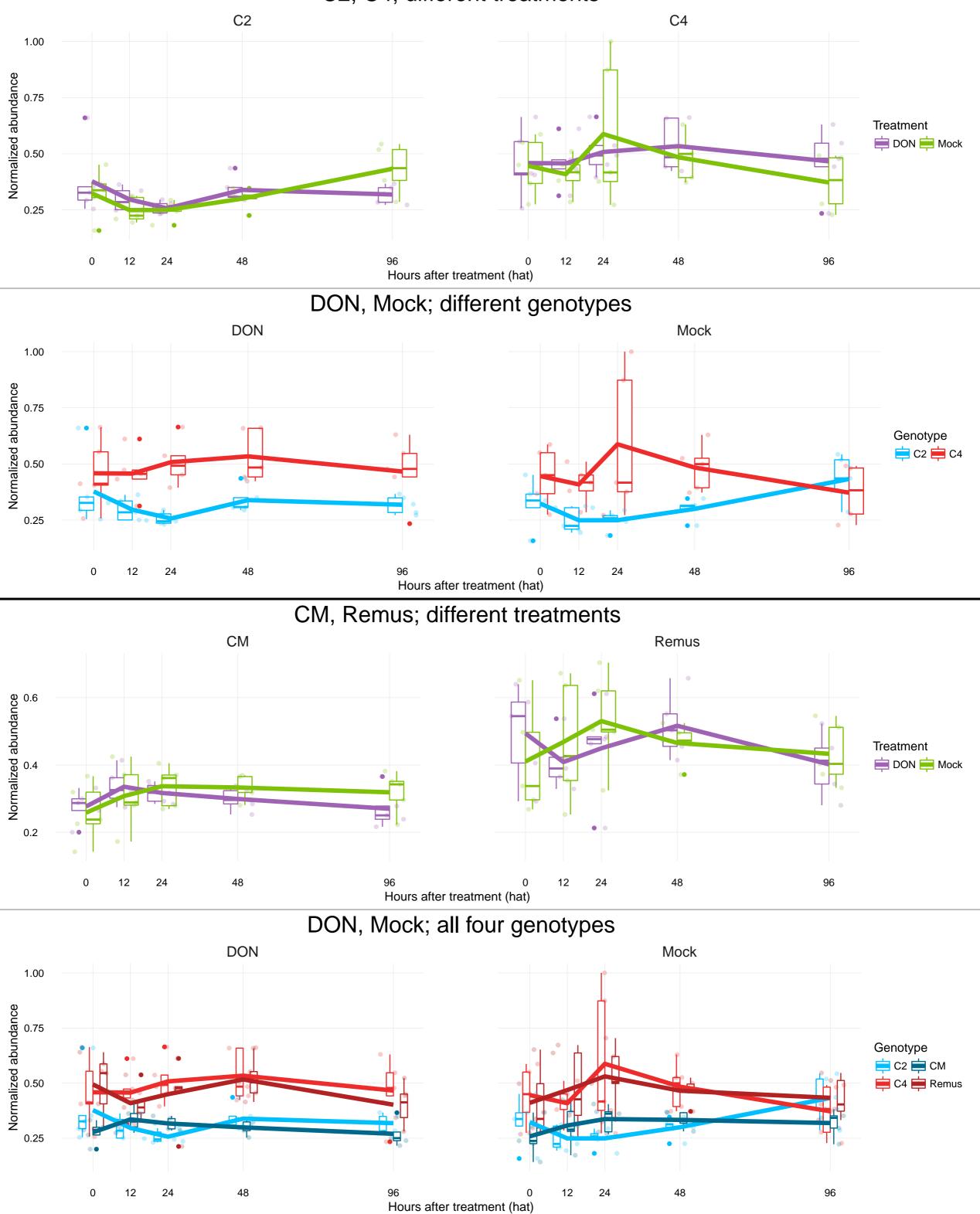


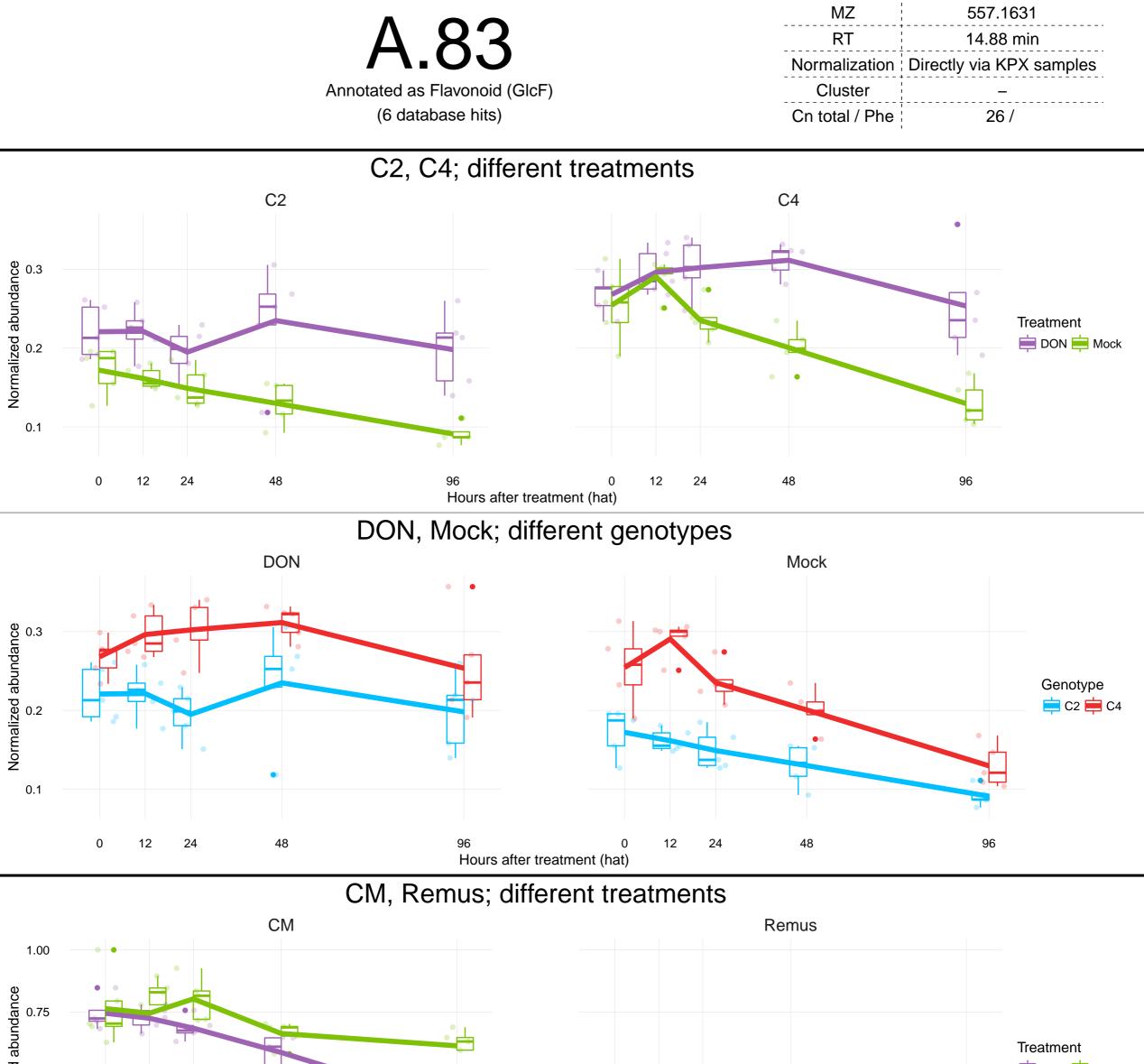
Genotype C2 CM C4 Remus

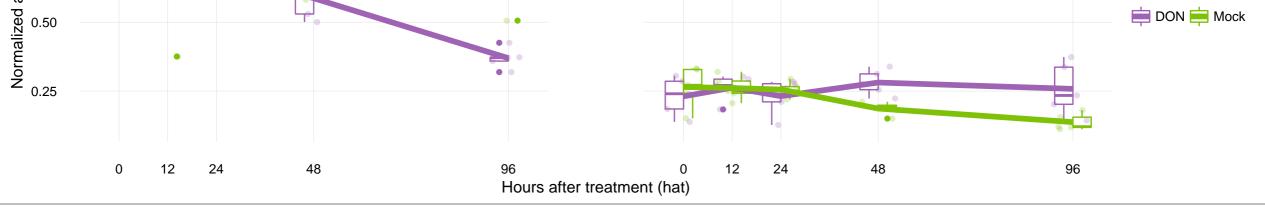




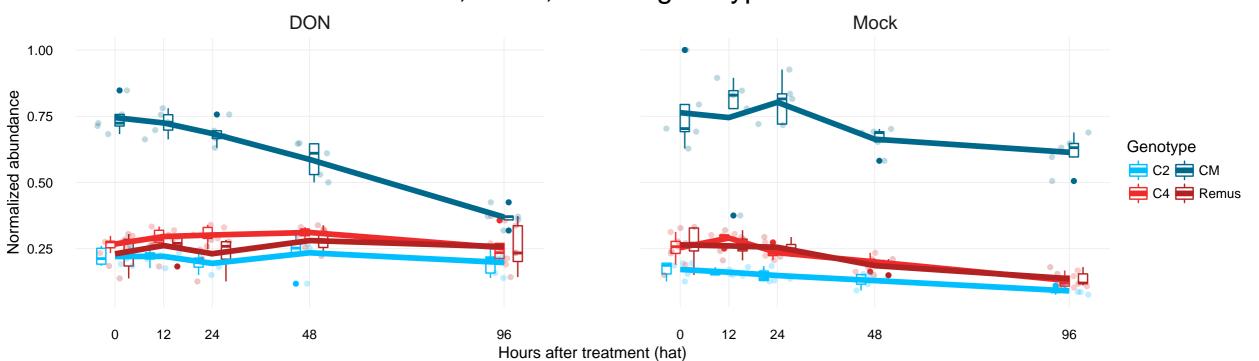


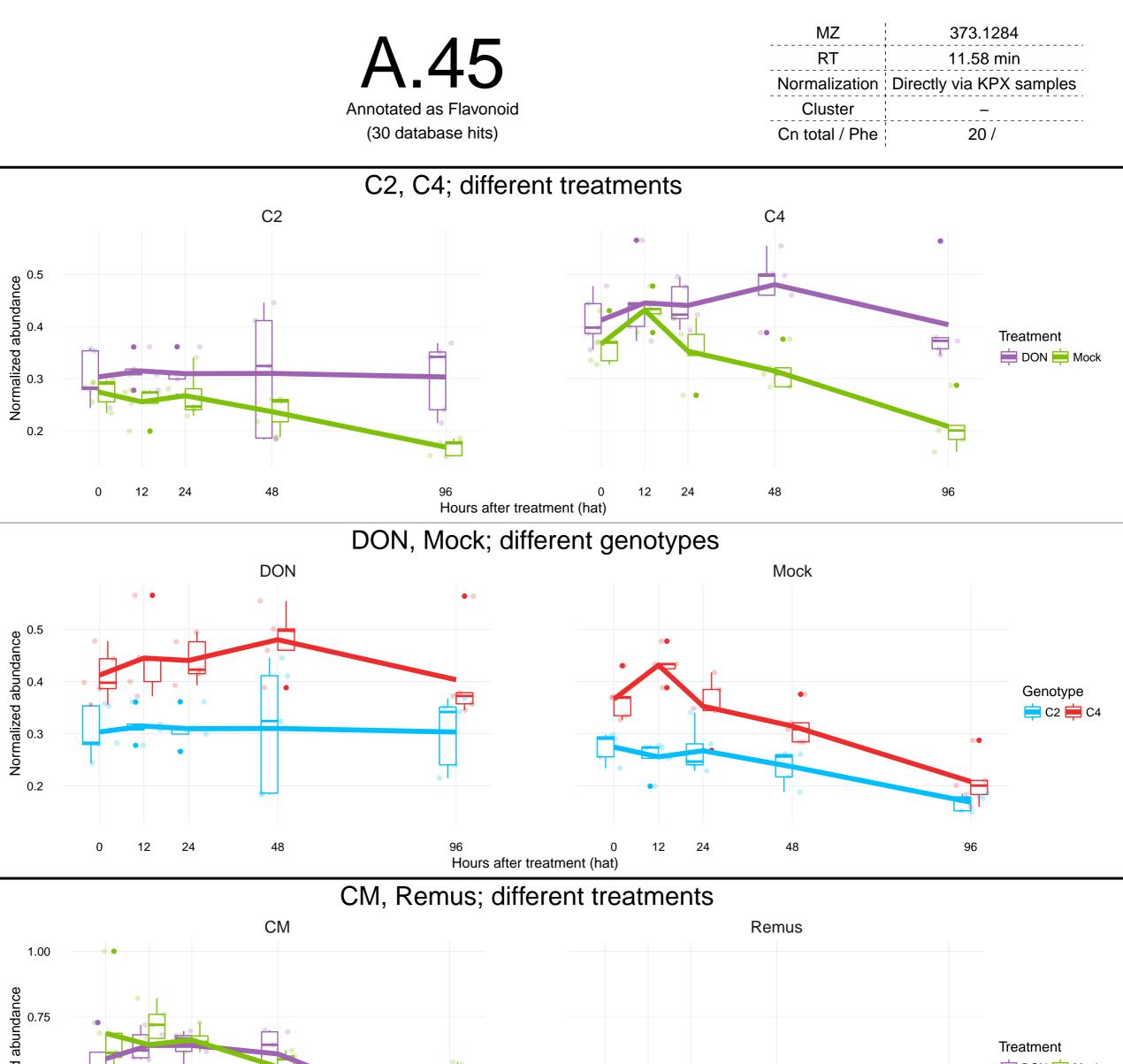


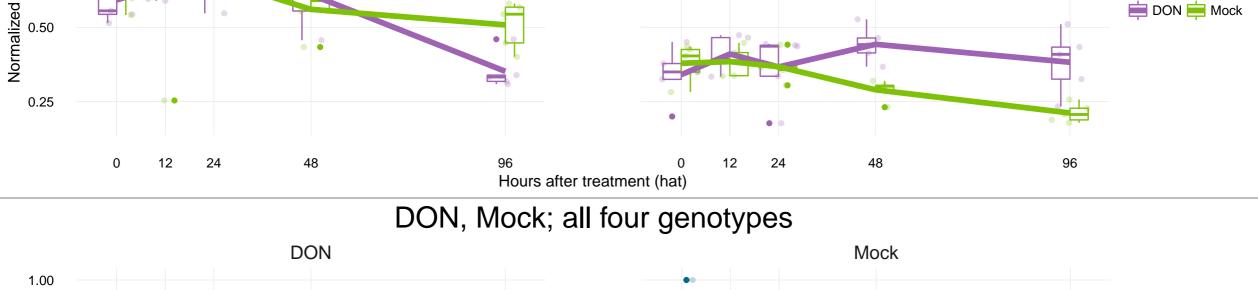


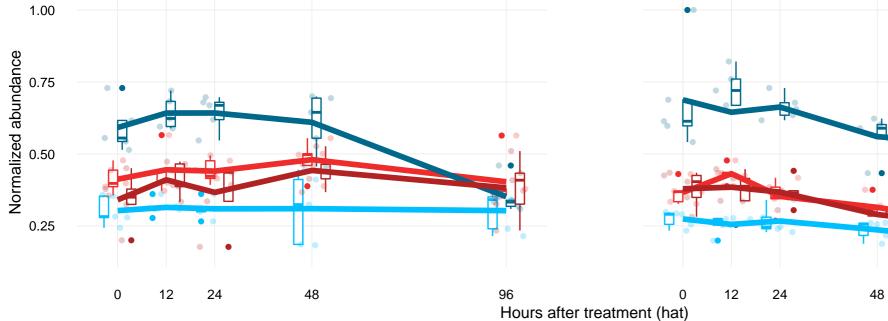


DON, Mock; all four genotypes

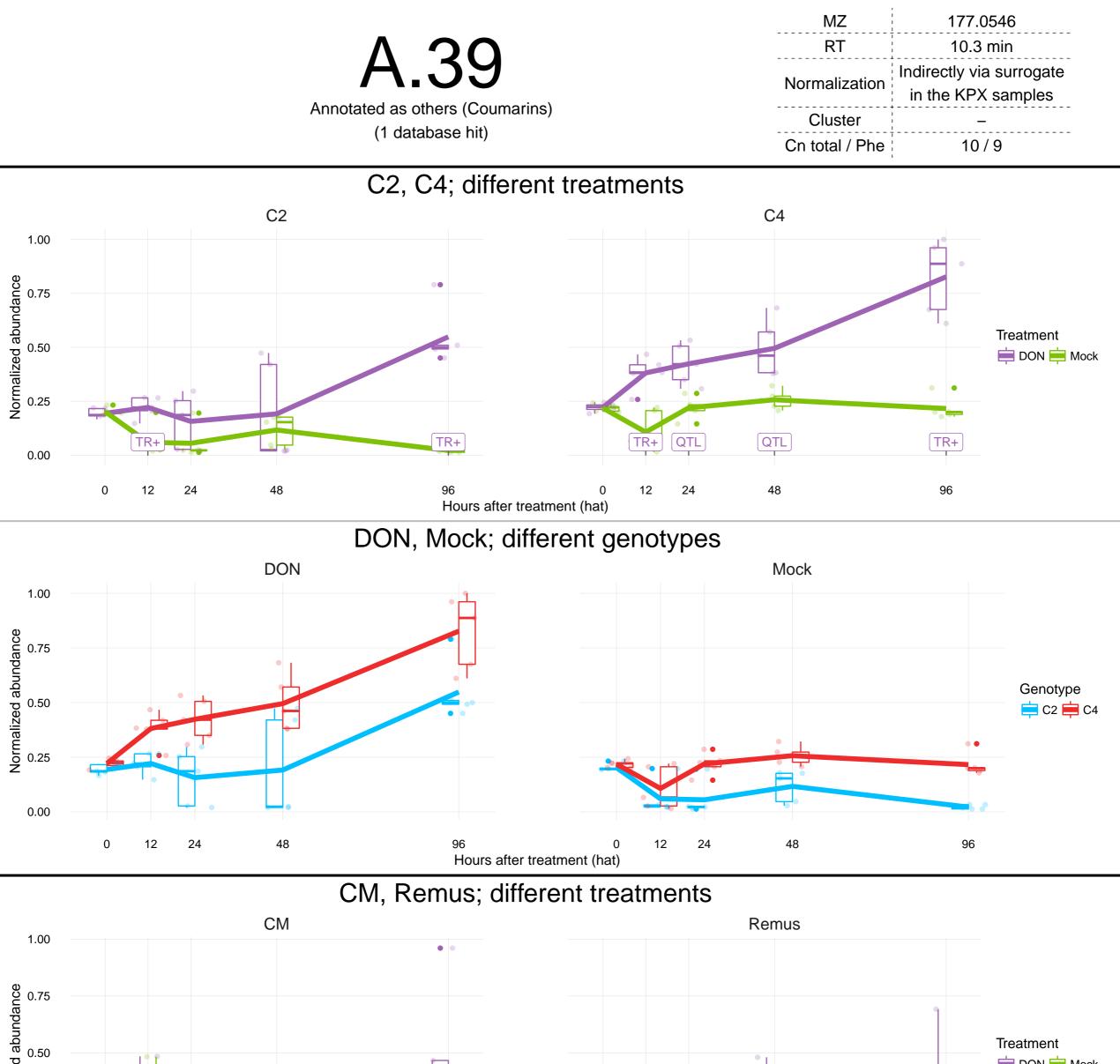


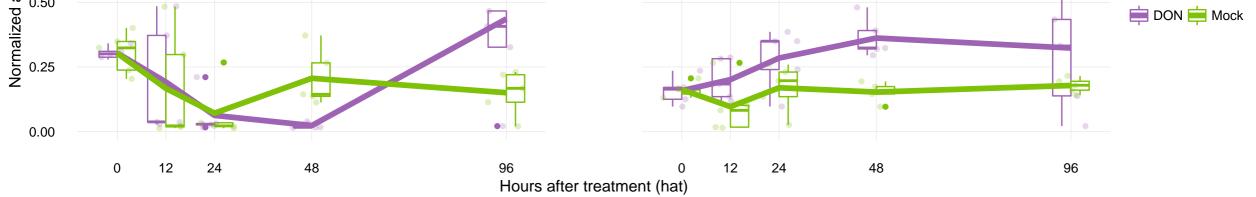




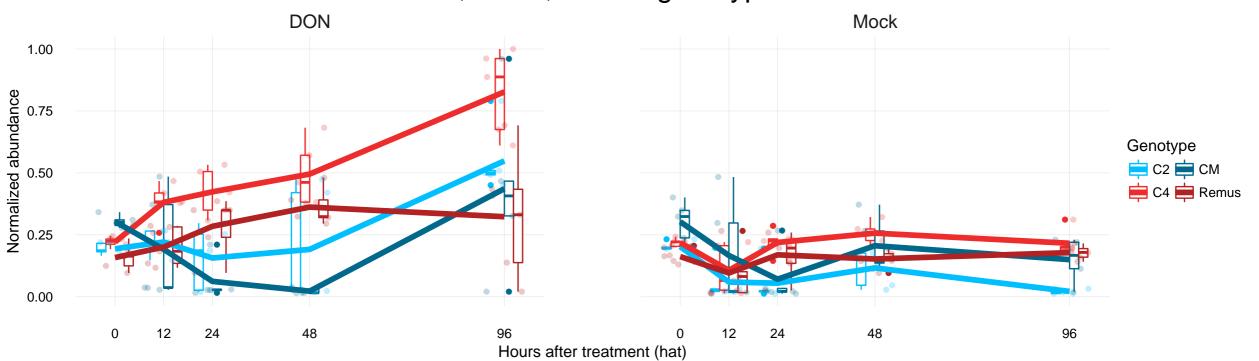


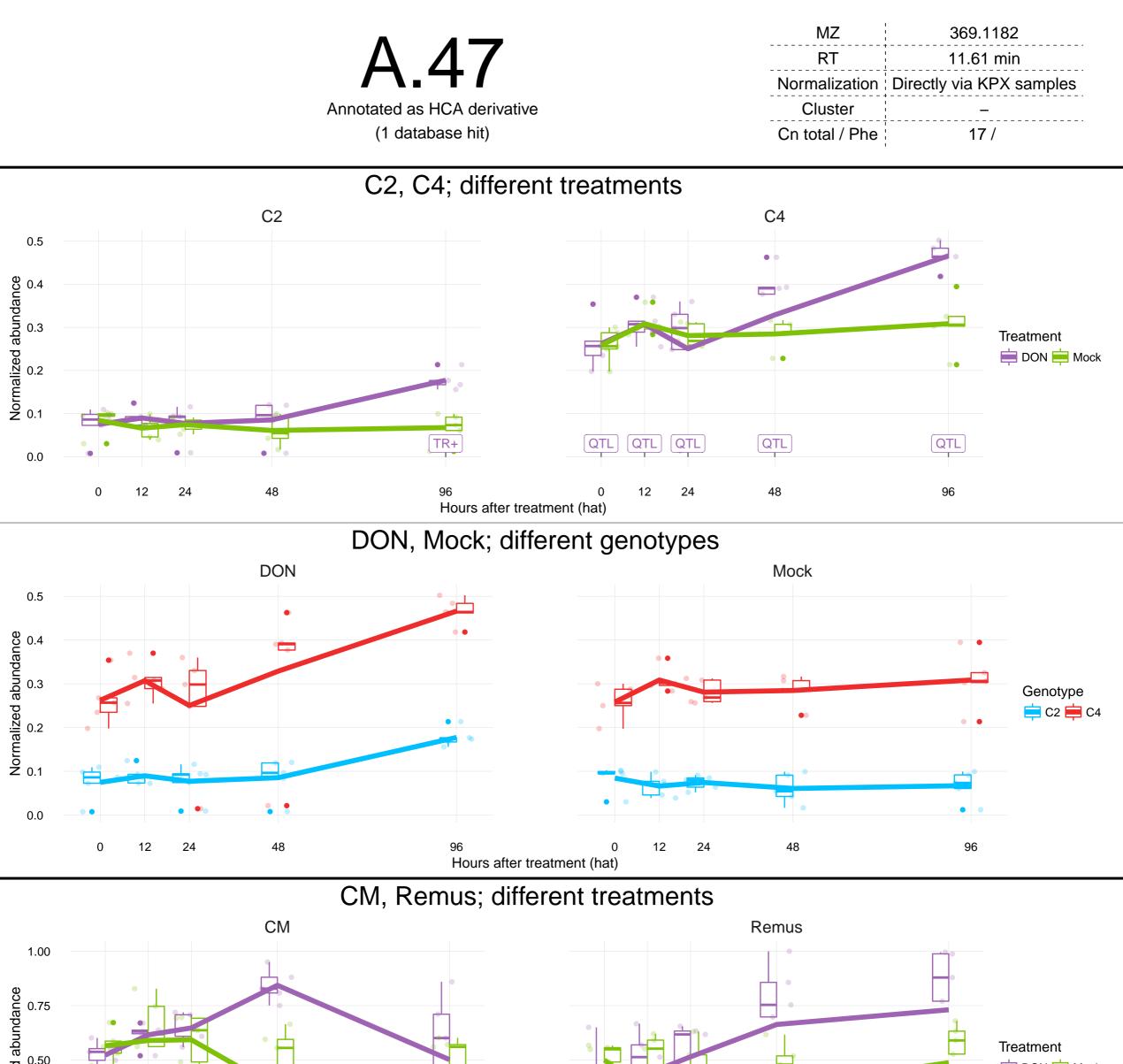
Genotype 럹 С2 🚔 СМ 🚔 C4 🚔 Remus

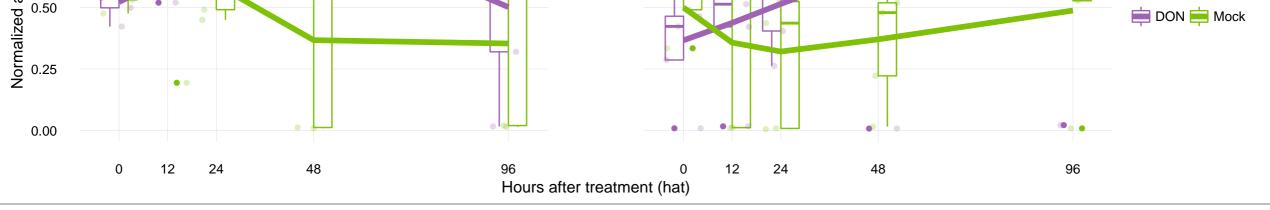




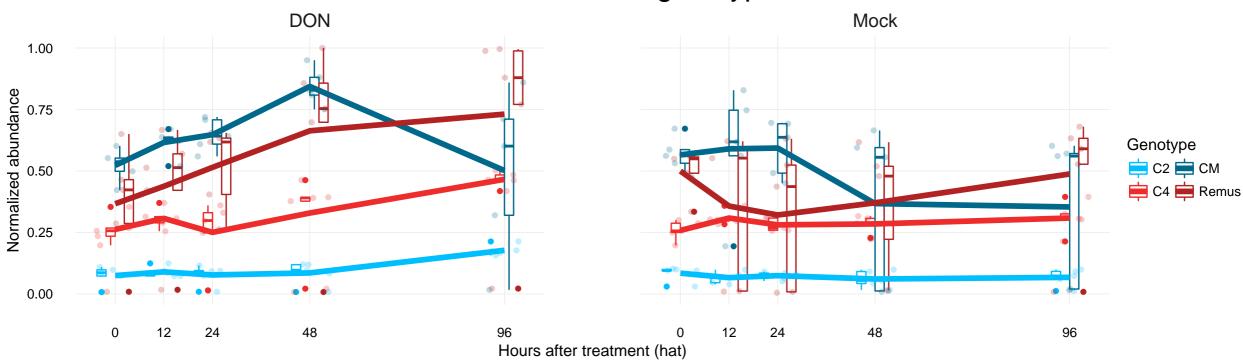
DON, Mock; all four genotypes

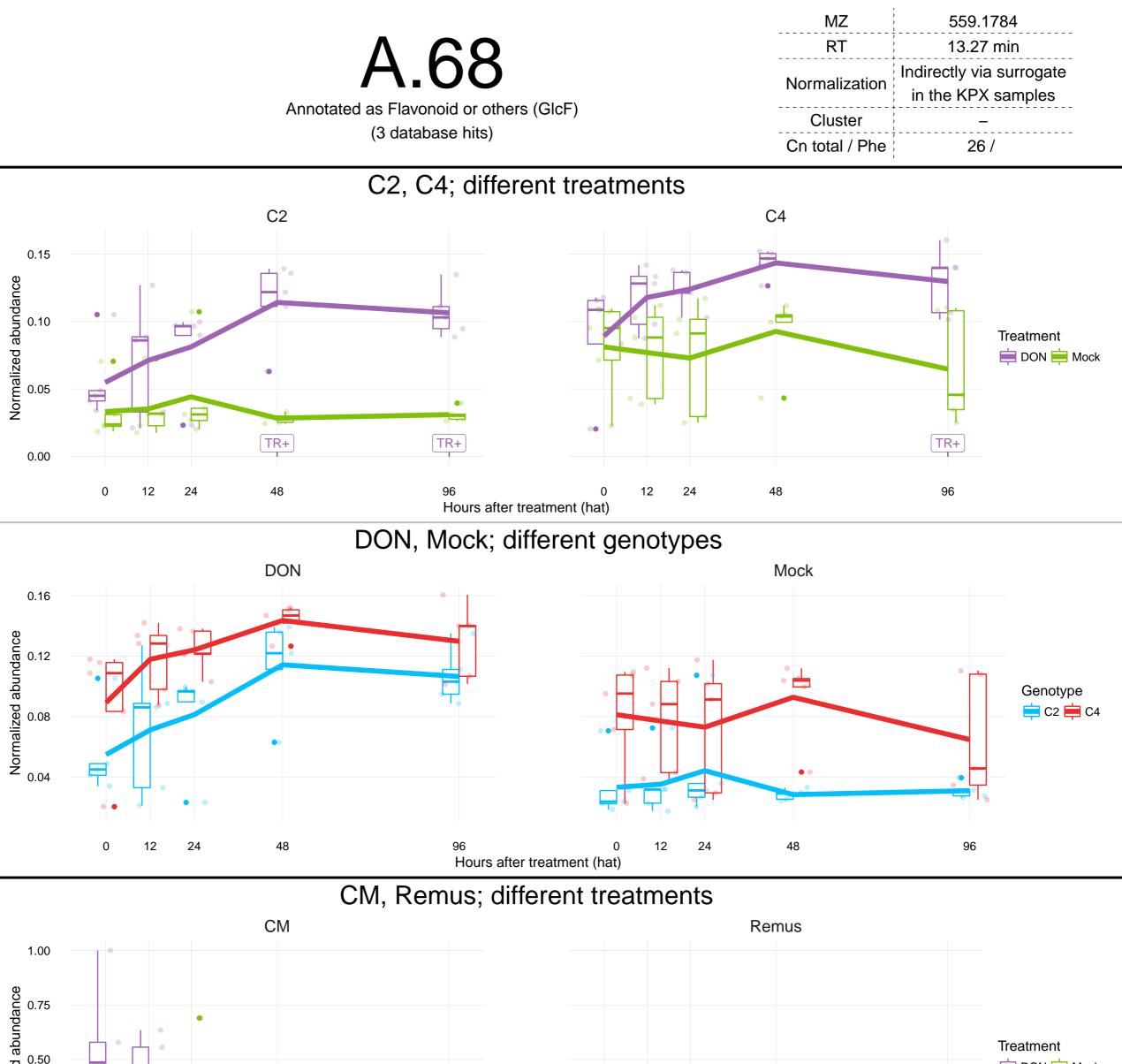


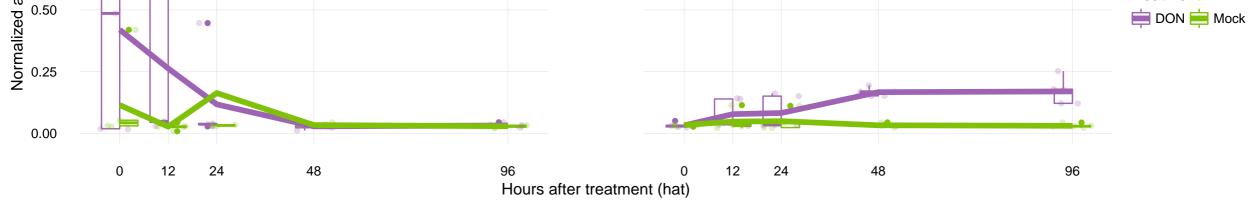




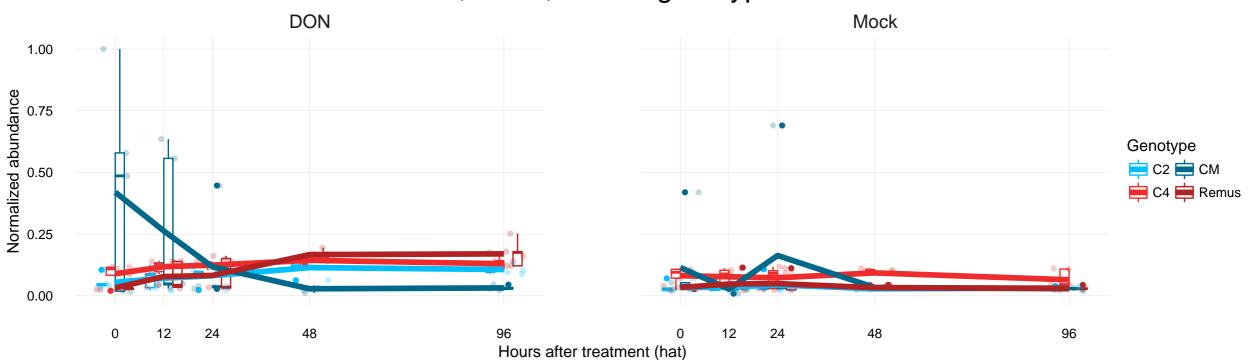
DON, Mock; all four genotypes







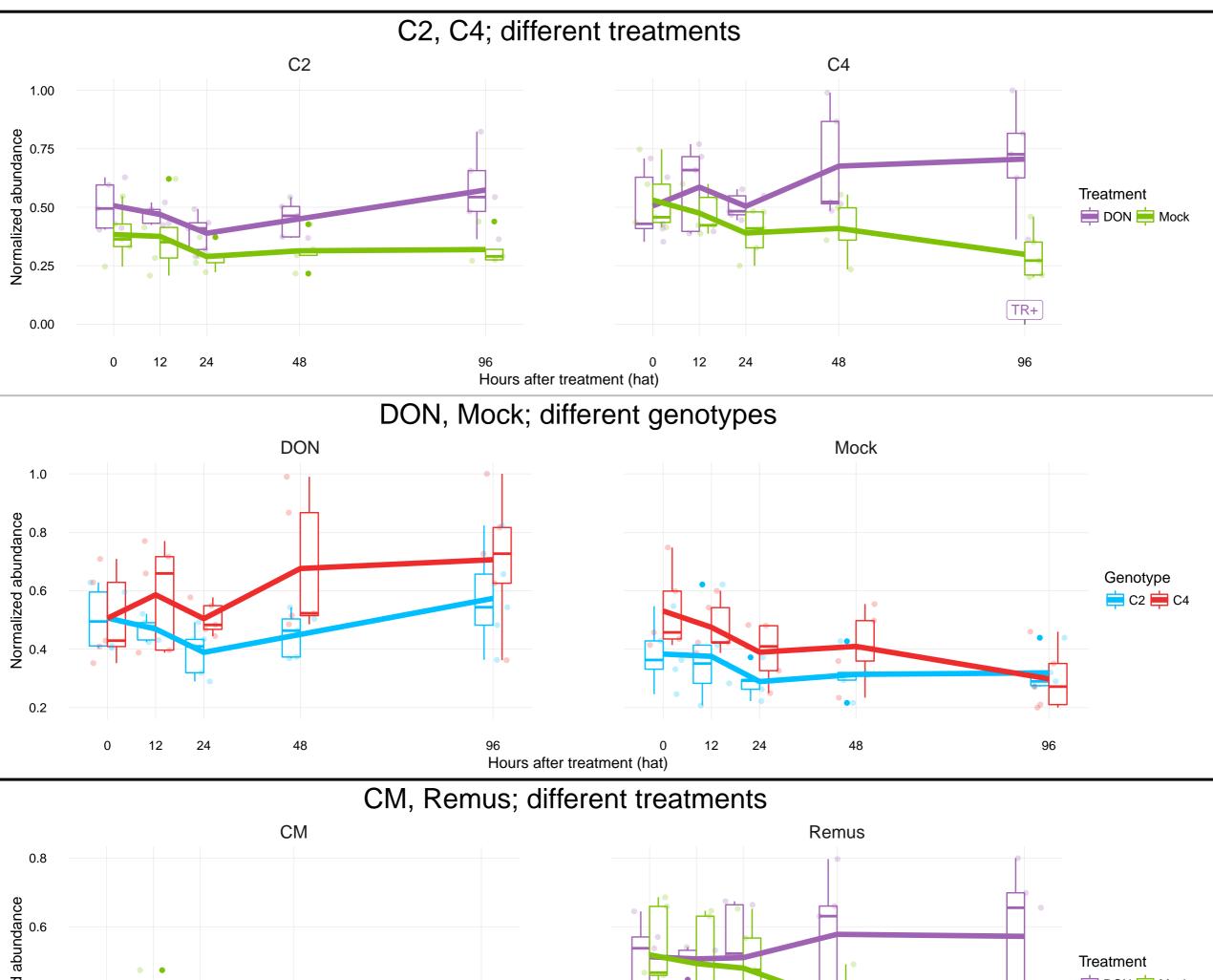
DON, Mock; all four genotypes

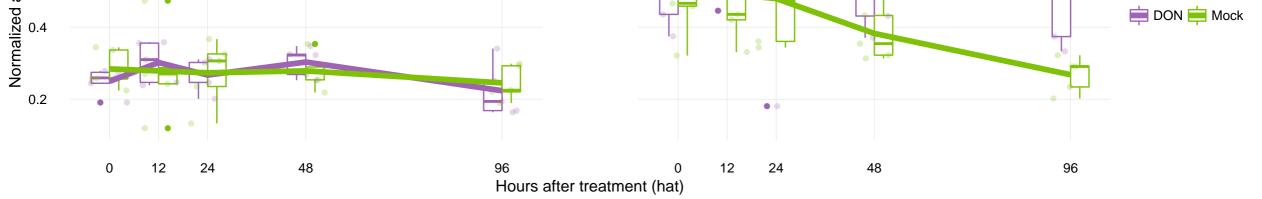


Trimethyltricetin

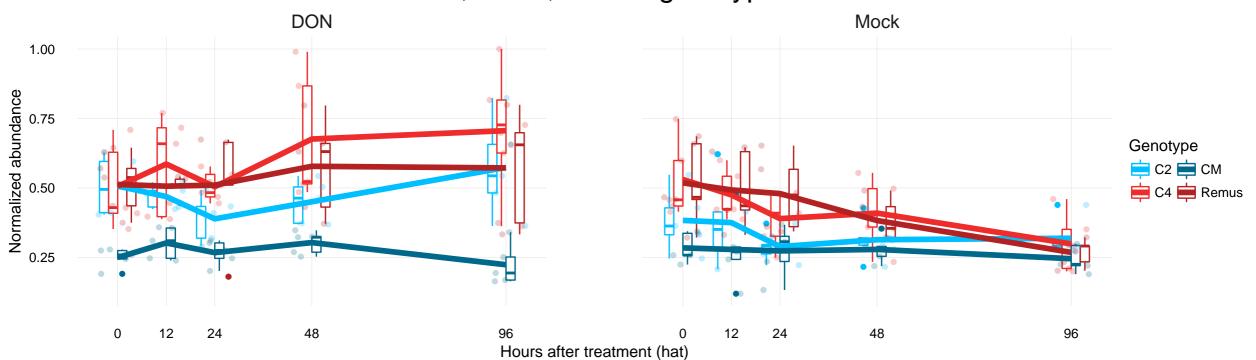
Identified metabolite (level 1)

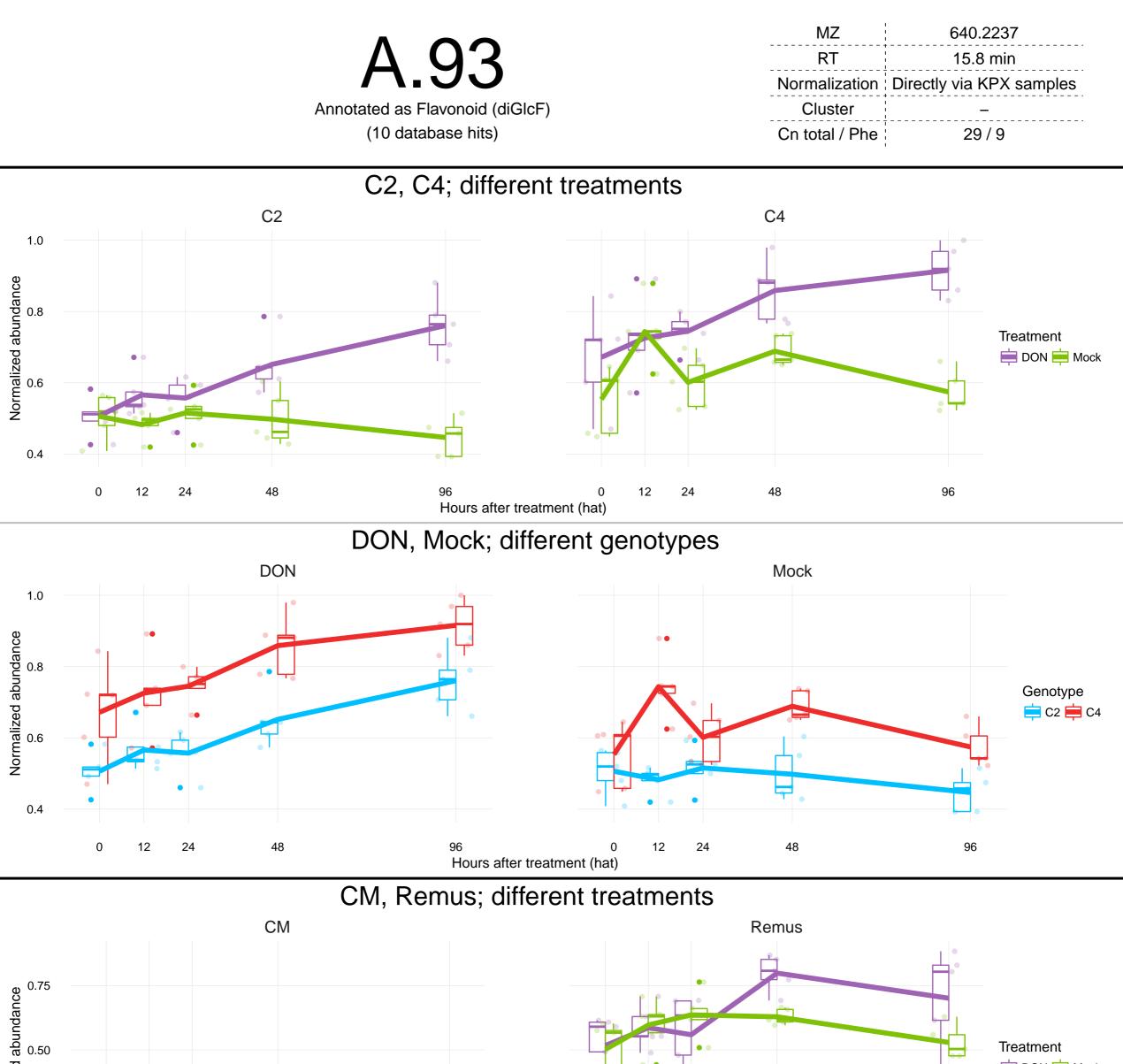
345.097
24.01 min
Directly via KPX samples
_
18 /

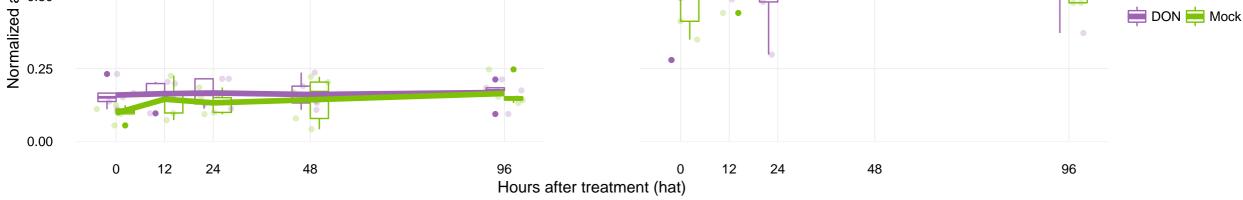




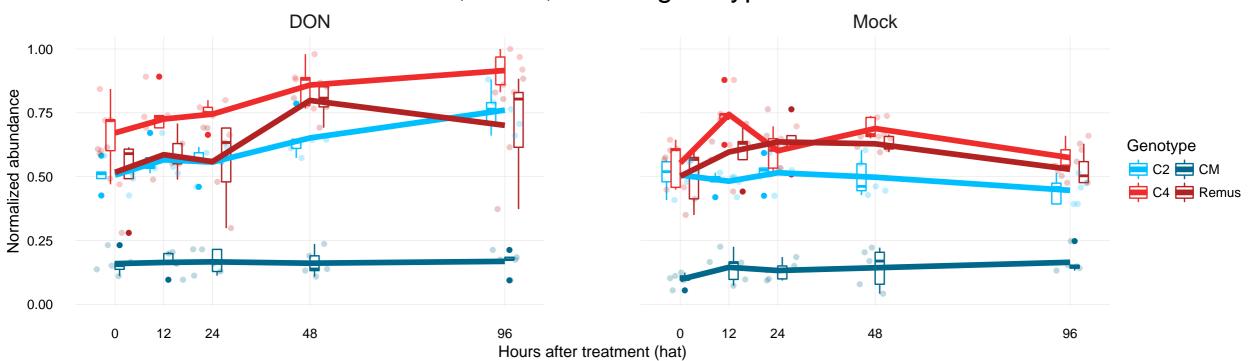
DON, Mock; all four genotypes

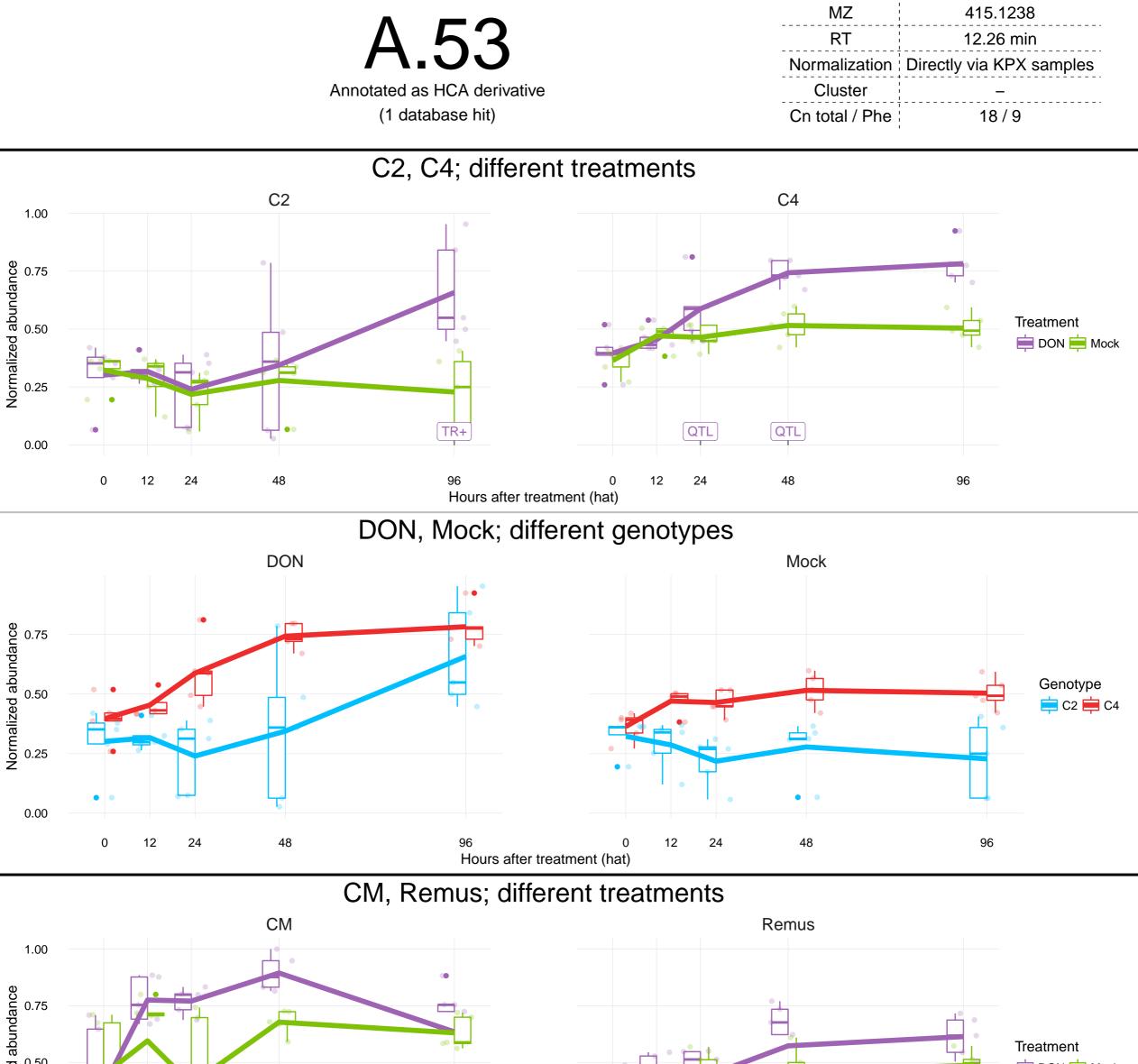


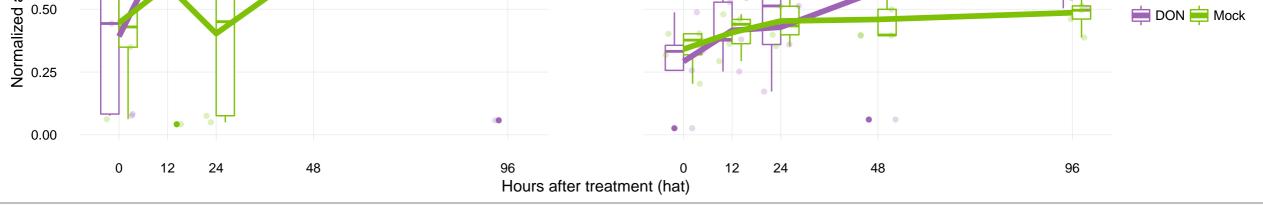




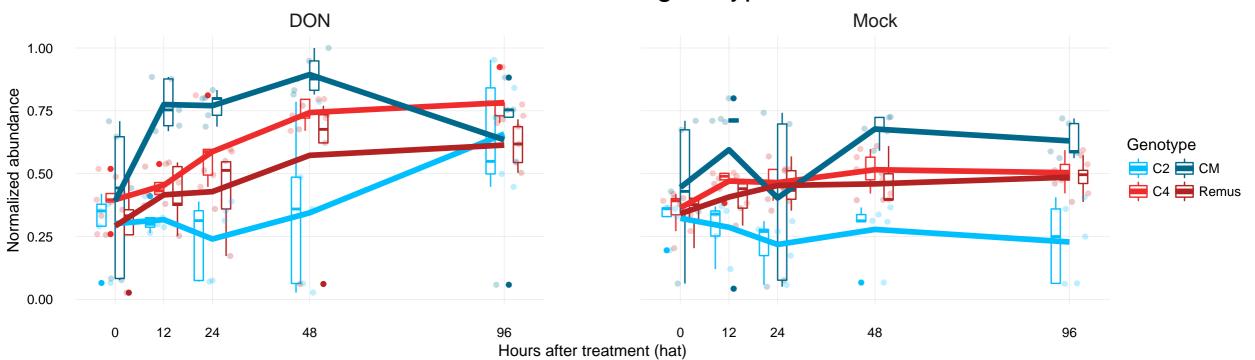
DON, Mock; all four genotypes

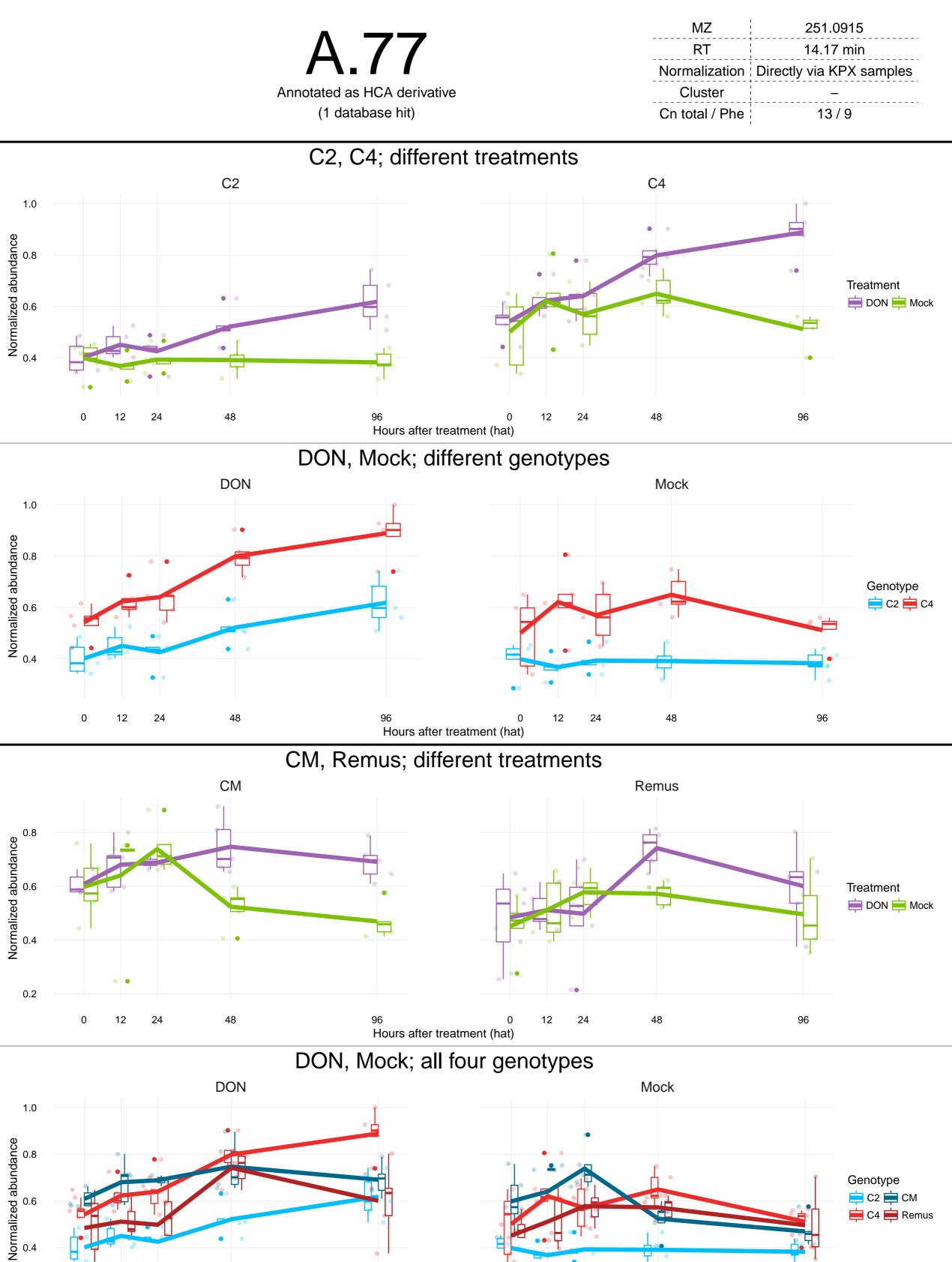


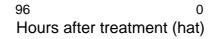




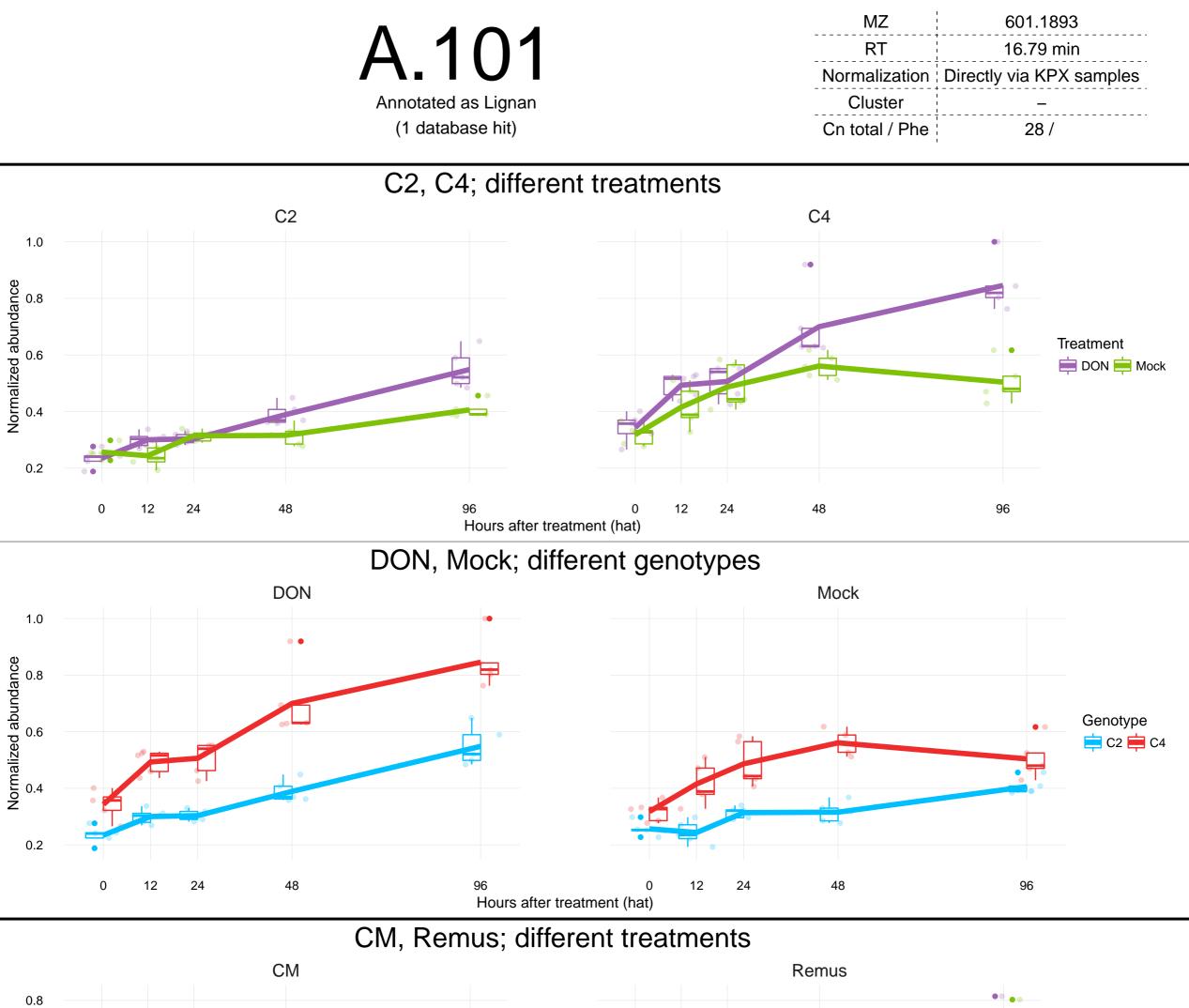
DON, Mock; all four genotypes

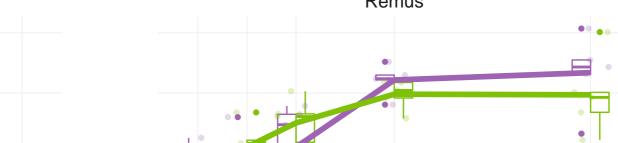


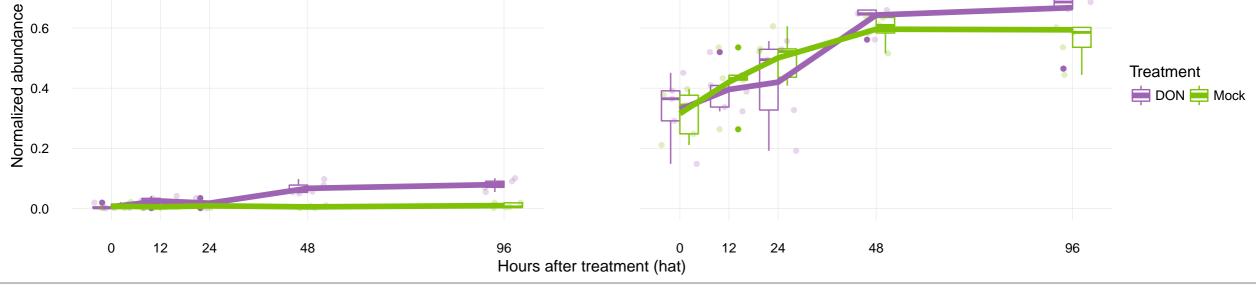




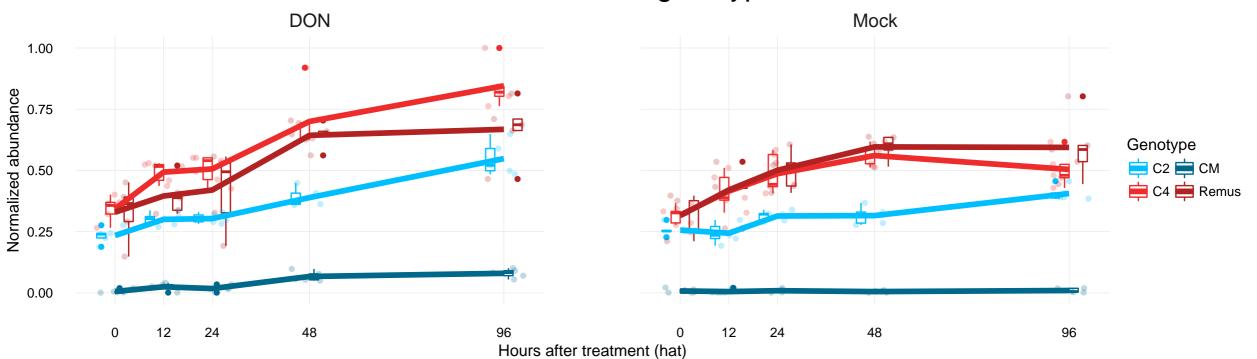
0.2

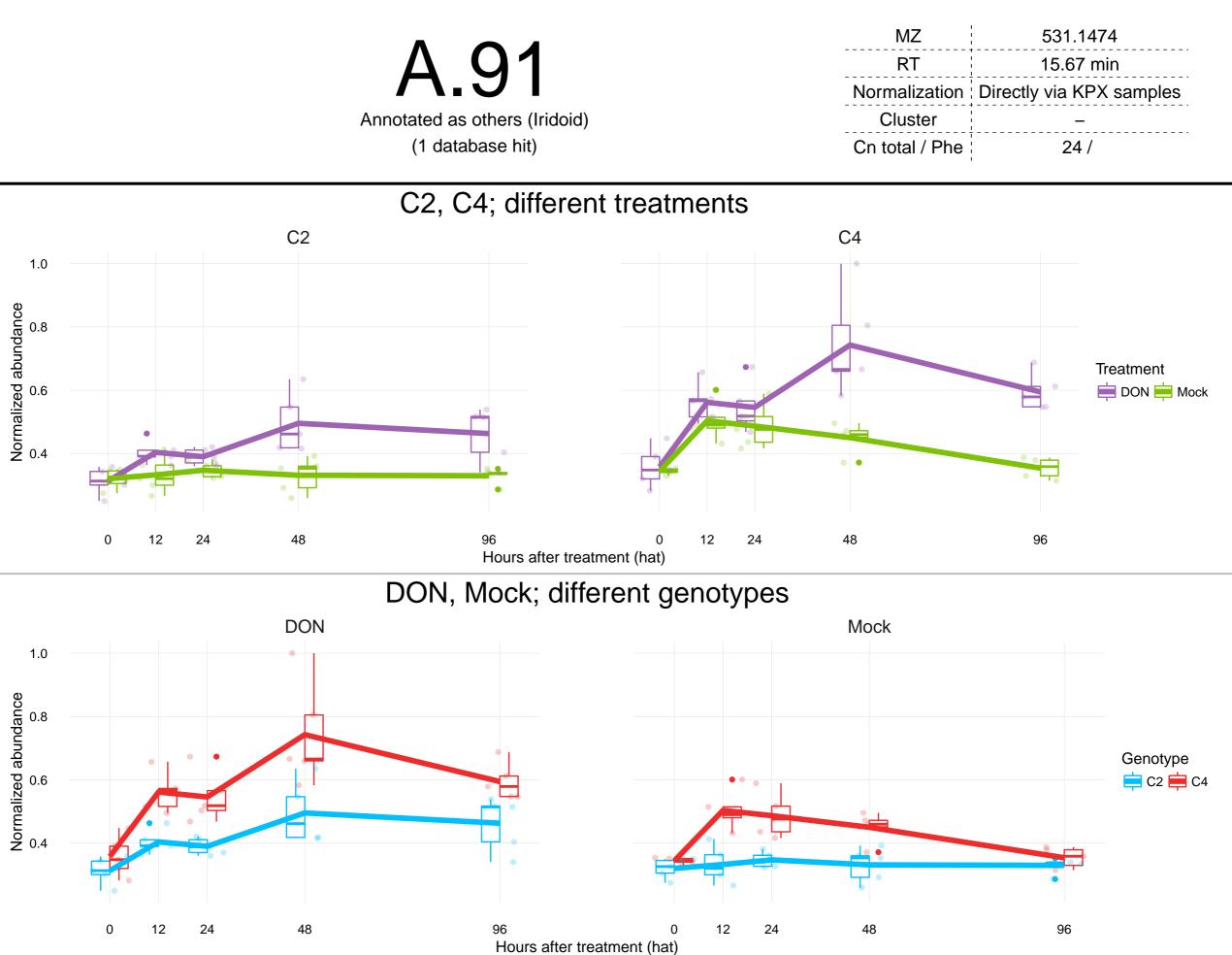




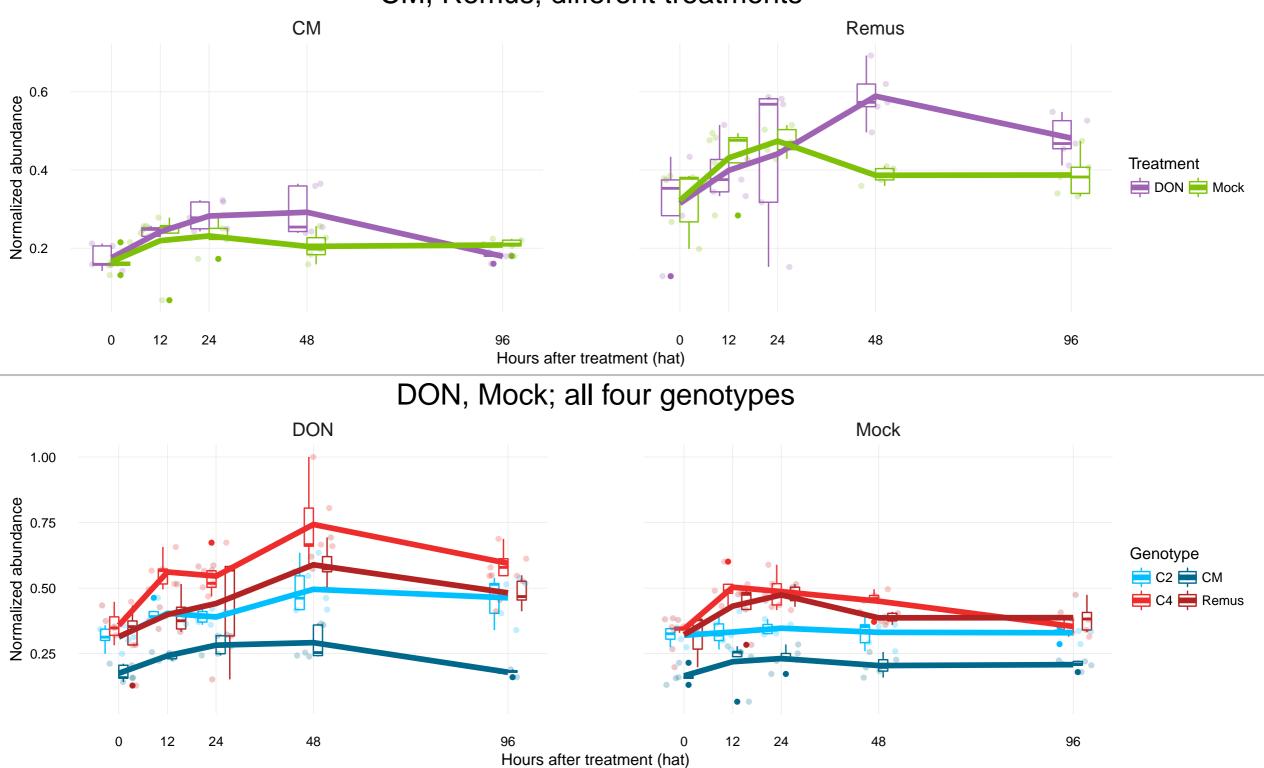


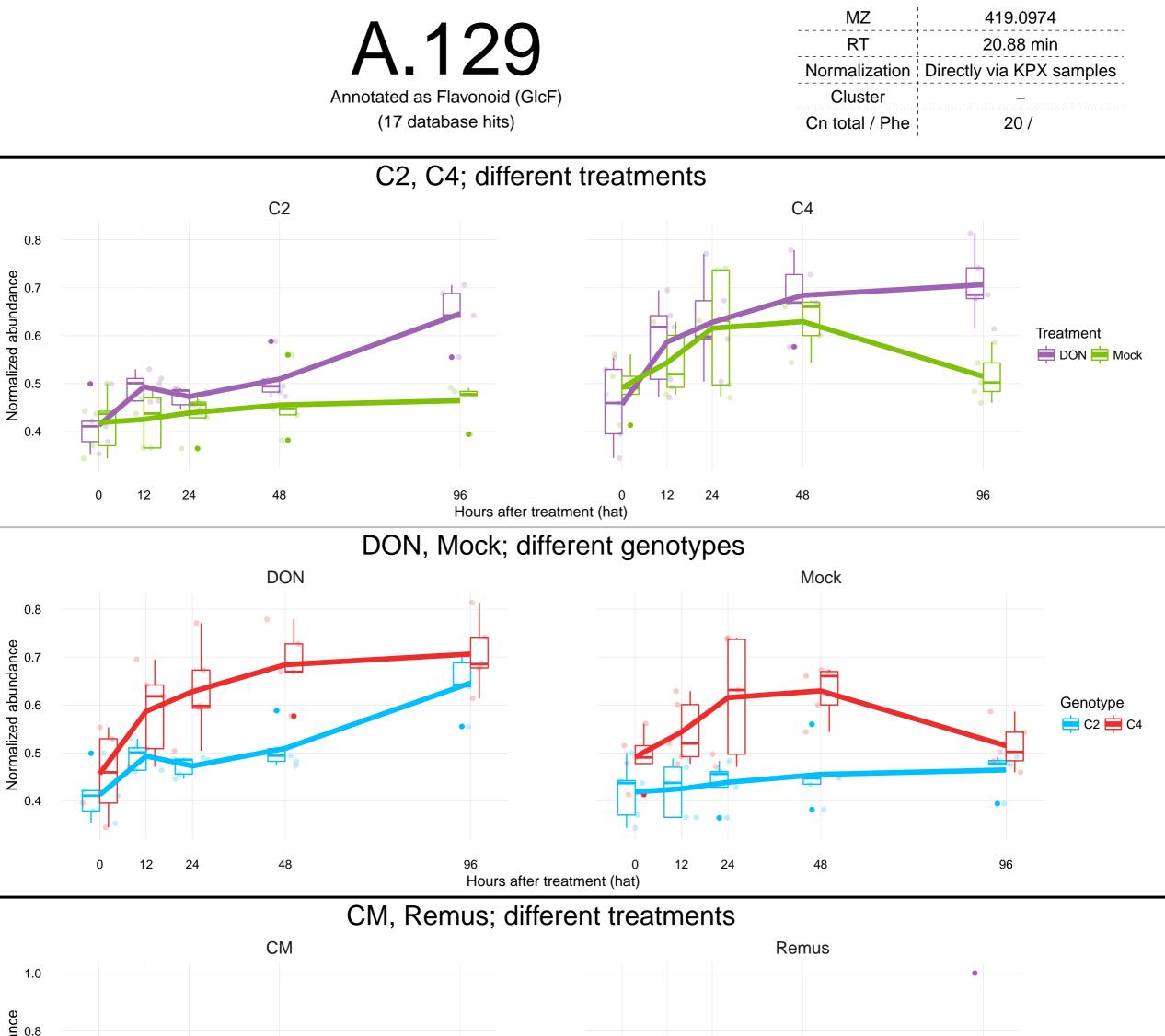
DON, Mock; all four genotypes

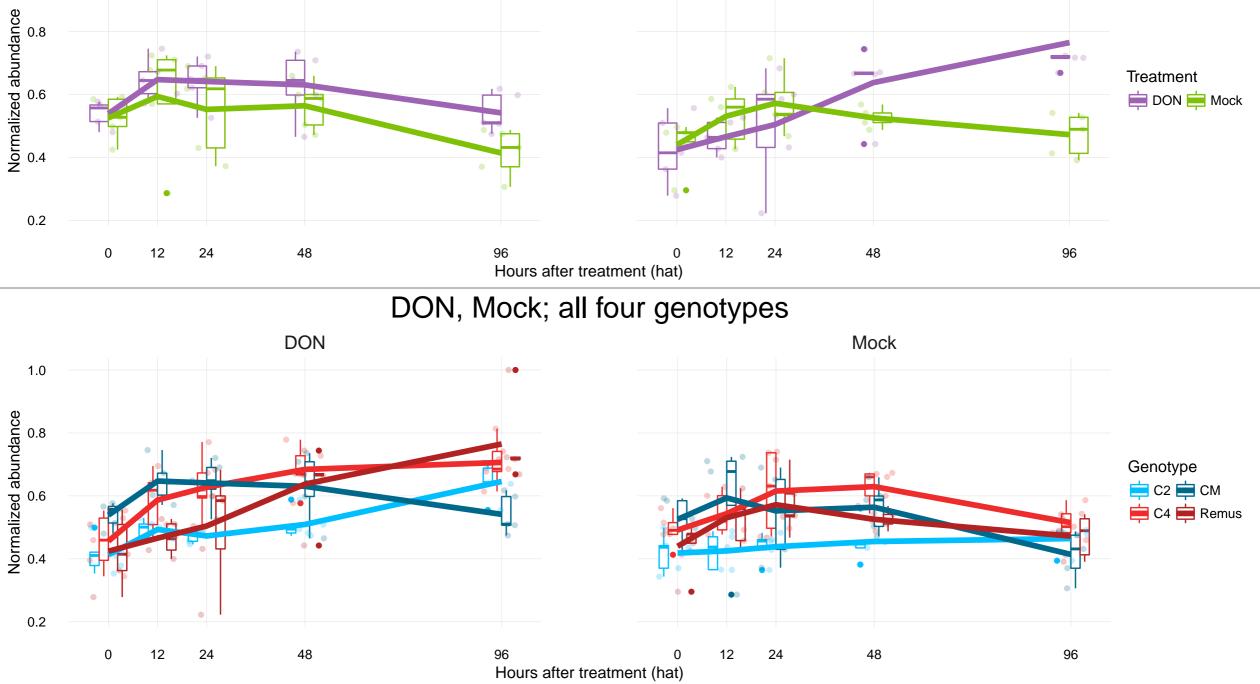


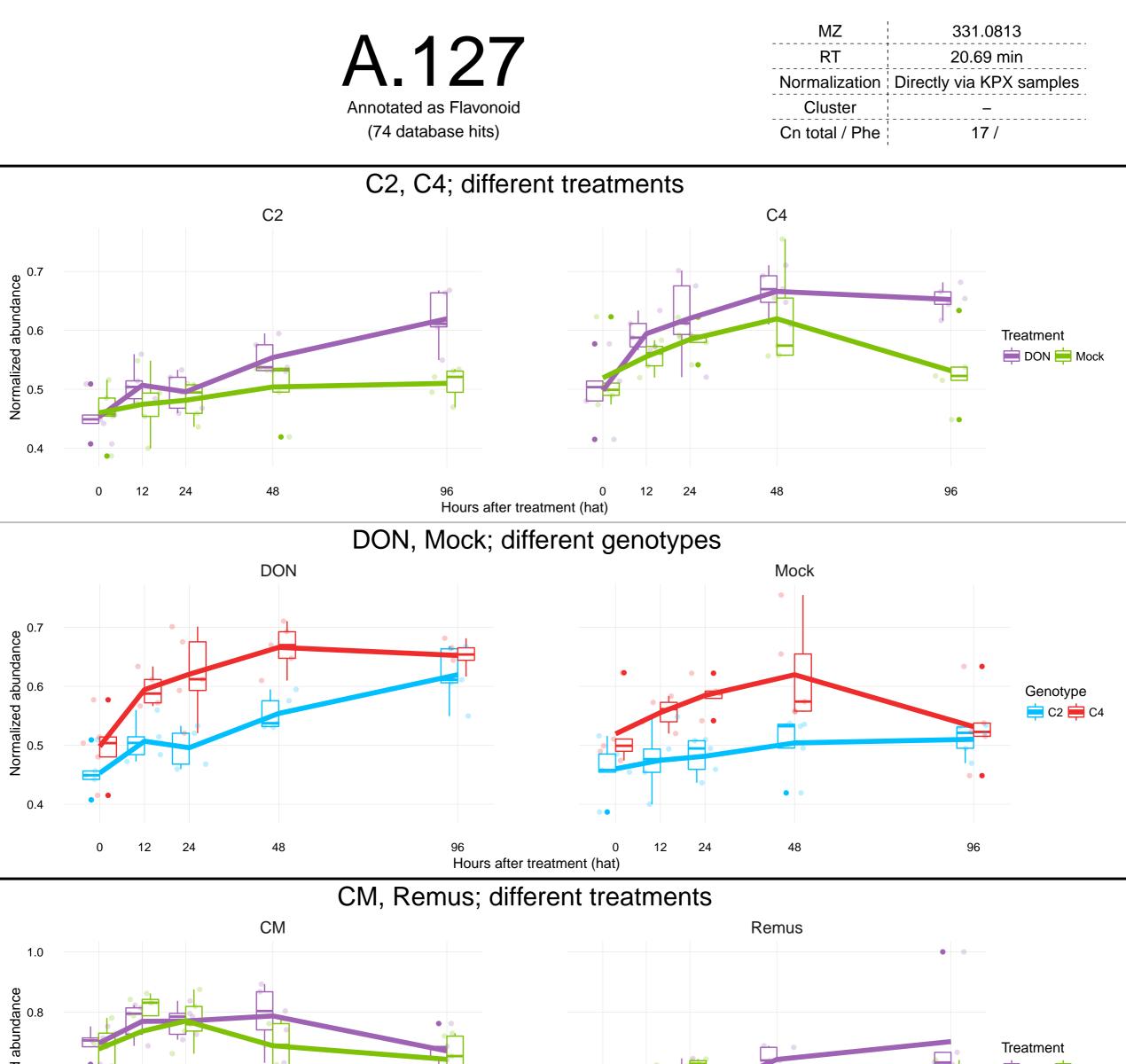


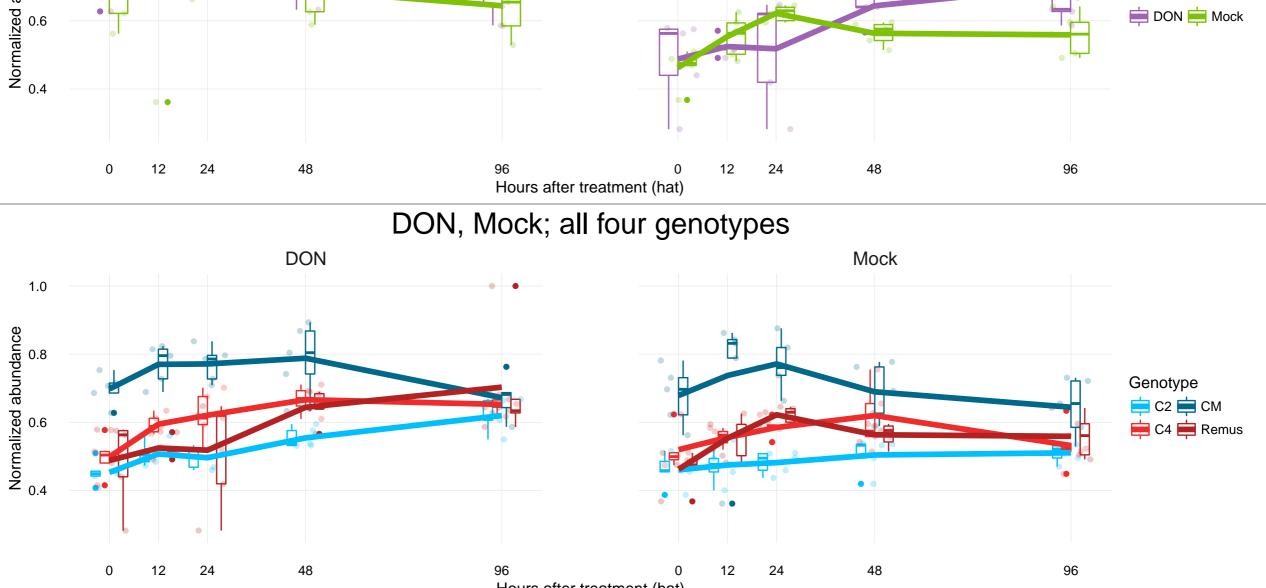
CM, Remus; different treatments

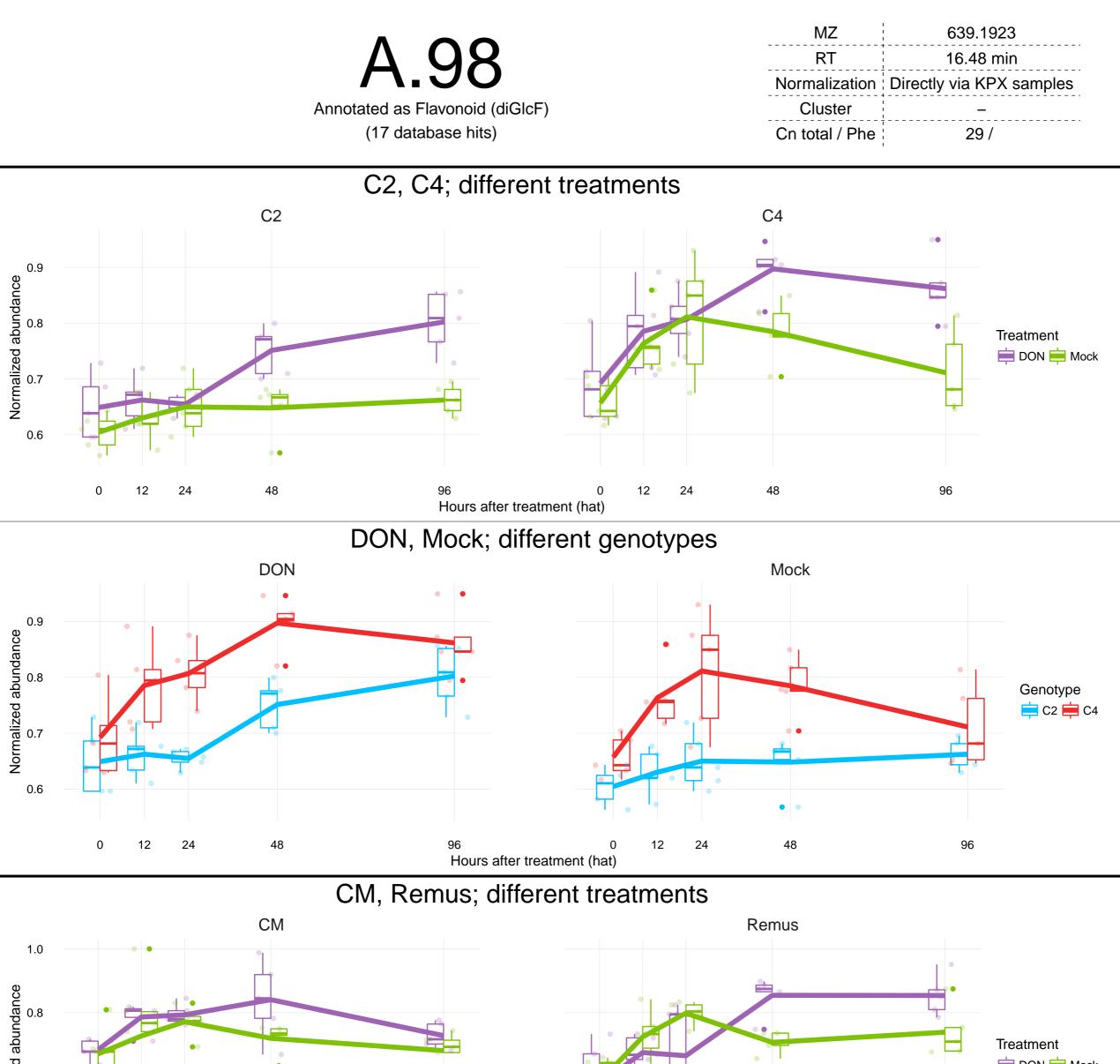


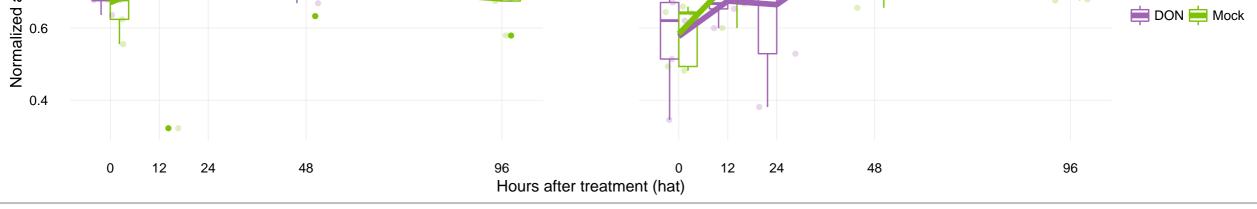




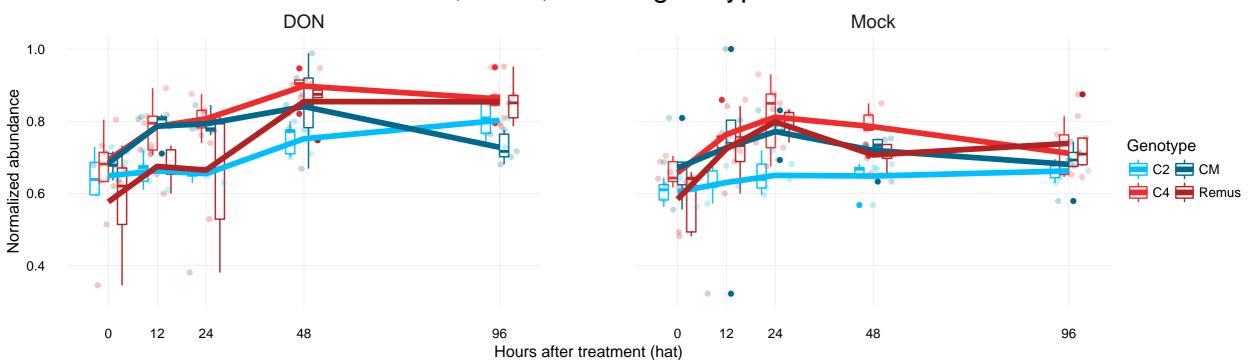


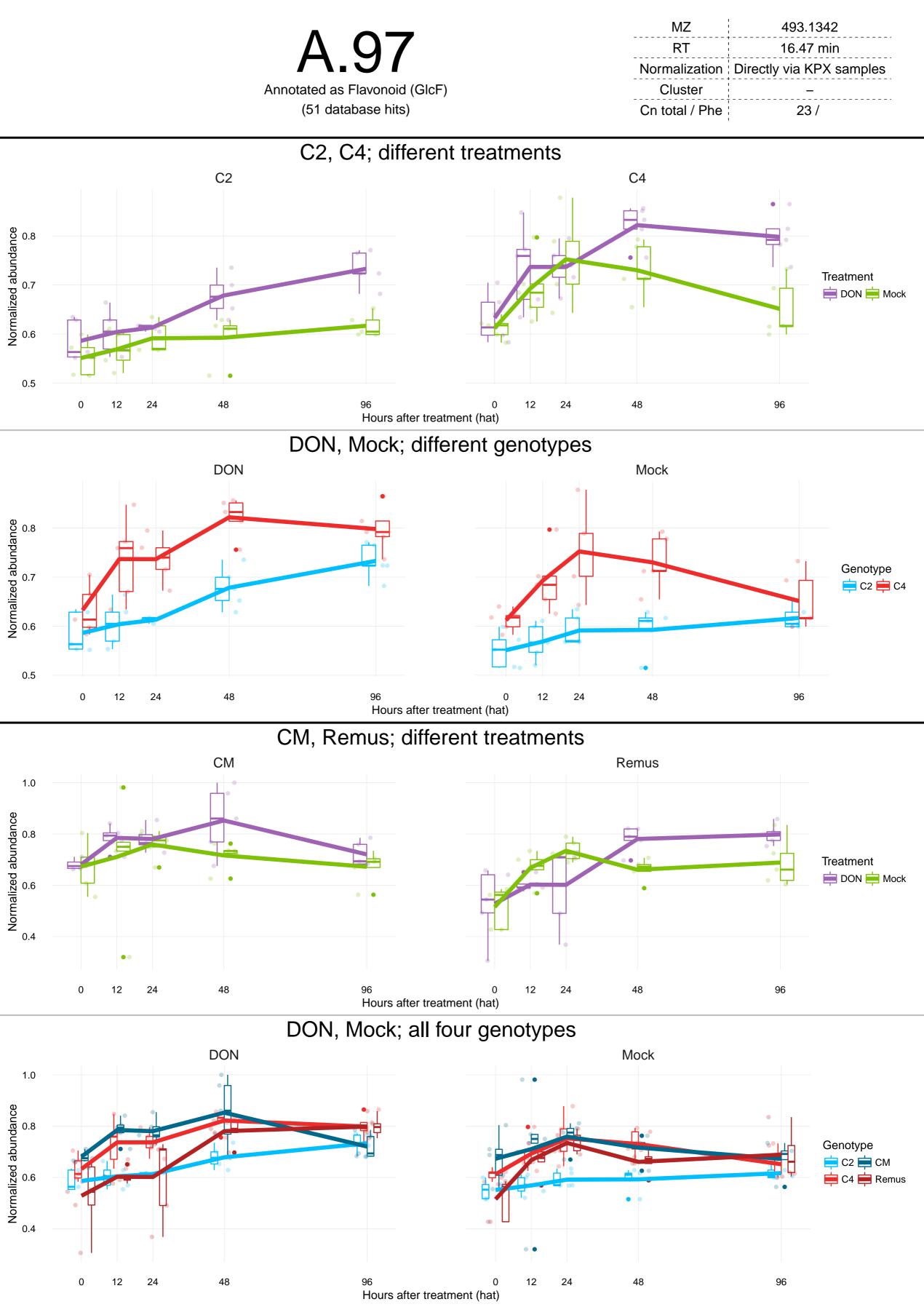


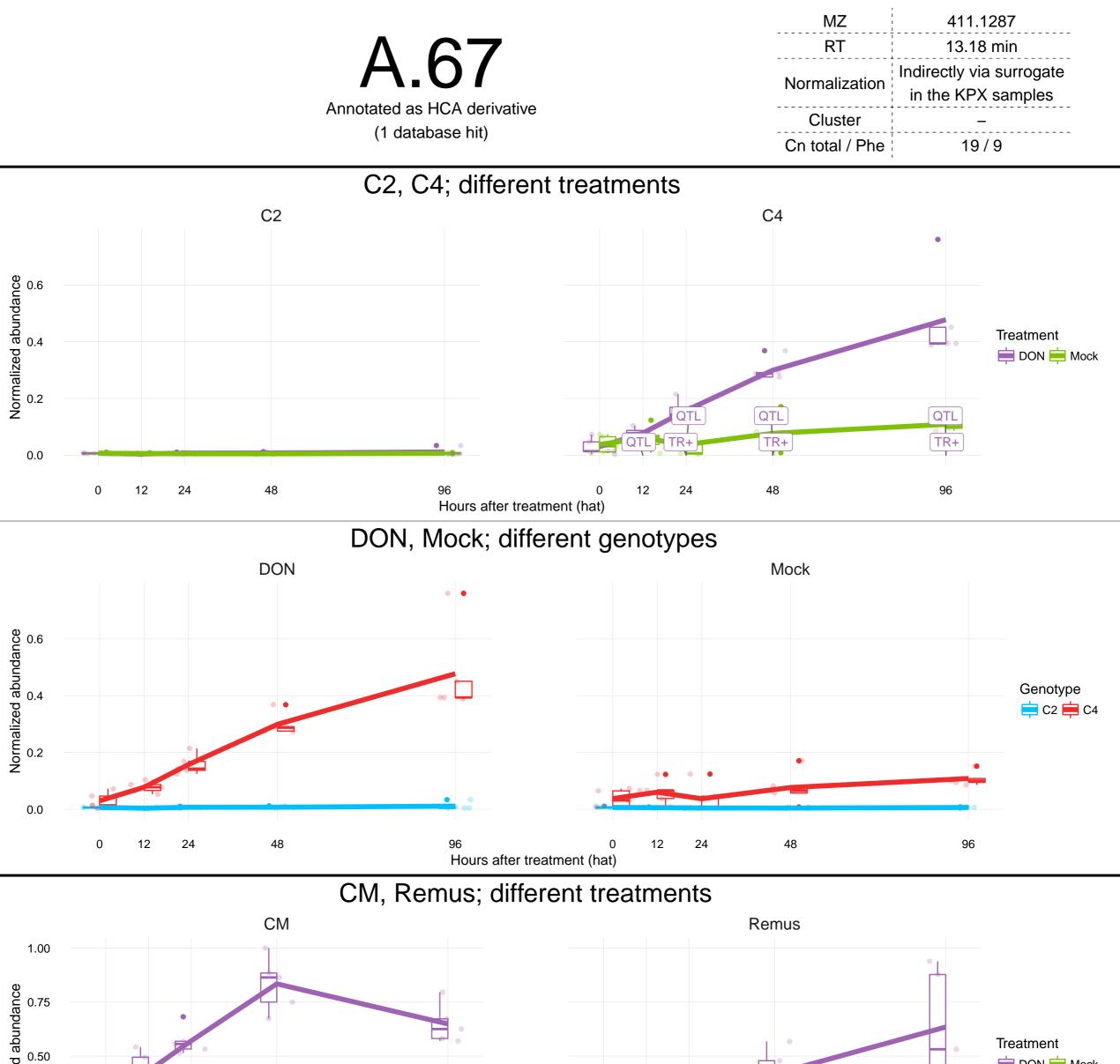


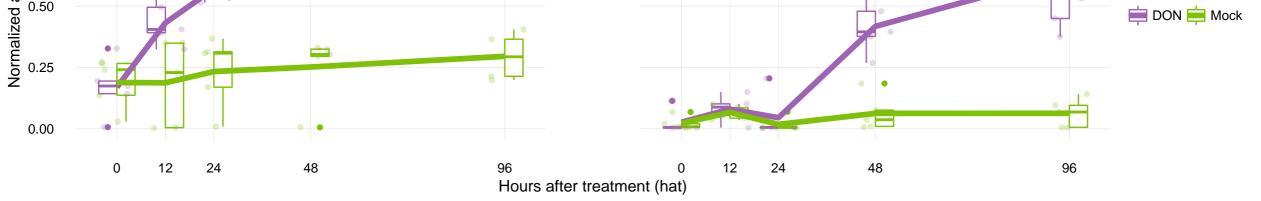


DON, Mock; all four genotypes

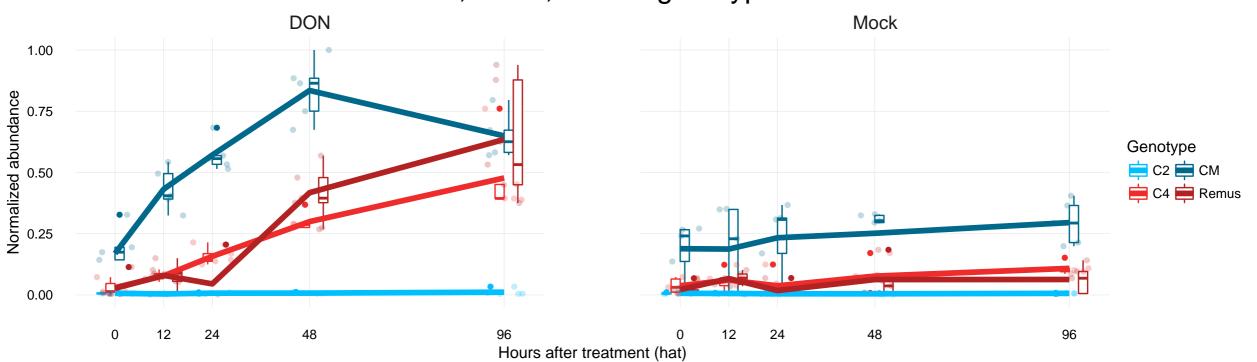


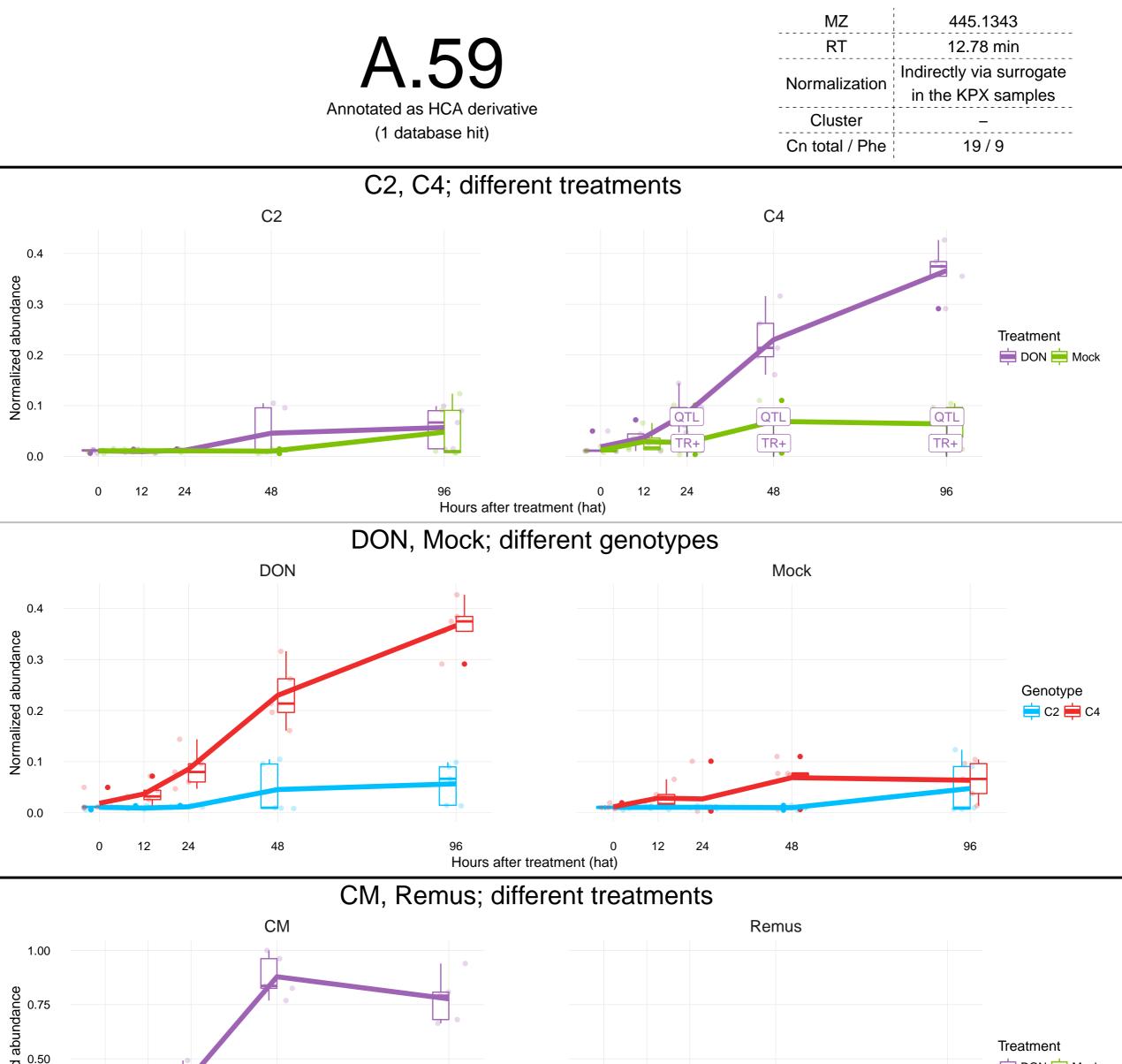


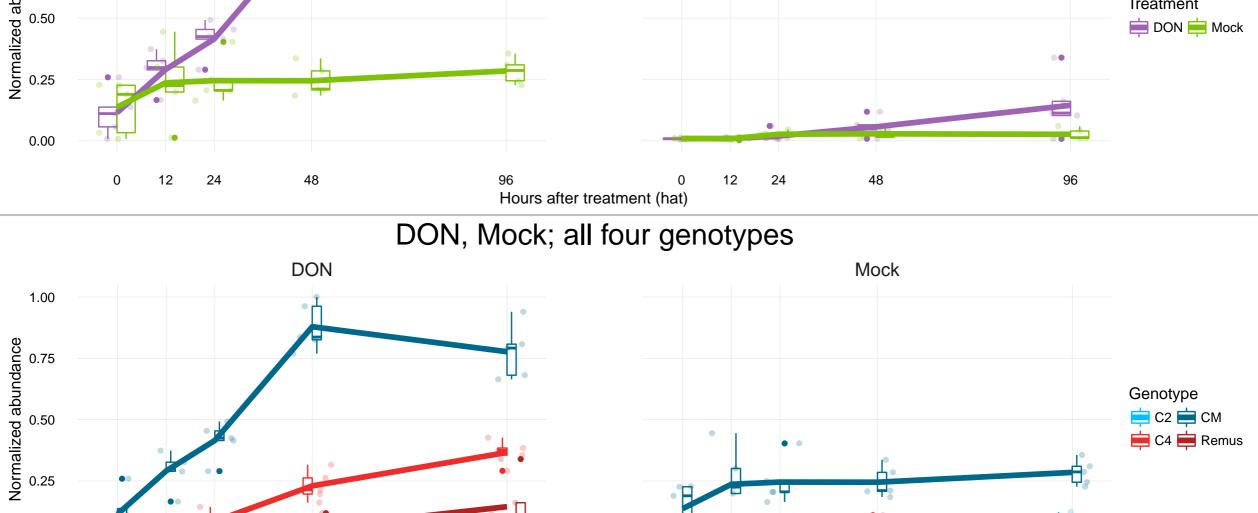


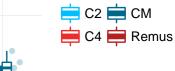


DON, Mock; all four genotypes

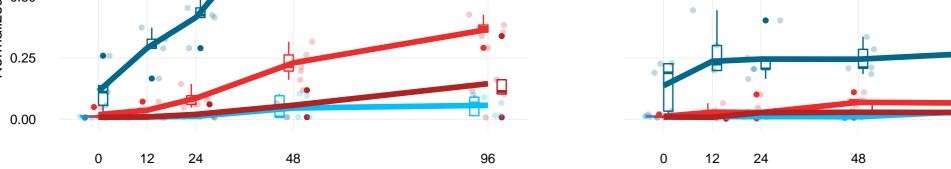








96



	A.74 Annotated as Lignan (2 database hits)	MZ RT Normalization Cluster Cn total / Phe	in the KPX samples
	C2, C4; differen	t treatments	
	C2	C4	
0.4 Outalized abundance 0.2 0.1 0.0		QTL QTL TR+	

96 0 12 24 Hours after treatment (hat)

48

96

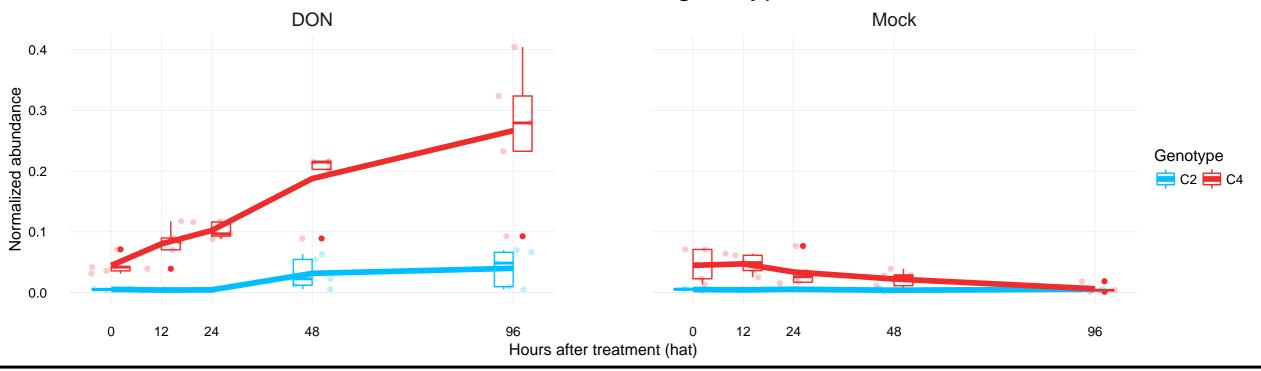
0.0

0

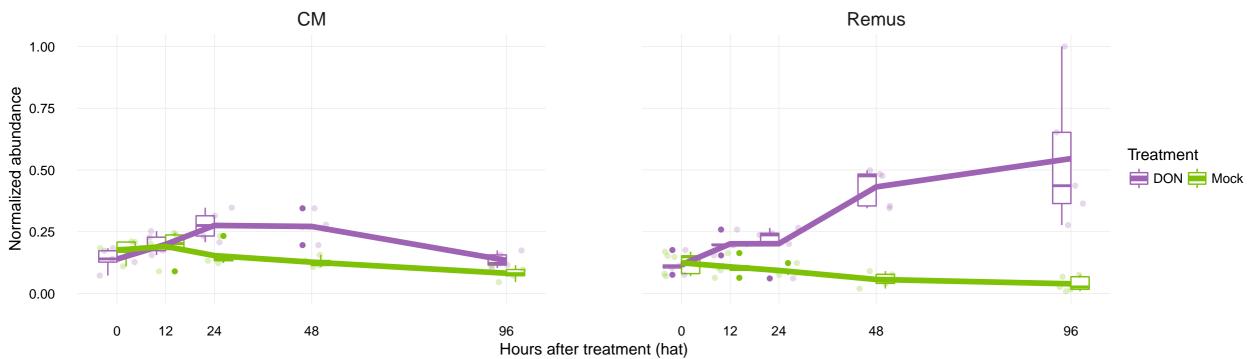
24

48

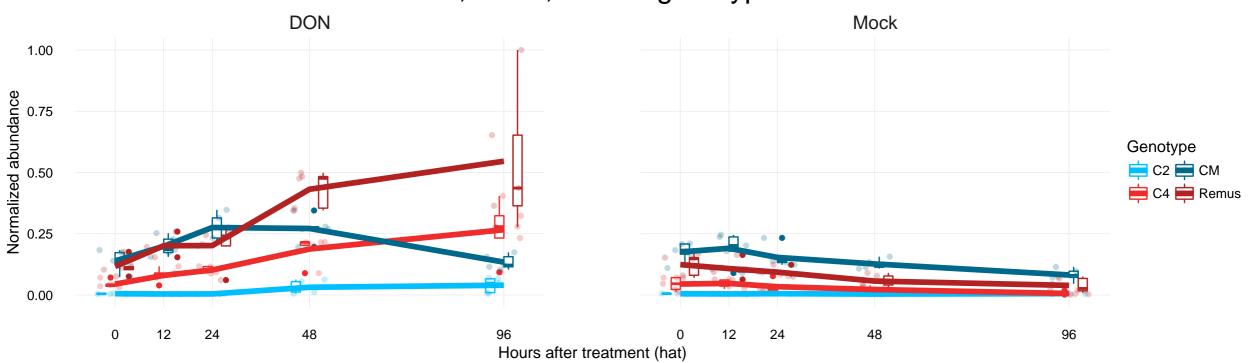
DON, Mock; different genotypes



CM, Remus; different treatments

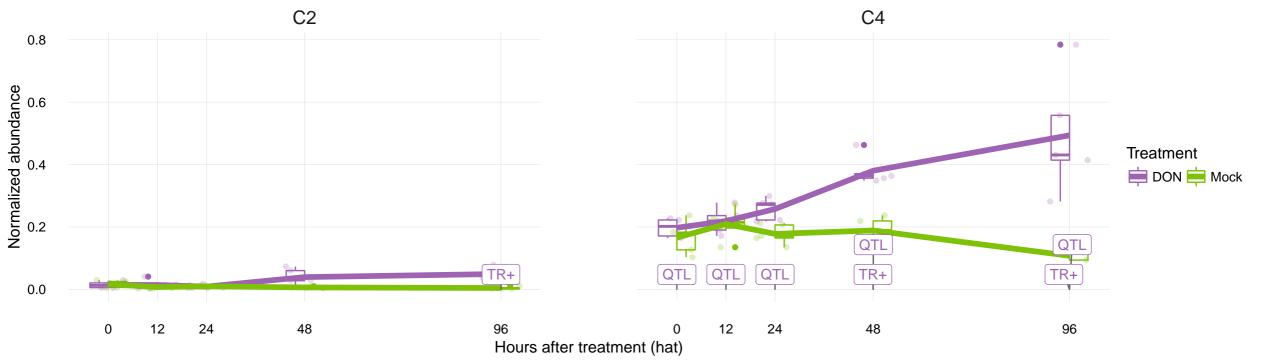


DON, Mock; all four genotypes

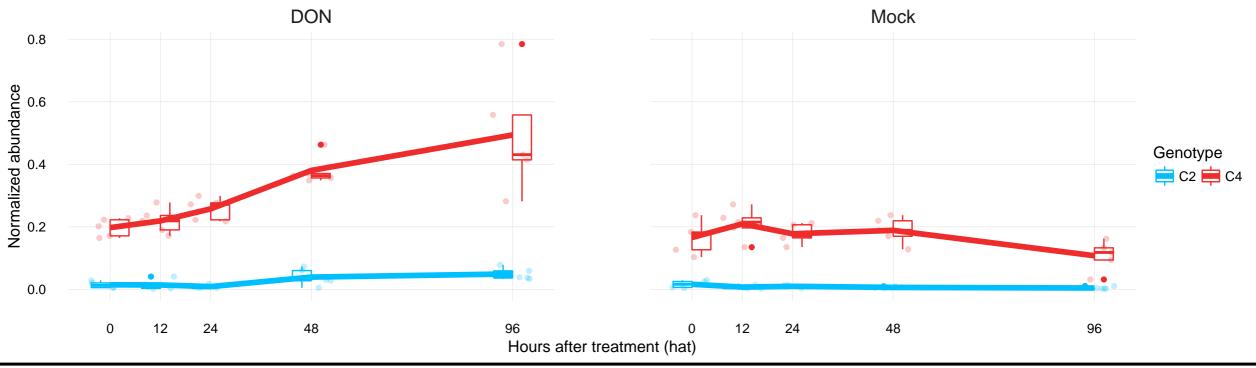


	MZ 540.2441
\wedge 70	RT 14.25 min
A.79	Normalization Indirectly via surrogate in the KPX samples
Annotated as Lignan (1 database hit)	Cluster –
(Tuatabase fiit)	Cn total / Phe 26 / 18

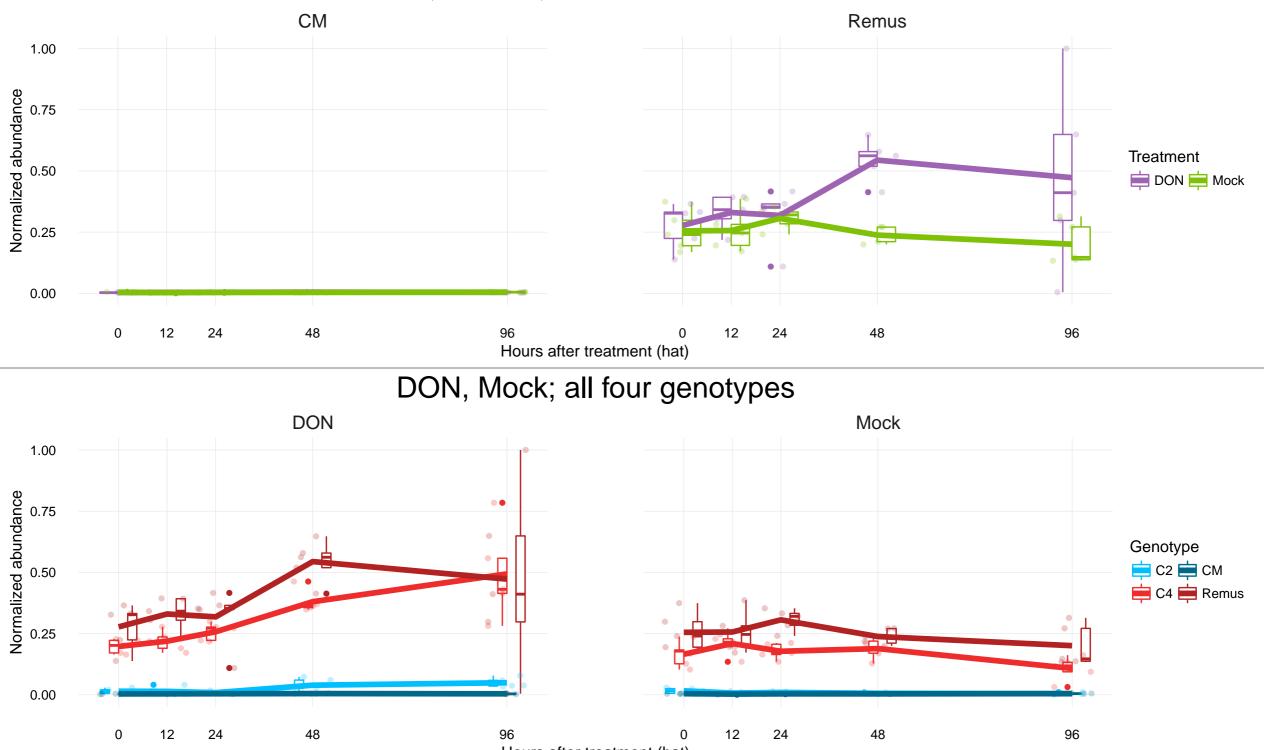




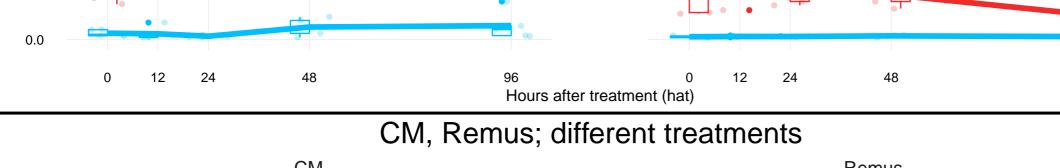
DON, Mock; different genotypes

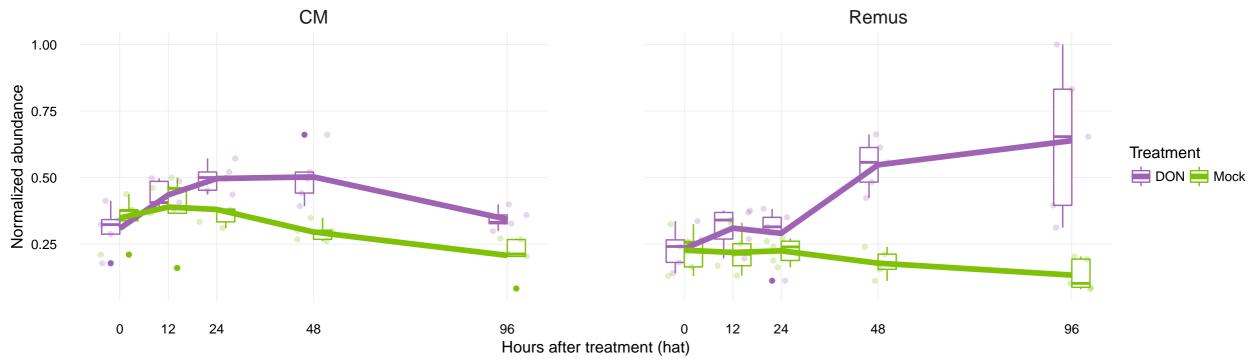


CM, Remus; different treatments

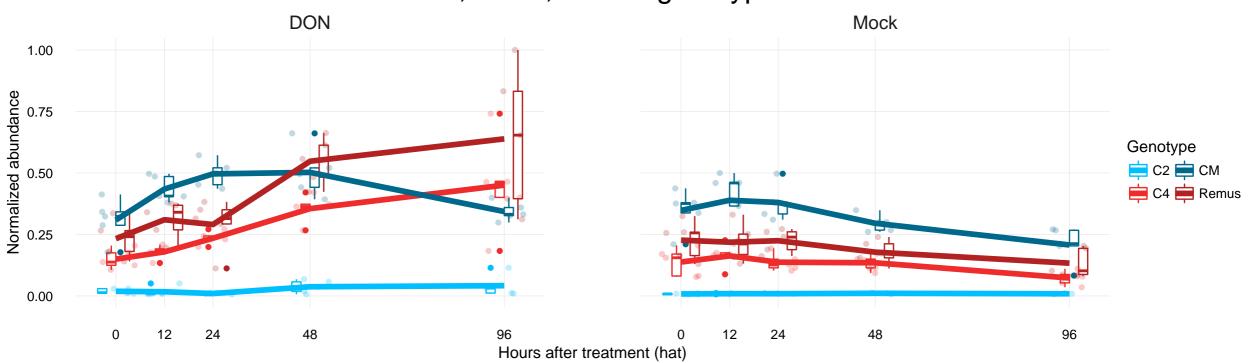


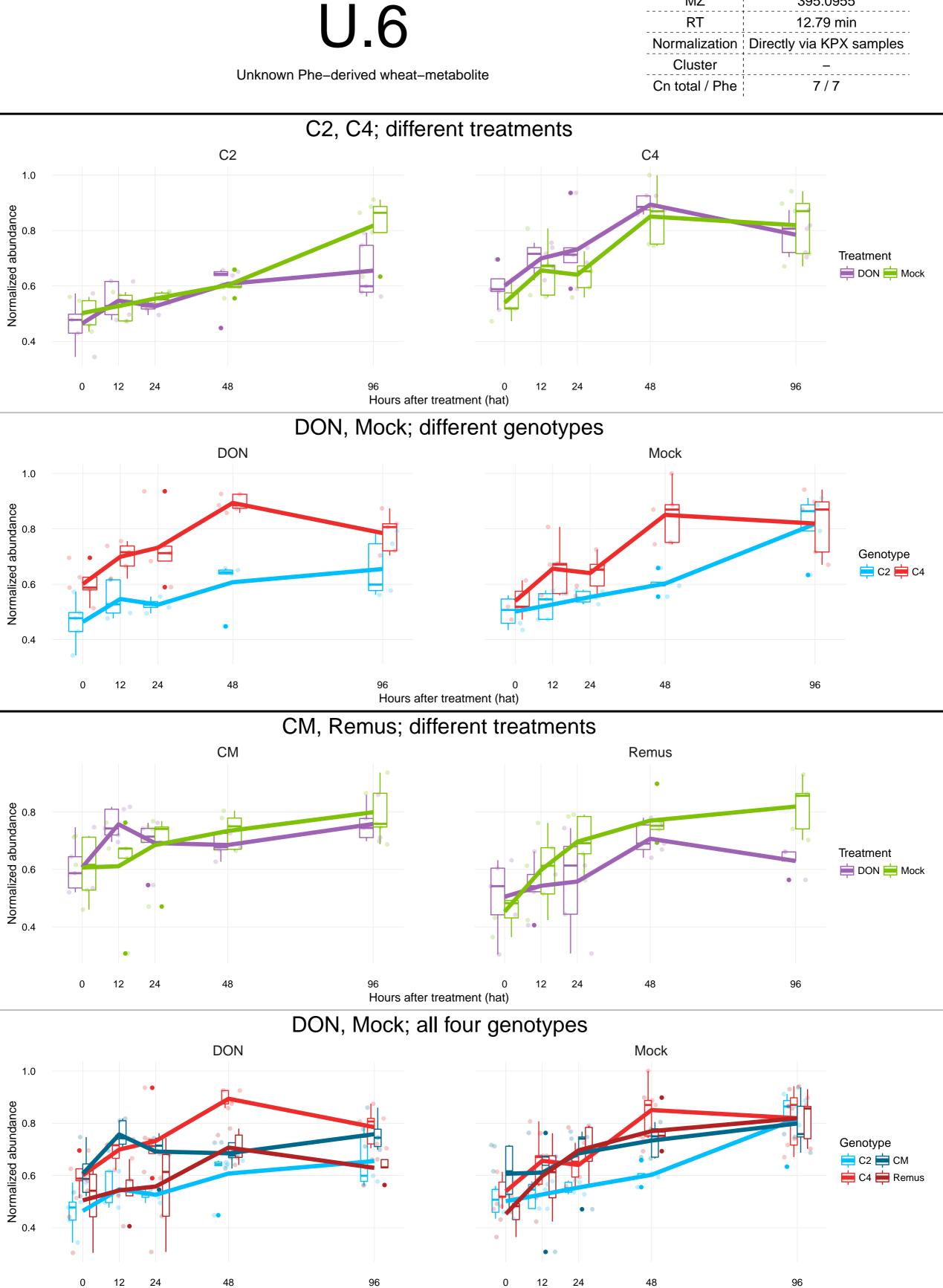
					MZ	÷	.2392
			4.43		RT Normalization	Indirectly v	19 min /ia surrogate PX samples
		Annotated as Lignan (1 database hit)			Cluster		
					Cn total / Phe	∠0	5/18
		(C2, C4; differe	nt treatments			
		C2			C4		
ወሳፍ						••	
9.0 abundance 7.0 br.0 br.0 br.0 br.0 br.0 br.0 br.0 br							
de 0.4				• •			Treatment
0.2 Norma		_ <u>_</u>	•			QTL (TR+)	
0.0							
	0 12 24	48	⁹⁶ Hours after tre	0 12 24 atment (hat)	48	96	
		D	ON, Mock; dif	ferent genotypes			
		DON	•		Mock		
6.0 e							
Normalized abundance 7.0 7.0 7.0		••					Genotype 럹 C2 🚔 C4
ormaliz		• •	• •		• 1		
Z			••			•	





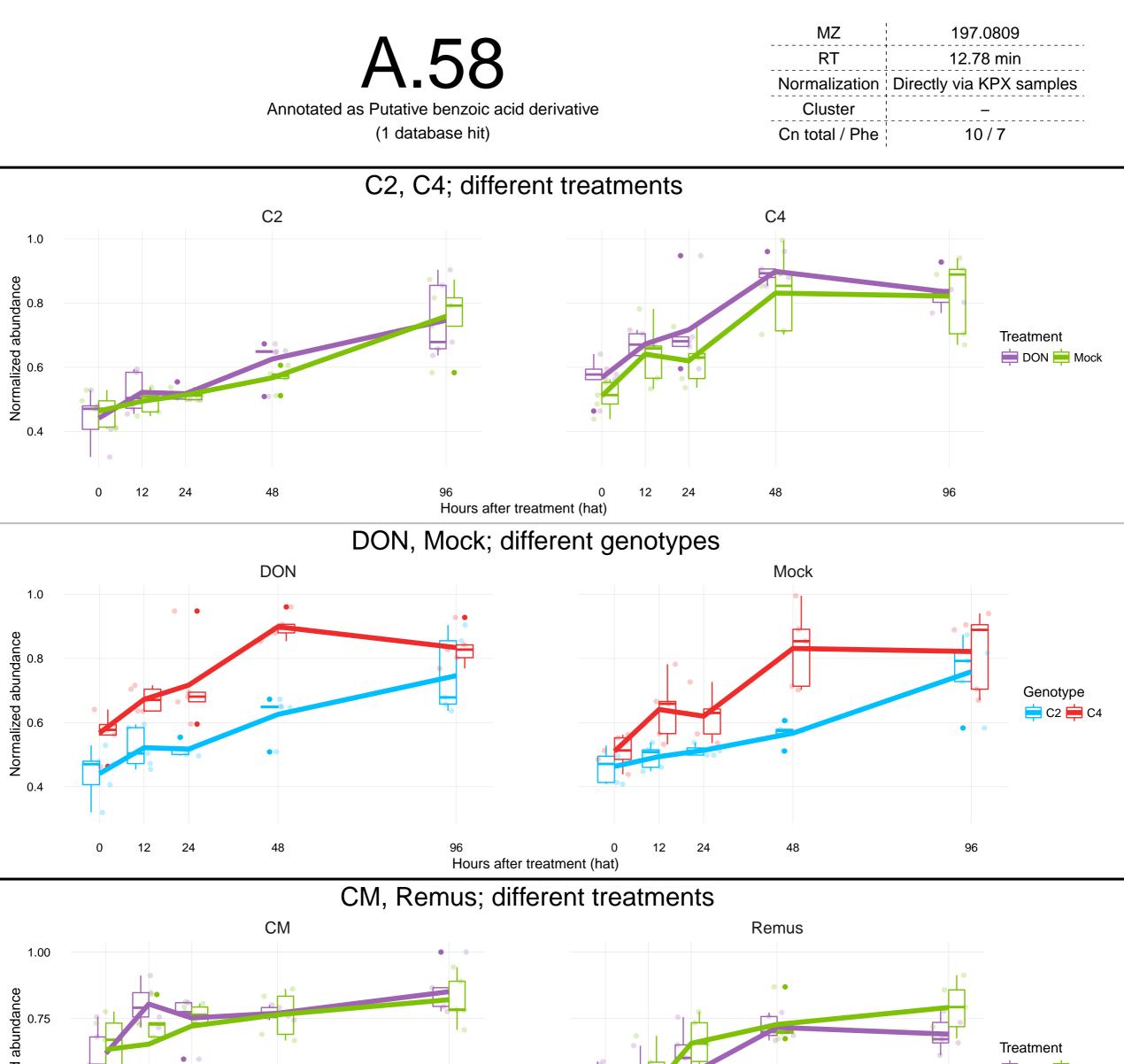
DON, Mock; all four genotypes

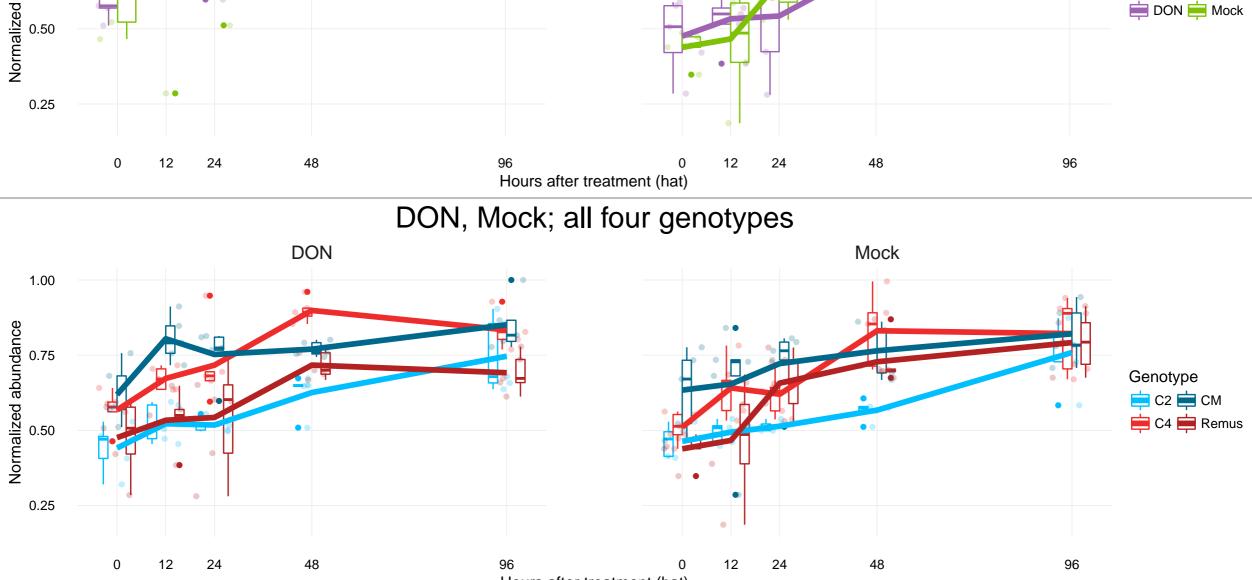


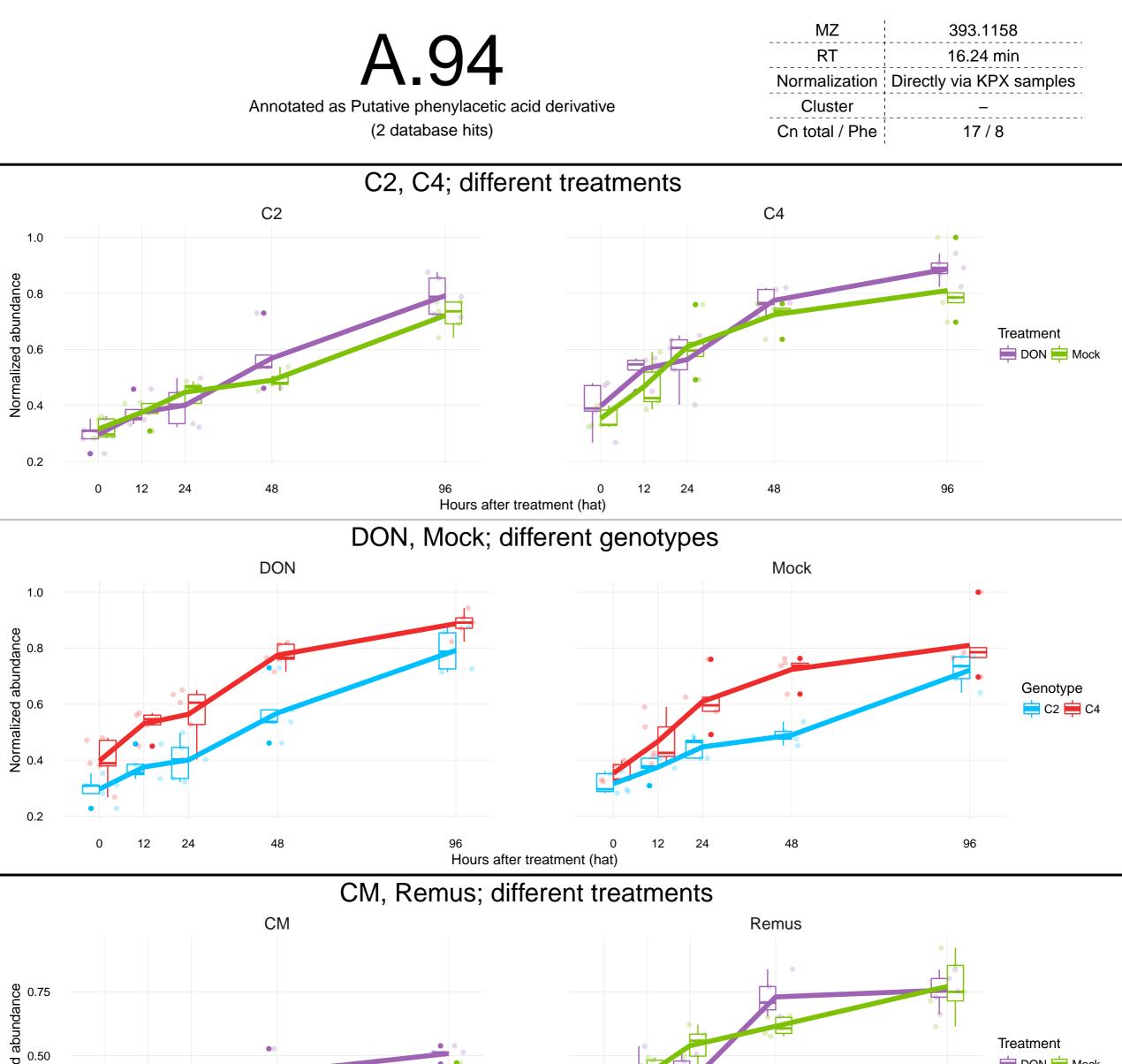


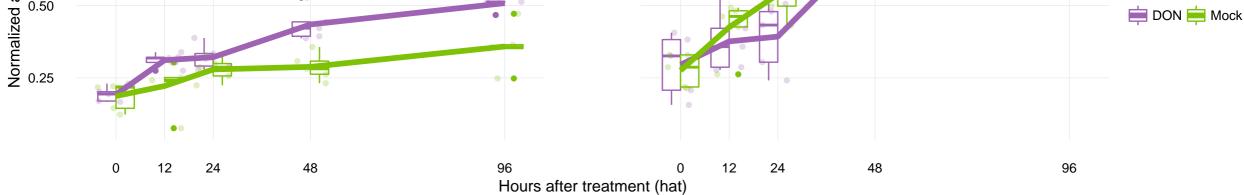
ΜZ

395.0955

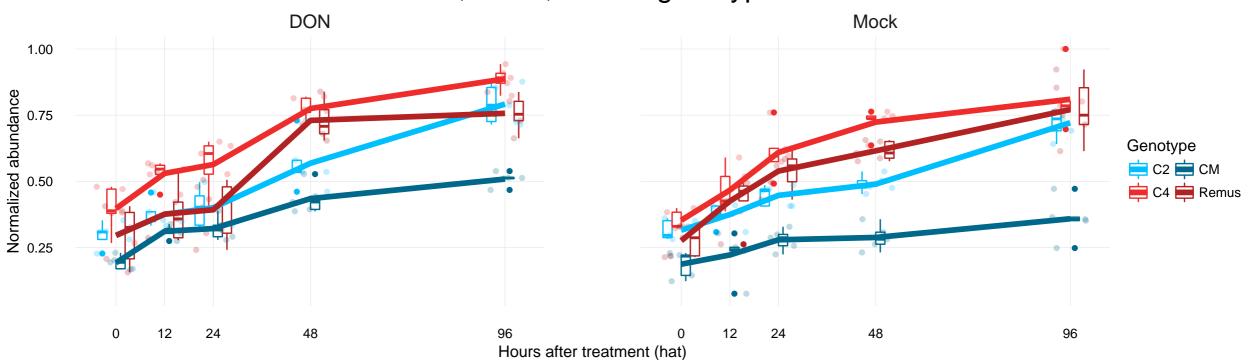


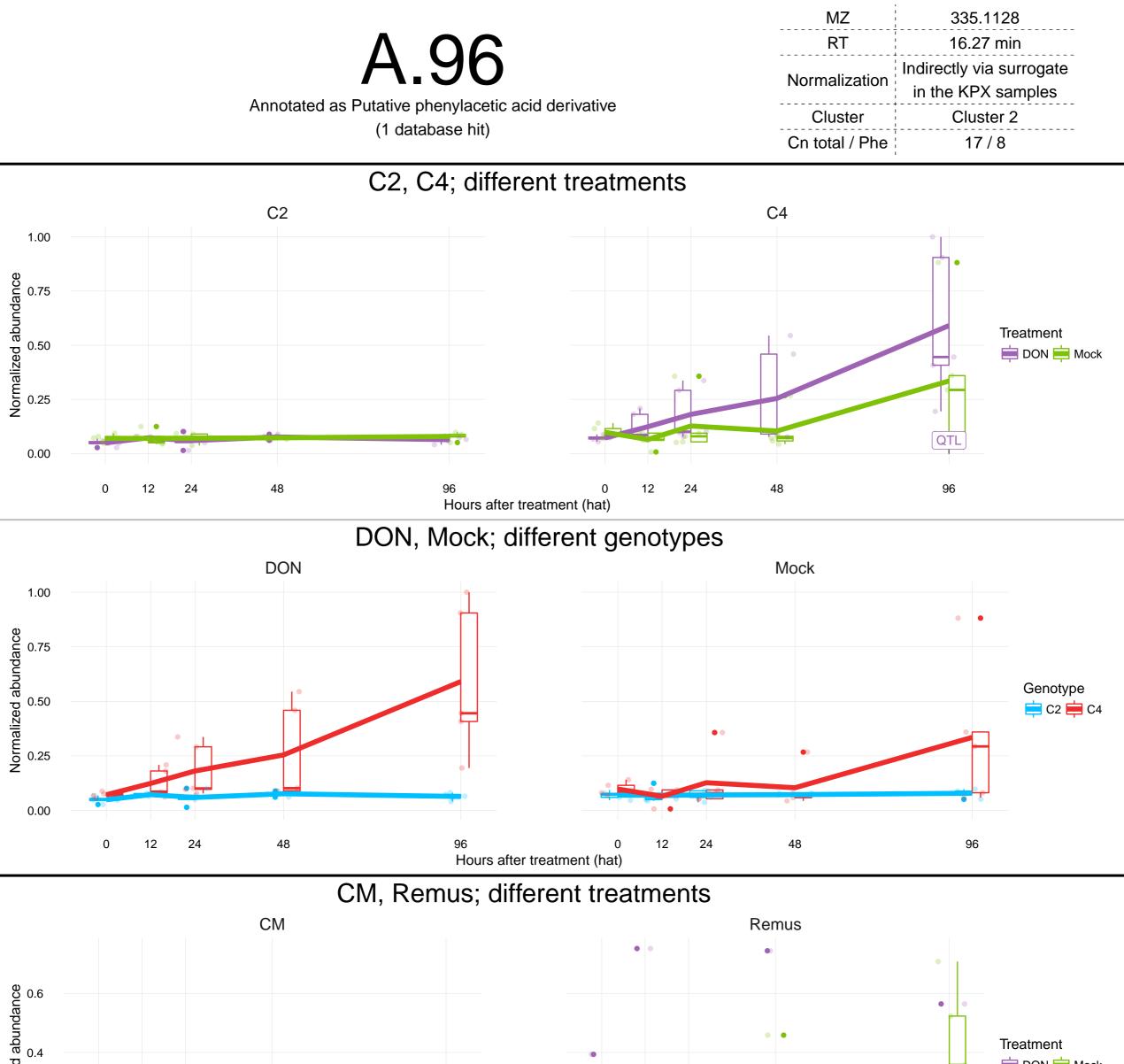


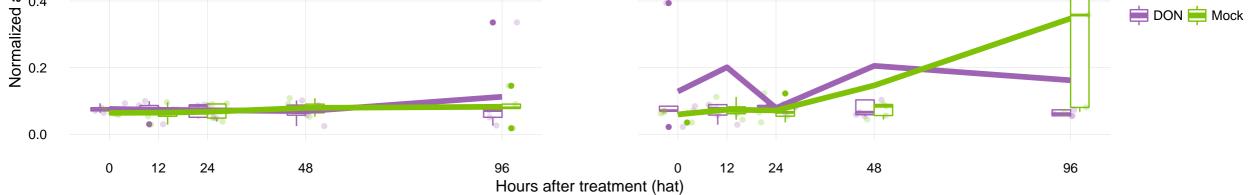




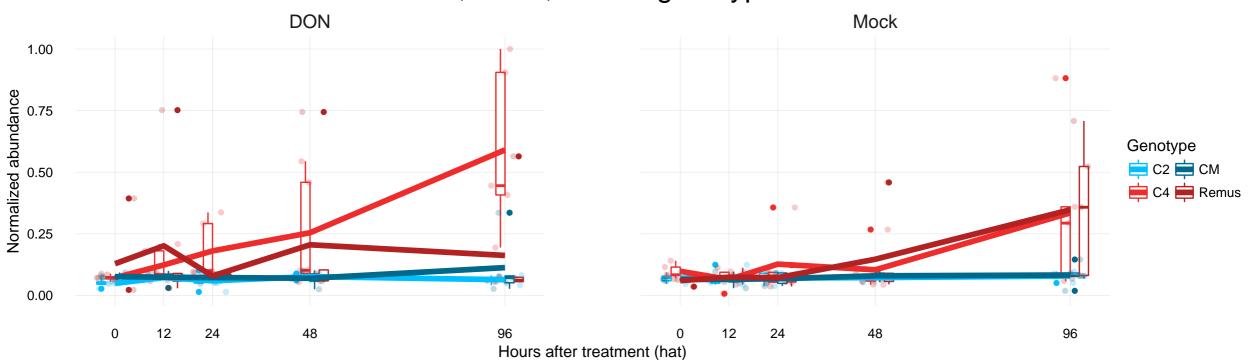
DON, Mock; all four genotypes



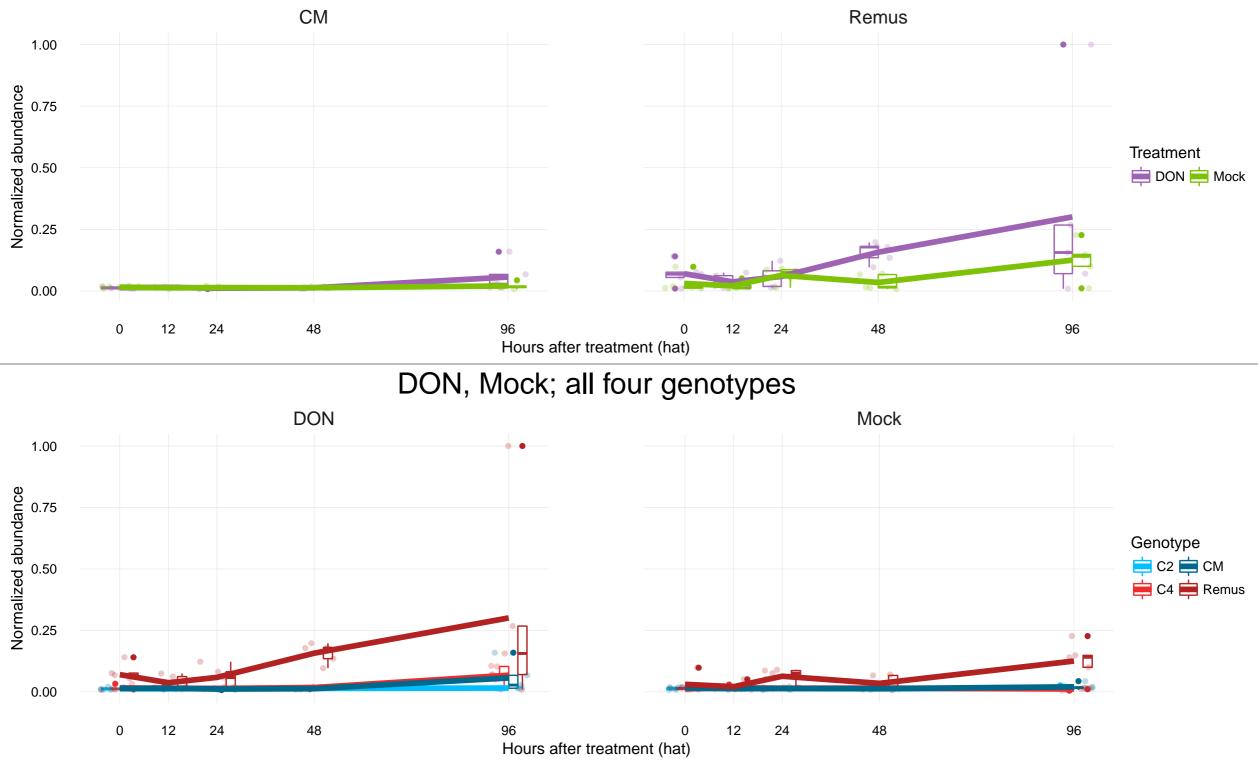


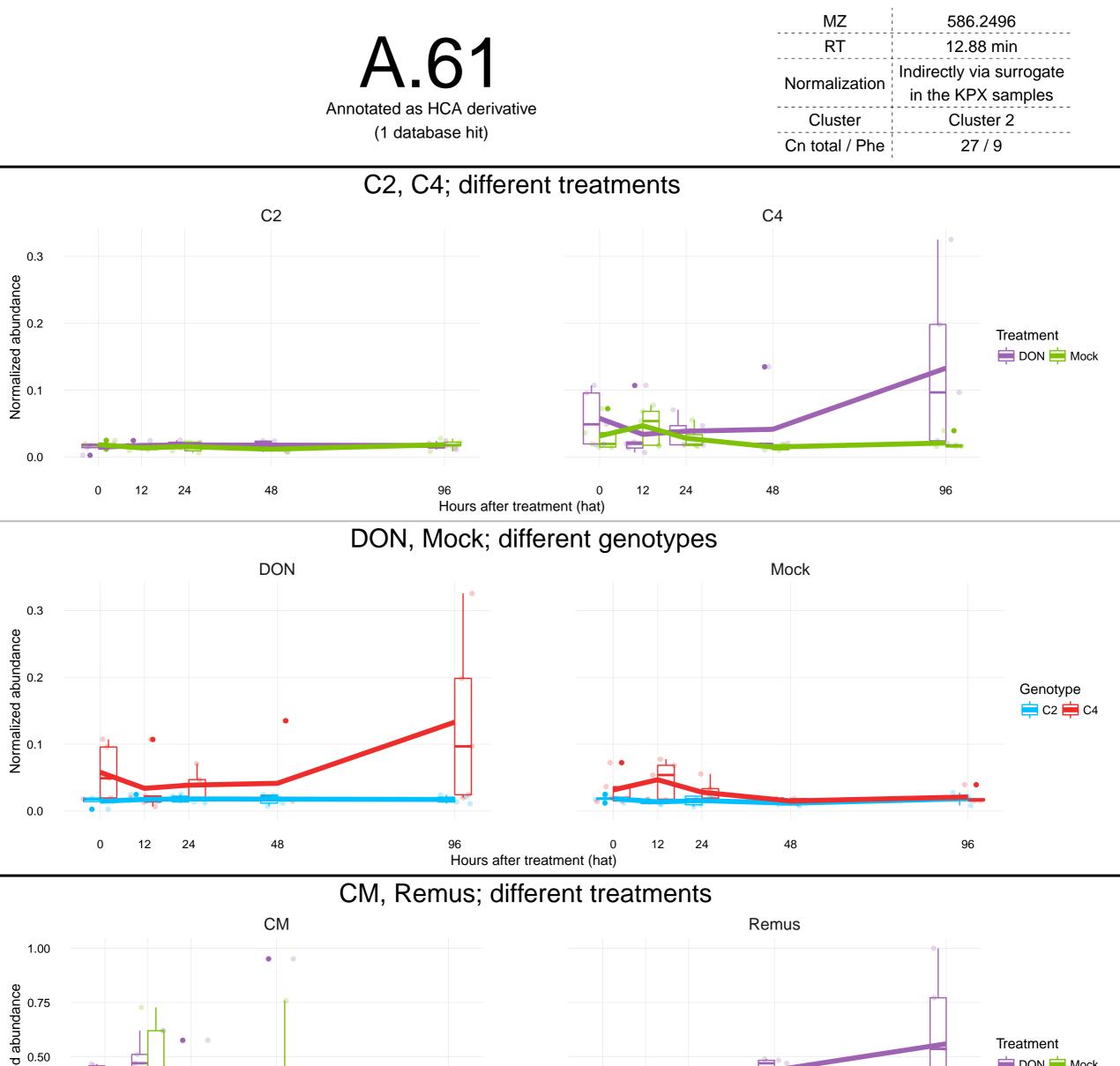


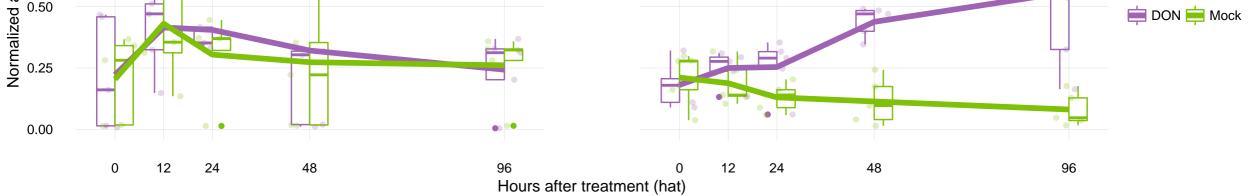
DON, Mock; all four genotypes



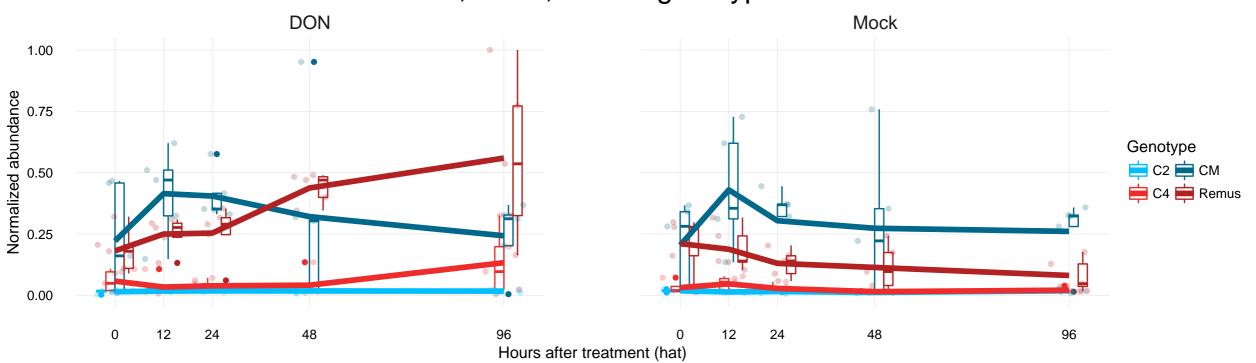
						MZ	600.2654
						RT	14.55 min
				A.80		Normalization	Indirectly via surrogate in the KPX samples
				Annotated as Lignan		Cluster	Cluster 2
				(1 database hit)		Cn total / Phe	28 / 9
				C2, C4; differer	t treatments		
			C2			C4	
			02			04	
0.100							
ce							
Normalized abundance 0.020 0.022							
abur							Treatment
0.050							DON 🚔 Mock
aliz							
0.025				• •	•		
2							QTL
0.000	•					•	TR+
	0	12 24	48	⁹⁶ Hours after treat	0 12 24 ment (hat)	48	96
				DON, Mock; diffe	erent genotypes		
			DON			Mock	
				•			
0.100							
JCe							
0.075 g							
abur							Genotype
Normalized abundance 0.020 0.022							——————————————————————————————————————
naliz							
UON 0.025	• •				• •		• •
∠ 0.020		••					
			•	•••		⊨ d _e	•
0.000							
	0	12 24	48	⁹⁶ Hours after tre	0 12 24 atment (hat)	48	96
			(CM, Remus; differ	ent treatments		
			СМ			emus	
1.00					R	GIIIUS	



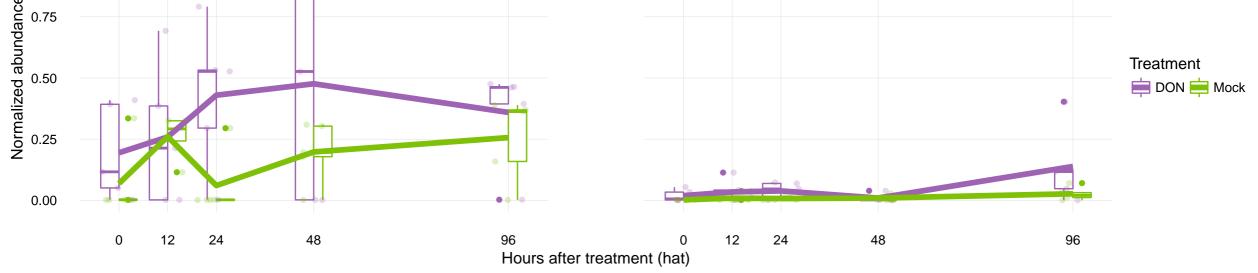




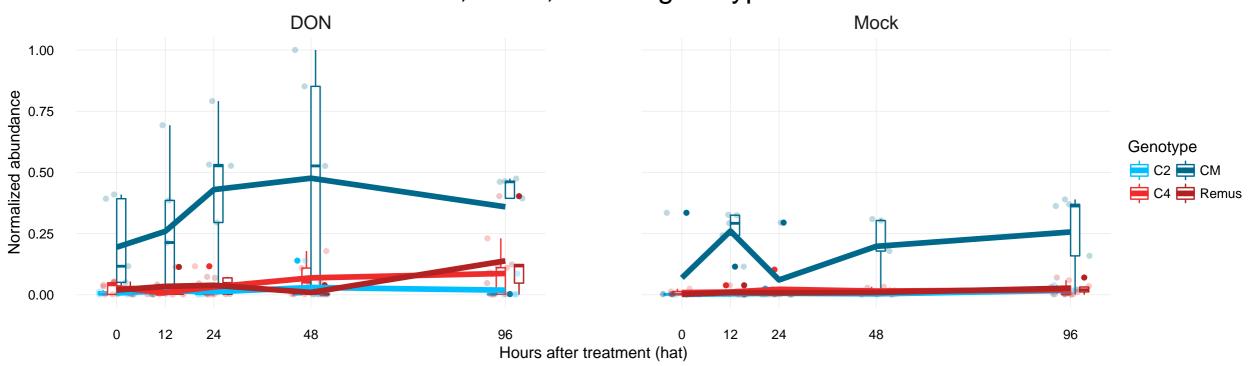
DON, Mock; all four genotypes



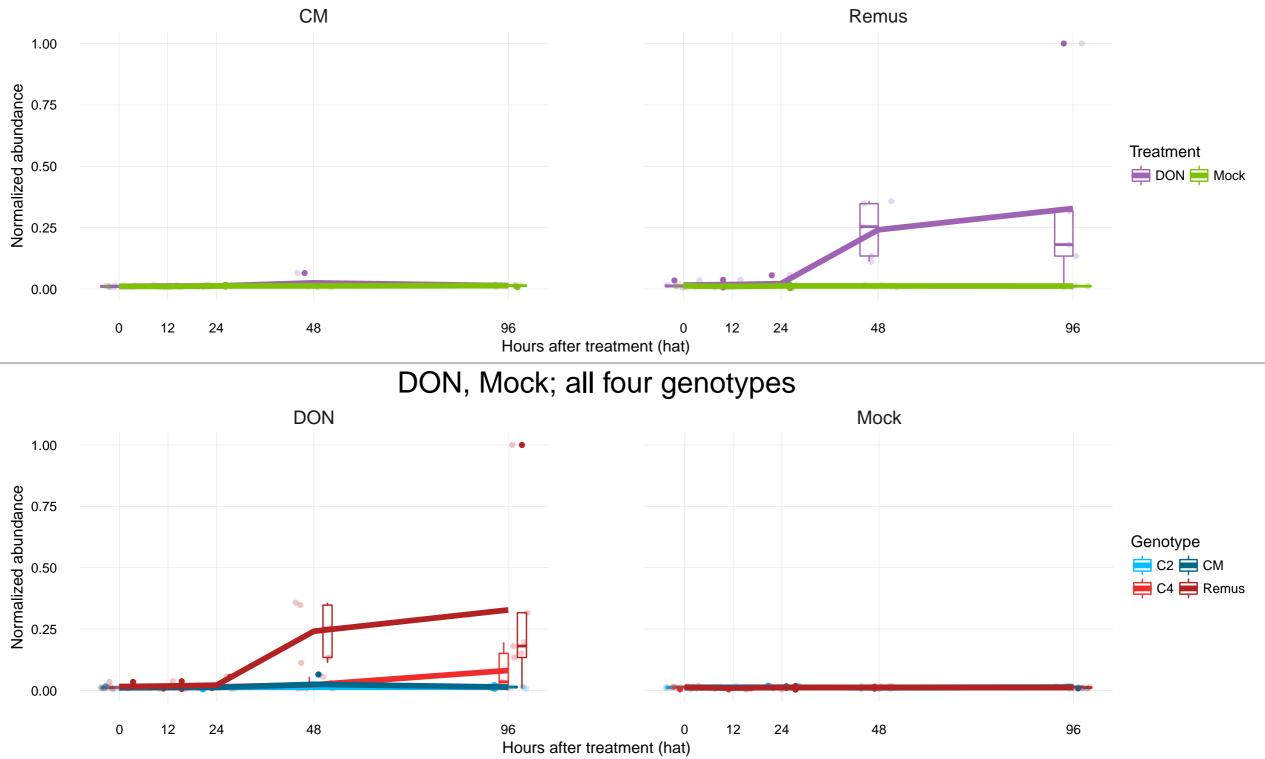
					MZ	371.149
		Λ	110		RT	19 min
			.119		Normalization	Indirectly via surrogate in the KPX samples
			ated as Flavonoid		Cluster	Cluster 2
		(21	database hits)		Cn total / Phe	
			2, C4; different t	rootmonte		
			Z, C4, Unterent t		64	
		C2			C4	
0.20 -						
0.20 0.15 0.10 0.10 0.05					r	
р и 0.15 –		• •				
d abı				•		Treatment
0.10 –			•	•		
						P
Z 0.00	•		1		•	
0.00						
	0 12 24	48	⁹⁶ Hours after treatmer	0 12 24 ht (hat)	48	96
		DC	N, Mock; differe	ent genotypes		
		DON		in generypee	Mock	
			•			
0.20						
ance		Ŷ				
pun 0.15 -		•				
0.20 0.15 0.10 0.10 0.05	•					Genotype 텆 C2 🚔 C4
0.05 -		•				
2						
0.00						• • •
	0 12 24	48	96 Hours after treatme	0 12 24 ent (hat)	48	96
		CM,	Remus; differer	nt treatments		
		CM	,		emus	
1.00		1				
D)		L.				
90 Ug 0.75 -	•					

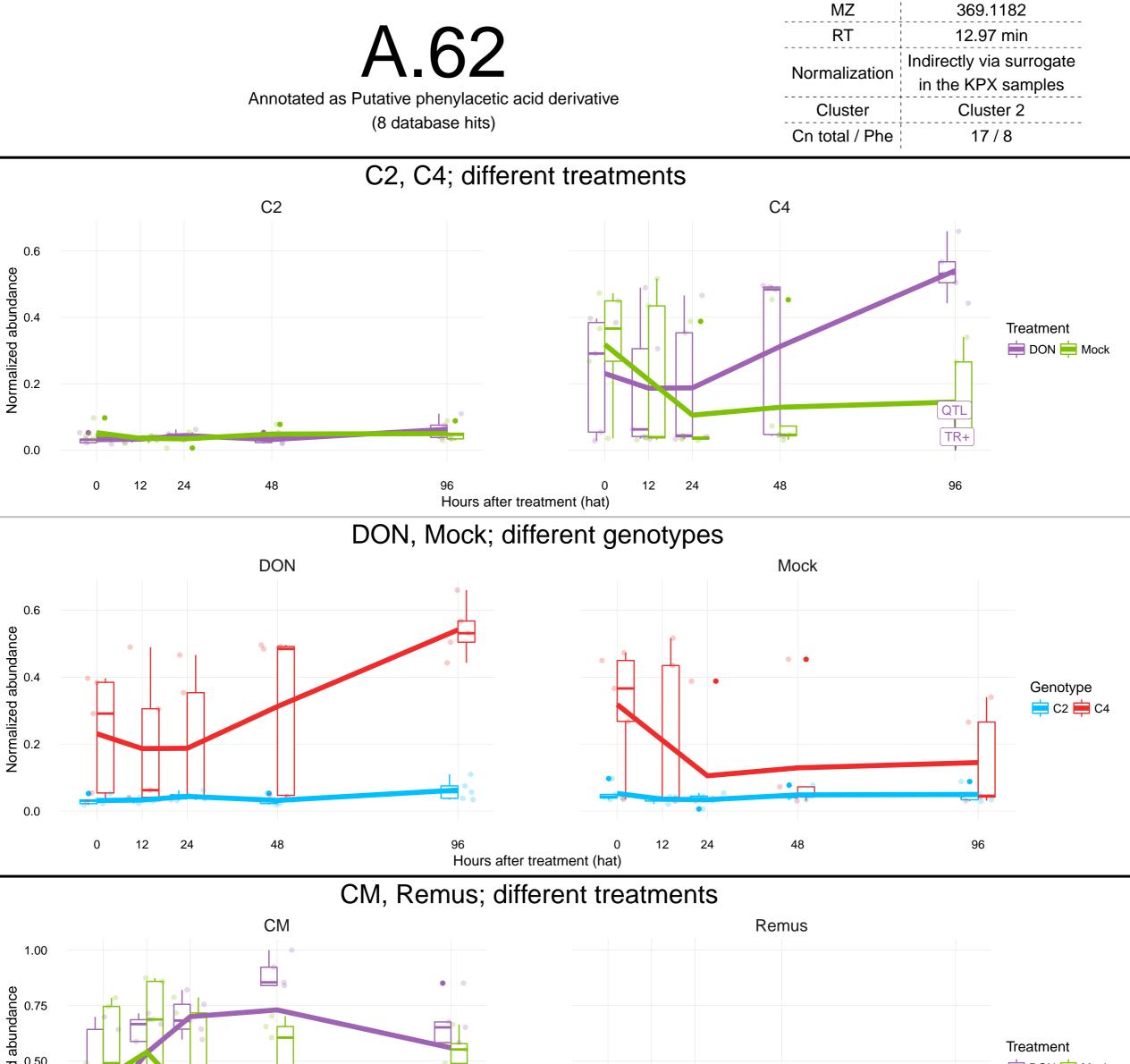


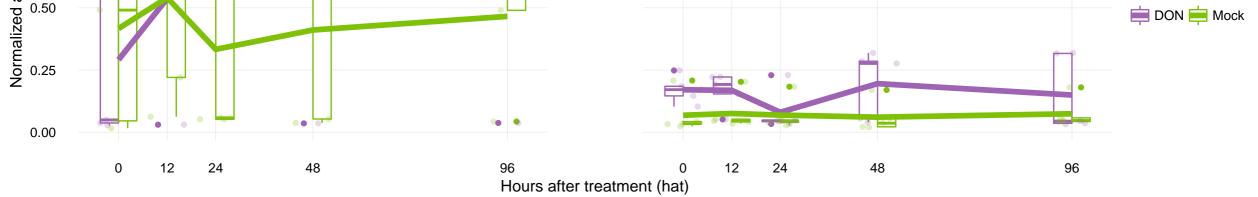
DON, Mock; all four genotypes



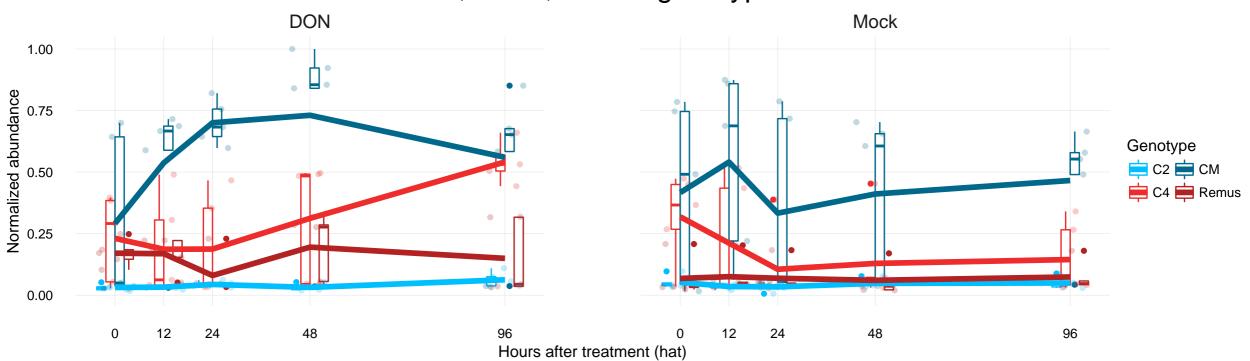
						MZ	540.24	39
						RT	13.15 r	nin
				A.65		Normalization	Indirectly via	
				Annotated as Lignan			in the KPX s	
				(1 database hit)		Cluster	Cluste	
				(1. 0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0		Cn total / Phe	26 / 1	8
				C2, C4; differe	nt treatments			
			C2			C4		
0.20							•	
Ð								
Normalized abundance 0.10 2000								
pund								Treatment
ອ ອີ ອີ								🚔 DON 🚔 Mock
aliz								
LO 0.05						•		
~				. <u>.</u>				
0.00		•		•		•		
	0 1	12 24	48	96 Hours after trea	0 12 24 atment (hat)	48	96	
				DON, Mock; diff	erent genotypes			
			DON			Mock		
0.20				•				
0								
0.15				•				
Normalized abundance 0.0 0.0 0.02								
אד ס 0.10								Genotype i C2 i C4
alize								
E 0.05								
Z								
0.00	-	• • •				• •		
	0	12 24	48	⁹⁶ Hours after ti	0 12 24 reatment (hat)	48	96	
			C	M Remus diffe	erent treatments			
			CM			Domus		



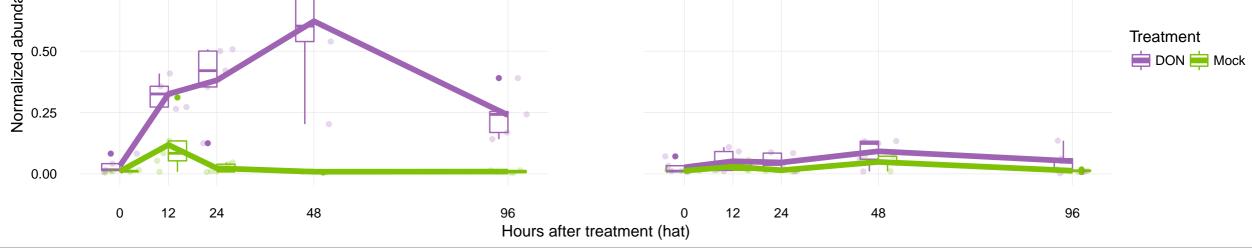




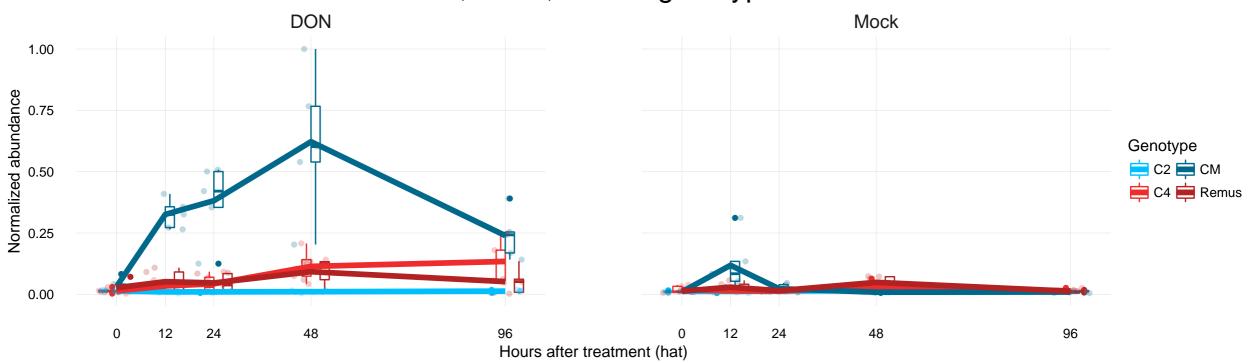
DON, Mock; all four genotypes

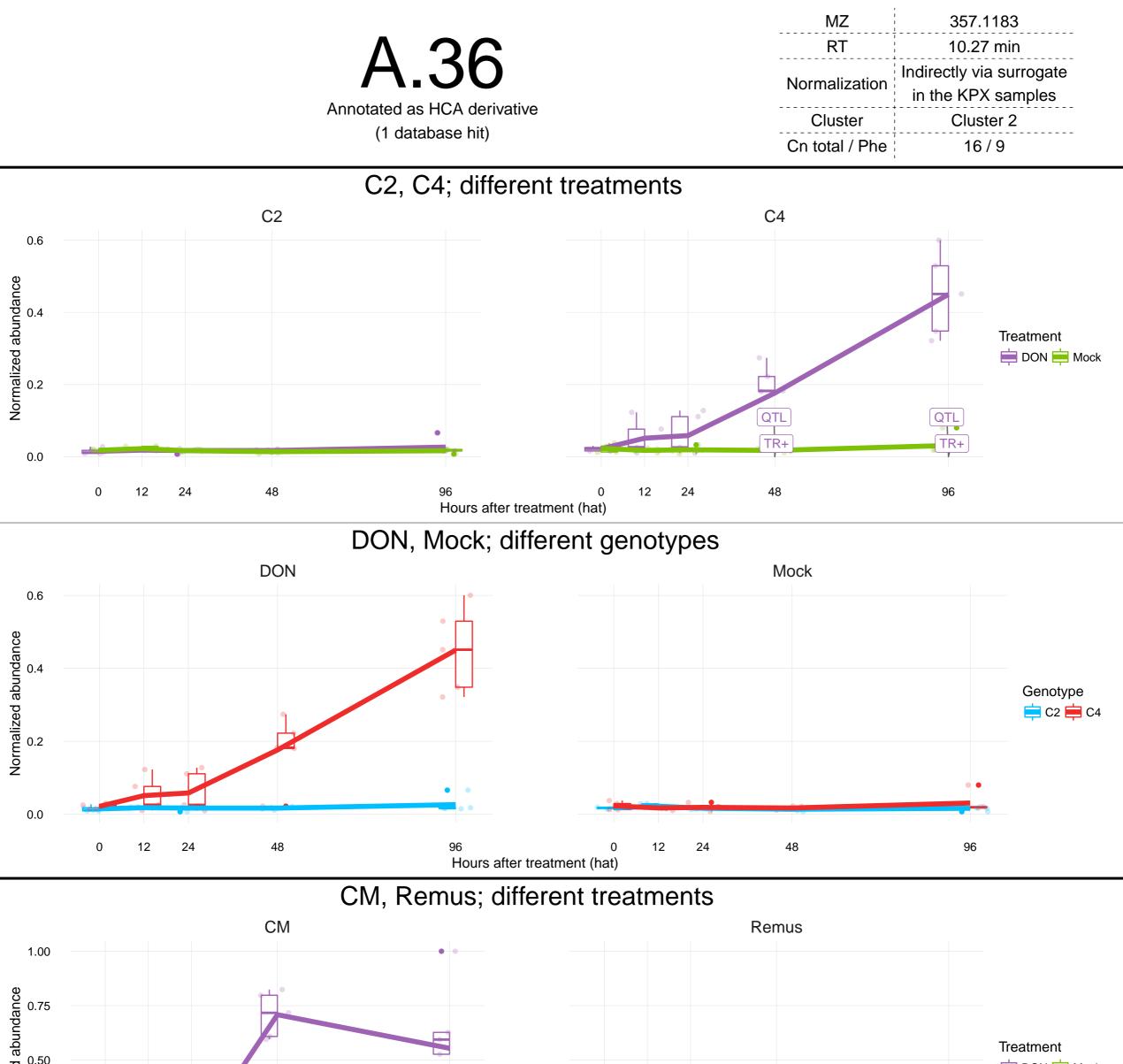


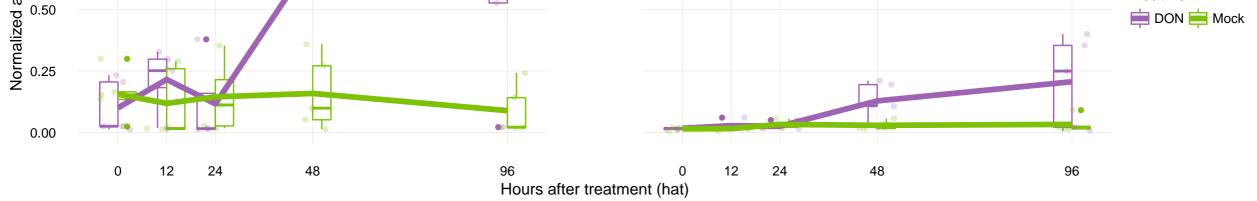
			-	MZ	565.1915
		A.10	Λ	RT	17.01 min
				Normalization	Indirectly via surrogate in the KPX samples
		Annotated as Flavonoid		Cluster	Cluster 2
		(3 database hits)	Cn total / Phe	
		C2. C4: di	fferent treatments		
	C	2 2		C4	
0.25					
<u>හ</u> 0.20				•	
udan 0.15					
d abt					Treatment
0.20 – 0.20 – 0.15 – 0.15 – 0.10 – 0.10 – 0.05 – 0.					
LION 0.05					
0.00			QTL	TR+	TR+
0.00					
	0 12 24 4	48 96 Hours a	0 12 24 after treatment (hat)	48	96
		DON, Mock	; different genotypes		
	D	ON		Mock	
0.25		•			
භී 0.20		P			
epun <u></u> 0.15					
∋d ab					Genotype 🖨 C2 🚔 C4
0.20					
LO N 0.05 —				•	
0.00		•			•
0.00	0 12 24	48 96	0 12 24	48	96
	0 12 27		s after treatment (hat)	-10	30
			different treatments		
1.00	C	Μ		Remus	
1.00 —					
0.75 –		•			
pur					



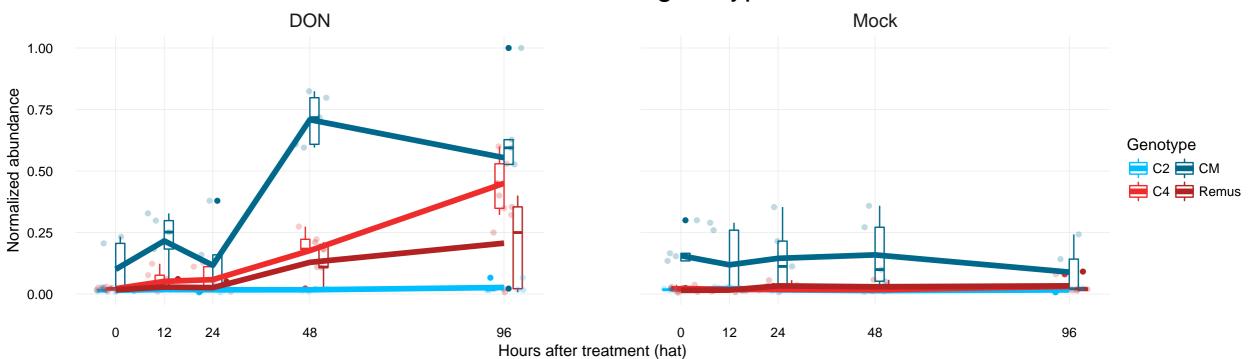
DON, Mock; all four genotypes

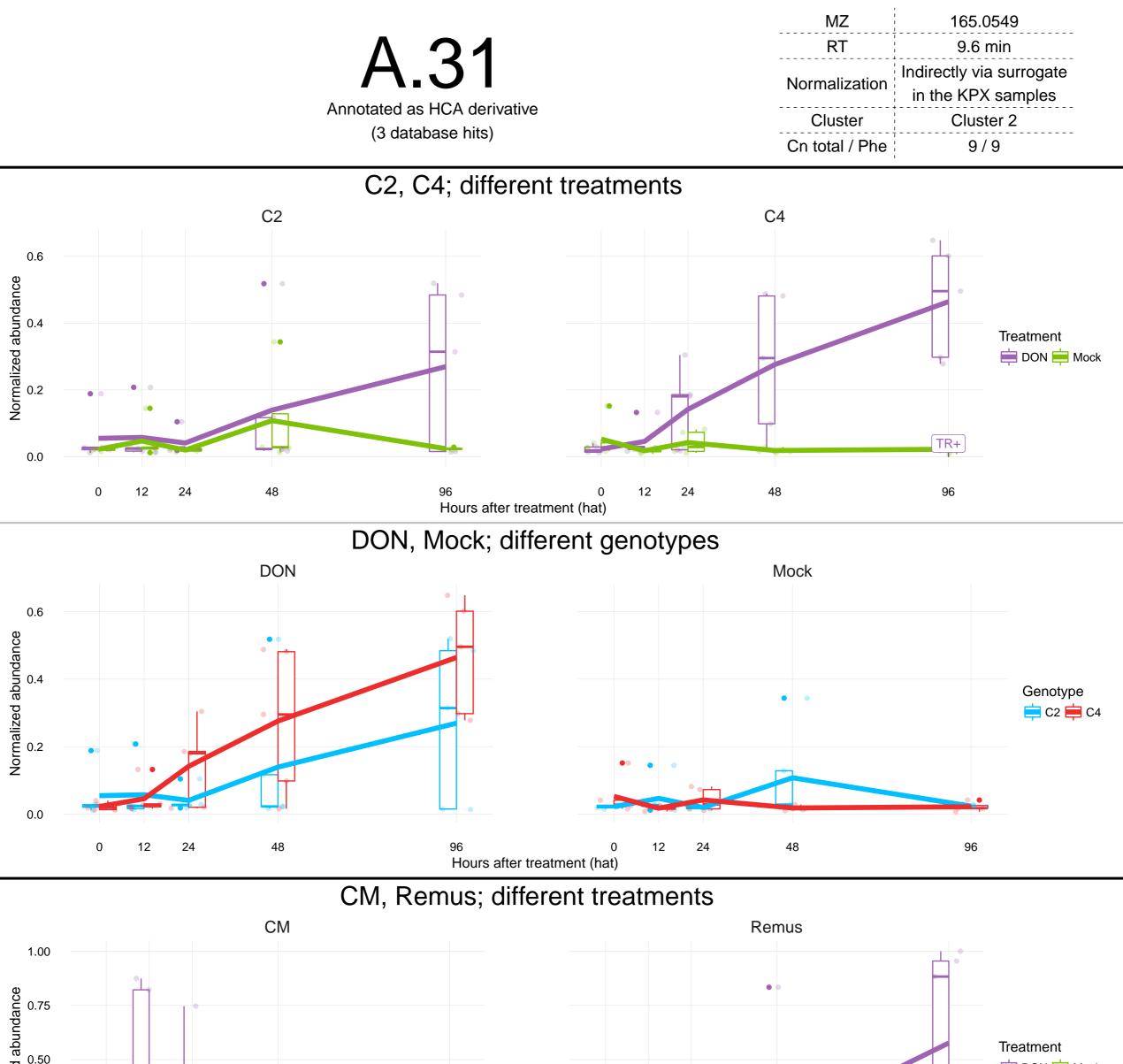


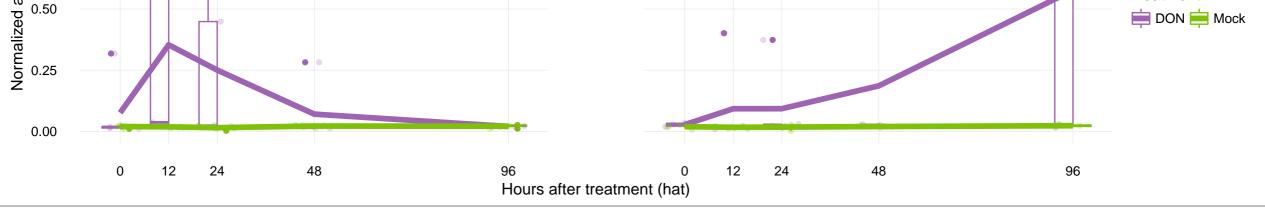




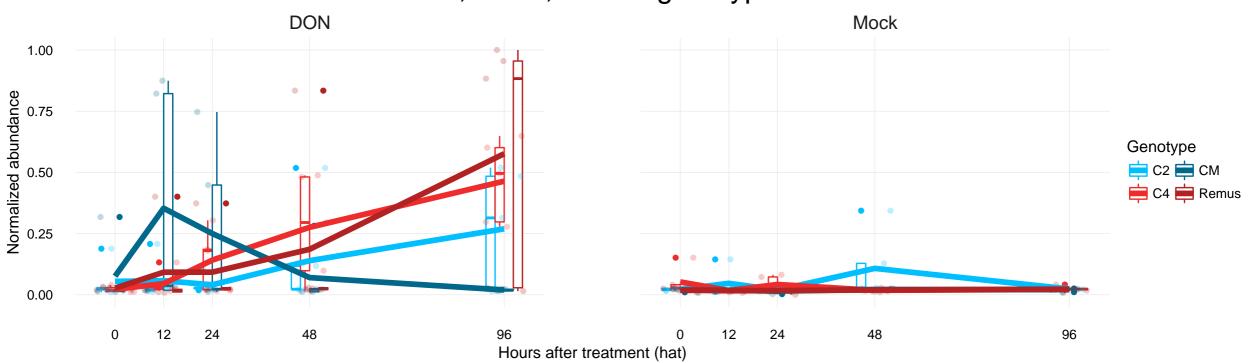
DON, Mock; all four genotypes



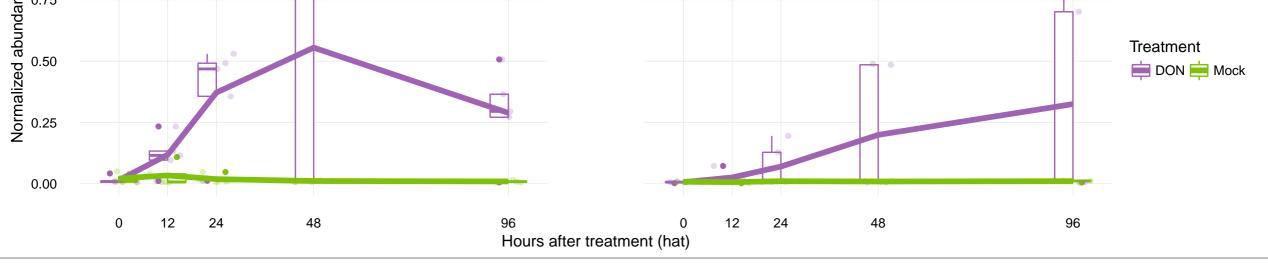




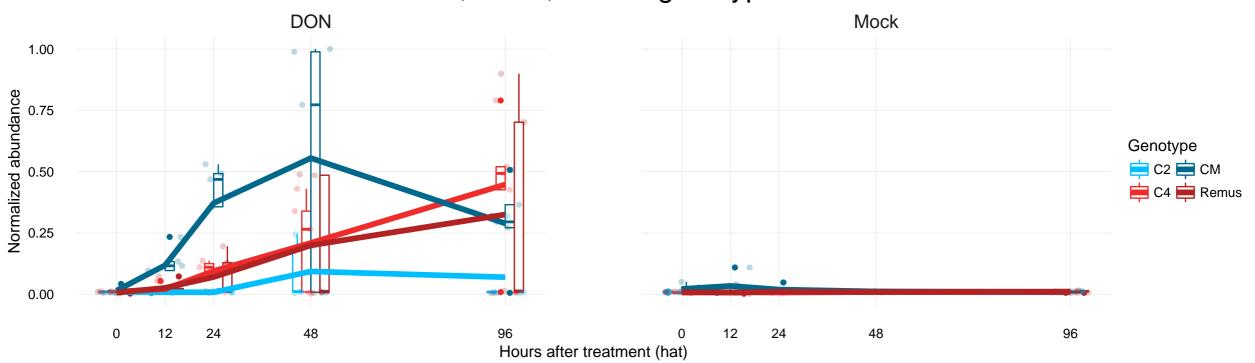
DON, Mock; all four genotypes



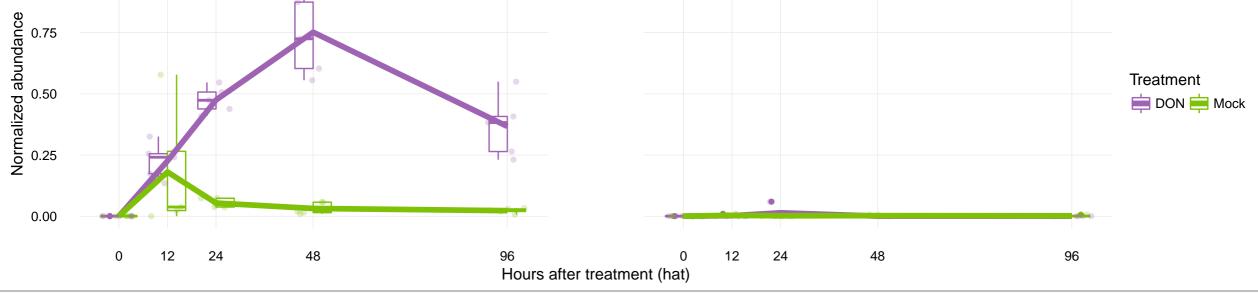
		Annota	A 13 ted as HCA derivative (1 database hit)		MZ RT Normalization Cluster Cn total / Phe	531.1 6.42 r Indirectly via in the KPX Cluste 23 /	nin surrogate samples er 2
		С	2, C4; different	treatments			
		C2			C4		
0.8						••	
Normalized abundance			•				Treatment
ō ^{0.2} Z				QTL		QTL	
0.0				• TR+		TR+	
	0 12 24	48	⁹⁶ Hours after treatn	0 12 24 nent (hat)	48	96	
		DC	DN, Mock; diffe	rent genotypes			
		DON	, ,	0 1	Mock		
0.8			•				
0.0 gu							
punq		•	F				Genotype
еро.4 родости – Срадини – С родости – Срадини – С							C2 🖨 C4
Normalized abundance 7.0 7.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8		•					
0 ^{0.2} Z	• -						
0.0			••				
	0 12 24	48	⁹⁶ Hours after trea	0 12 24 tment (hat)	48	96	
		CM	, Remus; differ	ent treatments			
		СМ	·		emus		
1.00		<u> </u>					
0.75							



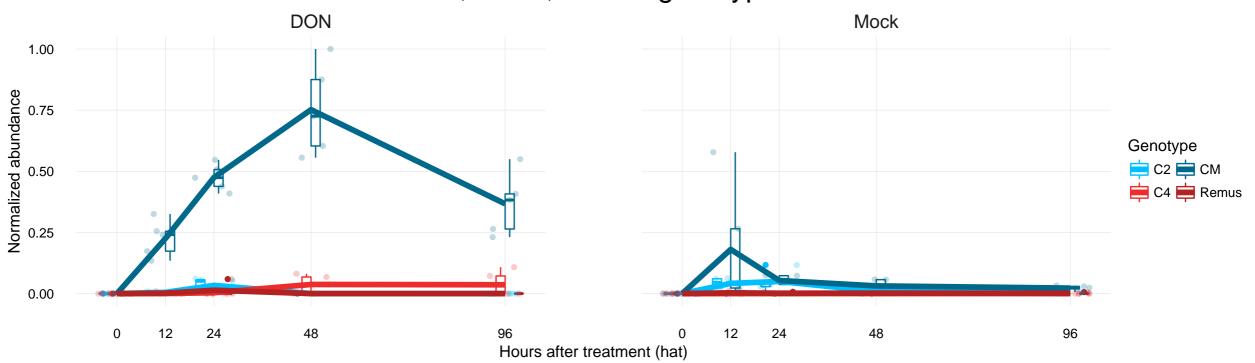
DON, Mock; all four genotypes



				MZ	251.1393	3
	Λ	1 /		RT	6.45 min	
	A.	14		Normalization	Indirectly via su	
		as HCAA			in the KPX sa	mples
	(2 datab			Cluster		
				Cn total / Phe	13/9	
	C2, C	4; different trea	atments			
0.12	C2		C4	4		
0.12					•	
Normalized abundance 0.00 0.03						
ndar			•			
ap 0.06			el.			eatment
ized					■	DON 뻗 Mock
2 ·····						
0.00		•		_		
0.00						
0 12	24 48	96 Hours after treatment (ha	0 12 24 48 t)	1	96	
	DON, I	Mock; different	genotypes			
	DON			/lock		
0.12			•			
		•				
Normalized abundance 0.00 0.03						
pun						
ab 20.0 م	et a					Genotype ≓ C2 븢 C4
alize						
E 0.03						
z				•		
0.00				•		
0 12	24 48	96	0 12 24	48	96	
		Hours after treatment (h	nat)			
	CM, Rei	mus; different t	reatments			
	CM		Rem	nus		
1.00						
e						



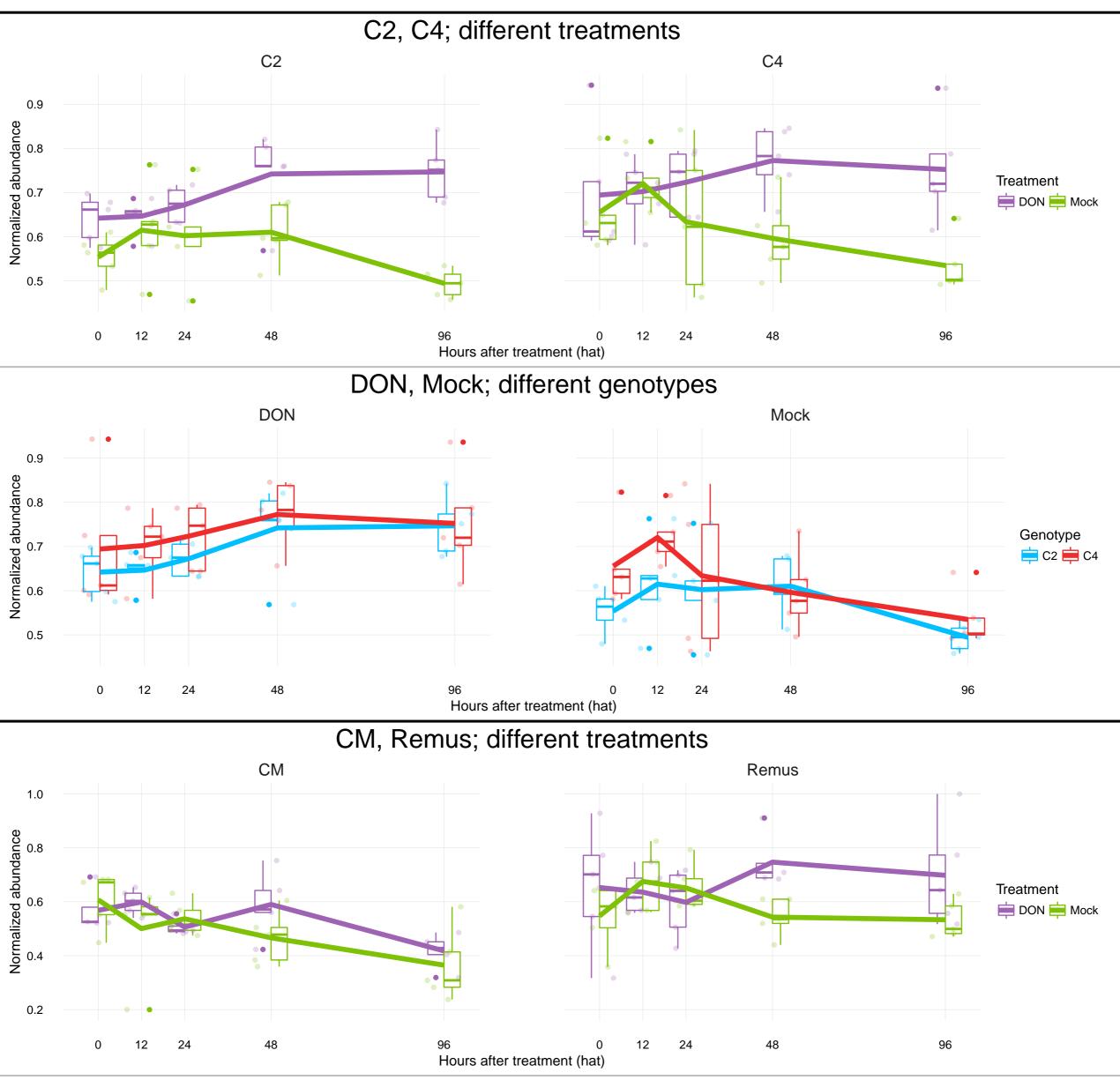
DON, Mock; all four genotypes



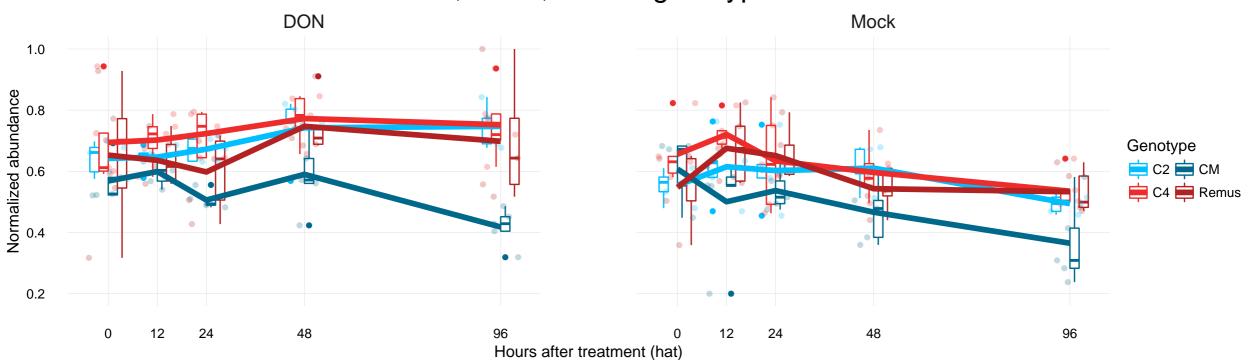
Sinapaldehyde

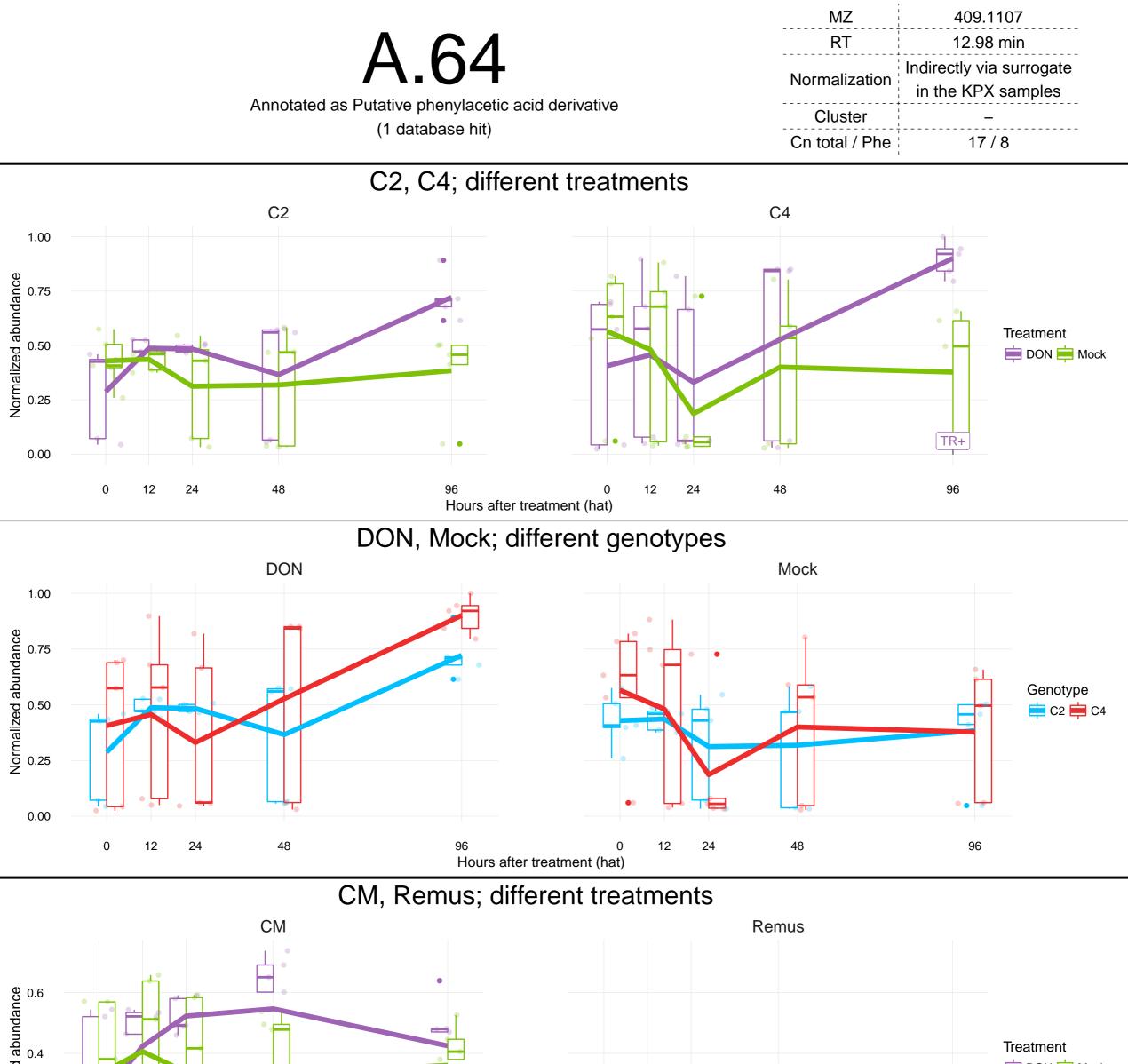
Identified metabolite (level 1)

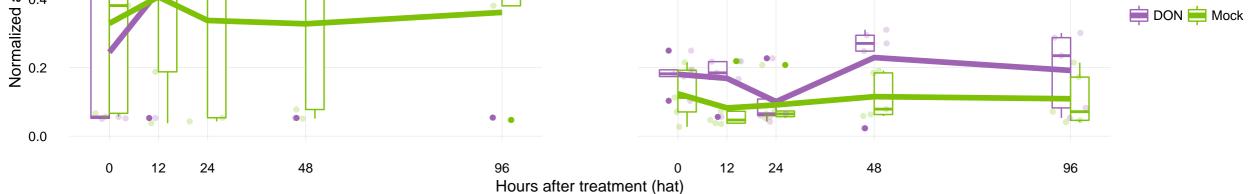
MZ	209.0809		
RT	14.46 min		
Normalization	Directly via KPX samples		
Cluster	_		
Cn total / Phe	11 /		



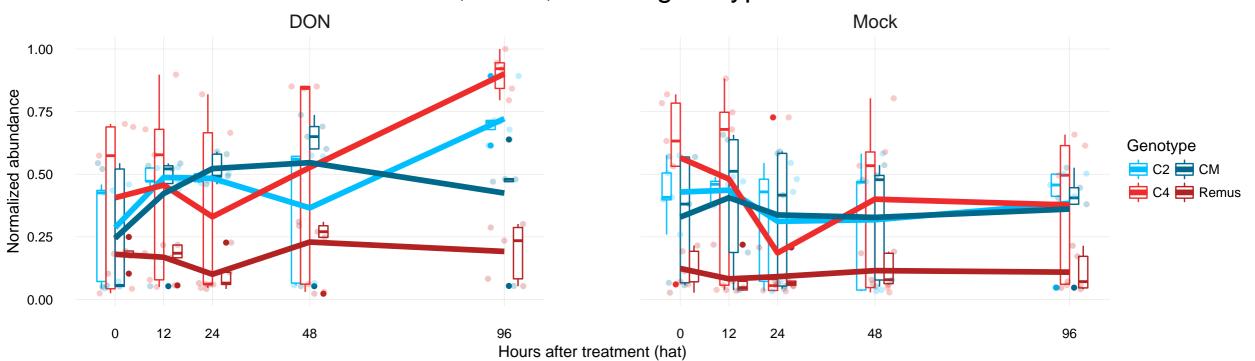
DON, Mock; all four genotypes







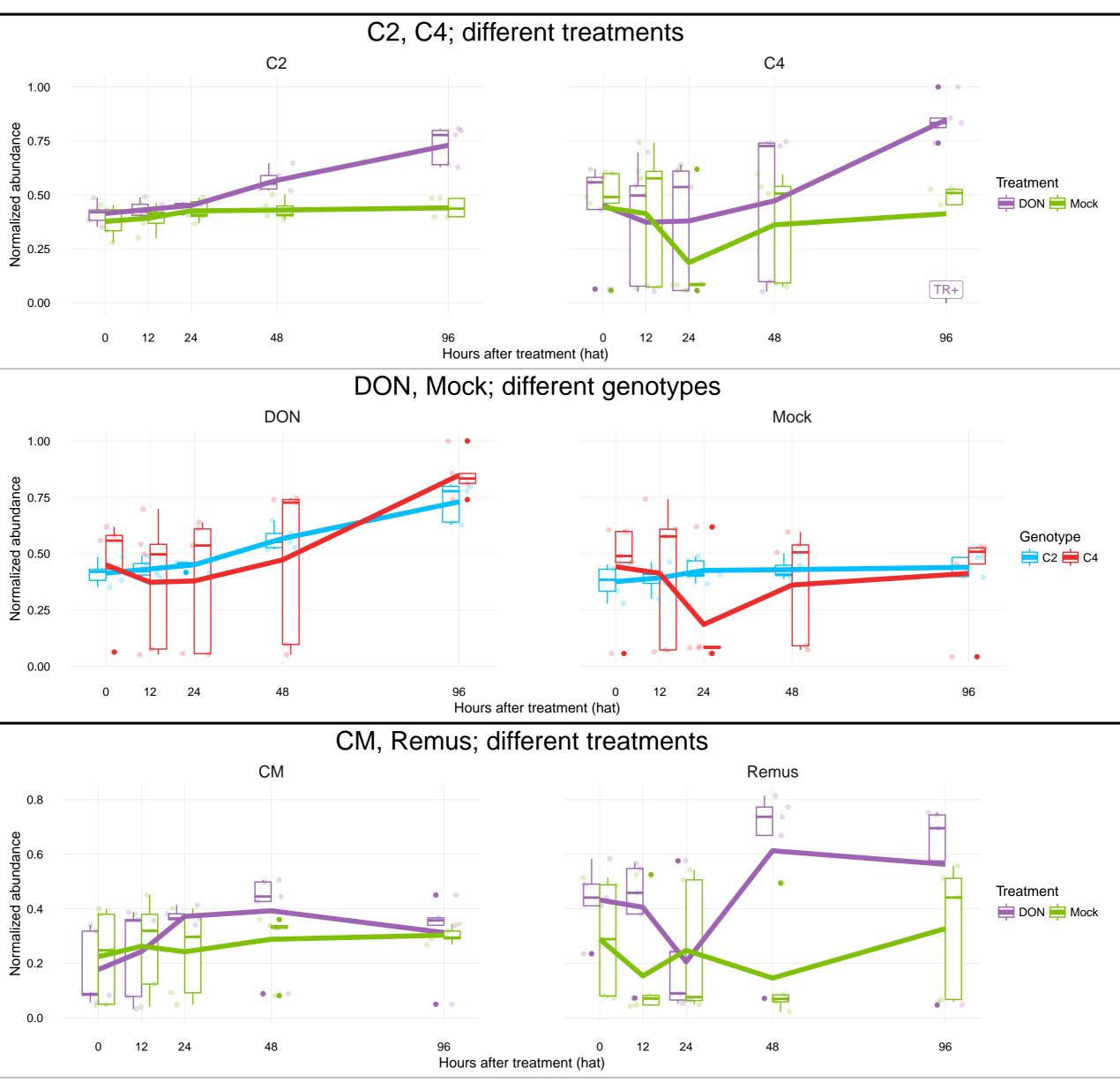
DON, Mock; all four genotypes



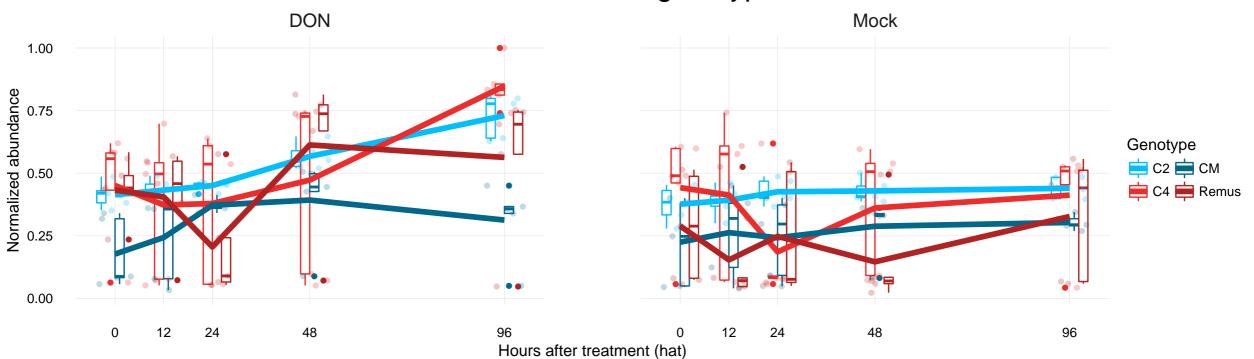
Sinapyl alcohol

Identified metabolite (level 1)

MZ	211.0966		
RT	12.97 min		
Normalization	Directly via KPX samples		
Cluster	—		
Cn total / Phe	11 /		



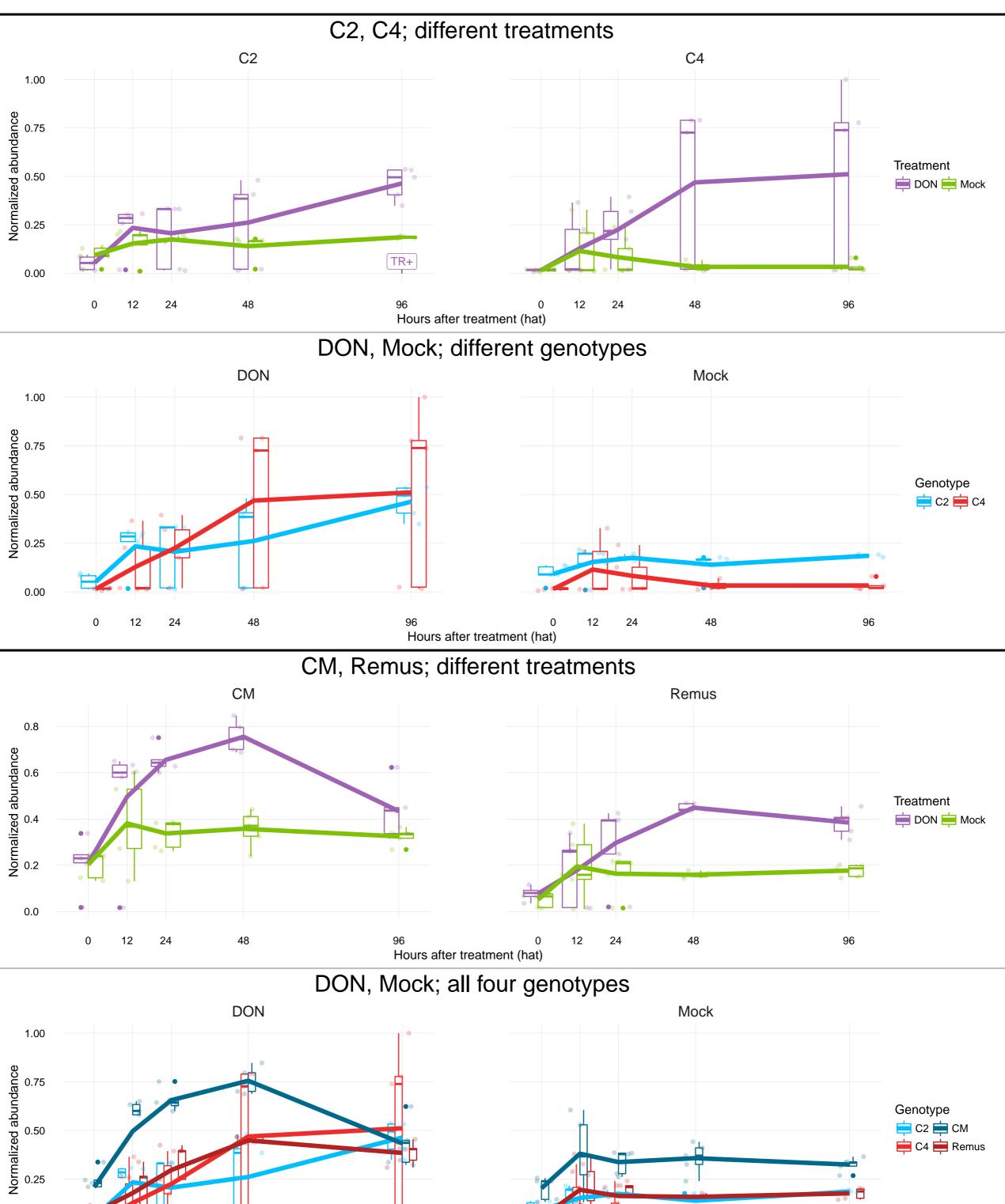
DON, Mock; all four genotypes



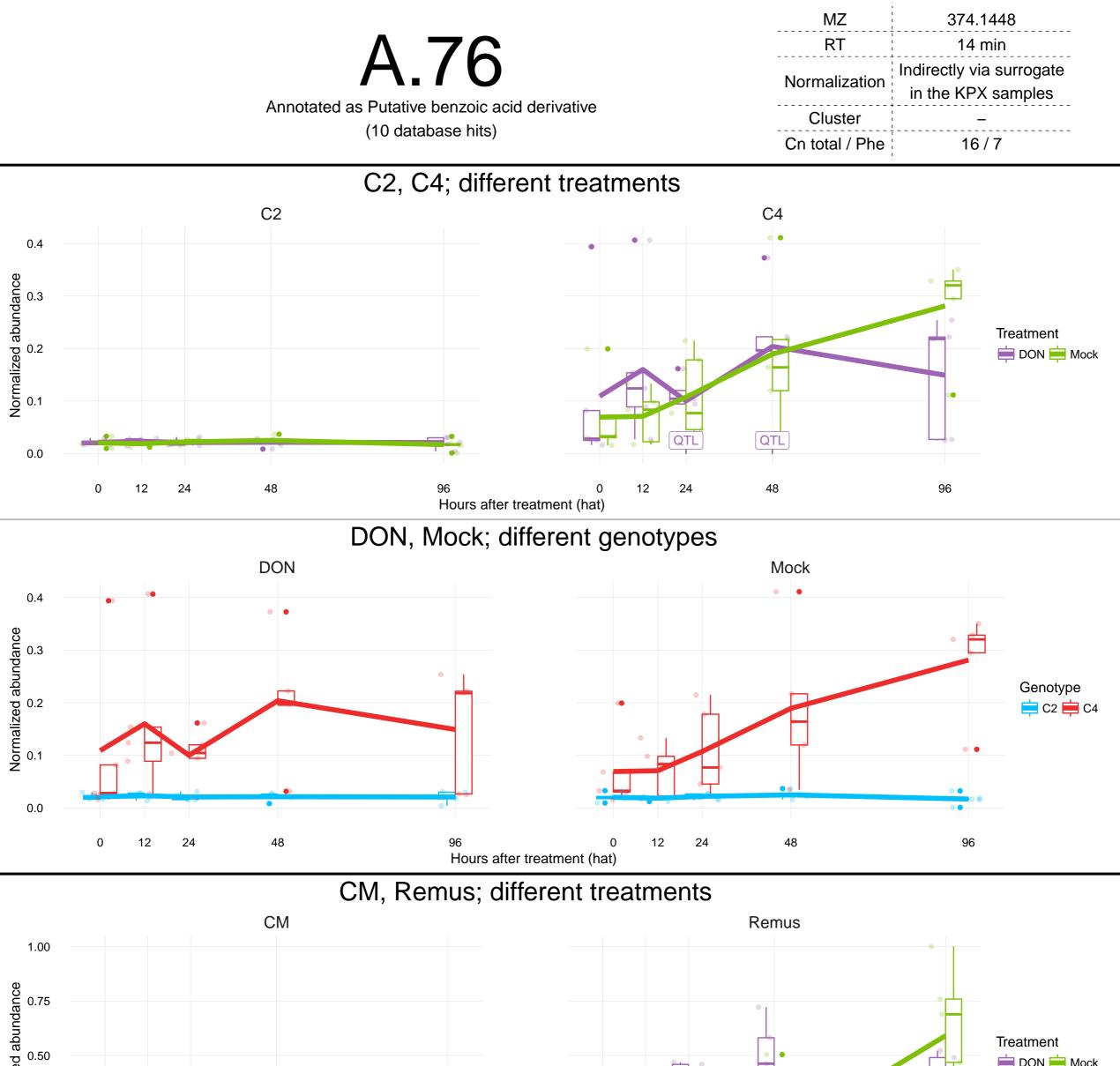
Phenylalanine

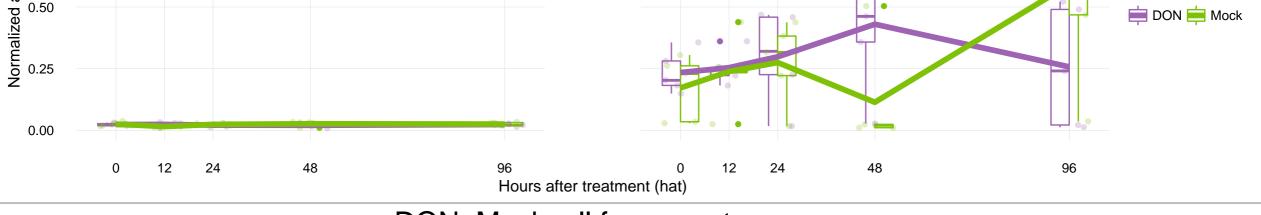
Identified metabolite (level 1)

166.0864	
4.46 min	
Not normalized	
_	
9/9	

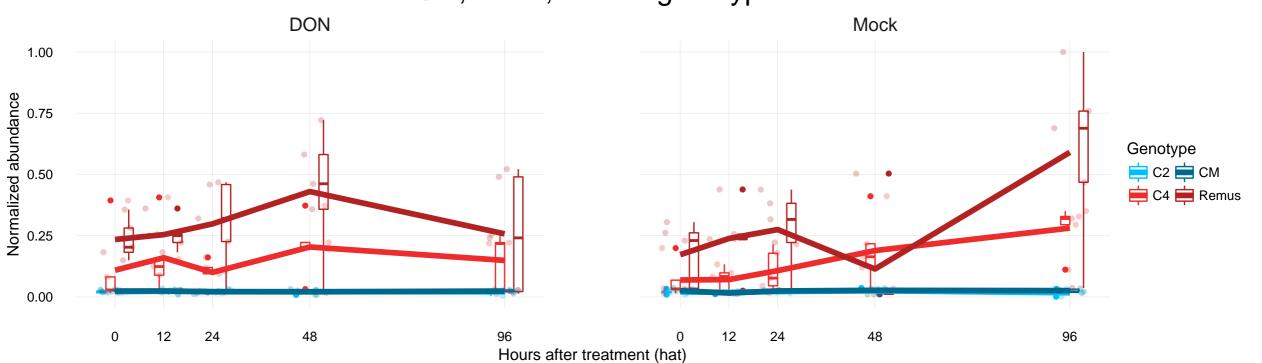


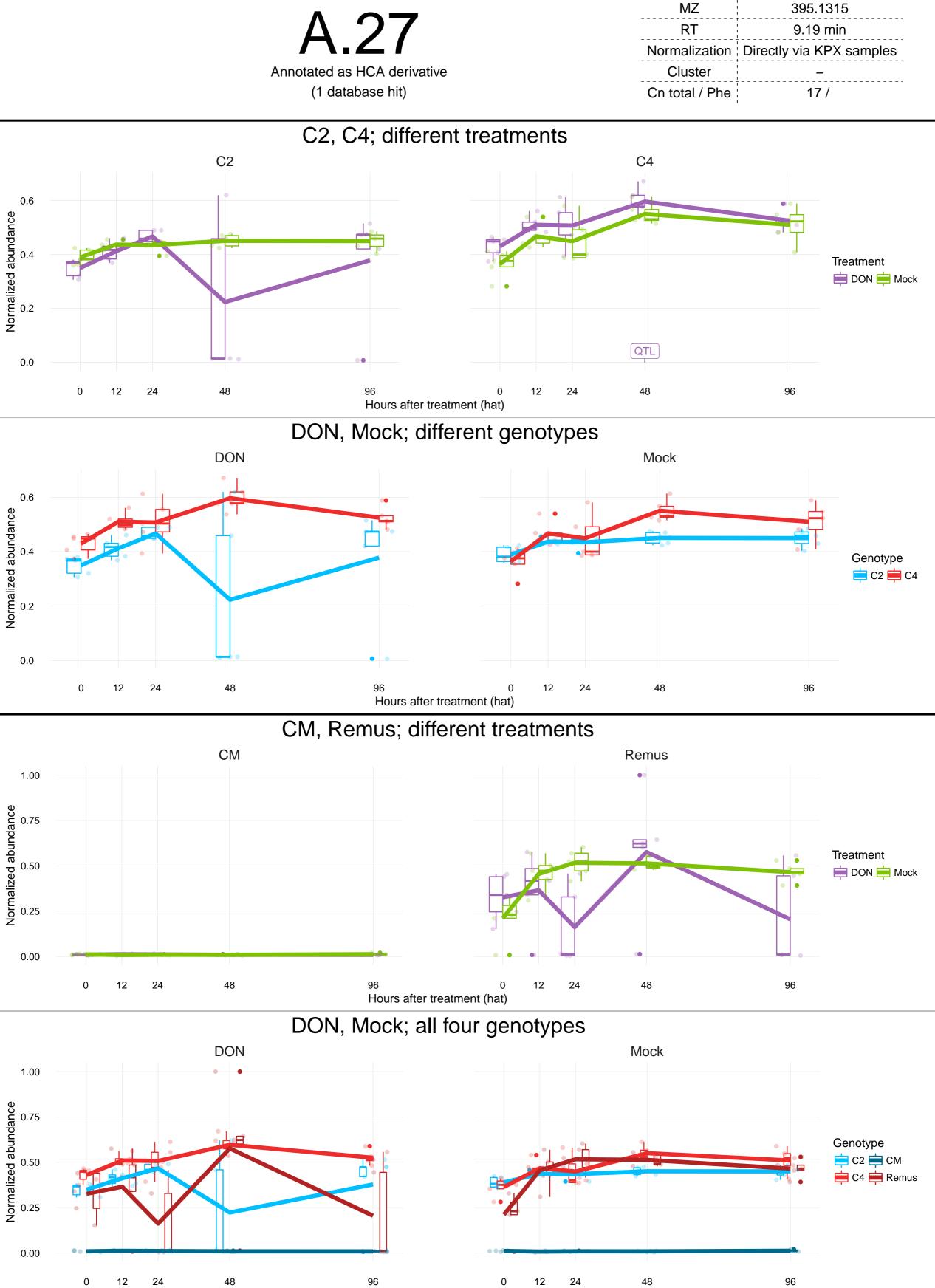
96 0 Hours after treatment (hat) 0.00



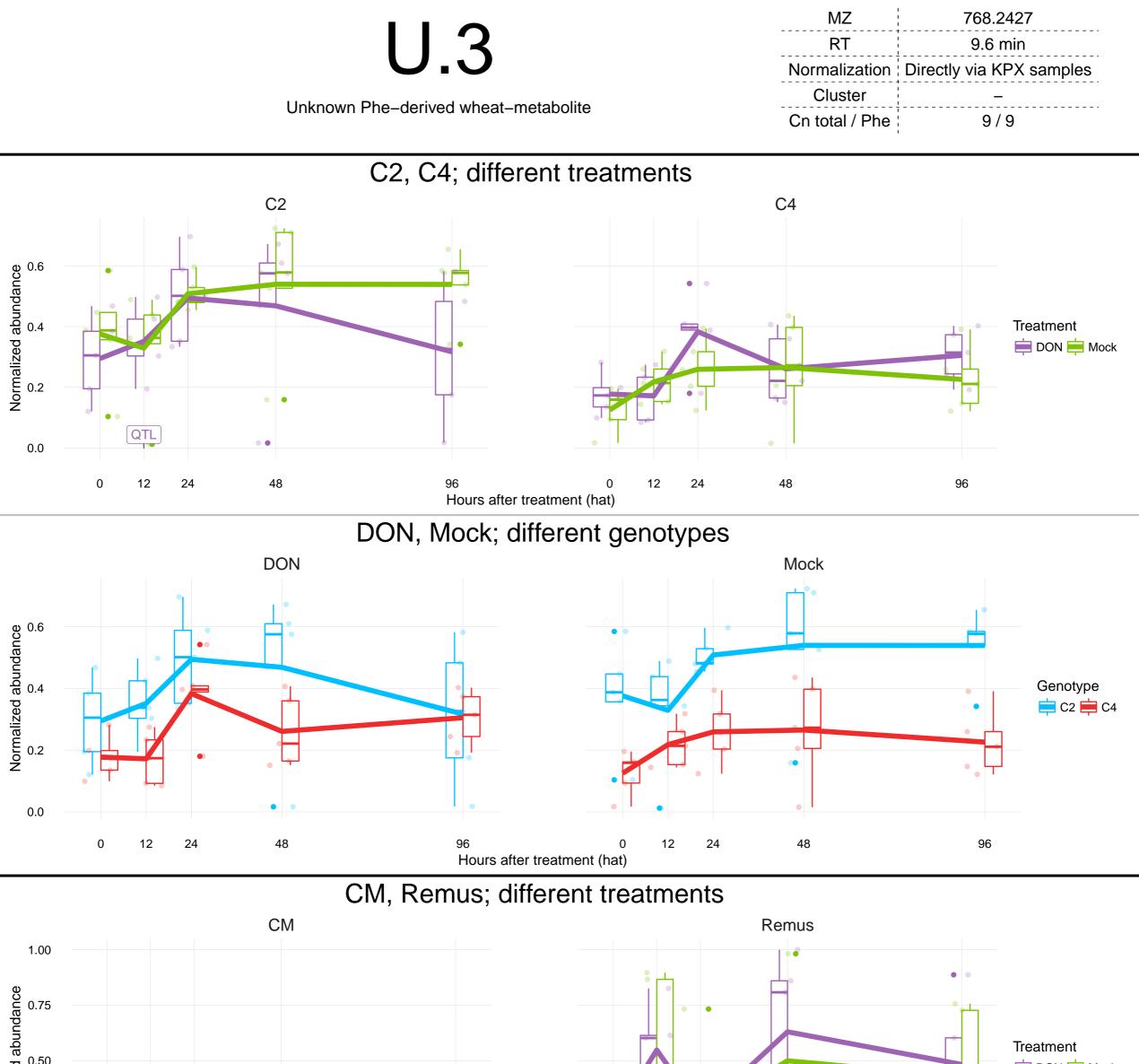


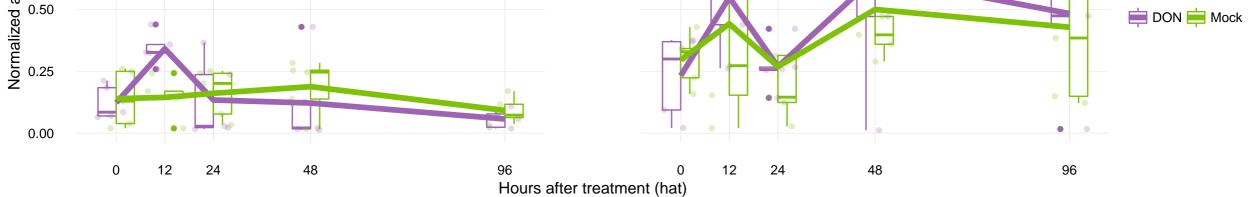
DON, Mock; all four genotypes



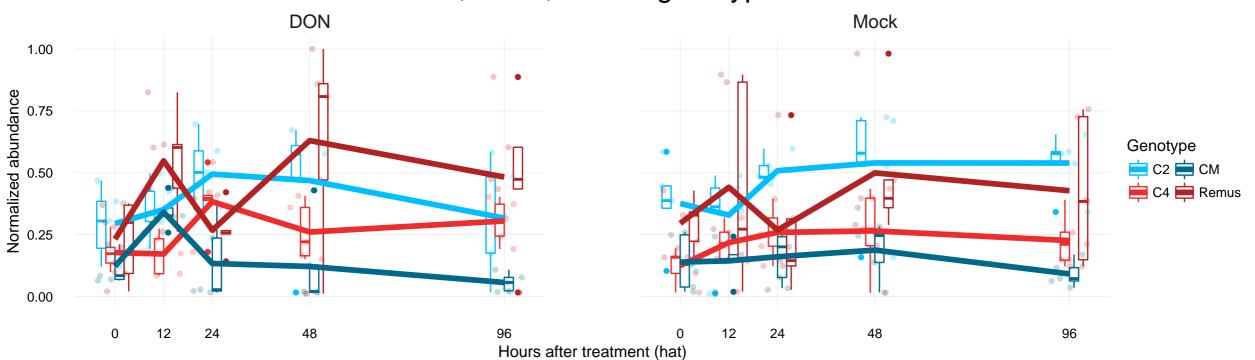


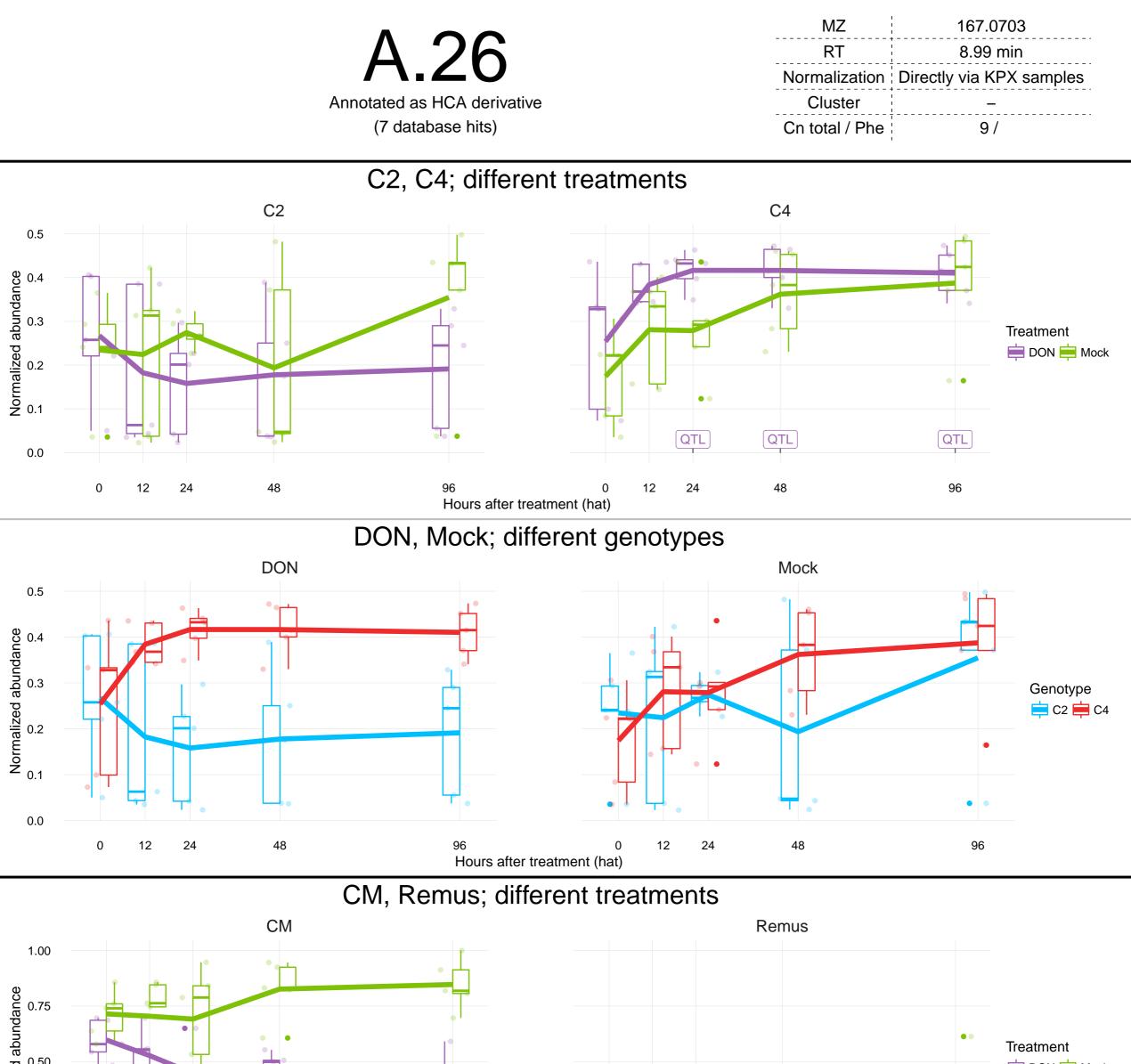
Hours after treatment (hat)

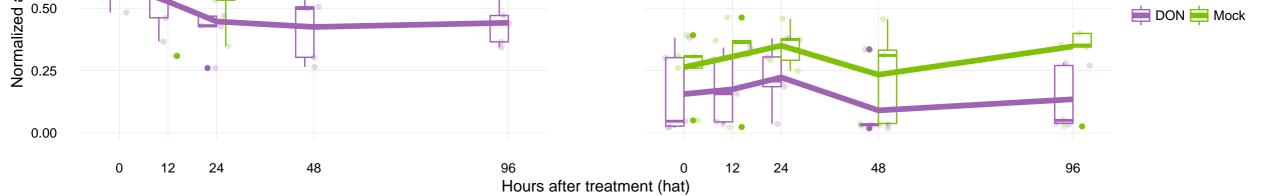




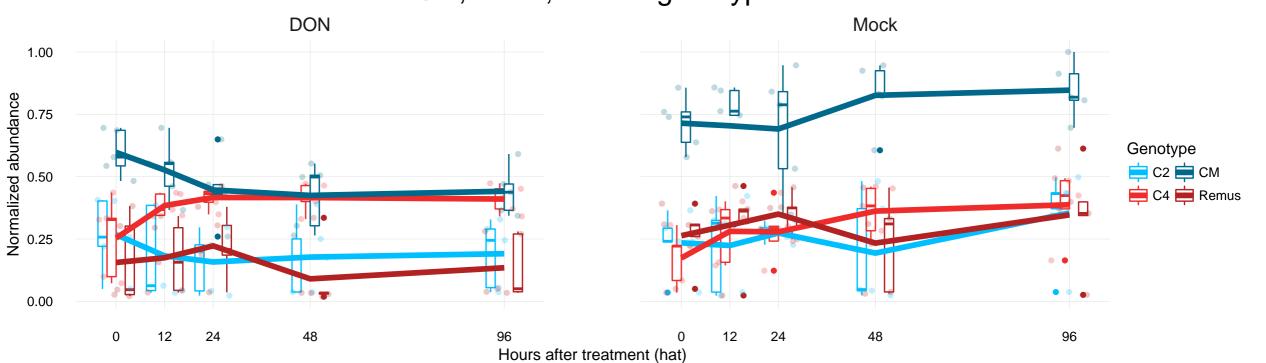
DON, Mock; all four genotypes

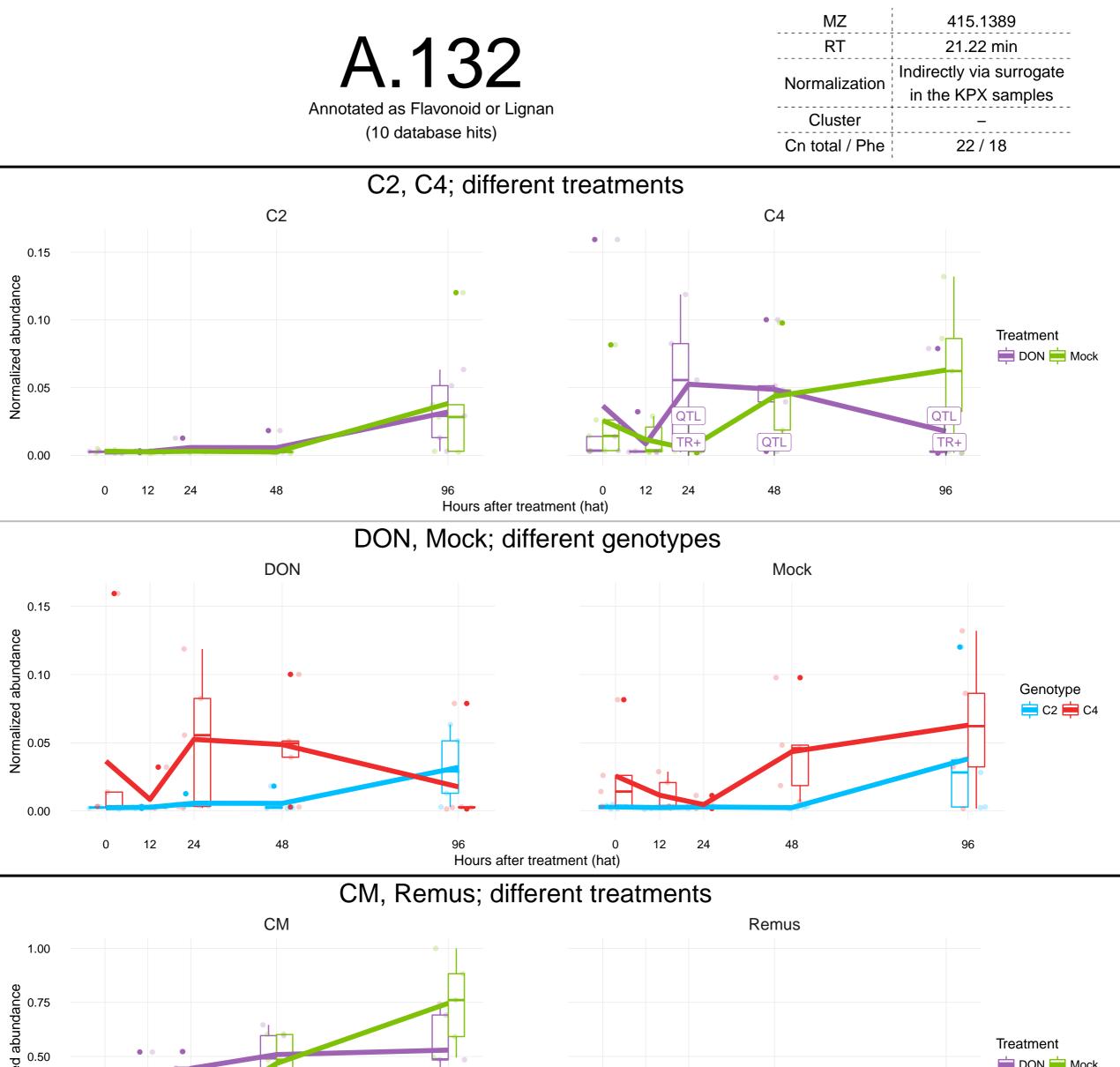


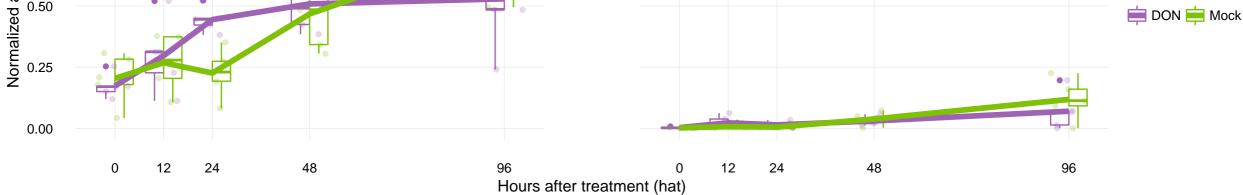




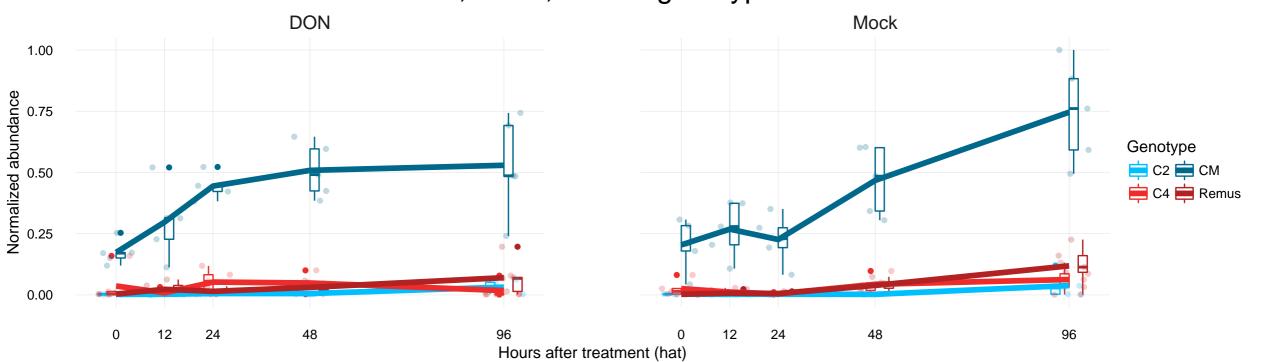
DON, Mock; all four genotypes







DON, Mock; all four genotypes

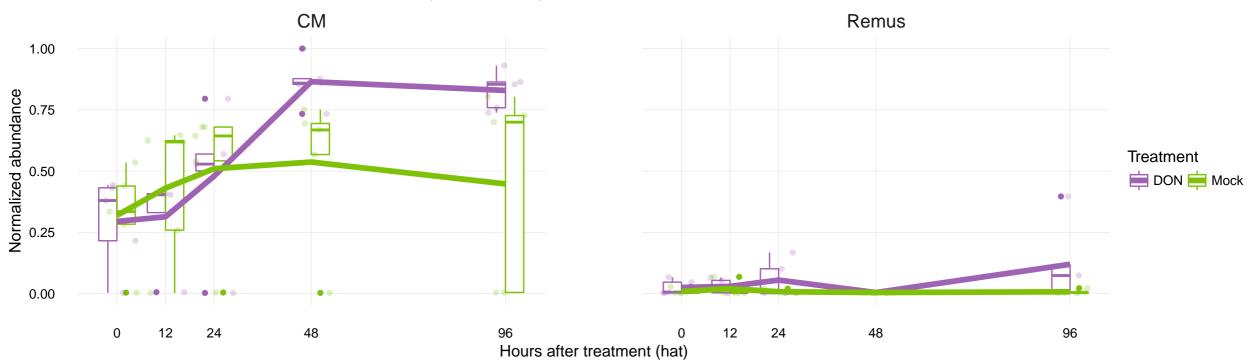


			A 108 nnotated as Flavonoid (30 database hits)		MZ RT Normalization Cluster Cn total / Phe	395.1102 17.59 min Indirectly via surrogate in the KPX samples – 20 /
			C2, C4; differe	ent treatments		
		C2			C4	
0.25						
april april					2-1	Treatment
0.10						DON 🚔 Mock
Z 0.03	••		TR+			
	0 12 24	48	96 Hours after tre	0 12 24 eatment (hat)	48	96
		[DON, Mock; dif	ferent genotypes		
0.25		DON			Mock	
	•					
0.20 0.15 0.10 0.05						Genotype
й О 0.05 —			<u> </u>			

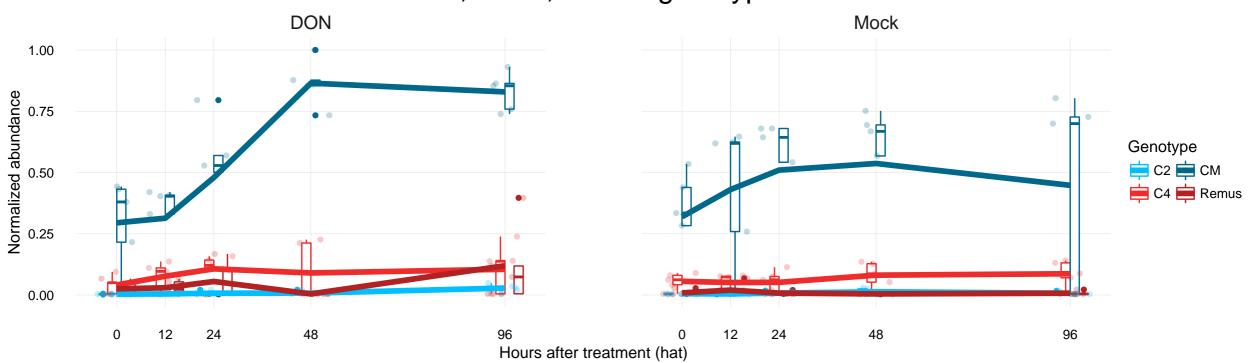
CM, Remus; different treatments

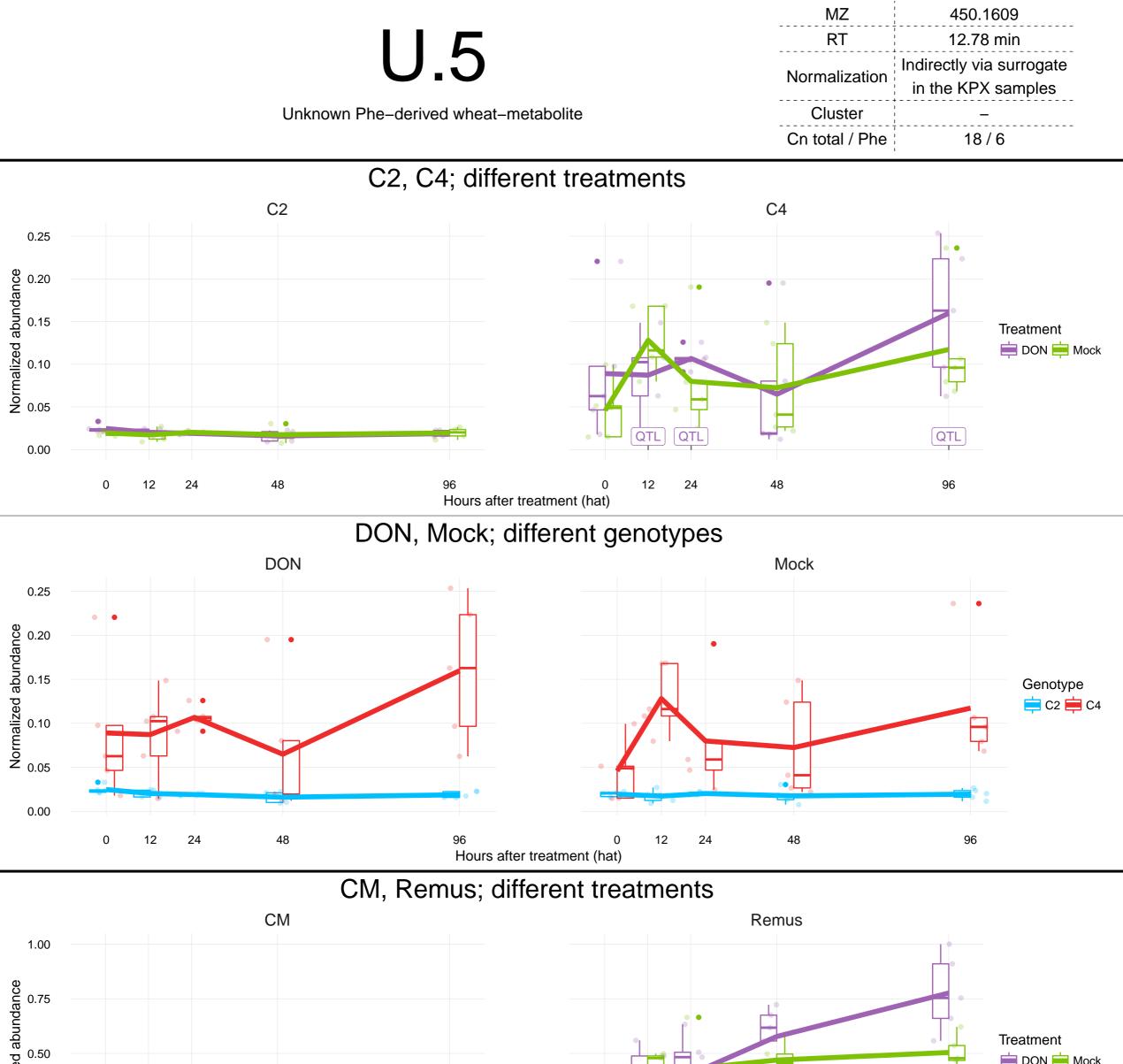
96 0 Hours after treatment (hat)

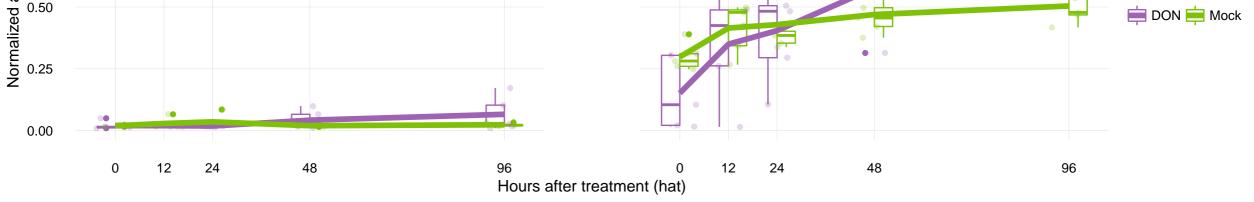
0.00



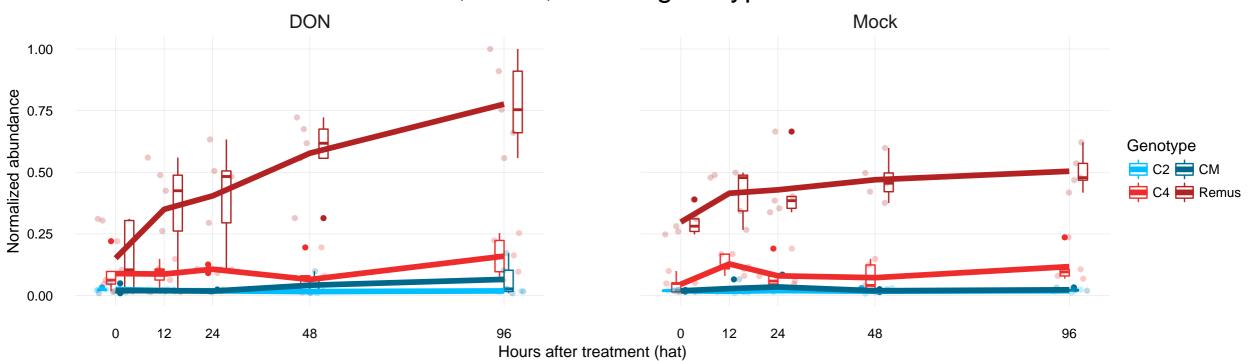
DON, Mock; all four genotypes





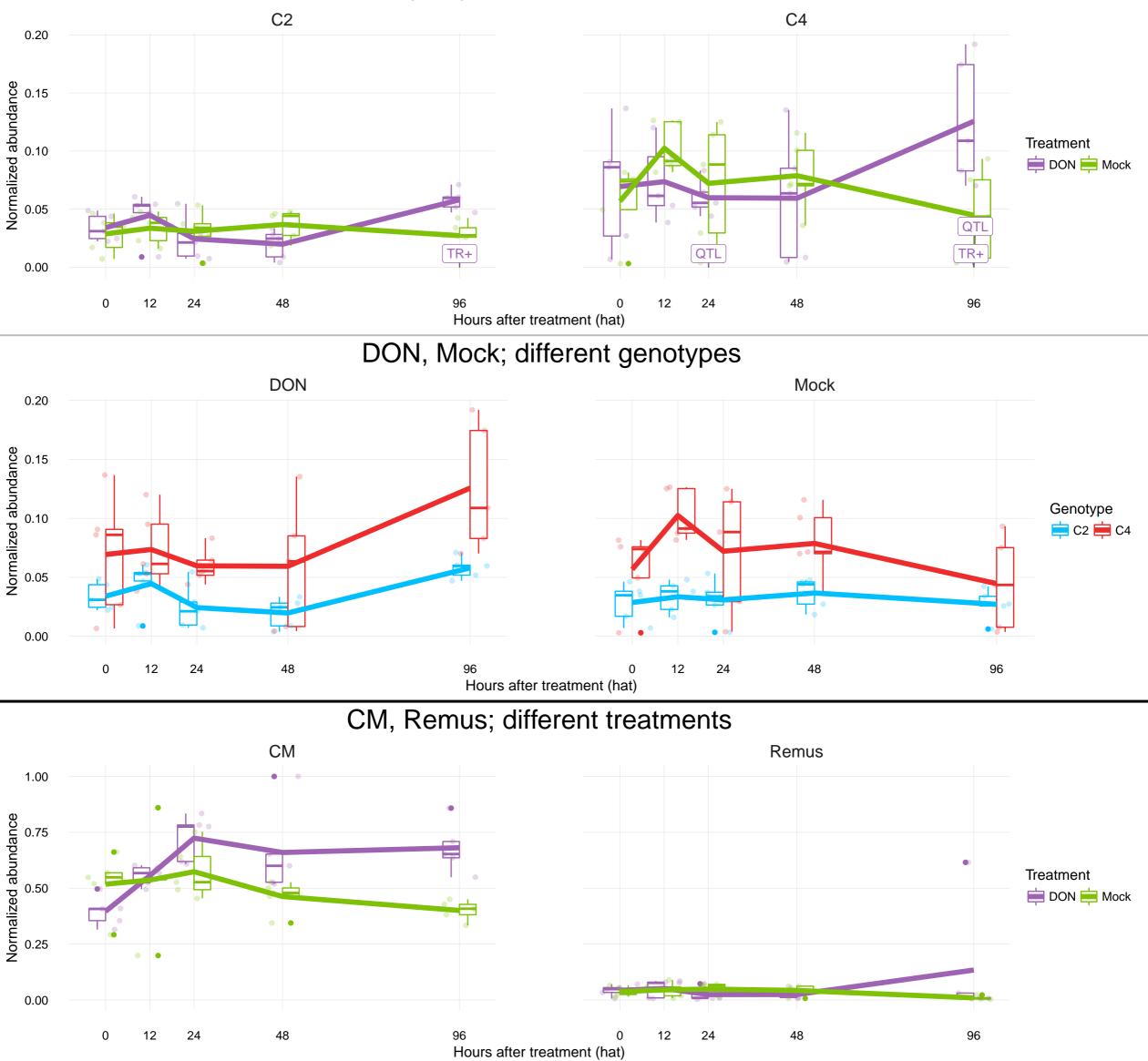


DON, Mock; all four genotypes

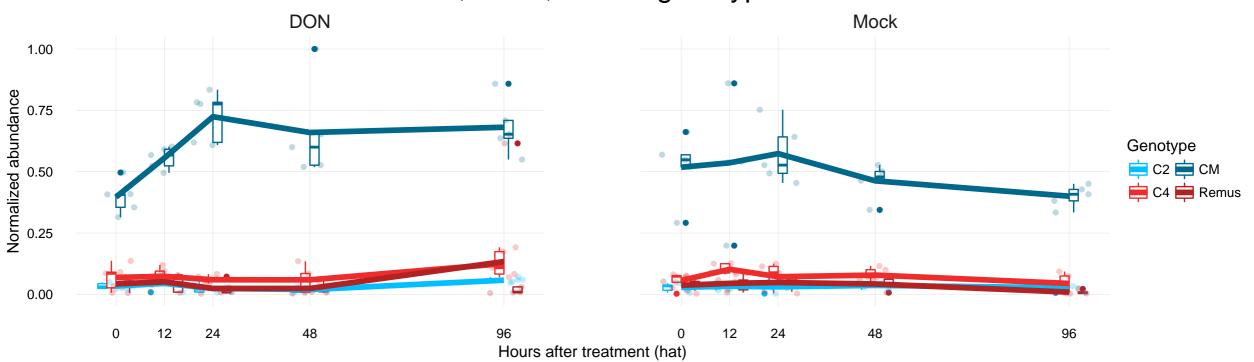


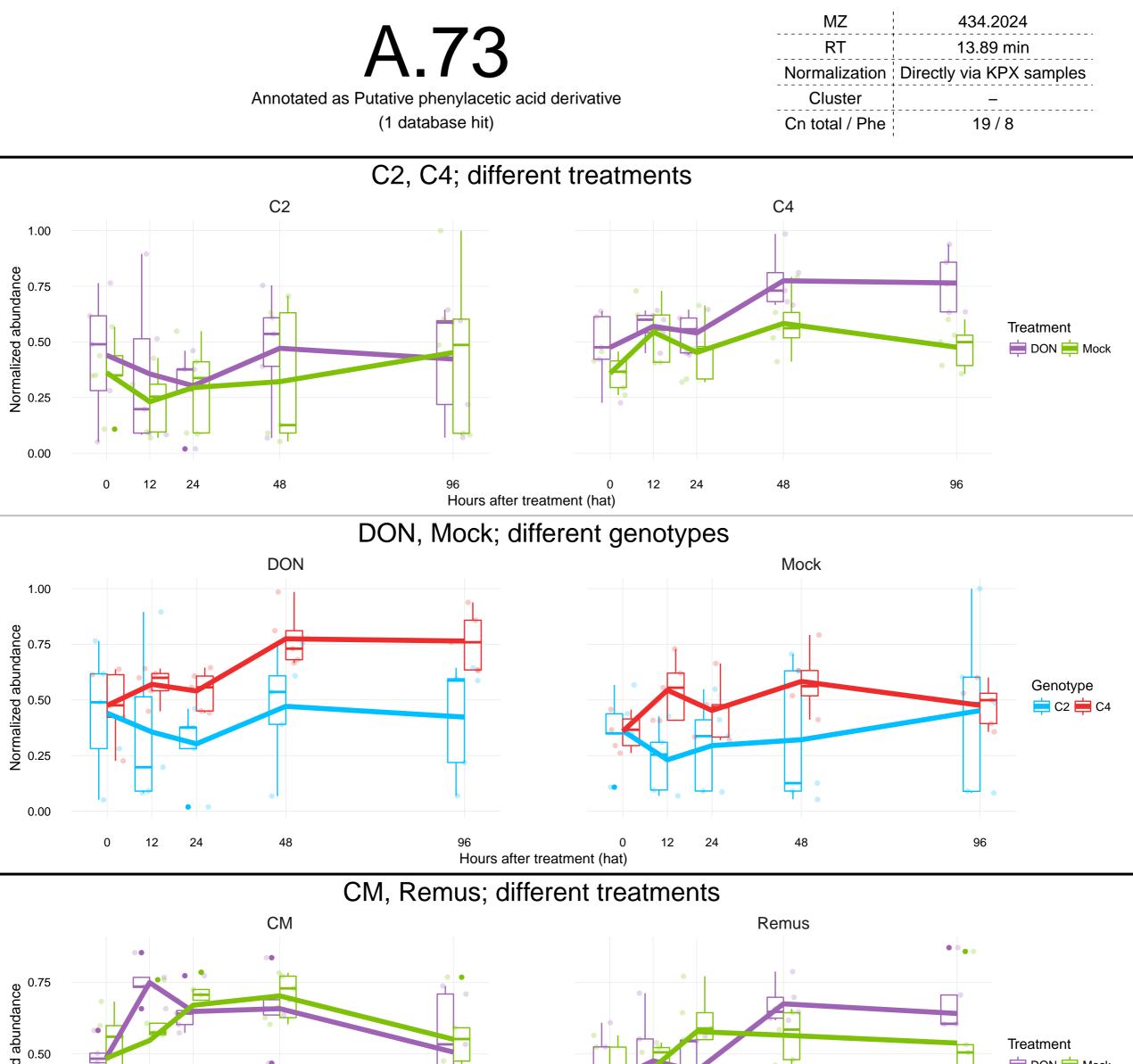


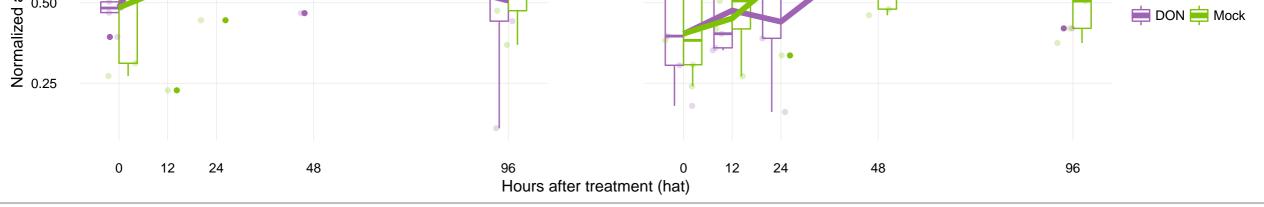




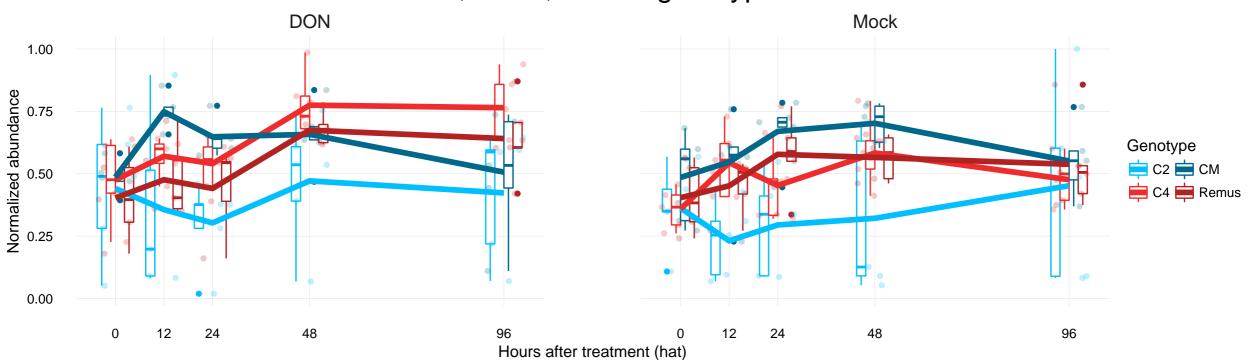
DON, Mock; all four genotypes

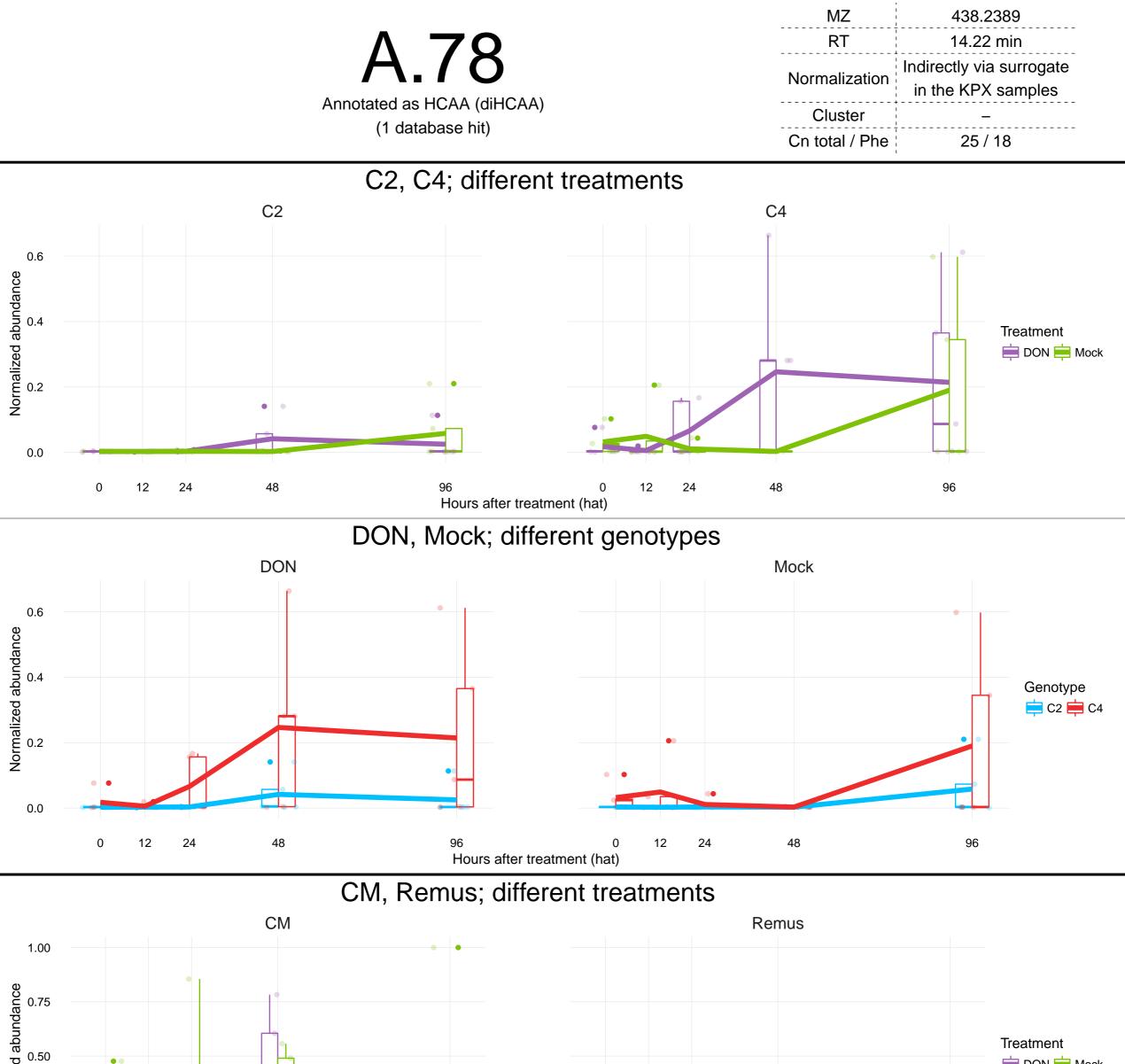


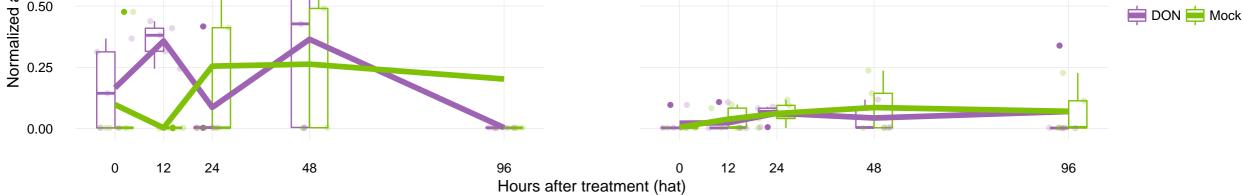




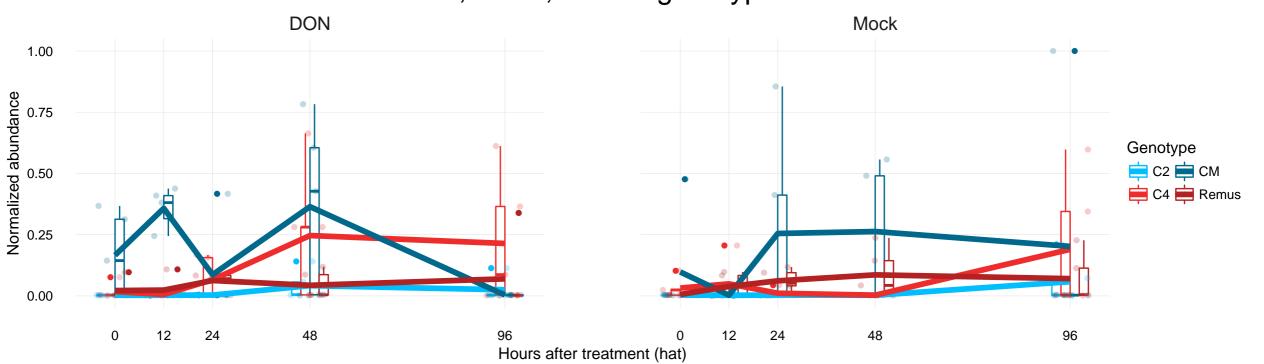
DON, Mock; all four genotypes







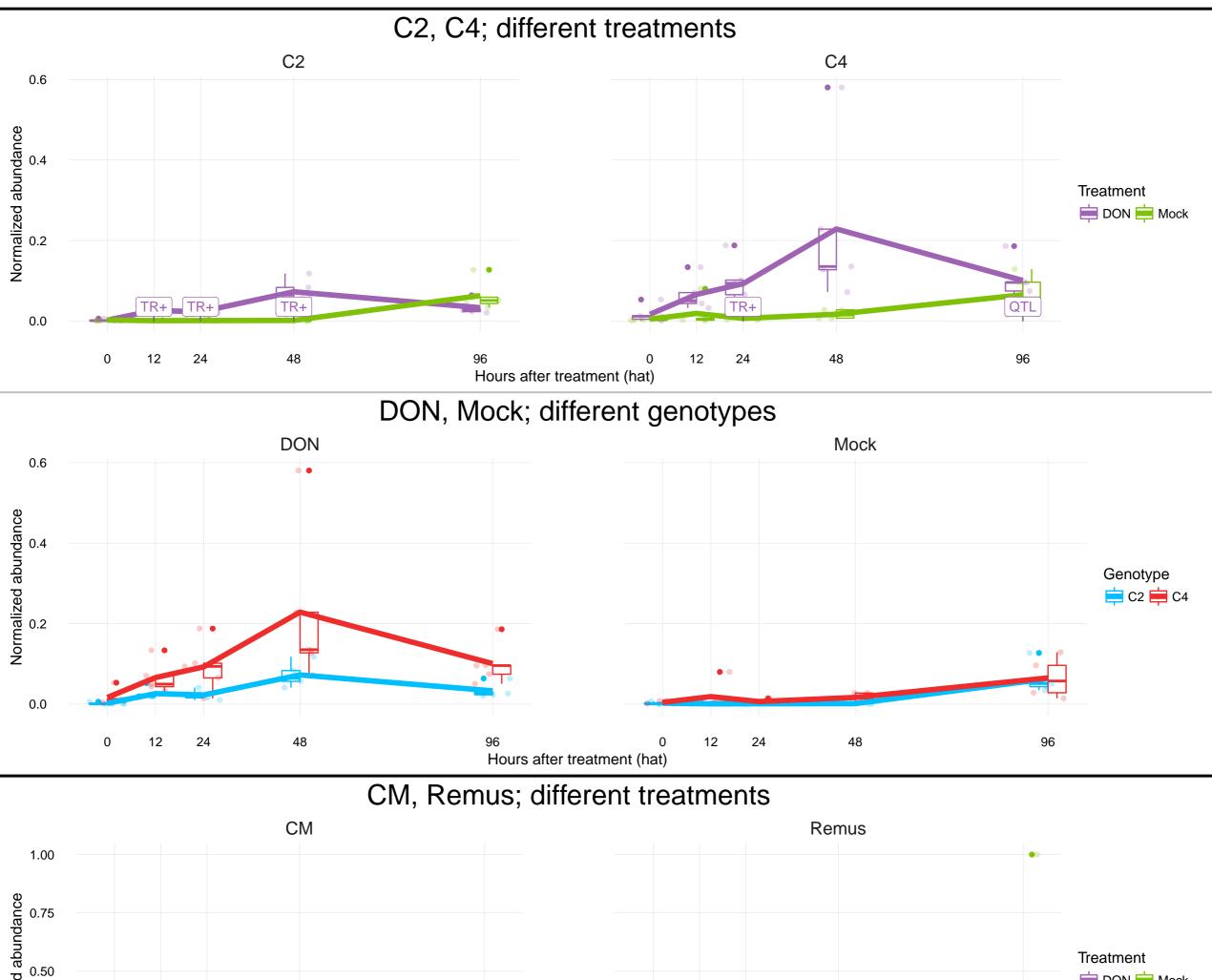
DON, Mock; all four genotypes

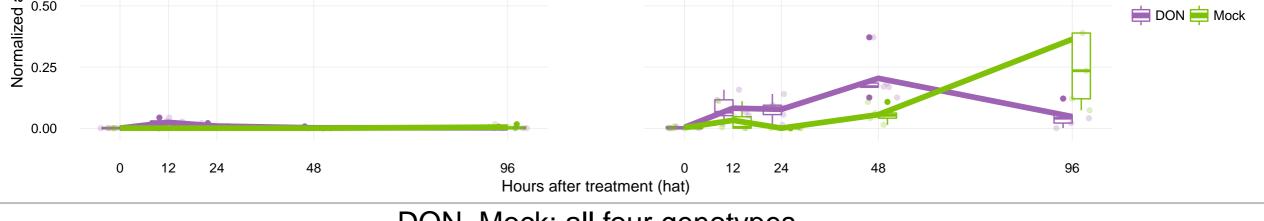


Chlorogenic acid

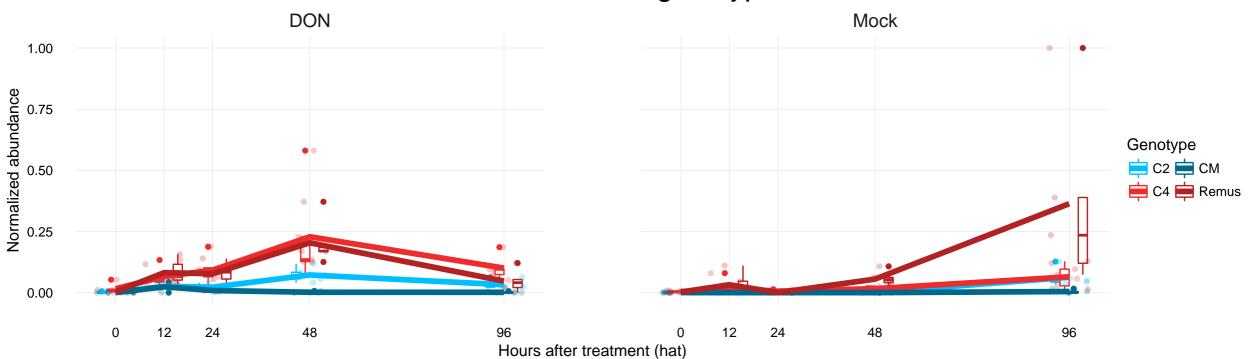
Identified metabolite (level 1)

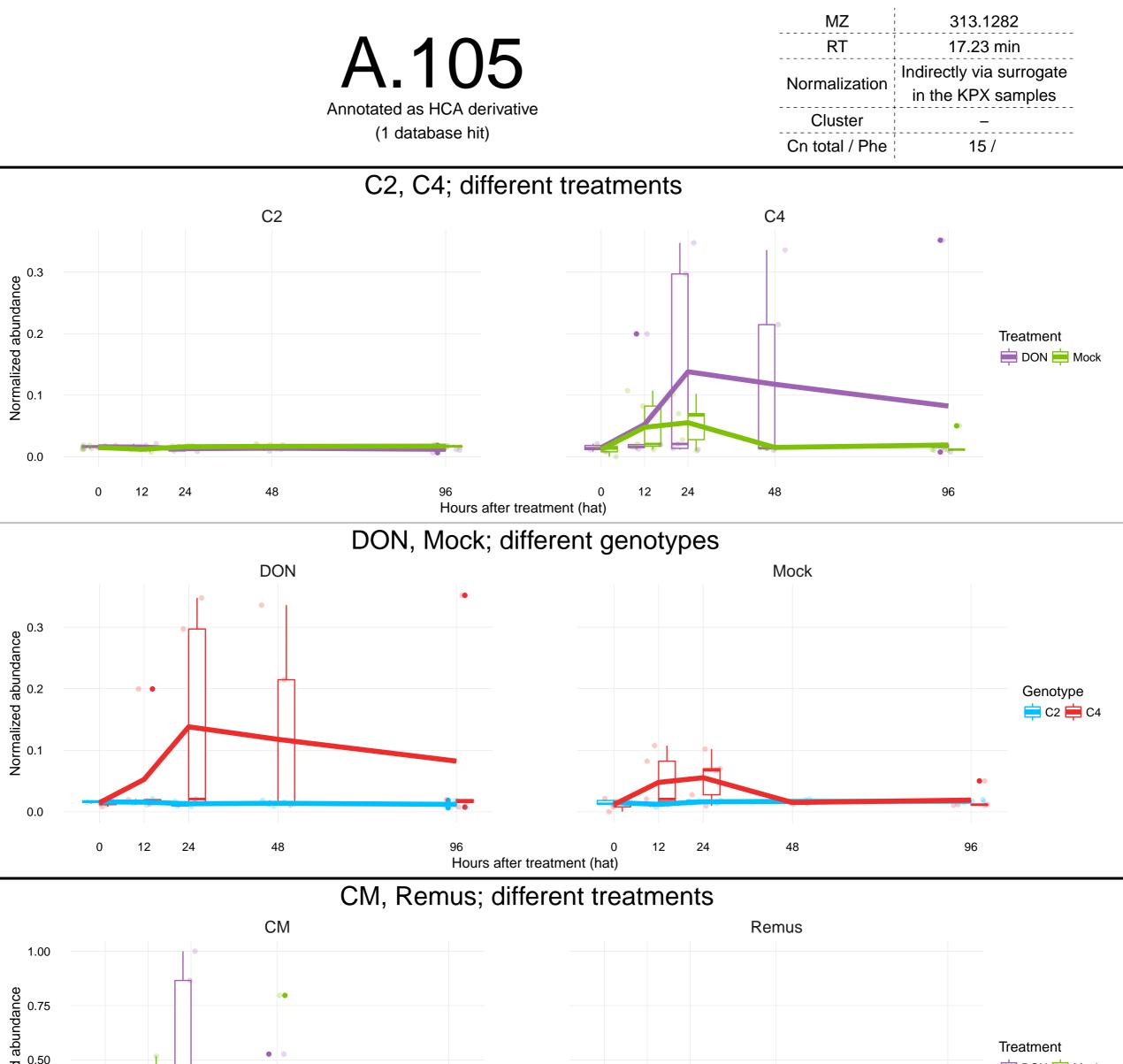
377.0846
9.54 min
Directly via KPX samples
_
16 /

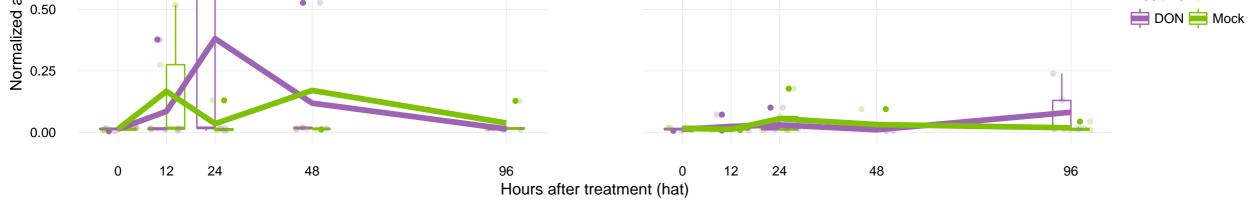




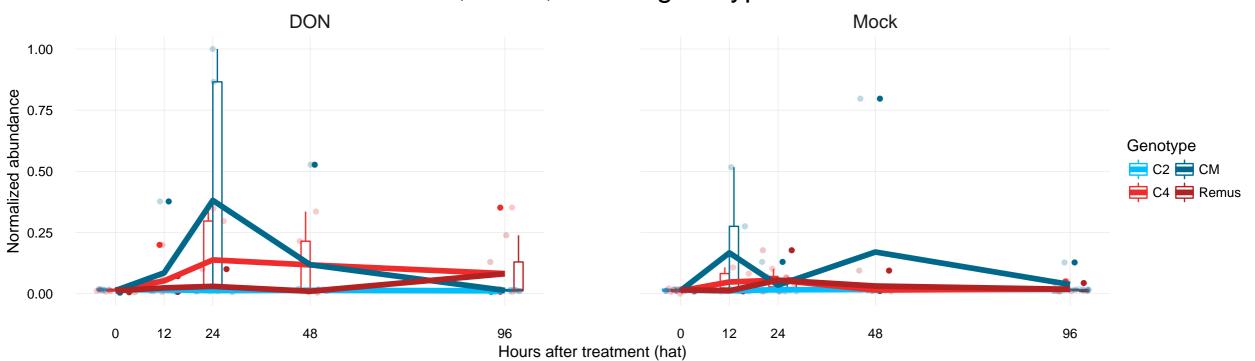
DON, Mock; all four genotypes

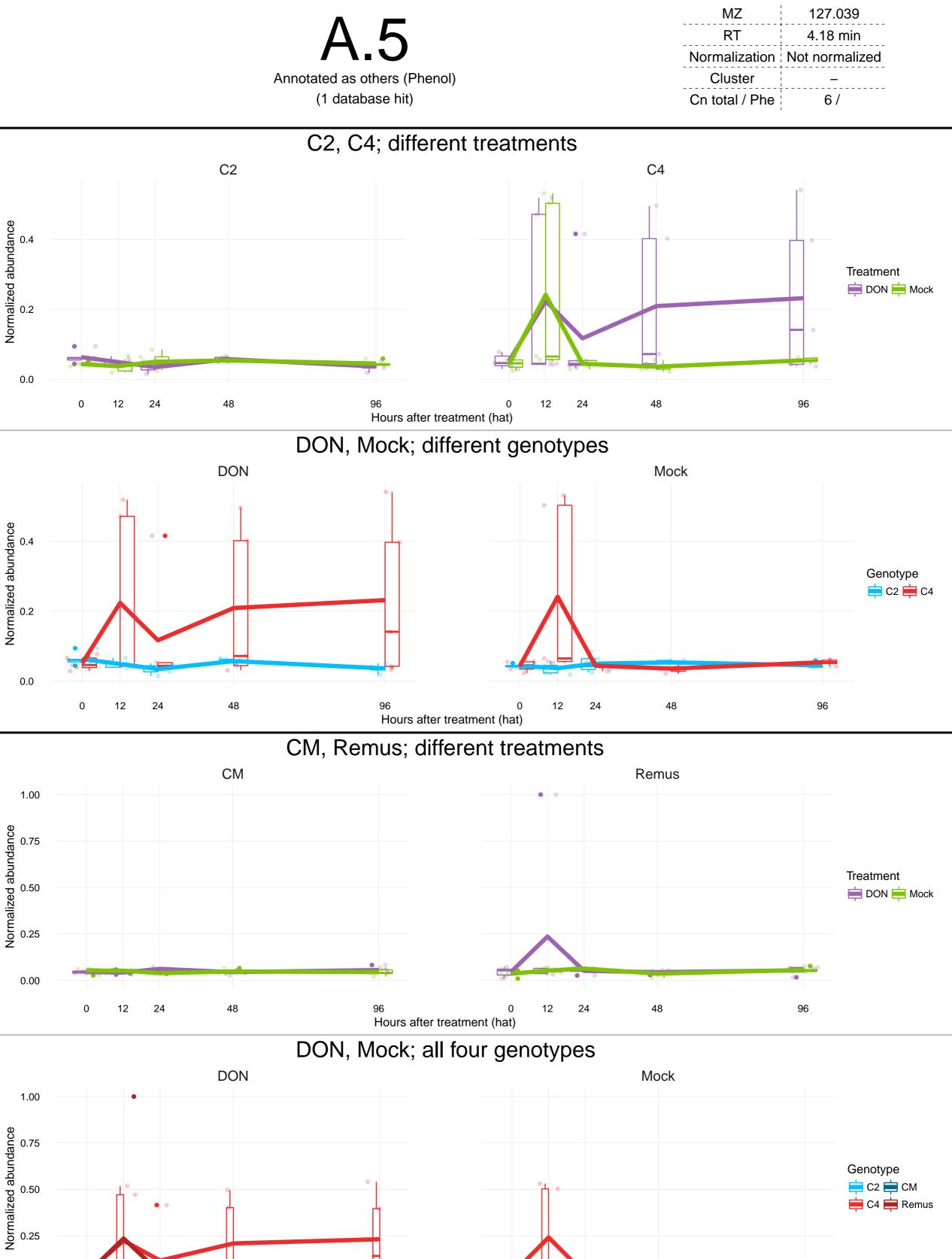






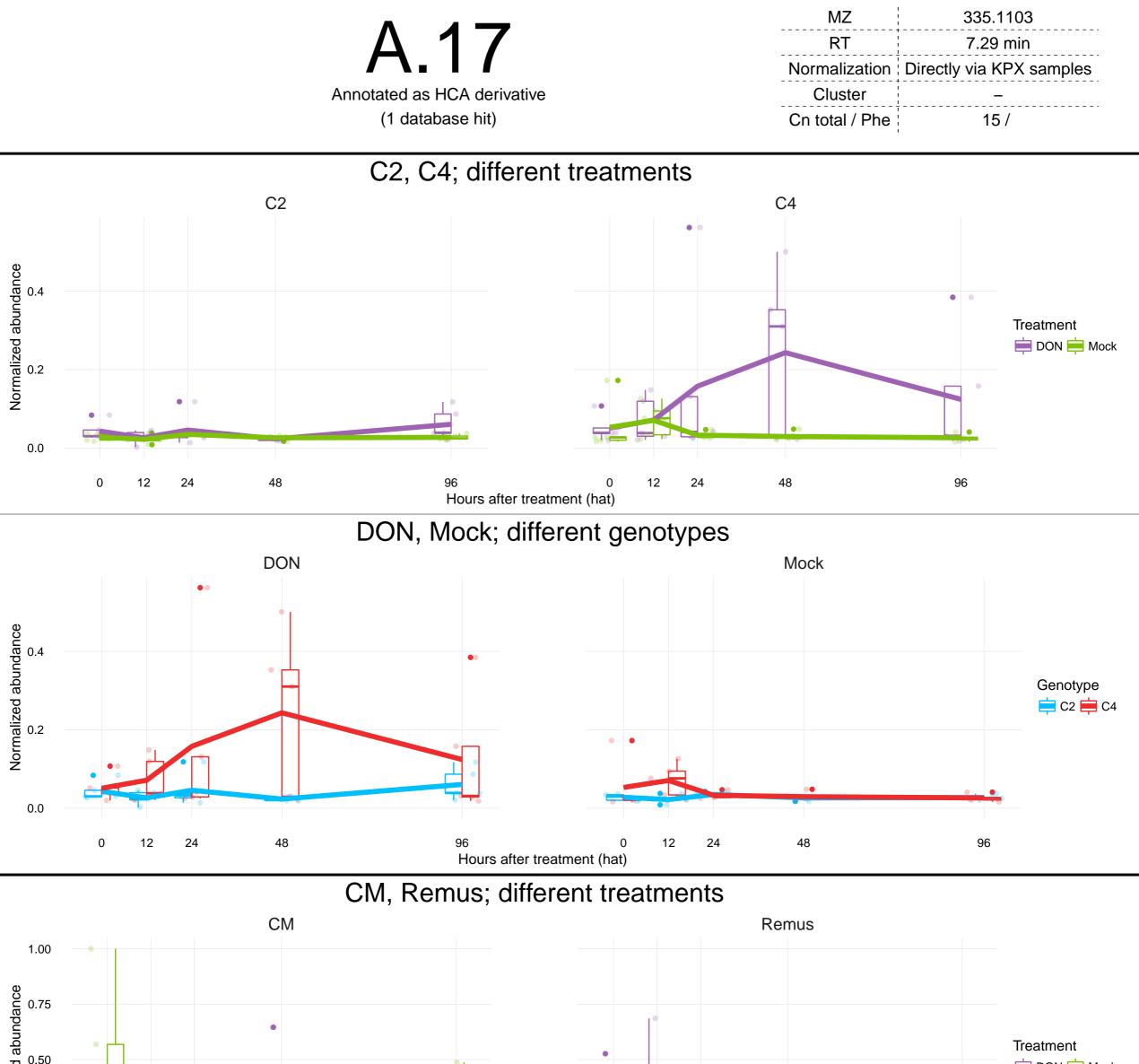
DON, Mock; all four genotypes

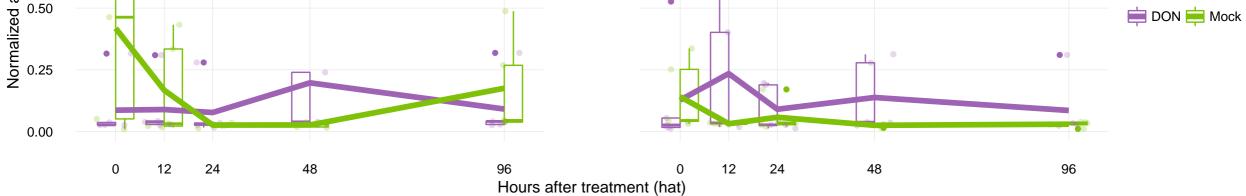




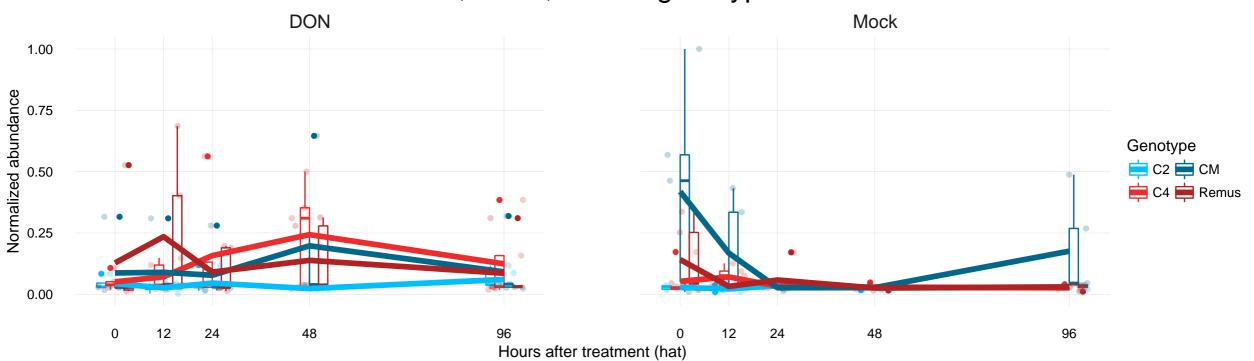


0.00

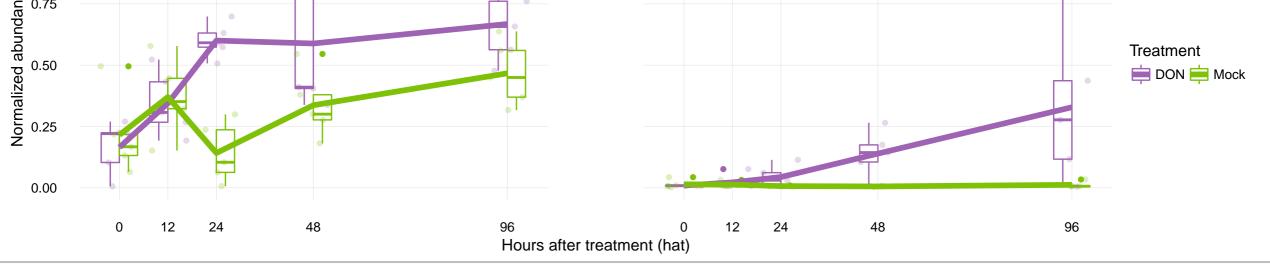




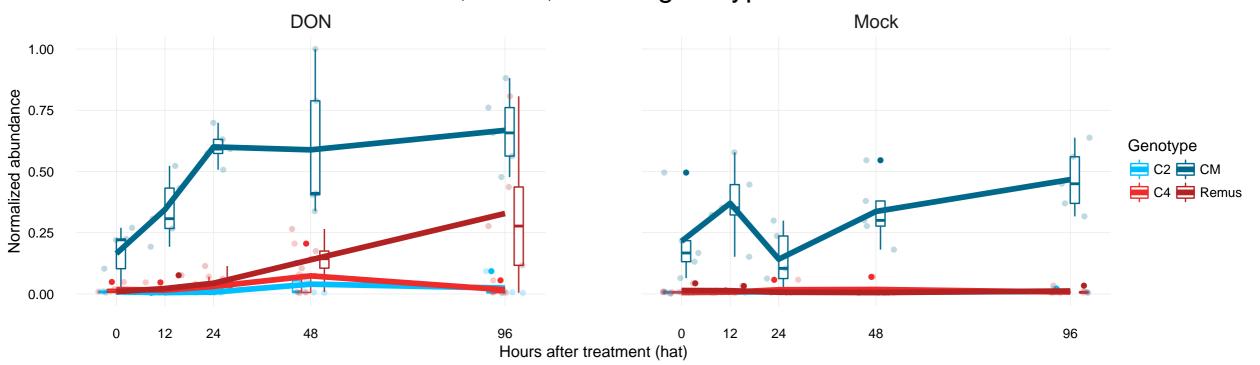
DON, Mock; all four genotypes

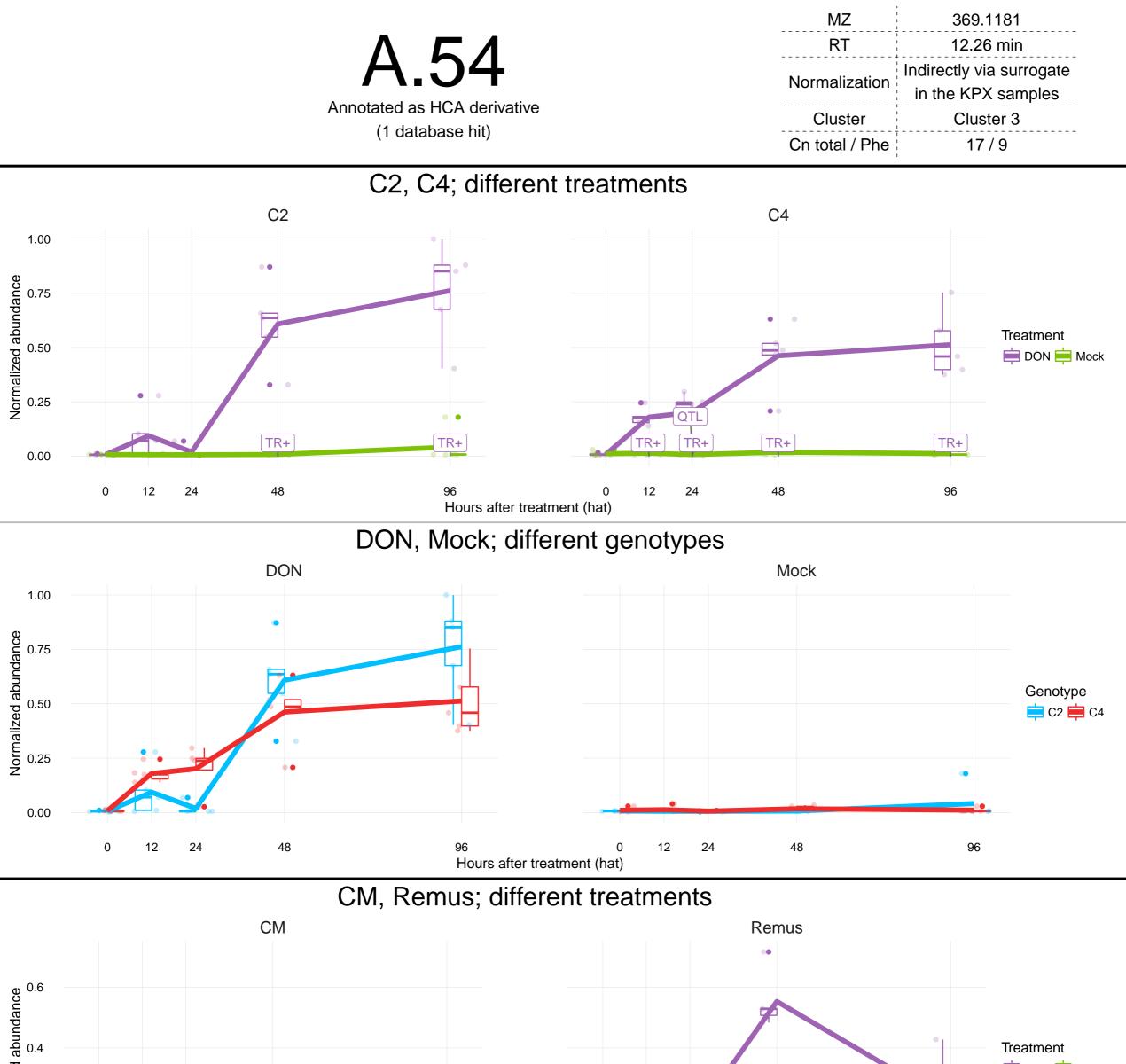


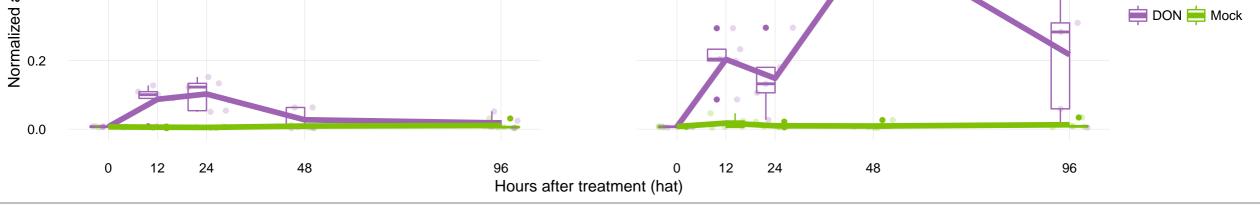
					MZ	549.2118
		/	\ 117		RT	17.96 min
			1.112		Normalization	Indirectly via surrogate in the KPX samples
		P	Annotated as Lignan		Cluster	_
			(1 database hit)		Cn total / Phe	31 / 18
			C2, C4; differen	t treatments		
		C2			C4	
0.20					•	
ě						
Normalized abundance 0.10 - 0 0.05 -						
unqu		• •				Treatment
ອ ອີ ອີ			•			DON 🚔 Mock
naliz				•		
L 0.05 -						• •
2			•			
0.00						
	0 12 24	48	96	0 12 24	48	96
			Hours after treat			
		E	DON, Mock; diffe	erent genotypes		
		DON			Mock	
0.20		••				
Φ						
0.15 -						
pund		• •				Ormatima
ק ק 0.10 –						Genotype C2 🚔 C4
Normalized abundance 0.10 - 0.02 -	. •				• •	
E 0.05 -			•	•		
Z						• •
0.00 -		╘╾╘╼				
	0 10 01	40	00	0 40 04	49	06
	0 12 24	48	96 Hours after trea	0 12 24 atment (hat)	48	96
		CI	M, Remus; differ	ent treatments		
		СМ			Remus	
1.00		•				
			•			
9 0.75 –						



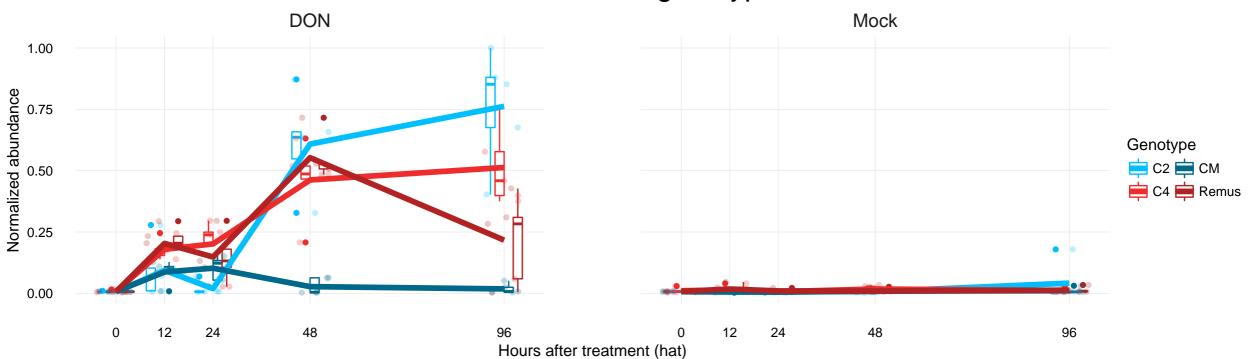
DON, Mock; all four genotypes

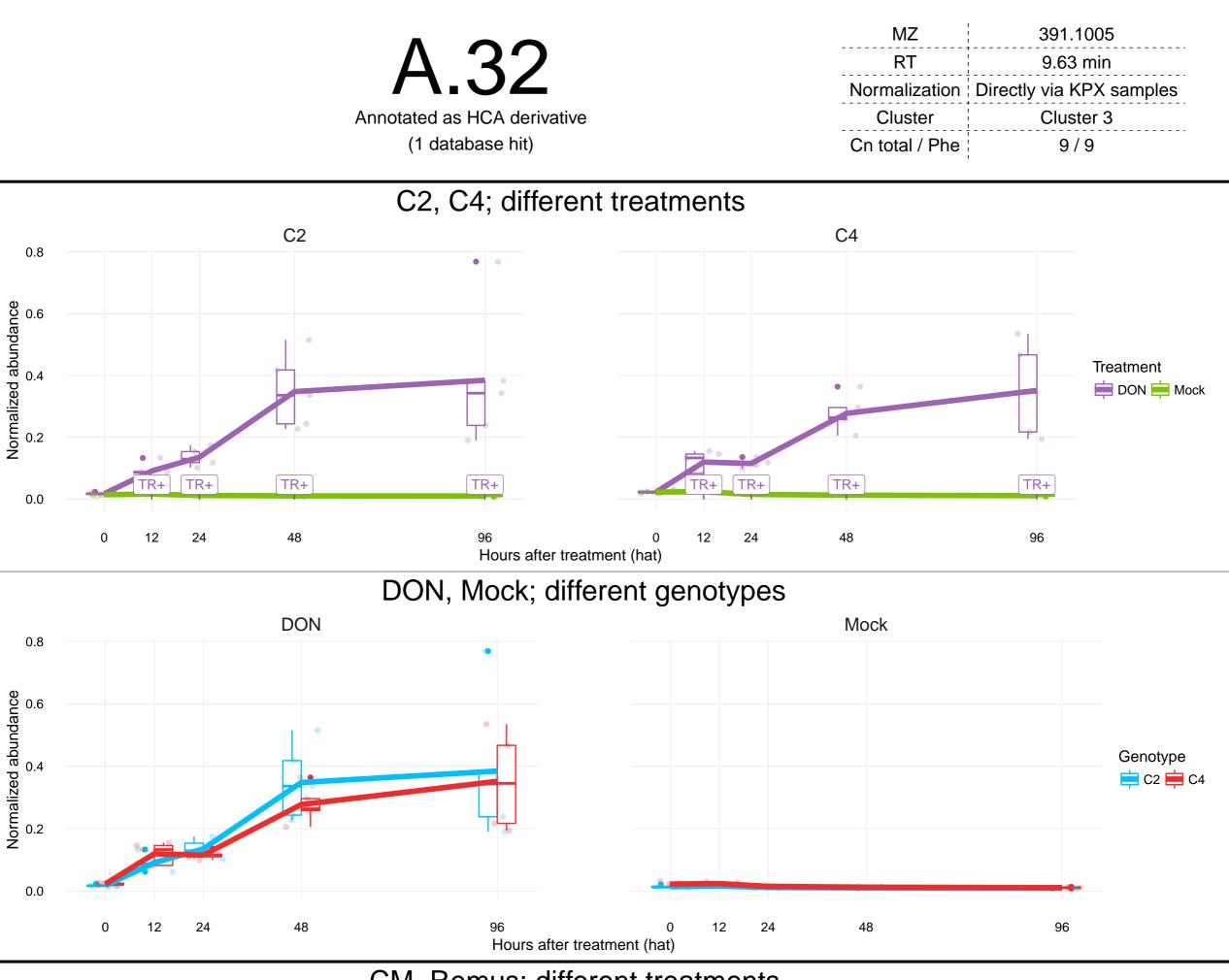




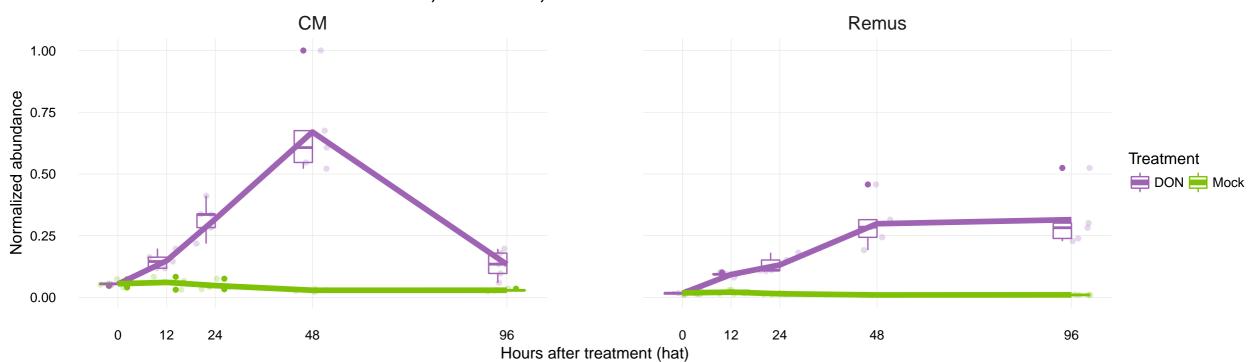


DON, Mock; all four genotypes

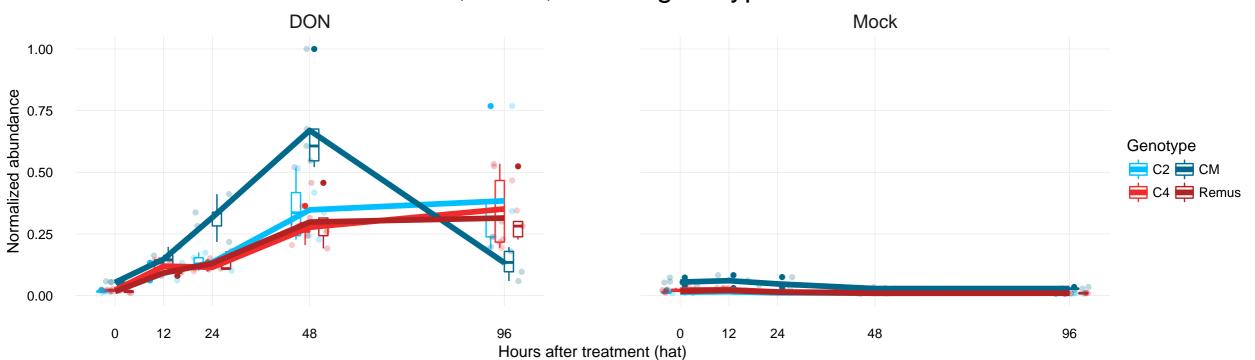


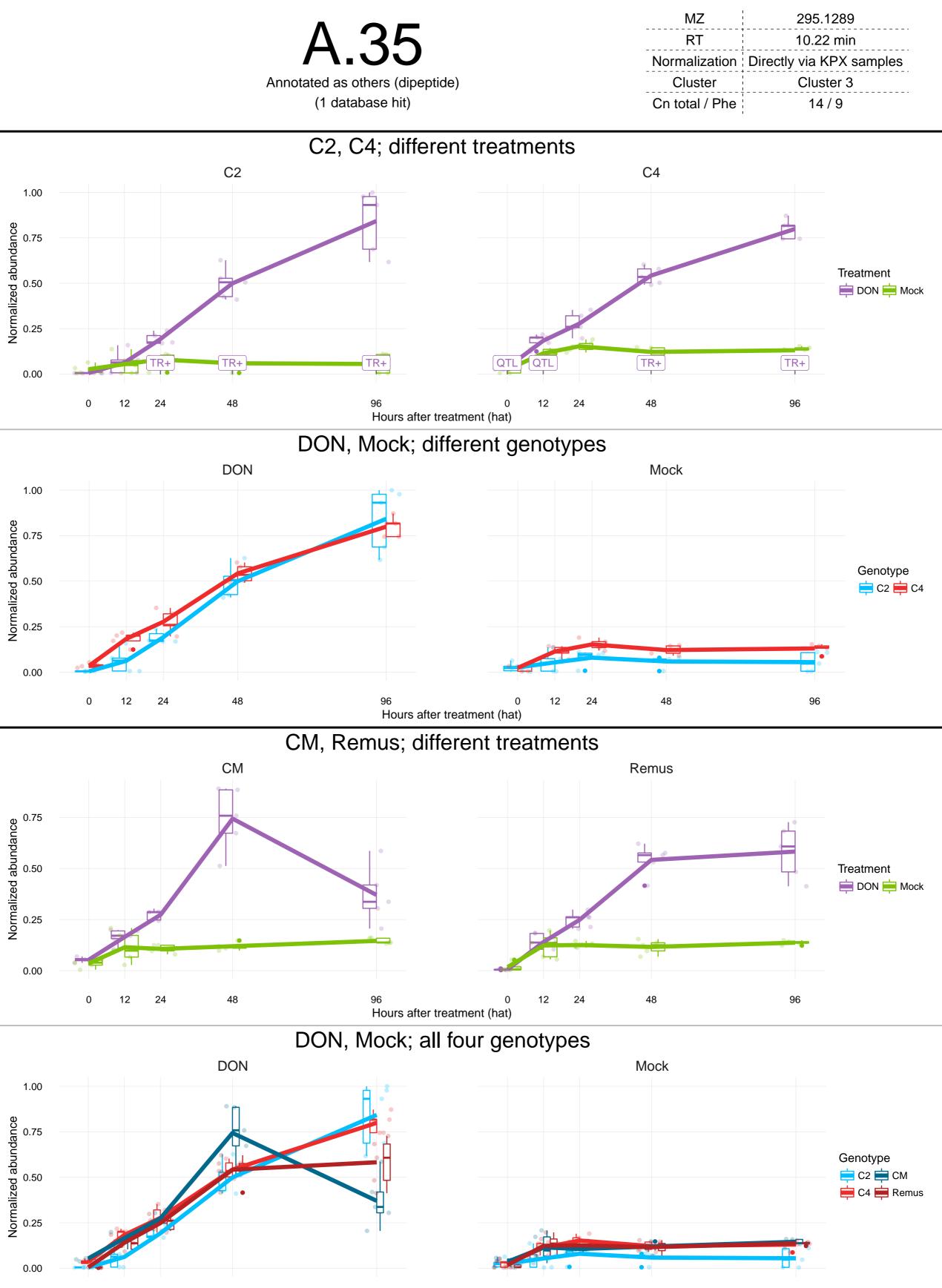


CM, Remus; different treatments

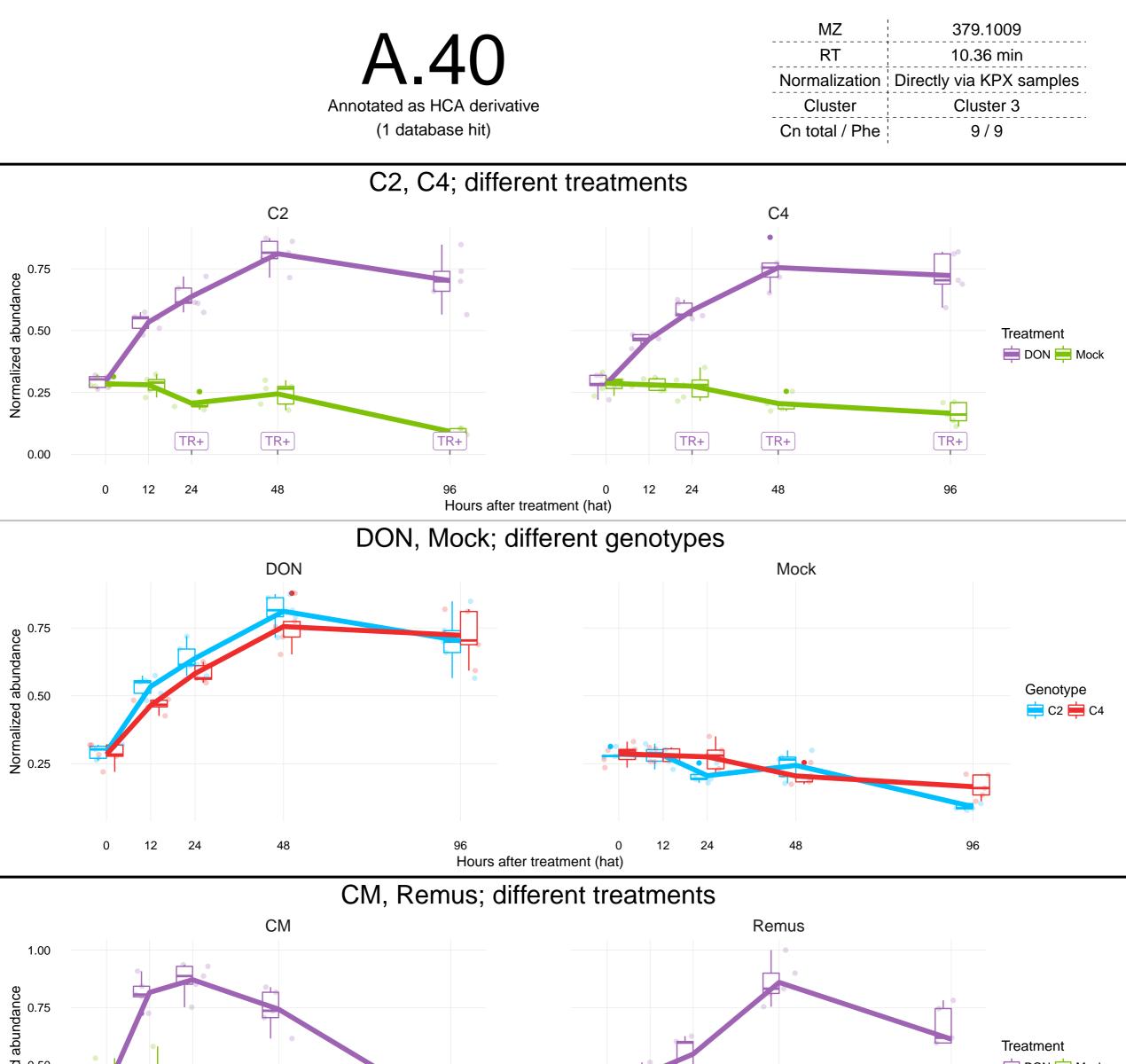


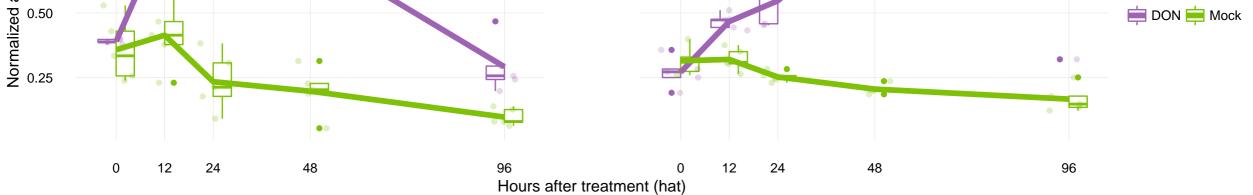
DON, Mock; all four genotypes



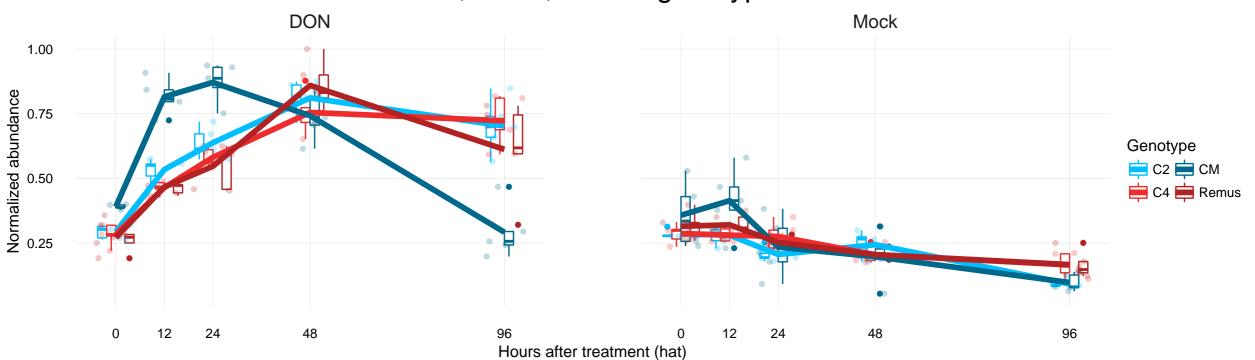


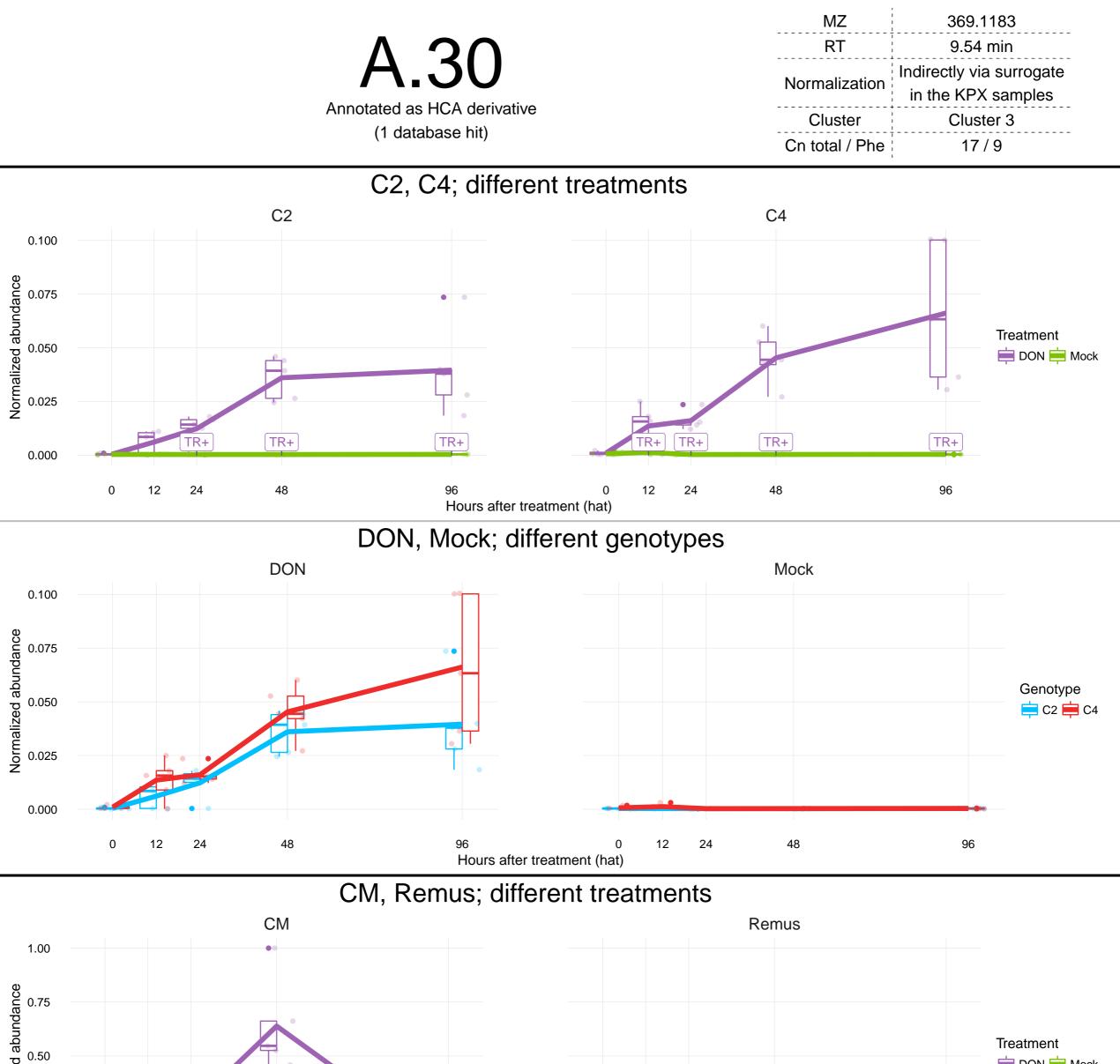
96 0 12 Hours after treatment (hat)

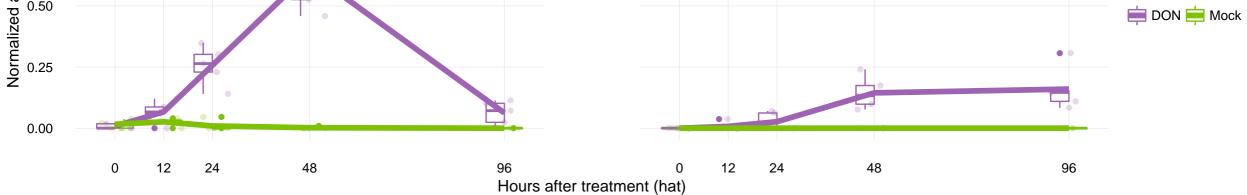




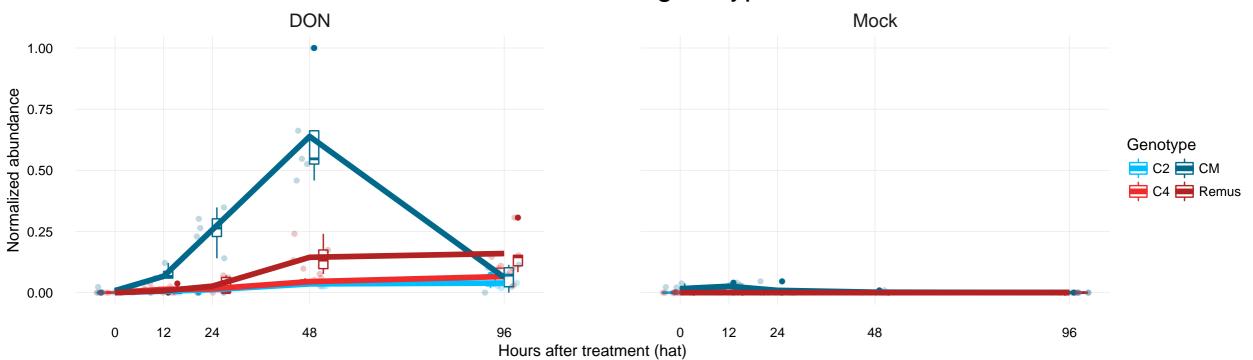
DON, Mock; all four genotypes

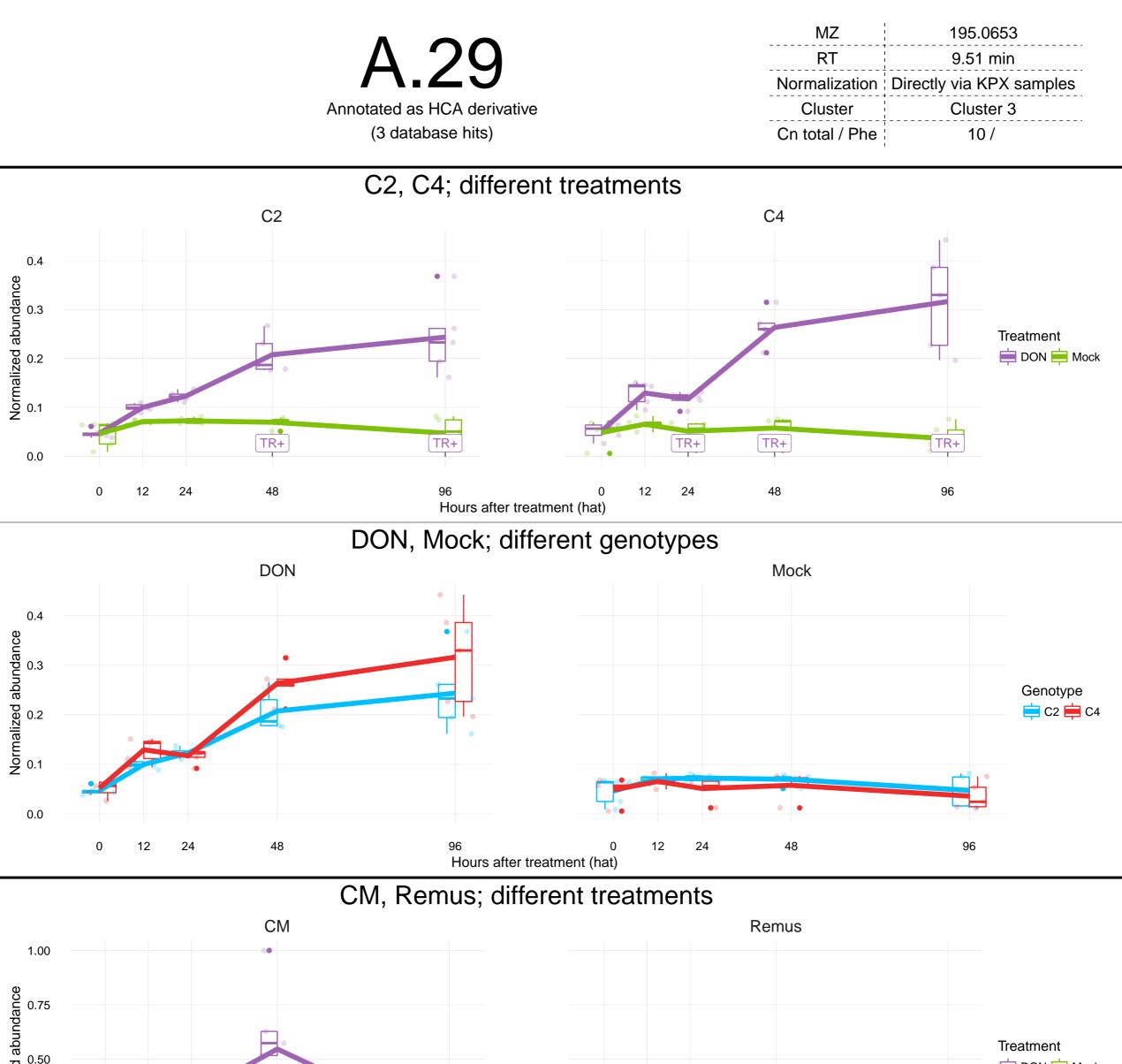


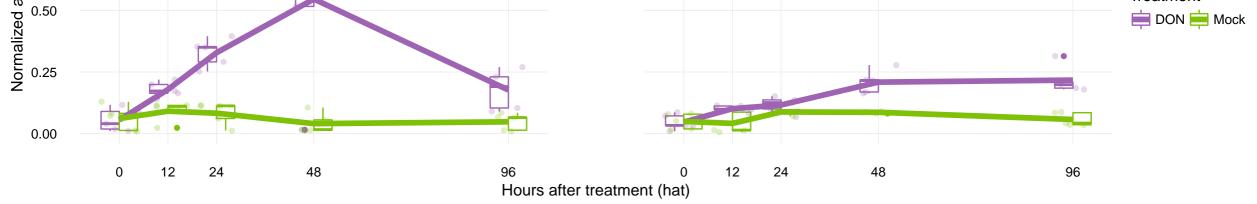




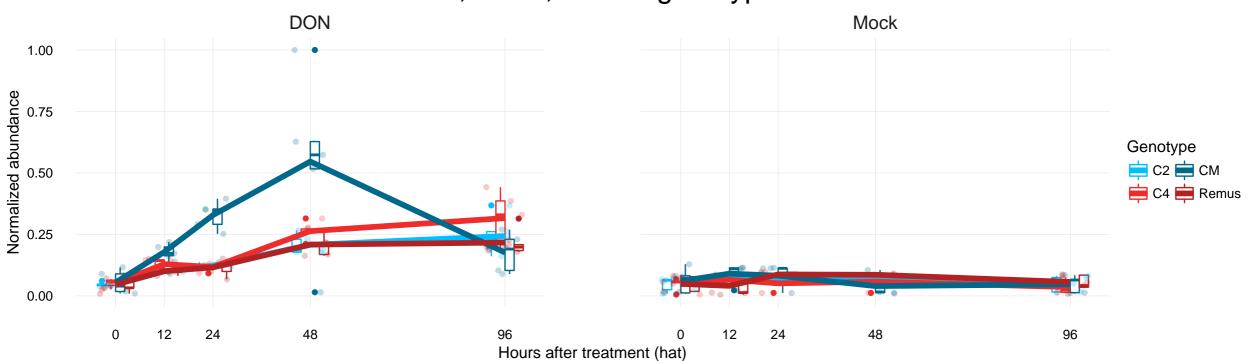
DON, Mock; all four genotypes

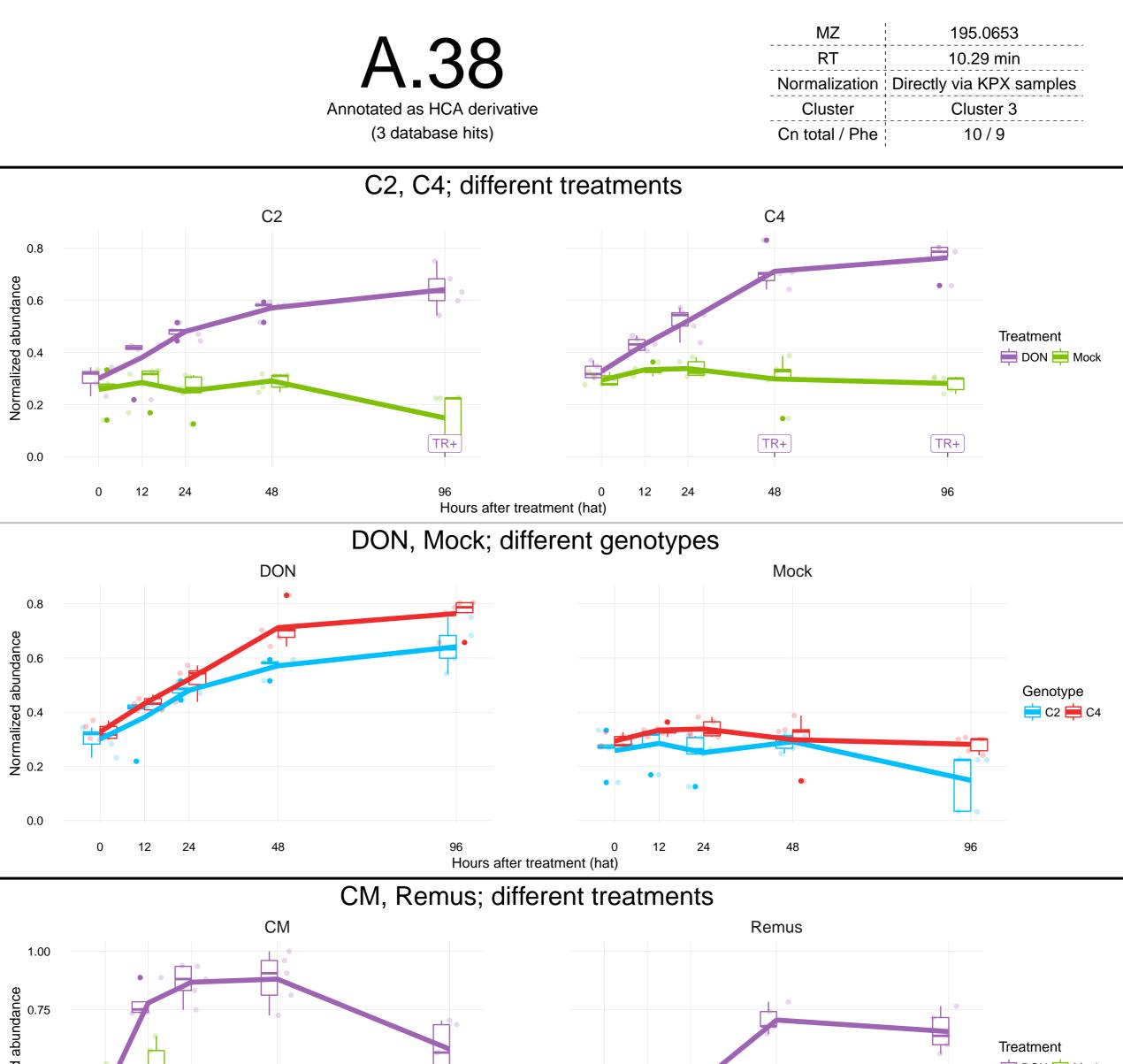


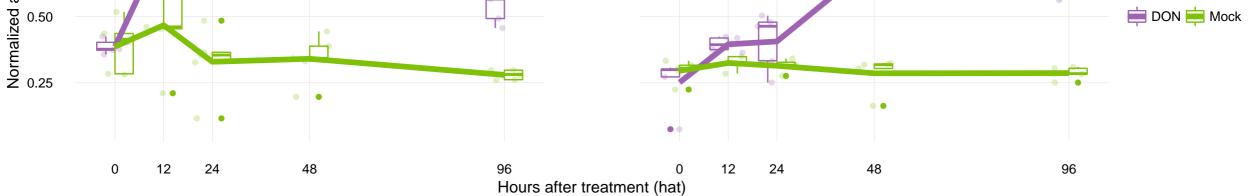




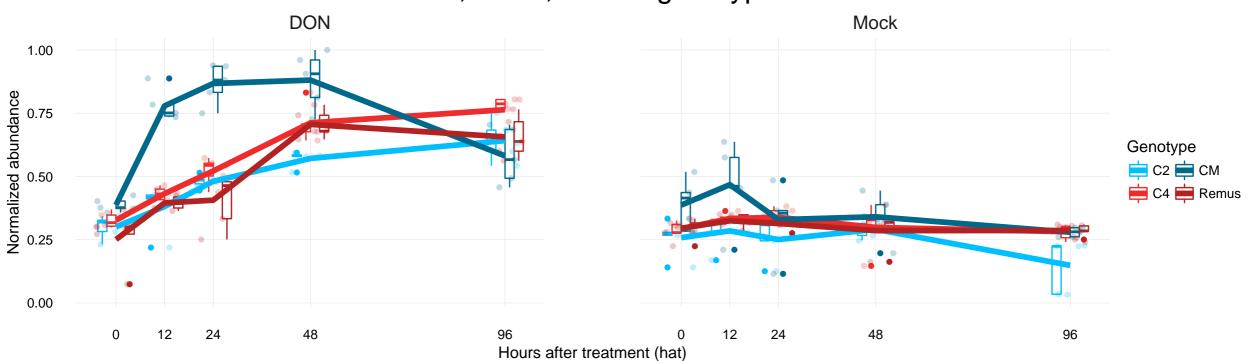
DON, Mock; all four genotypes

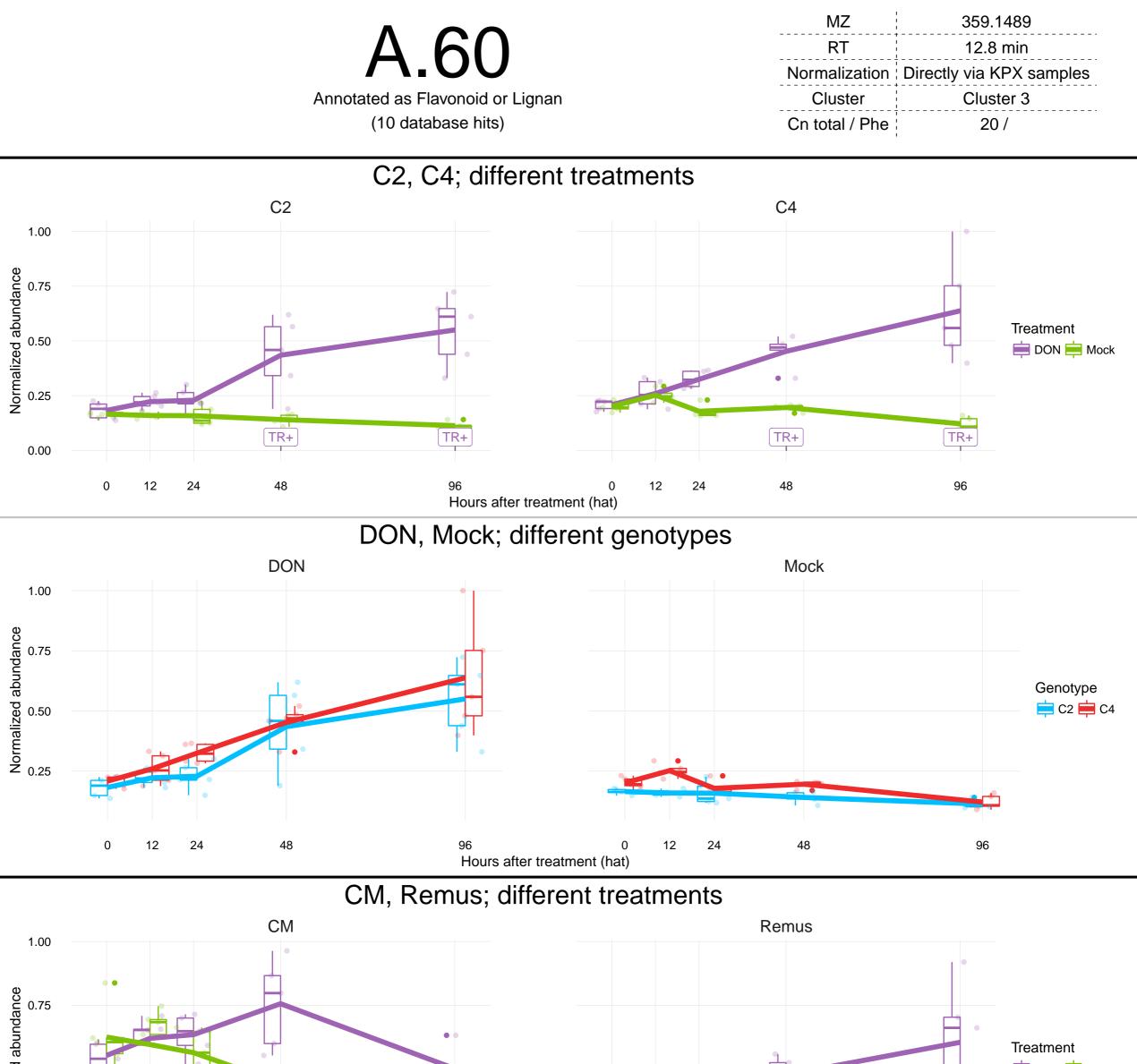


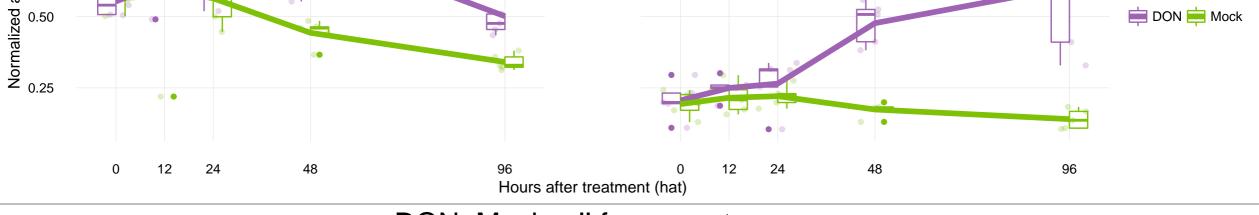




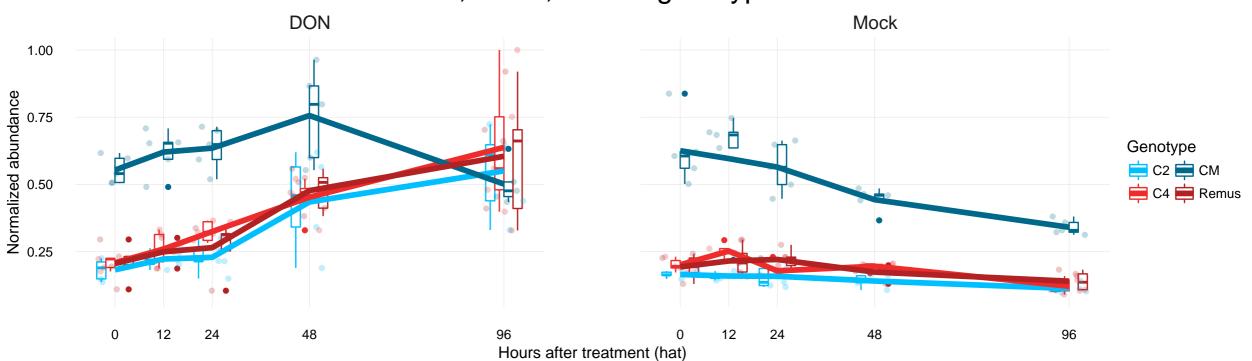
DON, Mock; all four genotypes

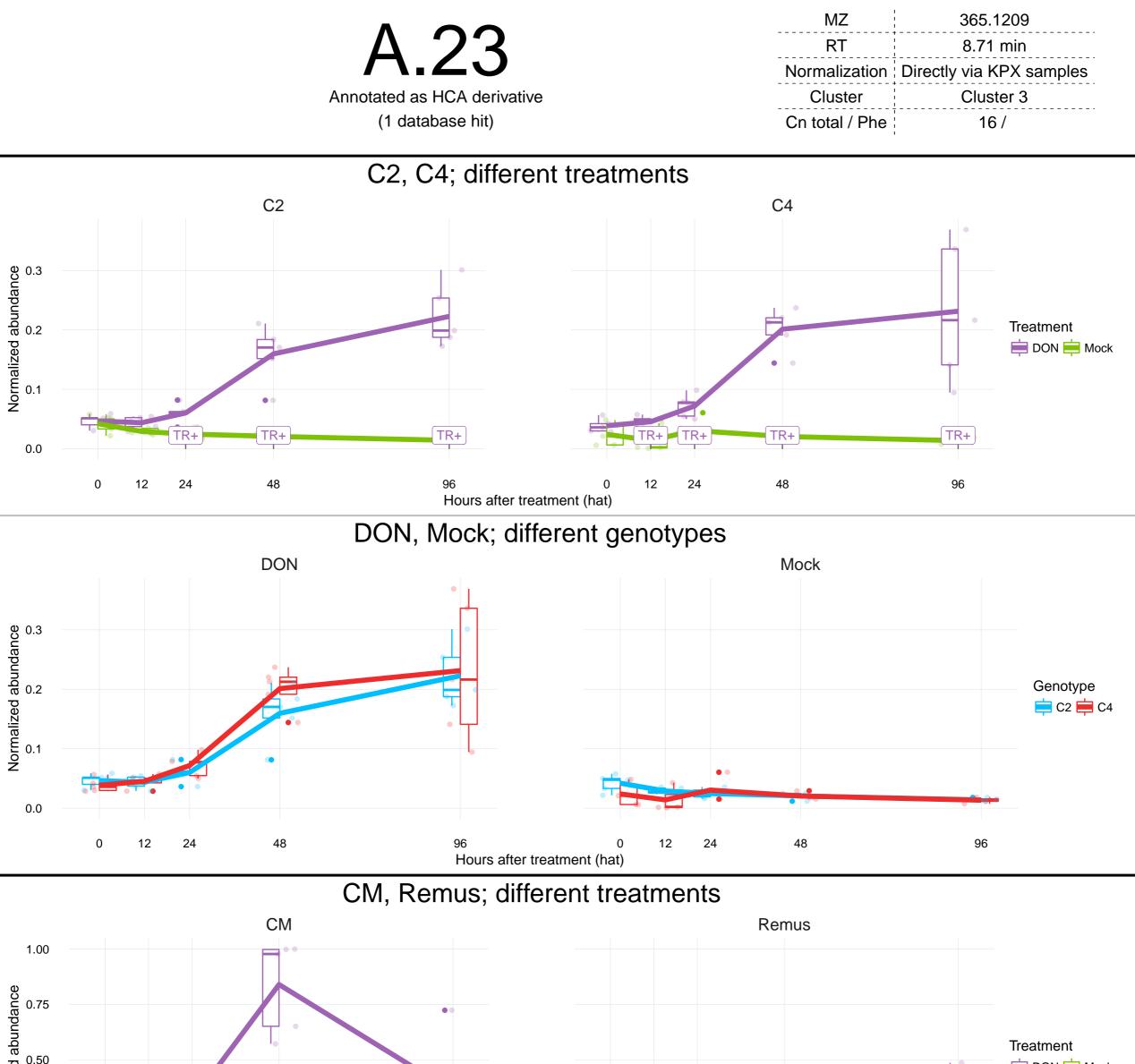


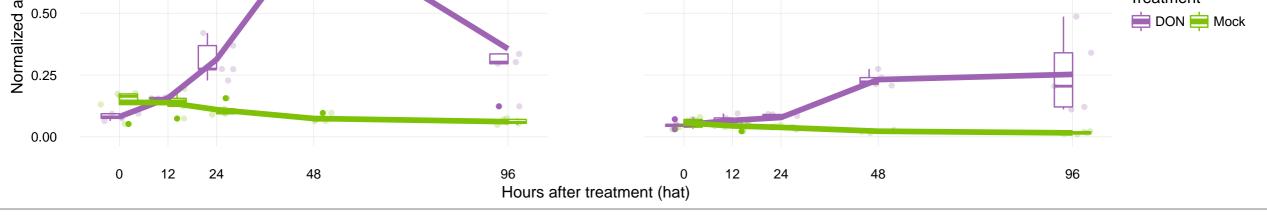




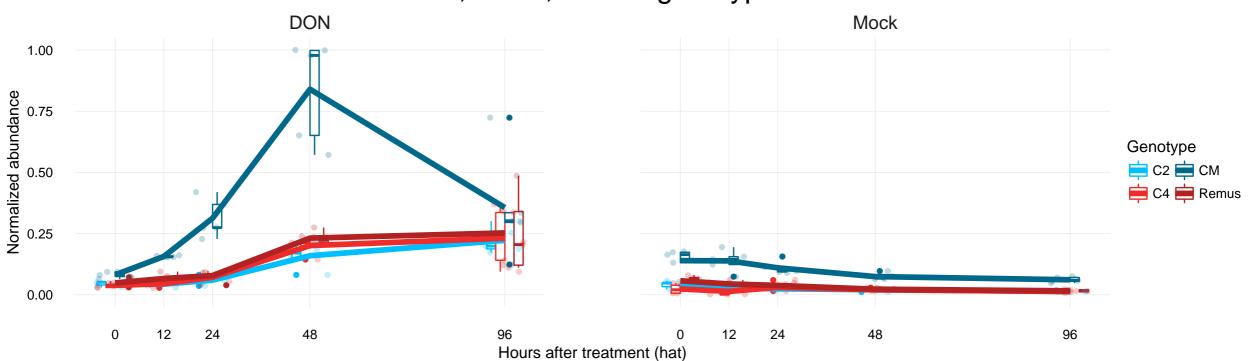
DON, Mock; all four genotypes

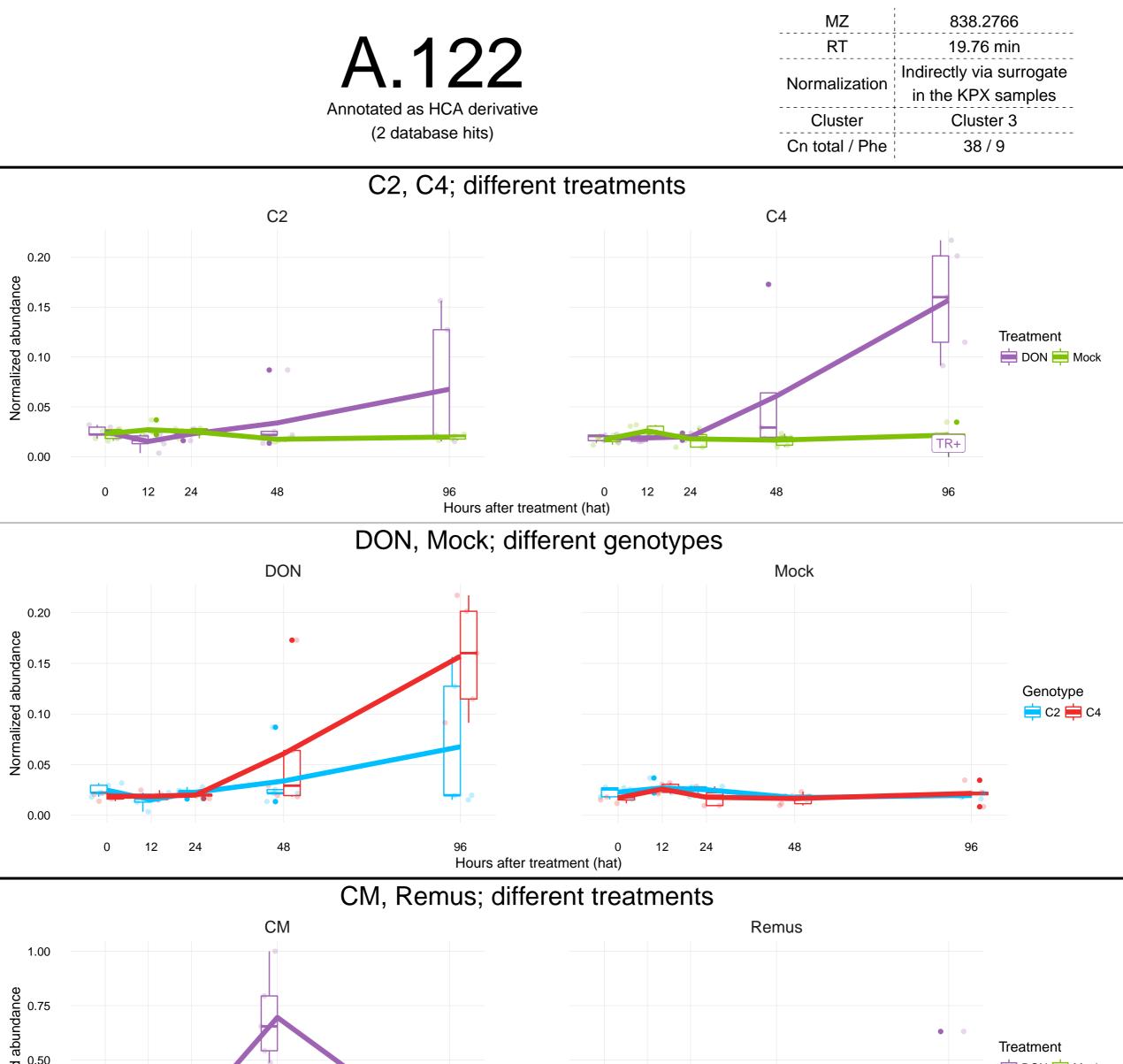


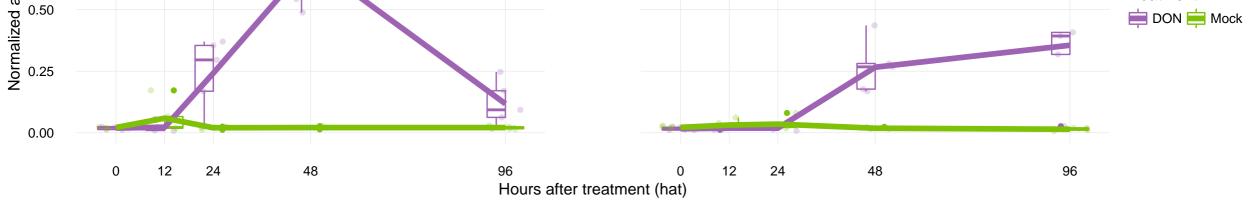




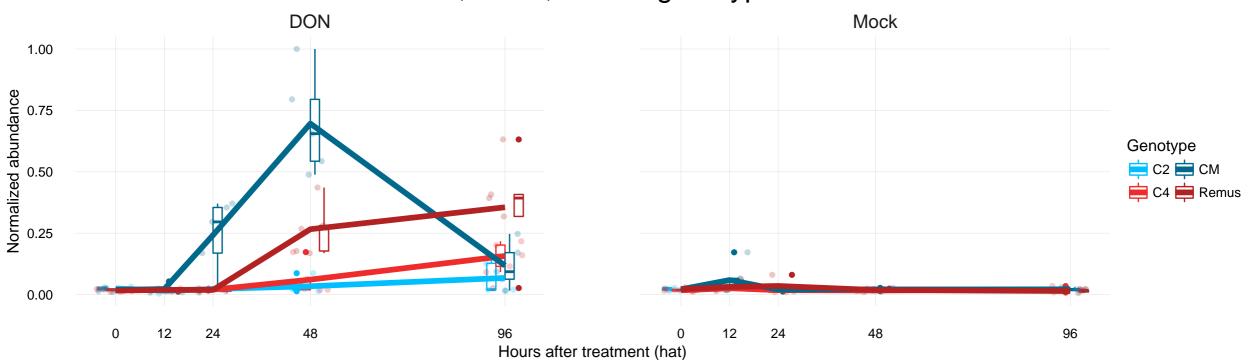
DON, Mock; all four genotypes



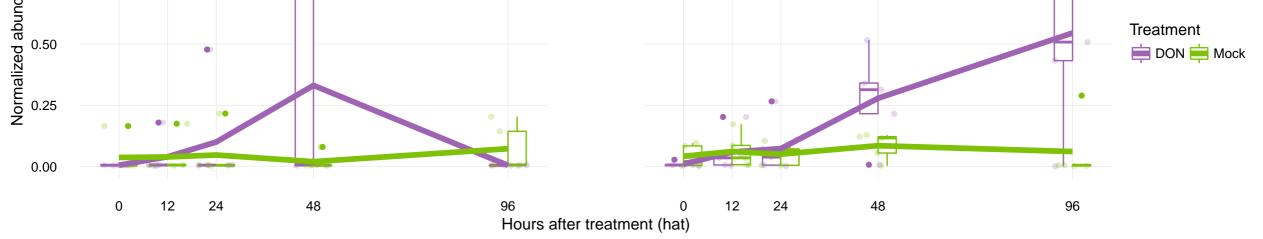




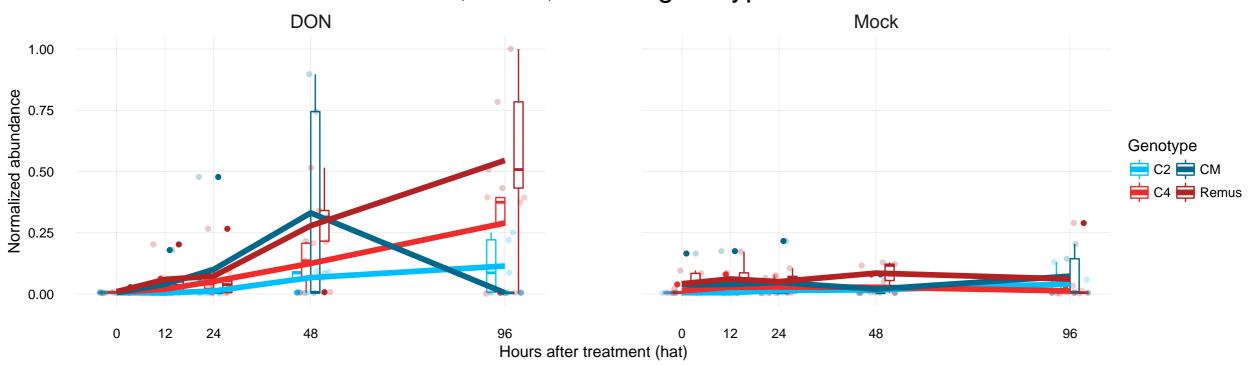
DON, Mock; all four genotypes

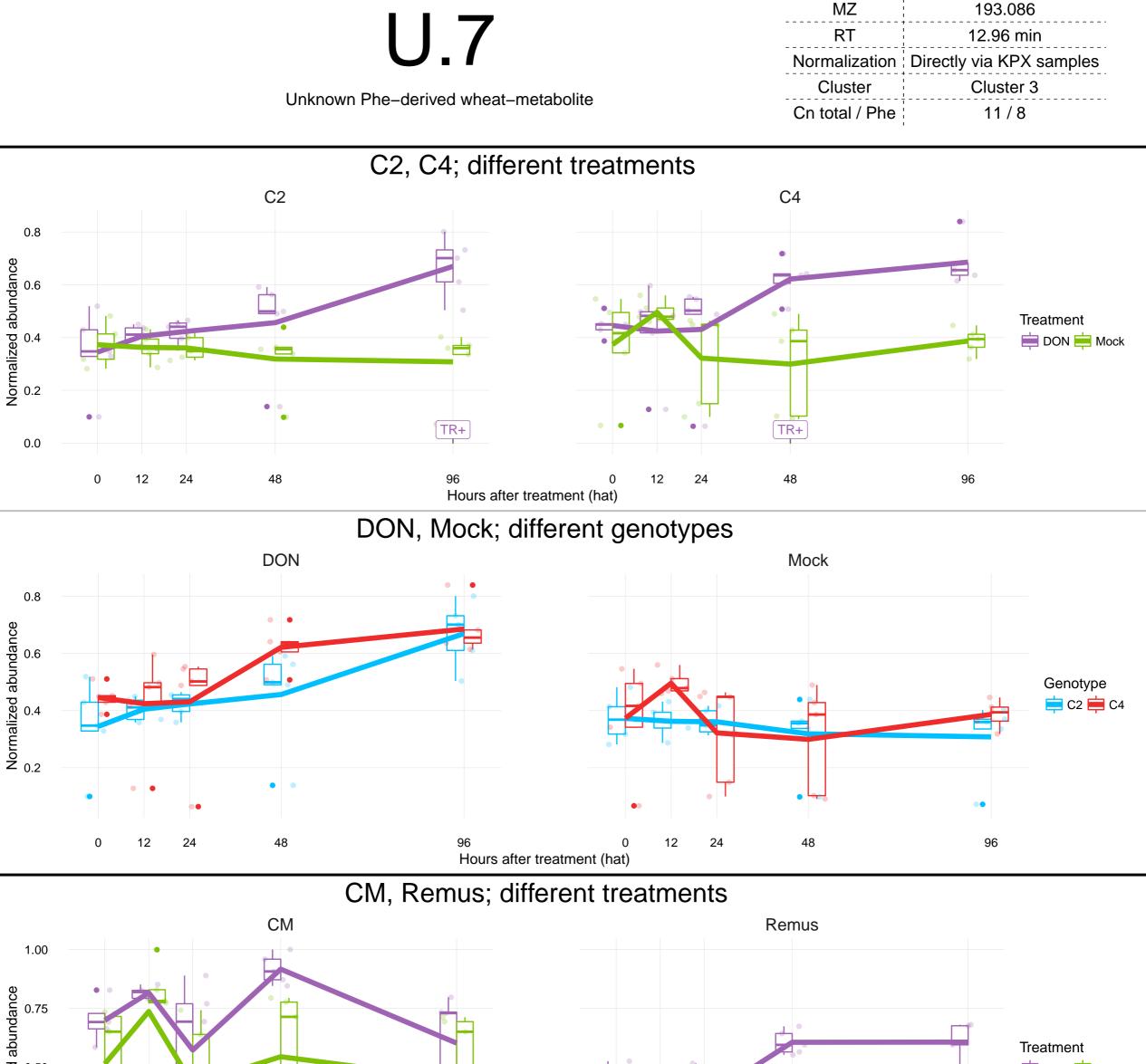


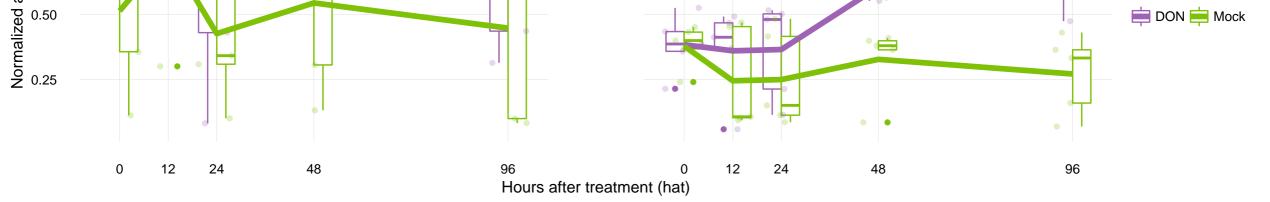
		MZ	339.1076	
		RT	11.79 min	
	A.49	Normalization	Indirectly via surrogate in the KPX samples	
	Annotated as HCA derivative	Cluster	Cluster 3	
	(1 database hit)	Cn total / Phe	16 /	
	C2, C4; different tr	reatments		
	C2	C4		
0.4 —				
es o o				
Normalized abundance 7.0 = 0.			•	
nqa po 0.2			Treatment	
alizeo			🚔 DON 🚔 Mock	
й 0.1 —				
Z				
0.0			TR+	
	0 12 24 48 96 Hours after treatment	0 12 24 48 : (hat)	96	
	DON, Mock; differe	nt genotypes		
	DON	Mock		
0.4				
e				
Normalized abundance				
abur			Genotype	
lized			텆 C2 🗮 C4	
0.1 -			•	
ž				
0.0				
	0 12 24 48 96	0 12 24 48	96	
Hours after treatment (hat) CM, Remus; different treatments				
	CM CM	Remus		
1.00			•	
۵.				
0.75 nudance				
nnc				



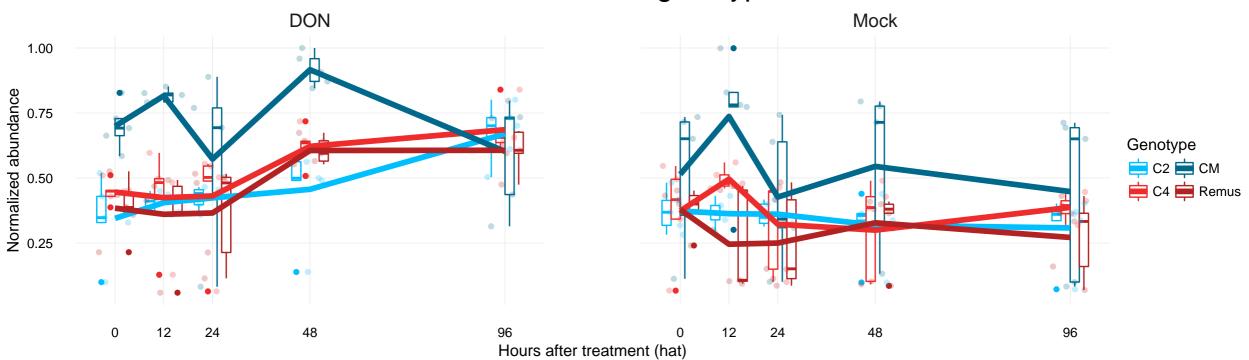
DON, Mock; all four genotypes

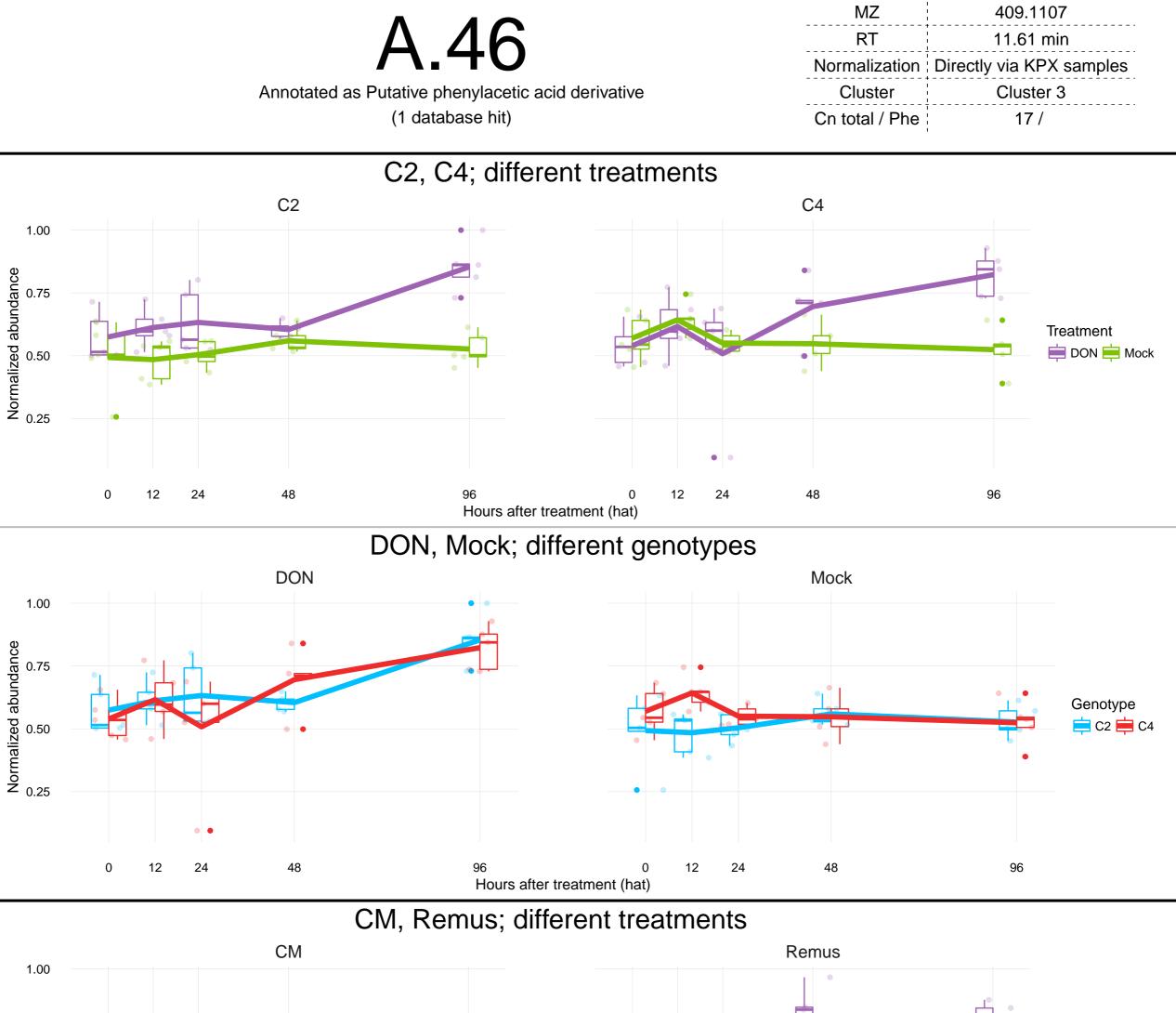


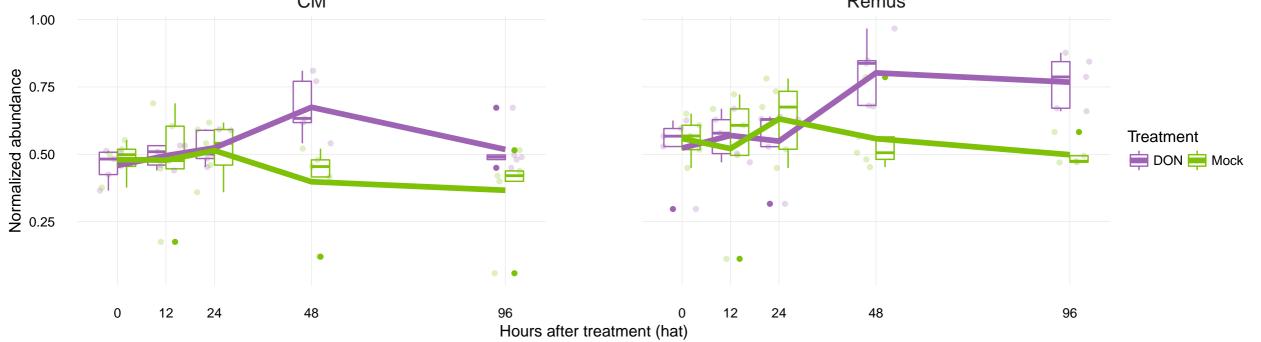




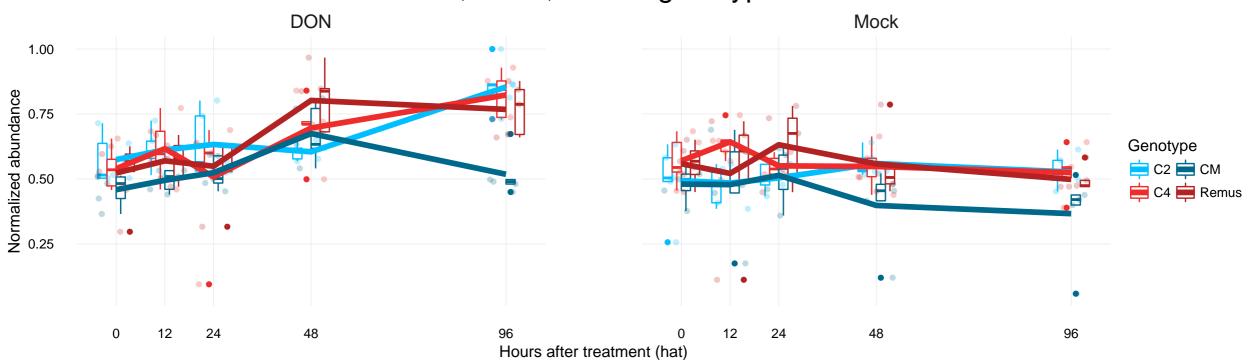
DON, Mock; all four genotypes

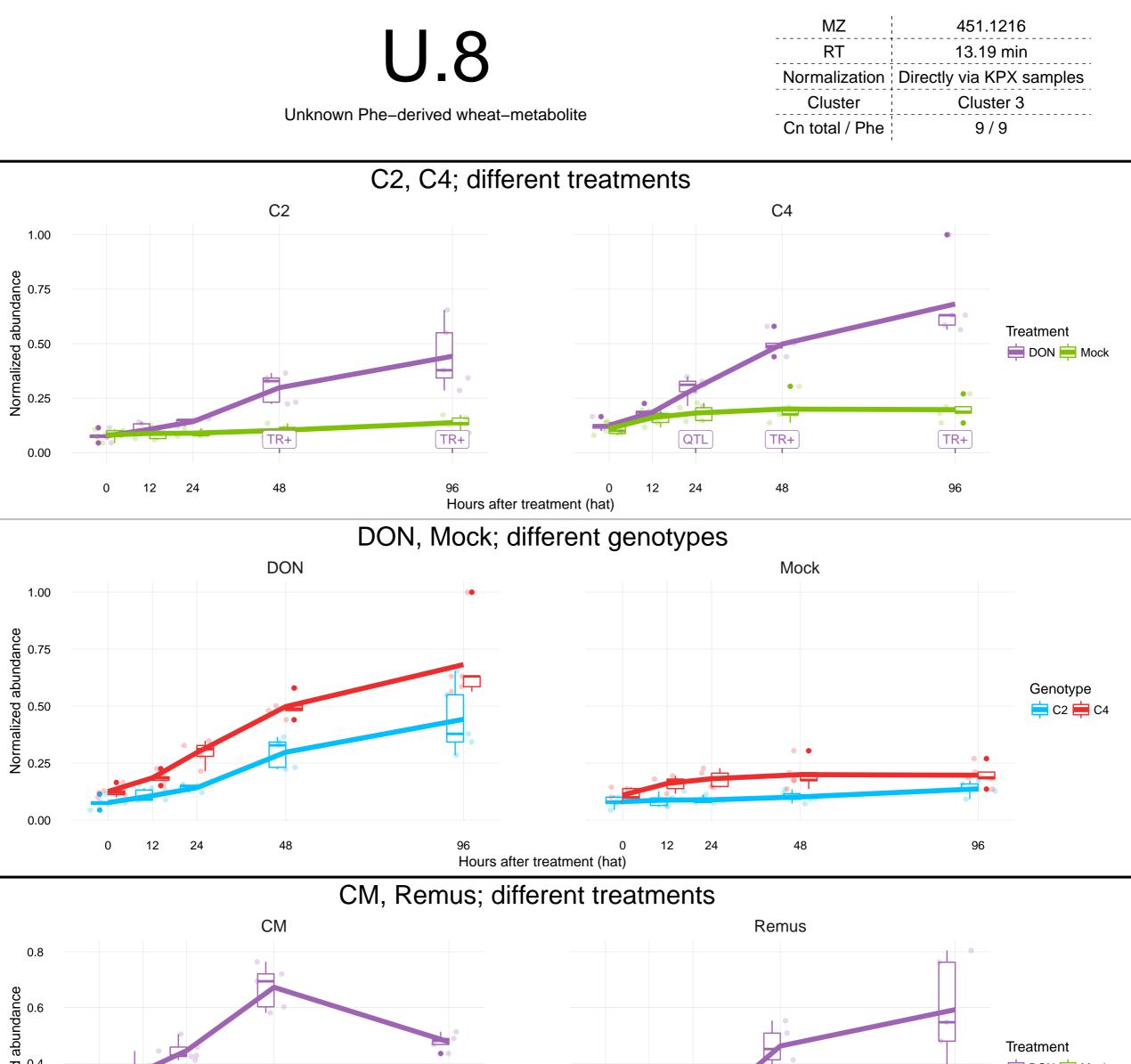


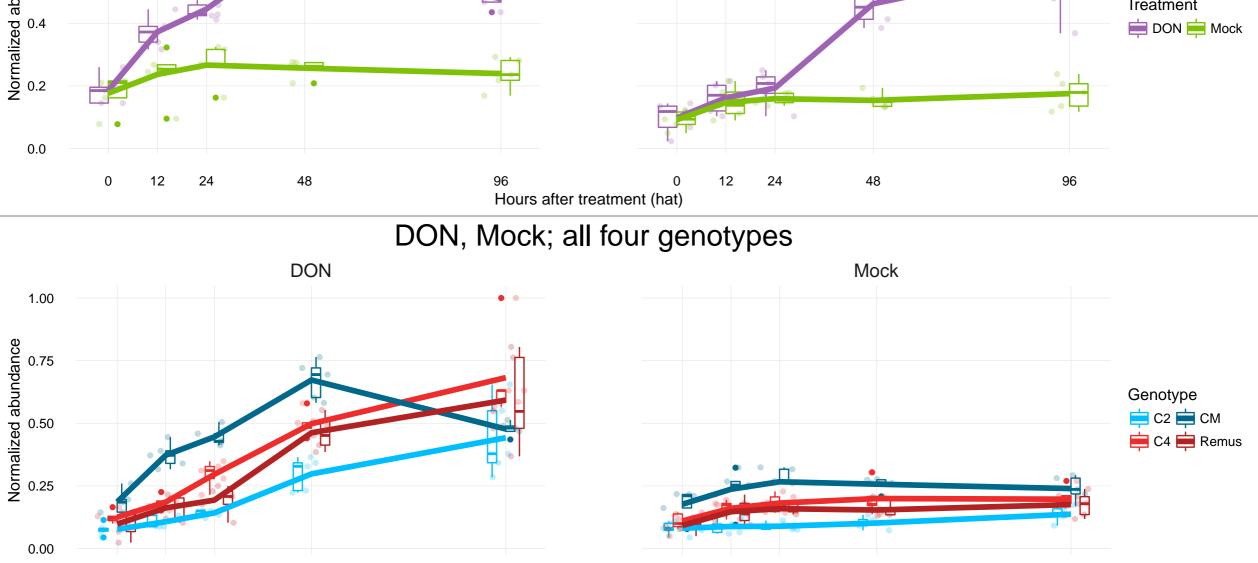


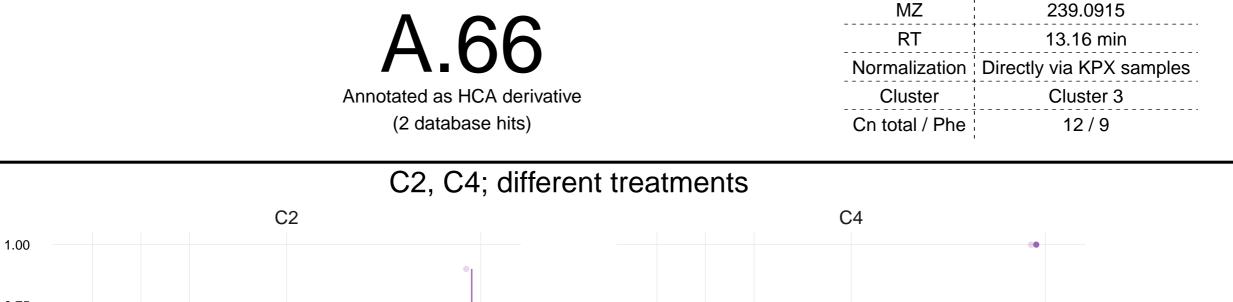


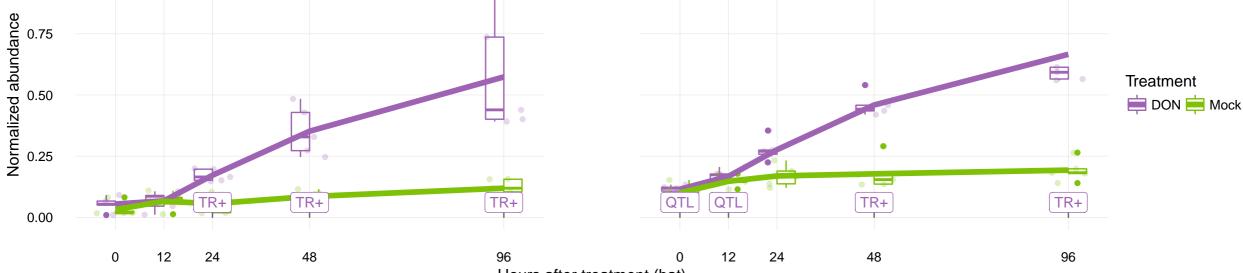
DON, Mock; all four genotypes





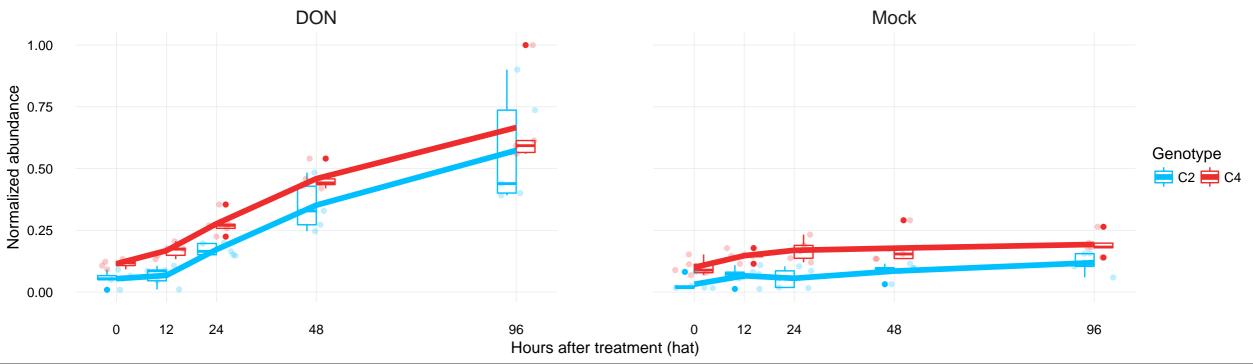


Hours after treatment (hat) 

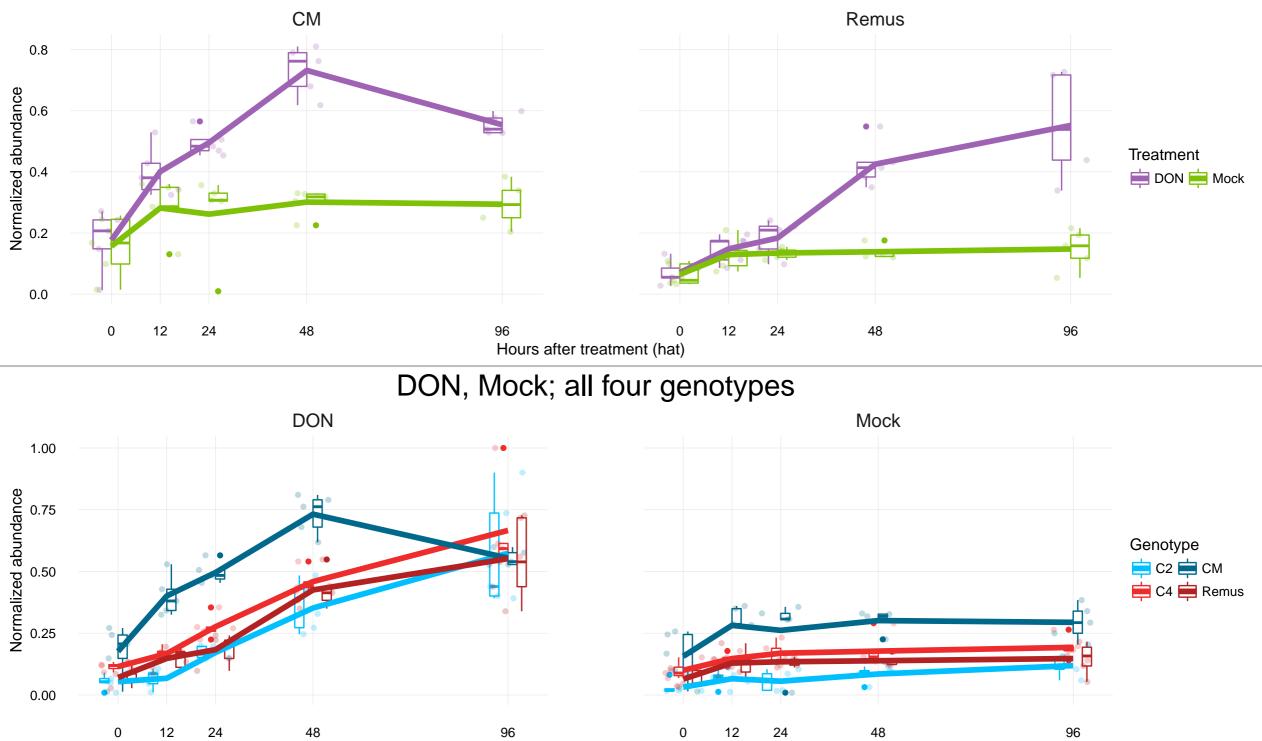


Hours after treatment (hat)

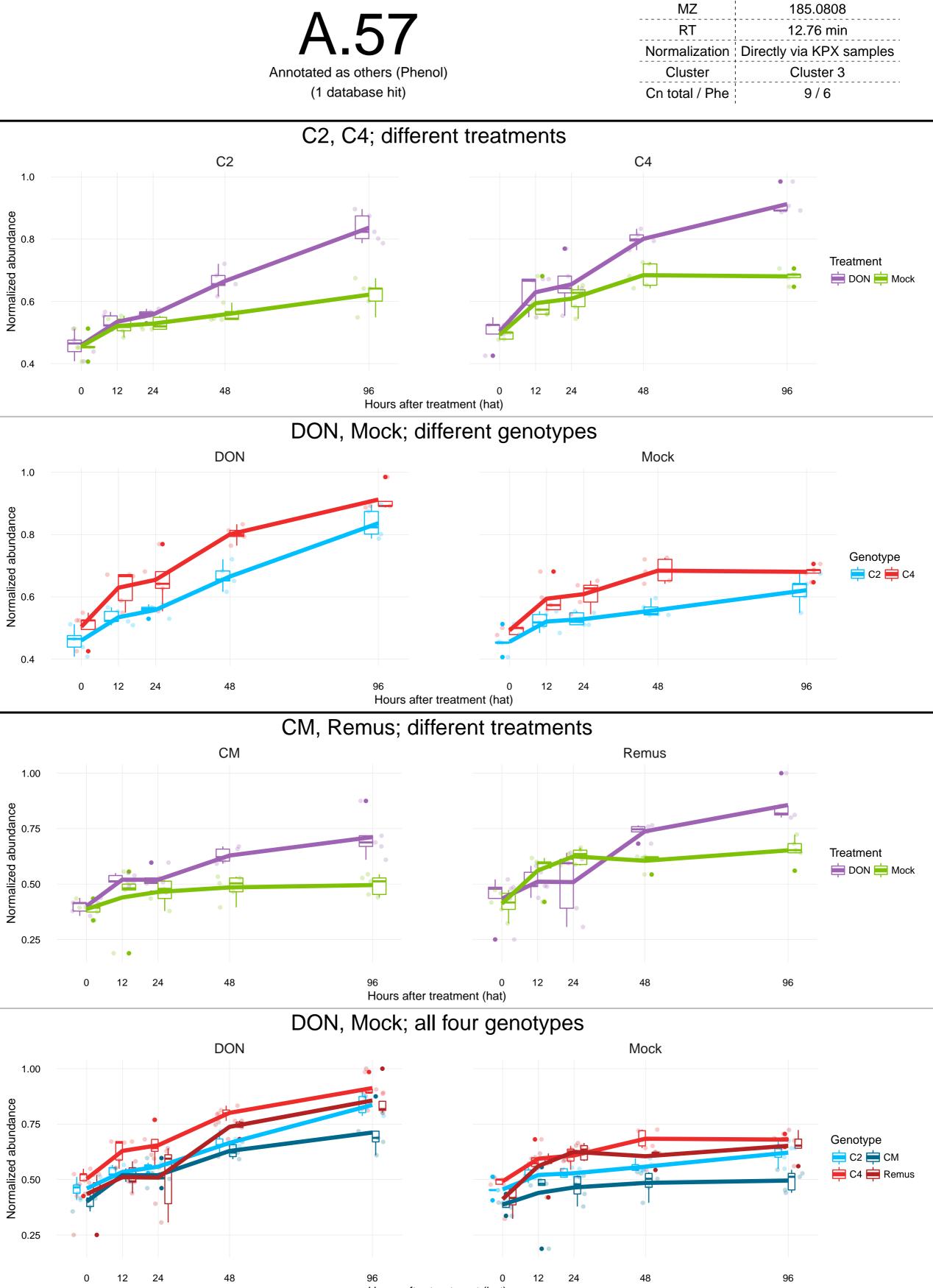
DON, Mock; different genotypes



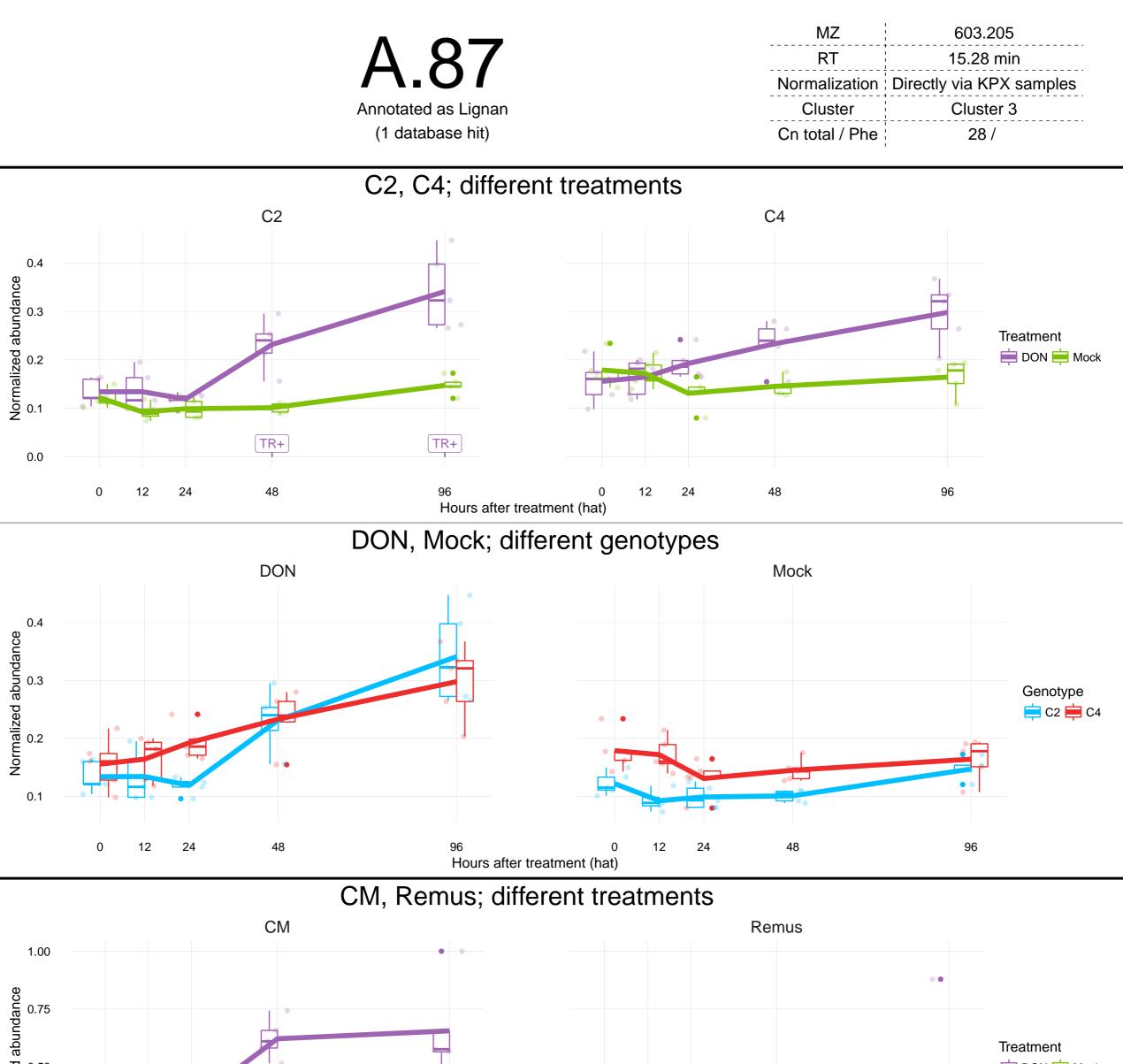
CM, Remus; different treatments

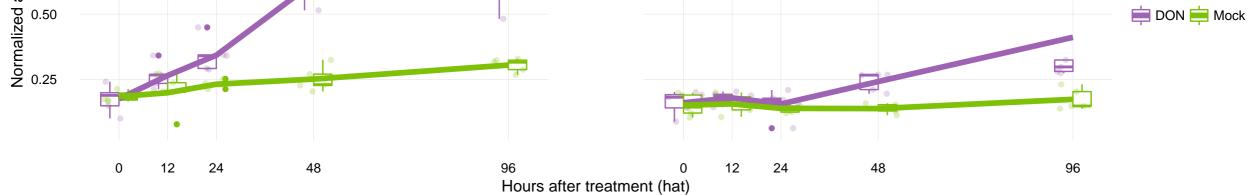


Hours after treatment (hat)

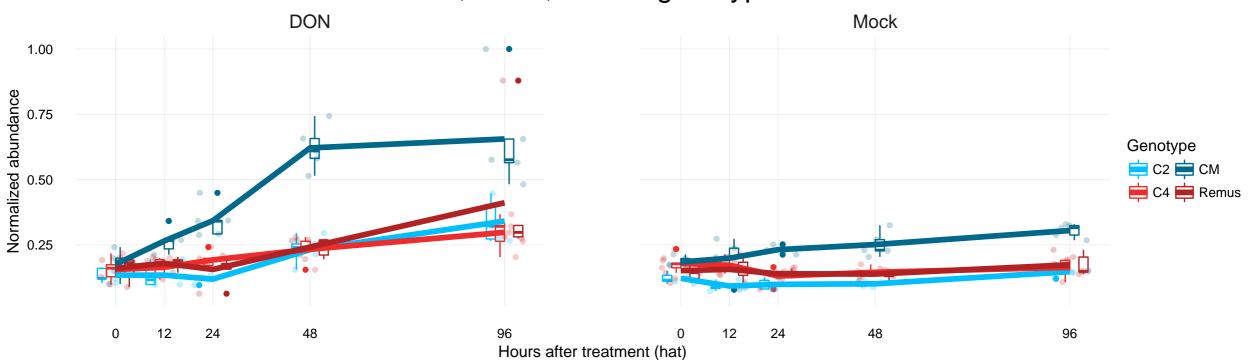


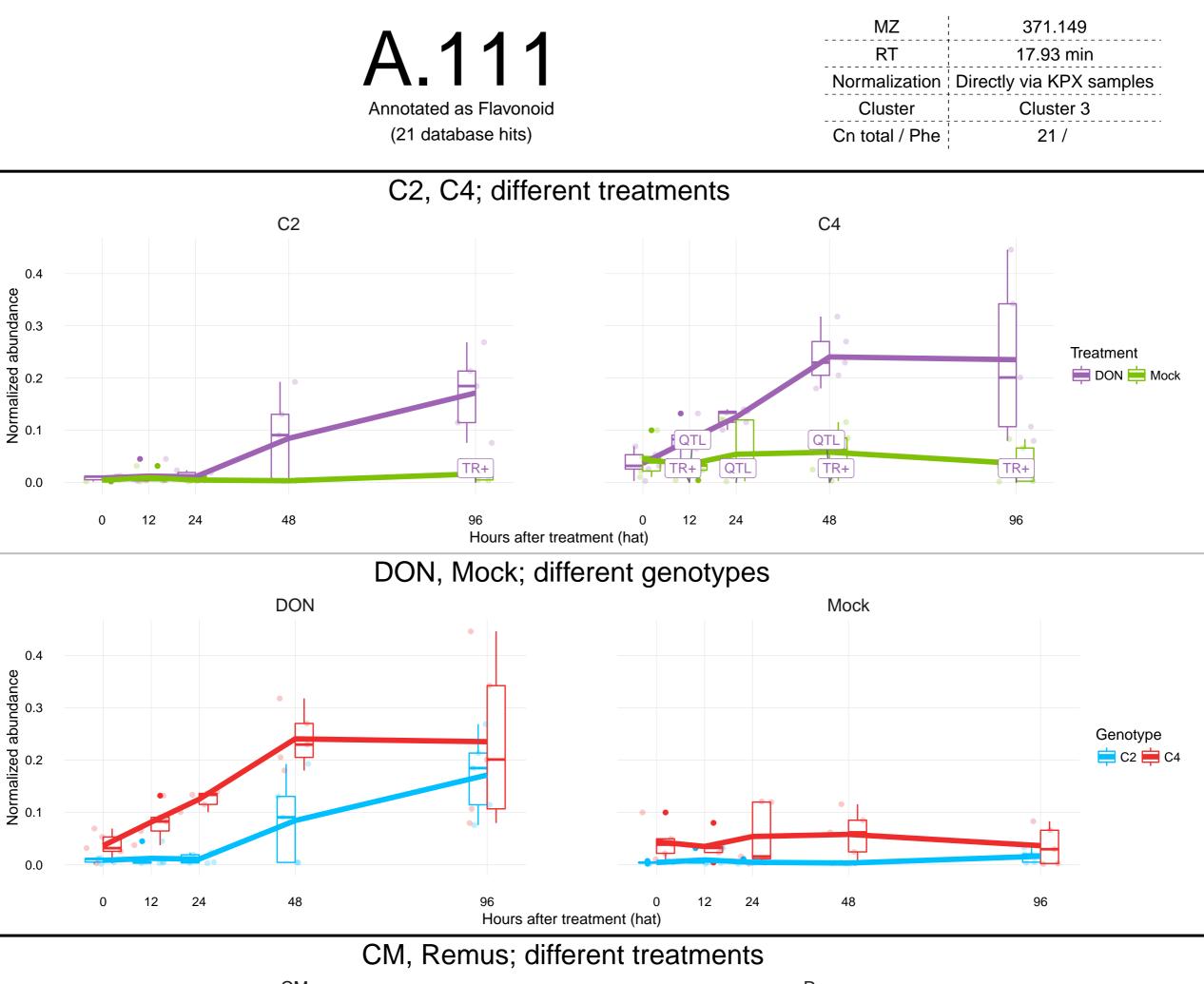
Hours after treatment (hat)

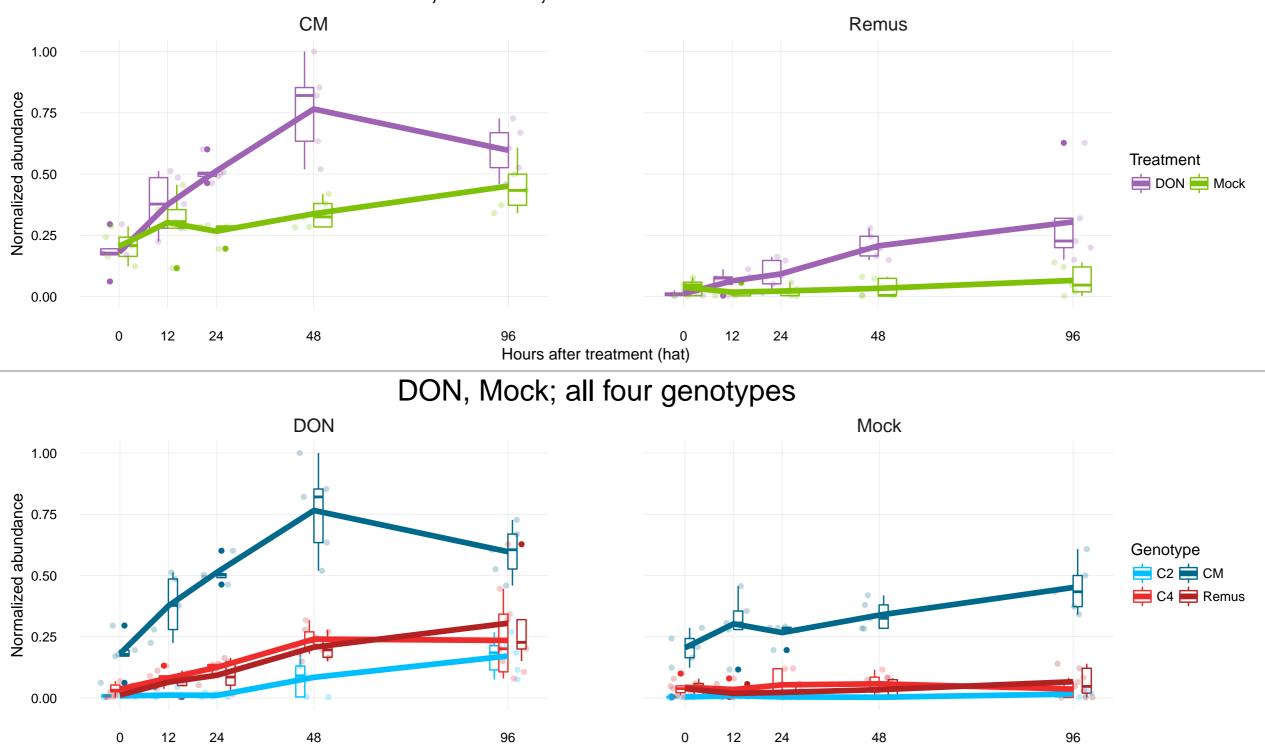




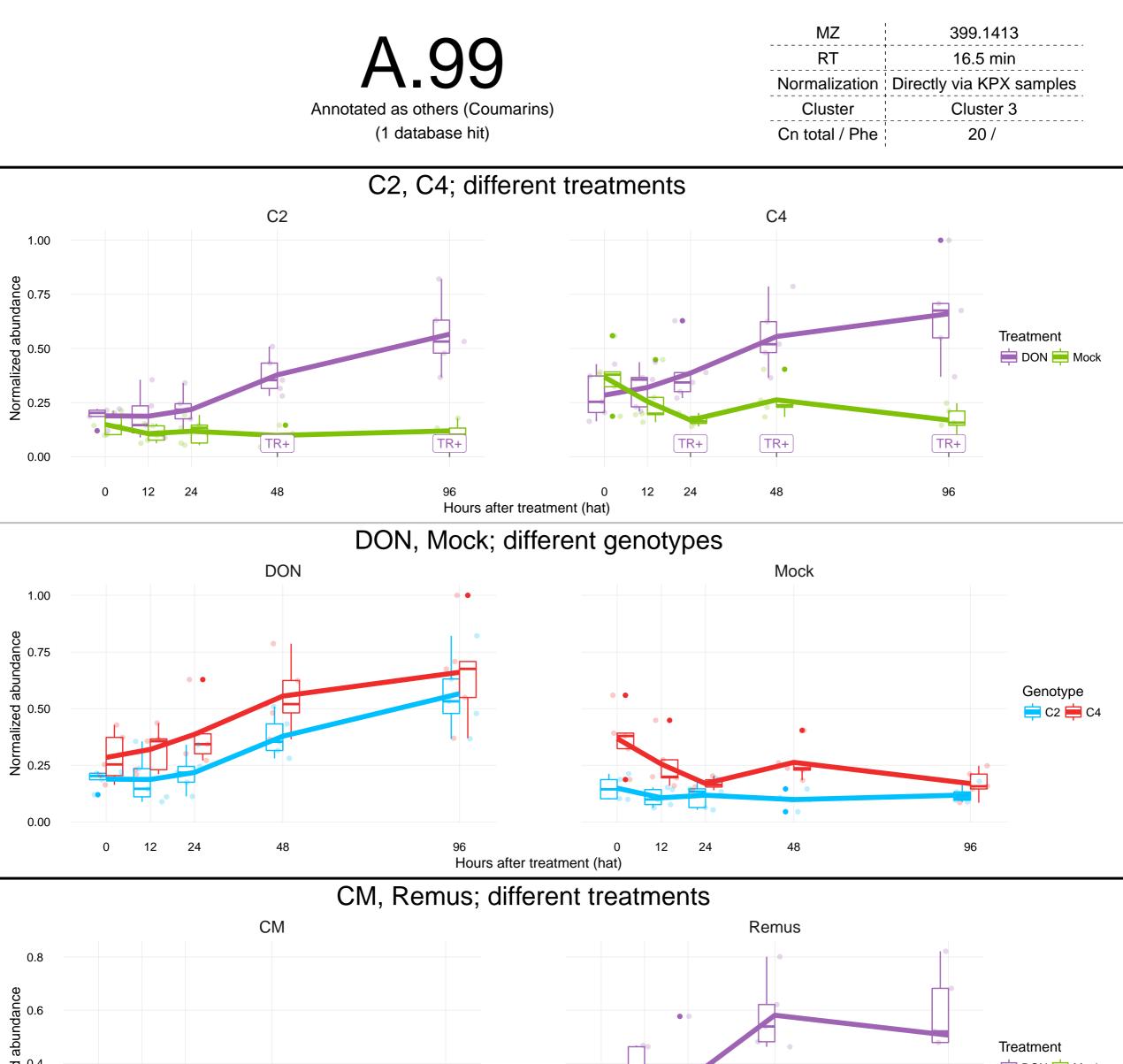
DON, Mock; all four genotypes



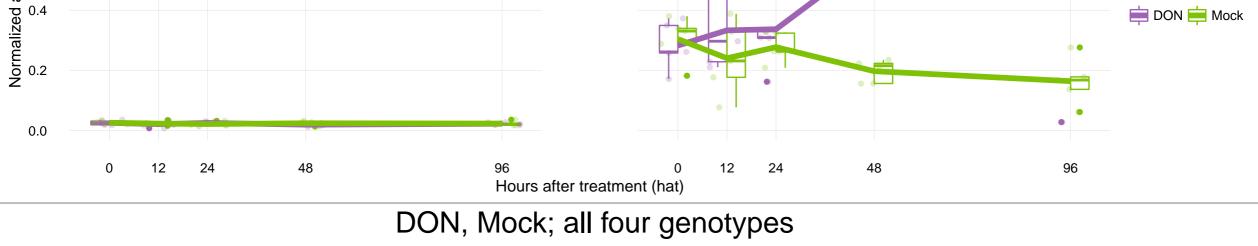


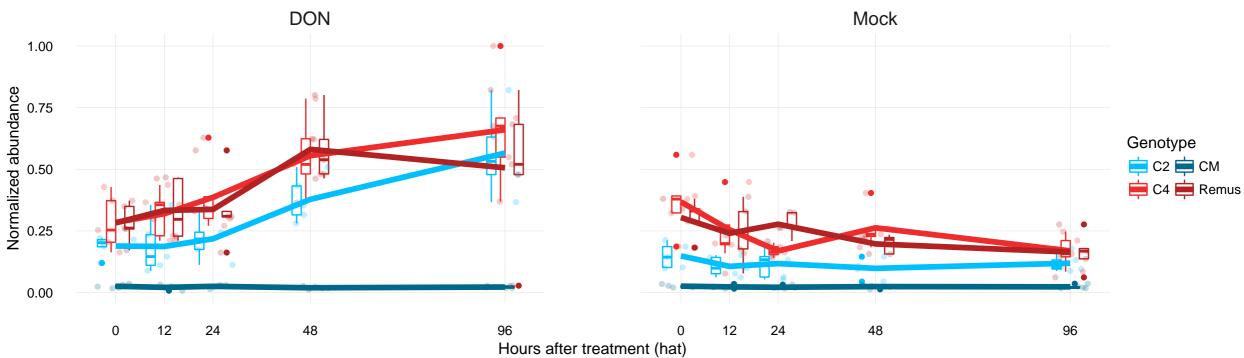


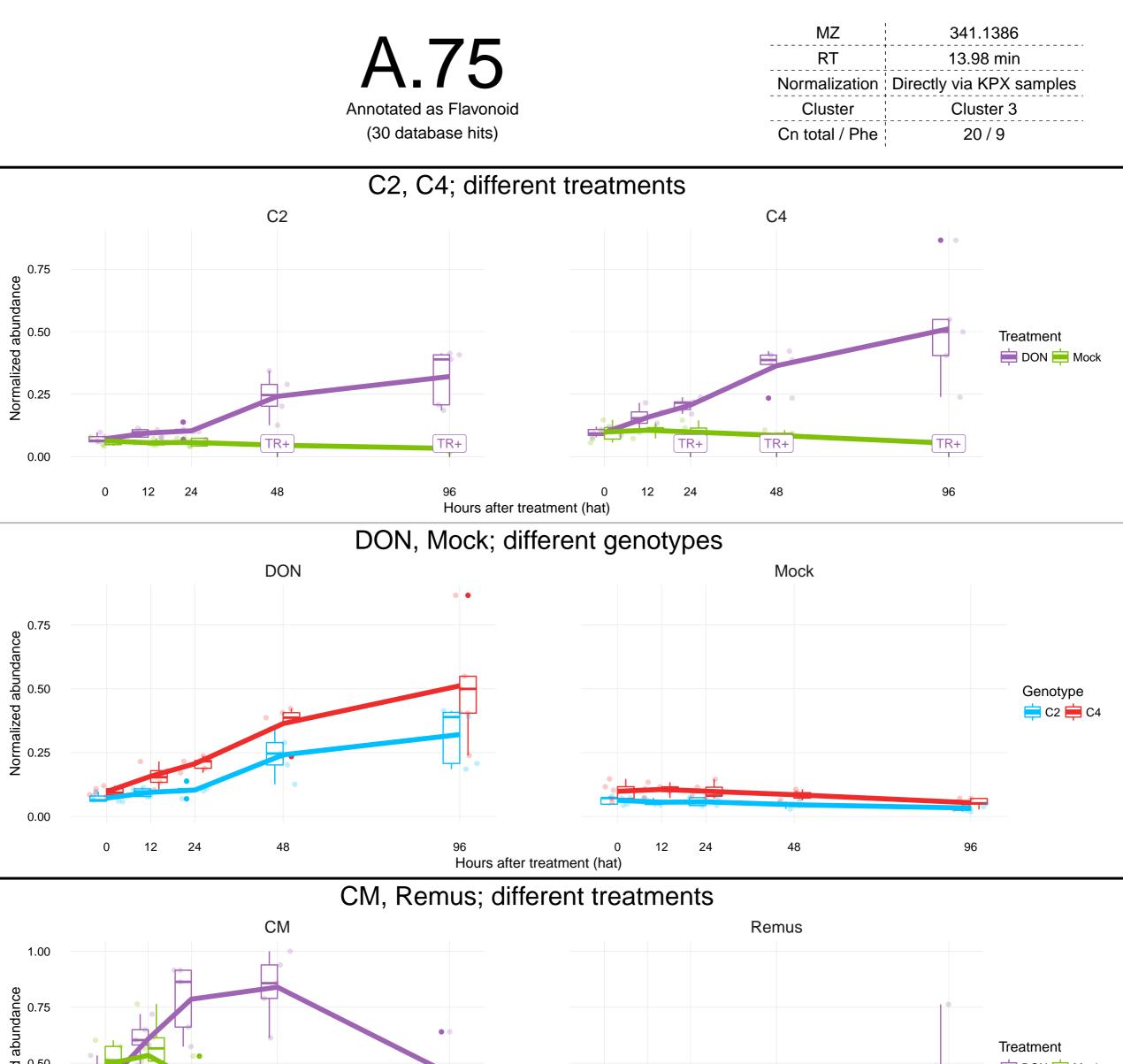
Hours after treatment (hat)

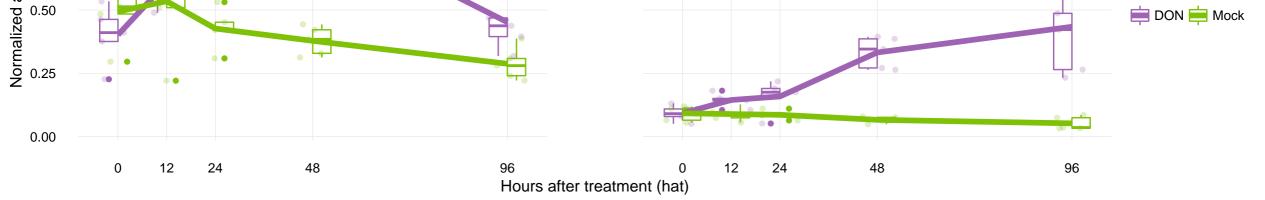


Treatment

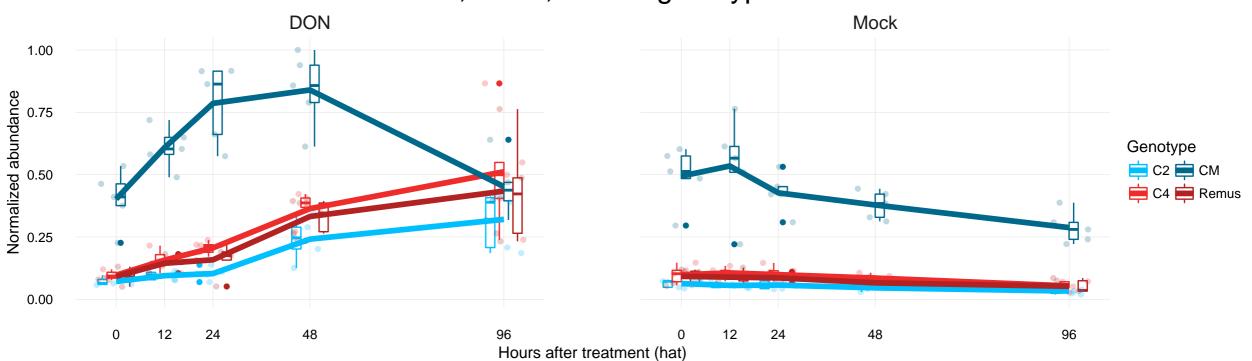


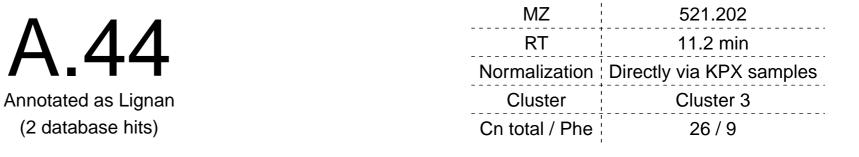


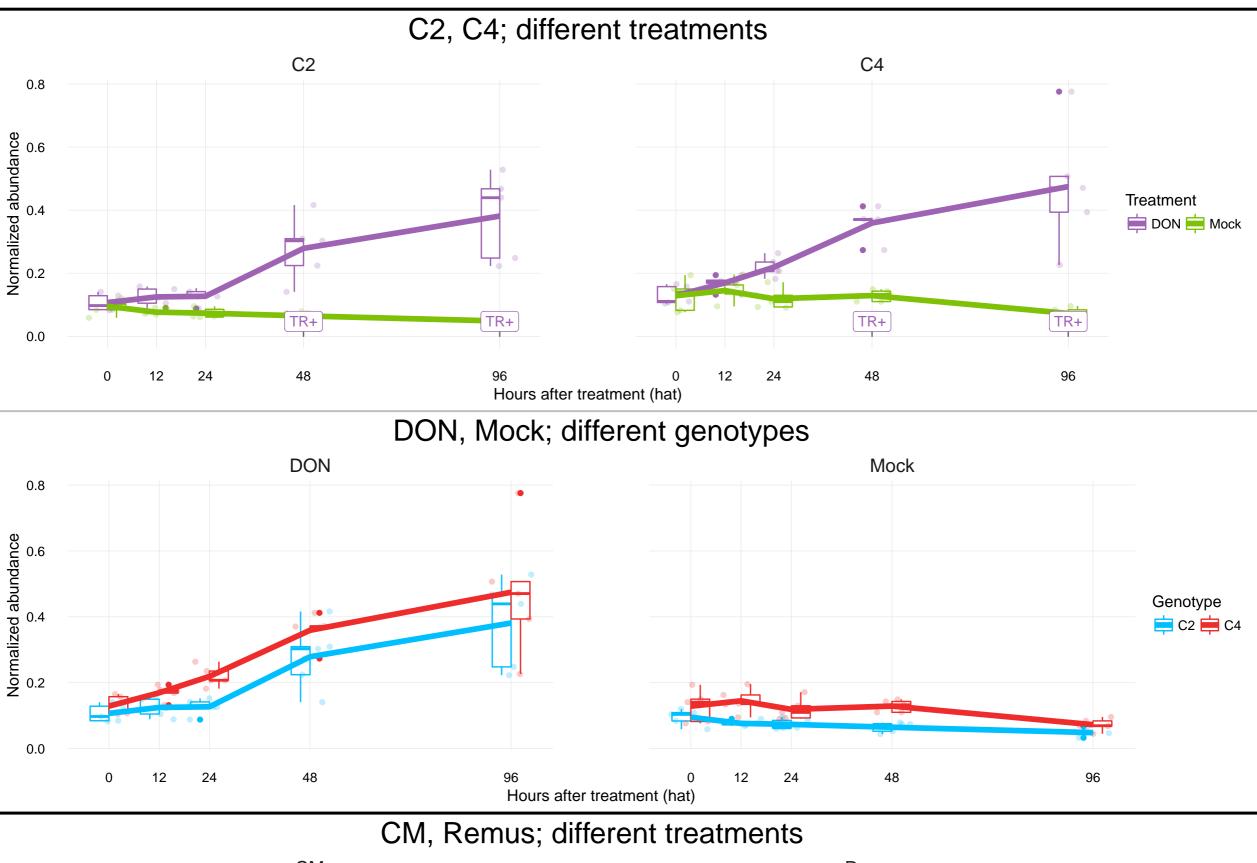


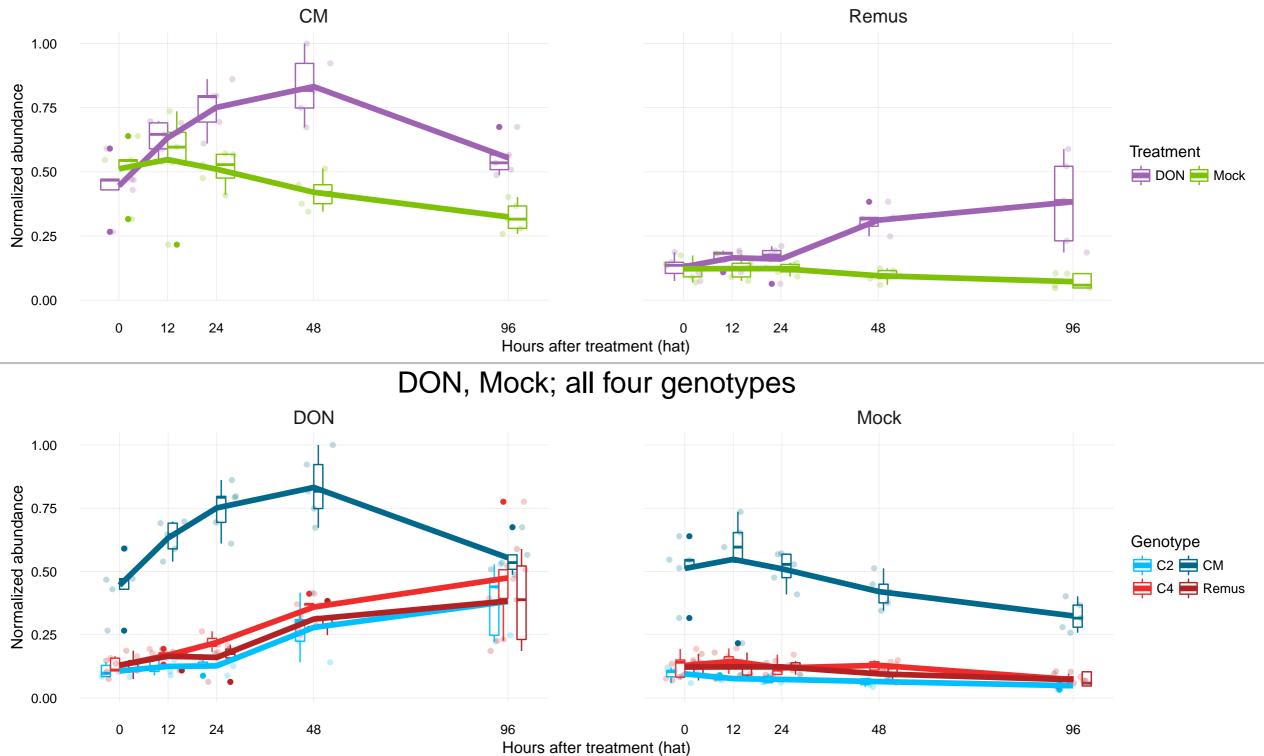


DON, Mock; all four genotypes





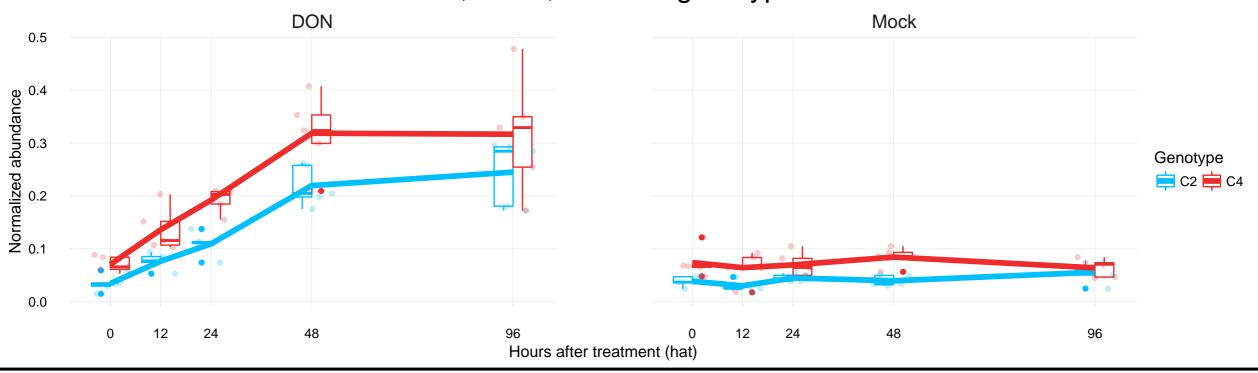




A.102 Annotated as Putative benzoic acid derivative (1 database hit)	MZ RT Normalization Dire Cluster Cn total / Phe	137.0597 16.81 min ectly via KPX samples Cluster 3 8 / 7			
C2, C4; different treatments					
0.5 C2	C4				
, 0.4		•			
		Treatment			
0.2					
0.0 TR+ TR+ TR+ QTL	TR+ TR+	TR+			

Hours after treatment (hat)
DON, Mock; different genotypes

Normalized abundance



CM, Remus; different treatments

