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Screening for seedling stage salinity tolerance and comparative transcriptome analysis in Rice, *Oryza sativa* L.

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Supplementary Data

Suppl. Table S1 — Analysis of variance for nine characters in rice genotypes under *in vitro* and *in vivo*

Source	Df	Germination percentage *in vitro*	Root length *in vitro*	Shoot length *in vitro*	Germination percentage *in vivo*	Root length *in vivo*	Shoot length *in vivo*	Seedling vigour*in vivo*	Fresh weight *in vivo*	Dry Weight *in vivo*
						MSS				
Replication	2	5.37	4.36	1.78	5.46	1.75	1.86	0.98	4.58	1.76
Genotype	9	198.54**	78.53**	37.46**	245.74**	89.45**	120.23**	4.49**	98.45**	280.21**
Error	18	9.87	5.85	2.45	7.89	5.26	3.11	1.24	6.89	2.83

[**Significant at 1%]

Suppl. Table S2 — Effect of salinity level on germination rate of different rice genotypes at different salt concentrations *in vitro*

Genotypes	Germination rate (per cent) at different salt concentration							
	control	EC2	EC4	EC6	EC8	EC10	EC12	EC14
IRLON GSR 9	82.01 (100.00)	93.3 (79.25)	80 (86.79)	86.67 (76.42)	100 (61.32)	86.67 (49.06)	80 (38.68)	35 (30.19)
IRLON GSR 5	82.50 (100.00)	81 (86.84)	76.5 (88.60)	74.2 (80.70)	62.5 (64.04)	52.8 (57.02)	50.5 (45.61)	43 (35.96)
CSR 2016 IR 18 18	80.50 (100.00)	70.5 (84.82)	68.4 (88.39)	59.5 (78.57)	51.4 (63.39)	48.5 (55.36)	46.8 (43.75)	42 (34.82)
CR 3878-245-2-4-1	89.00 (100.00)	88.5 (96.12)	90.4 (92.25)	81.2 (73.64)	70.5 (63.57)	60.8 (61.24)	57.6 (53.49)	48 (37.98)
CSR-11-143	88.50 (100.00)	86.5 (97.56)	82.6 (87.80)	79.4 (73.98)	65.8 (64.23)	58.7 (58.54)	53.7 (50.41)	47.5 (36.59)
CARIDHAN 7	91.50 (100.00)	90.5 (92.41)	91 (86.90)	85 (75.86)	76.5 (61.38)	65.4 (57.93)	62.5 (52.41)	61 (38.62)
CSR 2748-44-195	90.50 (100.00)	92.5 (92.81)	89.4 (87.05)	82.4 (71.22)	72.8 (61.15)	62.5 (59.71)	59.4 (51.80)	58 (37.41)
CR 3437-1*200 83	80.00 (100.00)	79.5 (81.65)	74.5 (87.16)	70.6 (77.06)	65.4 (63.30)	53.3 (53.21)	48.5 (42.20)	38 (32.11)
JK-58	85.50 (100.00)	83.5 (92.44)	80.5 (87.39)	76.5 (79.83)	63.8 (63.03)	53.6 (57.98)	49.8 (49.58)	45 (35.29)
NDRK 11-20	84.00 (100.00)	86.67 (74.26)	73.3 (88.12)	86.67 (77.23)	100 (58.42)	93.3 (48.51)	86.67 (38.61)	33.5 (28.71)
CV	3.96	4.68	5.24	6.45	7.36	7.89	8.23	8.56
SE(D)	3.86	4.12	4.68	5.24	5.78	6.58	6.78	7.23s
CD 5%	8.34	8.12	7.78	7.26	6.94	6.34	5.91	5.26
CD1%	9.22	9.36	8.54	7.93	7.56	7.04	6.24	5..95

[Figures in parentheses indicate percentage over control]

Suppl. Table S3 — Effect of salinity level on root length of different rice genotypes at different salt concentrations *in vitro*

Genotypes	Root length(mm) at different salt concentration							
	control	EC2	EC4	EC6	EC8	EC10	EC12	EC14
IRLON GSR 9	4.59 (100.00)	4.05 (88.24)	3.89 (84.75)	3.58 (78.00)	3.18 (69.28)	2.99 (65.14)	2.59 (56.43)	2.17 (47.28)
IRLON GSR 5	4.76 (100.00)	4.19 (88.03)	4.02 (84.45)	3.75 (78.78)	3.29 (69.12)	3.05 (64.08)	2.72 (57.14)	2.31 (48.53)
CSR 2016 IR 18 18	4.69 (100.00)	4.15 (88.49)	3.99 (85.07)	3.65 (77.83)	3.25 (69.30)	3.02 (64.39)	2.69 (57.36)	2.28 (48.61)
CR 3878-245-2-4-1	4.99 (100.00)	4.55 (91.18)	4.15 (83.17)	3.99 (79.96)	3.55 (71.14)	3.25 (65.13)	2.99 (59.92)	2.55 (51.10)
CSR-11-143	4.85 (100.00)	4.35 (89.69)	4.09 (84.33)	3.85 (79.38)	3.44 (70.93)	3.18 (65.57)	2.82 (58.14)	2.42 (49.90)
CARIDHAN 7	5.25 (100.00)	4.85 (92.38)	4.35 (82.86)	4.2 (80.00)	4.1 (78.10)	3.8 (72.38)	3.25 (61.90)	2.45 (46.67)
CSR 2748-44-195	5.15 (100.00)	4.8 (93.20)	4.29 (83.30)	4.19 (81.36)	3.99 (77.48)	3.78 (73.40)	3.19 (61.94)	2.38 (46.21)
CR 3437-1*200 83	4.65 (100.00)	4.09 (87.96)	3.95 (84.95)	3.62 (77.85)	3.22 (69.25)	3.01 (64.73)	2.65 (56.99)	2.25 (48.39)
JK-58	4.81 (100.00)	4.29 (89.19)	4.05 (84.20)	3.81 (79.21)	3.38 (70.27)	3.12 (64.86)	2.79 (58.00)	2.38 (49.48)
NDRK 11-20	4.35 (100.00)	4.01 (92.18)	3.85 (88.51)	3.45 (79.31)	3.15 (72.41)	2.95 (67.82)	2.45 (56.32)	2.05 (47.13)
CV	4.53	4.26	5.12	5.61	6.47	6.78	6.93	7.23
SE(D)	3.86	4.12	4.68	5.24	5.78	6.58	6.78	7.23s
CD 5%	5.26	5.21	4.68	4.35	4.18	3.78	3.55	3.45
CD1%	7.15	6.87	6.71	6.45	6.12	5.89	5.36	5.24

[Figures in parentheses indicate percentage over control]

Suppl. Table S4 — Effect of salinity level on shoot length of different rice genotypes at different salt concentrations *in vitro*

Genotypes	Shoot length(mm) at different salt concentration							
	control	EC2	EC4	EC6	EC8	EC10	EC12	EC14
IRLON GSR 9	1.06 (100.00)	0.84 (113.78)	0.92 (97.56)	0.81 (105.70)	0.65 (90.85)	0.52 (77.32)	0.41 (71.22)	0.32 (42.68)
IRLON GSR 5	1.14 (100.00)	0.99 (98.18)	1.01 (92.73)	0.92 (89.94)	0.73 (75.76)	0.65 (64.00)	0.52 (61.21)	0.41 (52.12)
CSR 2016 IR 18 18	1.12 (100.00)	0.95 (87.58)	0.99 (84.97)	0.88 (73.91)	0.71 (63.85)	0.62 (60.25)	0.49 (58.14)	0.39 (52.17)
CR 3878-245-2-4-1	1.29 (100.00)	1.24 (99.44)	1.19 (101.57)	0.95 (91.24)	0.82 (79.21)	0.79 (68.31)	0.69 (64.72)	0.49 (53.93)
CSR-11-143	1.23 (100.00)	1.2 (97.74)	1.08 (93.33)	0.91 (89.72)	0.79 (74.35)	0.72 (66.33)	0.62 (60.68)	0.45 (53.67)
CARIDHAN 7	1.45 (100.00)	1.34 (98.91)	1.26 (99.45)	1.1 (92.20)	0.89 (83.61)	0.84 (71.48)	0.76 (68.31)	0.56 (66.67)
CSR 2748-44-195	1.39 (100.00)	1.29 (102.21)	1.21 (98.78)	0.99 (91.05)	0.85 (80.44)	0.83 (69.06)	0.72 (65.64)	0.52 (64.09)
CR 3437-1*200 83	1.09 (100.00)	0.89 (99.38)	0.95 (93.13)	0.84 (88.25)	0.69 (81.75)	0.58 (66.63)	0.46 (60.63)	0.35 (47.50)
JK-58	1.19 (100.00)	1.1 (97.66)	1.04 (94.15)	0.95 (89.47)	0.75 (74.62)	0.69 (62.69)	0.59 (58.25)	0.42 (52.63)
NDRK 11-20	1.01 (100.00)	0.75 (103.18)	0.89 (87.26)	0.78 (103.18)	0.59 (93.45)	0.49 (111.07)	0.39 (103.18)	0.29 (39.88)
CV	4.28	4.46	4.85	5.12	5.34	5.68	5.93	6.14
SE(D)	2.79	3.12	3.34	3.62	3.94	4.23	4.68	4.98
CD 5%	5.98	5.74	5.68	5.46	5.23	4.84	4.68	3.33
CD1%	7.43	6.12	5.96	5.89	5.68	5.45	5.13	4.76

[Figures in parentheses indicate percentage over control]

Suppl. Table S5 — Effect of salinity level on Germination percentage of different rice genotypes at different salt concentrations *in vivo*

Genotypes	Germination percentage at different salt concentration							
	Control	EC2	EC4	EC6	EC8	EC10	EC12	EC14
IRLON GSR 9	78.95 (100.00)	79.25 (100.30)	80.25 (80.75)	80.12 (101.48)	80.45 (101.90)	67.95 (86.07)	61.85 (78.34)	63.92 (80.96)
IRLON GSR 5	79.25 (100.00)	79.85 (100.76)	80.01 (100.96)	80.84 (102.01)	80.75 (101.89)	68.50 (86.44)	62.53 (78.90)	64.25 (81.07)
CSR 2016 IR 18 18	79.10 (100.00)	79.45 (100.44)	79.85 (100.95)	80.54 (101.82)	80.62 (101.92)	68.12 (86.12)	62.35 (78.82)	64.12 (81.06)
CR 3878-245-2-4-1	86.40 (100.00)	86.90 (100.58)	87.20 (100.93)	81.50 (94.33)	71.20 (82.41)	69.10 (79.98)	64.20 (74.31)	64.85 (75.06)
CSR-11-143	84.20 (100.00)	85.23 (101.22)	85.65 (101.72)	81.21 (96.45)	70.98 (84.30)	68.95 (81.89)	63.12 (74.96)	64.45 (76.54)
CARIDHAN 7	89.50 (100.00)	91.40 (102.12)	90.26 (100.85)	83.5 (93.30)	72.40 (80.89)	70.20 (78.44)	65.60 (73.30)	65.80 (73.52)
CSR 2748-44-195	88.54 (100.00)	89.50 (101.08)	90.01 (101.66)	82.5 (93.18)	71.30 (80.53)	69.3 (78.27)	64.30 (72.62)	64.99 (73.40)
CR 3437-1*200 83	79.00 (100.00)	79.35 (100.44)	79.50 (100.63)	80.25 (101.58)	80.56 (101.97)	68.00 (86.23)	62.00 (79.05)	64.00 (82.10)
JK-58	79.50 (100.00)	79.95 (100.57)	80.02 (100.65)	80.99 (101.87)	70.86 (89.13)	68.56 (86.24)	62.96 (79.19)	64.35 (80.94)
NDRK 11-20	78.01 (100.00)	78.12 (100.40)	78.32 (100.40)	80.1 (102.68)	80.21 (102.82)	67.45 (86.46)	61.65 (79.03)	62.5 (80.17)
CV	7.64	7.98	8.35	8.78	9.12	9.35	9.65	9.94
SE(D)	4.54	4.23	3.95	3.46	3.21	2.89	2.54	2.12
CD 5%	8.56	7.45	7.15	6.46	5.49	4.98	4.53	3.97
CD1%	10.5	9.64	8.95	8.25	7.85	7.12	6.93	6.35

[Figures in parentheses indicate percentage over control]

Suppl. Table S6 — Effect of salinity level on root length of different rice genotypes at different salt concentrations *in vivo*

Genotypes	Root length(mm) at different salt concentration							
	control	EC2	EC4	EC6	EC8	EC10	EC12	EC14
IRLON GSR 9	6.01 (100.00)	6.35 (105.66)	6.25 (103.99)	5.75 (95.67)	5.35 89.02)	5.15 (85.69)	4.25 70.72)	4.01 (66.72)
IRLON GSR 5	6.95 (100.00)	6.82 (98.13)	6.45 (92.81)	6.05 (87.05)	5.85 (84.17)	5.38 (77.41)	4.98 (71.65)	4.35 (62.59)
CSR 2016 IR 18 18	6.56 (100.00)	6.78 (103.35)	6.39 (97.81)	6.01 (91.62)	5.74 (87.50)	5.32 (81.10)	4.75 (72.41)	4.25 (64.79)
CR 3878-245-2-4-1	7.32 (100.00)	7.1 (97.18)	6.78 (93.42)	6.35 (87.79)	6.15 (83.89)	5.78 (80.00)	5.15 (70.87)	4.99 (68.99)
CSR-11-143	7.19 (100.00)	6.99 (97.22)	6.65 (92.49)	6.25 (86.93)	5.98 (83.17)	5.65 (78.58)	5.05 (70.24)	4.65 (64.67)
CARIDHAN 7	7.56 (100.00)	7.24 (99.14)	6.96 (93.58)	6.54 (87.73)	6.25 (84.88)	5.96 (77.75)	5.28 (71.47)	5.14 (63.48)
CSR 2748-44-195	7.45 (100.00)	7.13 (94.31)	6.89 (91.14)	6.48 (85.71)	6.19 (81.88)	5.89 (77.91)	5.19 (68.65)	5.02 (66.40)
CR 3437-1*200 83	6.25 (100.00)	6.45 (103.20)	6.31 (100.96)	5.95 (95.20)	5.45 (87.20)	5.25 (84.00)	4.65 (74.40)	4.15 (66.40)
JK-58	7.01 (100.00)	6.95 (90.79)	6.56 (86.70)	6.15 (81.20)	5.95 (78.64)	5.45 (73.91)	5.01 (65.86)	4.45 (63.81)
NDRK 11-20	5.98 (100.00)	6.25 (104.52)	6.11 (102.17)	5.25 (87.79)	5.25 (87.79)	5.1 (85.28)	4.15 (69.40)	3.98 (66.56)
CV	4.16	4.34	4.58	4.93	5.26	5.64	5.98	6.11
SE(D)	3.12	2.97	2.64	2.52	2.31	1.96	1.87	1.76
CD 5%	5.66	4.55	3.42	3.66	3.24	3.06	2.84	2.56
CD1%	6.74	6.54	5.36	5.78	5.27	5.06	4.74	3.86

[Figures in parentheses indicate percentage over control]

Suppl. Table S7 — Effect of salinity level on shoot length of different rice genotypes at different salt concentrations *in vivo*

Genotypes	Shoot length(mm) at different salt concentration							
	control	EC2	EC4	EC6	EC8	EC10	EC12	EC14
IRLON GSR 9	8.96 (100.00)	8.96 (100.00)	7.55 (84.26)	6.56 (73.21)	6.35 (70.87)	5.95 (66.41)	5.01 (55.92)	5.64 (62.95)
IRLON GSR 5	9.55 (100.00)	9.25 (99.01)	7.98 (83.00)	6.98 (72.92)	6.74 (70.65)	6.15 (69.07)	5.96 (65.51)	6.01 (63.74)
CSR 2016 IR 18 18	9.25 (100.00)	9.12 (98.59)	7.95 (85.95)	6.93 (74.92)	6.54 (70.70)	6.11 (66.05)	5.9 (63.78)	5.98 (64.65)
CR 3878-245-2-4-1	10.12 (100.00)	10.02 (96.86)	8.4 (83.56)	7.38 (73.09)	7.15 (70.58)	6.99 (64.40)	6.63 (62.41)	6.45 (62.93)
CSR-11-143	10.02 (100.00)	9.95 (99.30)	8.12 (81.04)	7.12 (71.06)	6.95 (69.36)	6.54 (65.27)	6.23 (62.18)	6.21 (61.98)
CARIDHAN 7	10.58 (100.00)	10.12 (95.65)	8.95 (84.59)	7.86 (74.29)	7.35 (69.47)	7.12 (67.30	6.85 (64.74)	6.54 (61.81)
CSR 2748-44-195	10.16 (100.00)	10.05 (99.89)	8.5 (87.03)	7.45 (73.73)	7.25 (71.51)	7.02 (67.52)	6.74 (64.03)	6.43 (65.96)
CR 3437-1*200 83	9.02 (100.00)	9.01 (98.92)	7.85 (83.66)	6.65 (73.33)	6.45 (71.36)	6.09 (69.09)	5.8 (66.34)	5.95 (63.29)
JK-58	9.98 (100.00)	9.45 (94.69)	8.1 (81.16)	7.01 (70.24)	6.81 (68.24)	6.35 (63.63)	6.01 (60.22)	6.05 (60.62)
NDRK 11-20	8.65 (100.00)	8.55 (98.84)	7.45 (86.13)	6.45 (74.57)	6.15 (71.10)	5.55 (64.16)	4.78 (55.26)	5.55 (64.16)
CV	4.36	4.48	4.96	5.12	5.23	5.46	5.78	6.14
SE(D)	5.54	5.31	5.19	4.86	5.23	5.54	5.76	5.98
CD 5%	7.86	7.34	7.12	6.94	6.52	6.31	5.94	5.76
CD1%	8.44	8.23	7.98	7.54	7.32	7.16	6.78	6.54

[Figures in parentheses indicate percentage over control]

Suppl. Table S8 — Effect of salinity level on seedling vigour index of different rice genotypes at different salt concentrations *in vivo*

Genotypes	Vigour at different salt concentration							
	control	EC2	EC4	EC6	EC8	EC10	EC12	EC14
IRLON GSR 9	17.25 (100.00)	17.45 (101.16)	14.12 (81.86)	13.02 (75.48)	11.95 (69.28)	9.12 (52.87)	8.12 (47.07)	6.56 (38.08)
IRLON GSR 5	18.04 (100.00)	18.01 (99.83)	15.45 (85.64)	14.12 (78.27)	12.45 (69.01)	9.65 (53.49)	8.65 (47.95)	7.12 (39.47)
CSR 2016 IR 18 18	17.89 (100.00)	17.89 (100.00)	14.35 (80.21)	13.98 (78.14)	12.12 (67.75)	9.55 (53.38)	8.55 (47.79)	7.01 (39.18)
CR 3878-245-2-4-1	18.39 (100.00)	18.57 (100.98)	16.02 (87.11)	14.35 (78.03)	13.02 (70.80)	10.15 (55.19)	9.02 (49.05)	7.65 (41.60)
CSR-11-143	18.21 (100.00)	18.32 (100.60)	15.98 (87.75)	14.21 (78.03)	12.96 (71.17)	9.94 (54.59)	8.89 (48.82)	7.45 (40.91)
CARIDHAN 7	18.56 (100.00)	18.84 (101.51)	16.54 (89.12)	14.56 (78.45)	13.24 (71.34)	10.45 (56.30)	9.26 (49.89)	7.86 (42.35)
CSR 2748-44-195	18.42 (100.00)	18.67 (101.36)	16.28 (88.38)	14.41 (78.23)	13.15 (71.39)	10.28 (55.81)	9.15 (49.67)	7.71 (41.86)
CR 3437-1*200 83	17.75 (100.00)	17.65 (99.44)	14.25 (80.28)	13.65 (77.84)	12.1 (69.74)	9.45 (53.69)	8.41 (48.18)	6.98 (40.46)
JK-58	18.14 (100.00)	18.15 (100.06)	15.74 (86.77)	14.12 (77.84)	12.65 (69.74)	9.74 (53.69)	8.74 (48.18)	7.34 (40.46)
NDRK 11-20	17.02 (100.00)	17.25 (101.35)	14.02 (82.37)	12.89 (75.73)	11.23 (65.98)	9 (53.64)	7.98 (46.89)	6.35 (37.31)
CV	4.94	5.66	6.84	6.98	7.23	7.54	8.12	8.36
SE(D)	6.78	6.44	6.32	6.17	5.98	5.79	5.46	5.32
CD 5%	11.38	10.17	9.56	9.34	8.87	7.96	7.24	6.58
CD1%	13.47	11.54	10.76	10.44	9.32	8.77	8.32	7.94

[Figures in parentheses indicate percentage over control]

Suppl. Table S9 — Effect of salinity level on fresh weight of shoot and root different rice genotypes at different salt concentrations *in vivo*

Genotypes	Fresh weight at different salt concentration							
	control	EC2	EC4	EC6	EC8	EC10	EC12	EC14
IRLON GSR 9	0.29 (100.00)	0.31 (106.90)	0.35 (120.69)	0.25 (86.21)	0.25 (86.21)	0.26 (89.66)	0.25 (86.21)	0.16 (55.17)
IRLON GSR 5	0.41 (100.00)	0.45 (109.76)	0.48 (117.07)	0.45 (109.76)	0.35 (85.37)	0.31 (75.61)	0.32 (78.05)	0.19 (46.34)
CSR 2016 IR 18 18	0.36 (100.00)	0.39 (108.33)	0.45 (125.00)	0.42 (116.67)	0.32 (88.89)	0.28 (77.78)	0.31 (86.11)	0.18 (50.00)
CR 3878-245-2-4-1	0.61 (100.00)	0.62 (101.64)	0.61 (100.00)	0.56 (91.80)	0.48 (78.69)	0.41 (67.21)	0.38 (62.30)	0.28 (45.90)
CSR-11-143	0.59 (100.00)	0.58 (98.31)	0.56 (94.92)	0.54 (91.53)	0.45 (76.27)	0.39 (66.10)	0.36 (61.02)	0.25 (42.37)
CARIDHAN 7	0.69 (100.00)	0.7 (101.45)	0.68 (98.55)	0.65 (94.20)	0.56 (81.16)	0.48 (69.57)	0.45 (65.22)	0.35 (50.72)
CSR 2748-44-195	0.64 (100.00)	0.67 (109.38)	0.64 (121.88)	0.59 (96.88)	0.51 (90.63)	0.44 (84.38)	0.41 (87.50)	0.31 (53.13)
CR 3437-1*200 83	0.32 (100.00)	0.35 (104.69)	0.39 (100.00)	0.31 (92.19)	0.29 (79.69)	0.27 (68.75)	0.28 (64.06)	0.17 (48.44)
JK-58	0.45 (100.00)	0.48 (106.67)	0.51 (113.33)	0.48 (106.67)	0.39 (86.67)	0.35 (77.78)	0.34 (75.56)	0.21 (46.67)
NDRK 11-20	0.25 (100.00)	0.24 (96.00)	0.31 (124.00)	0.24 (96.00)	0.21 (84.00)	0.24 (96.00)	0.24 (96.00)	0.14 (56.00)
CV	4.22	4.36	4.64	4.17	4.31	5.26	5.45	6.12
SE(D)	2.45	2.36	2.17	2.06	1.94	1.89	1.76	1.65
CD 5%	3.39	3.30	3.28	3.22	3.16	3.05	2.94	2.76
CD1%	4.76	4.58	4.37	4.18	3.94	3.76	3.54	3.29

[Figures in parentheses indicate percentage over control]

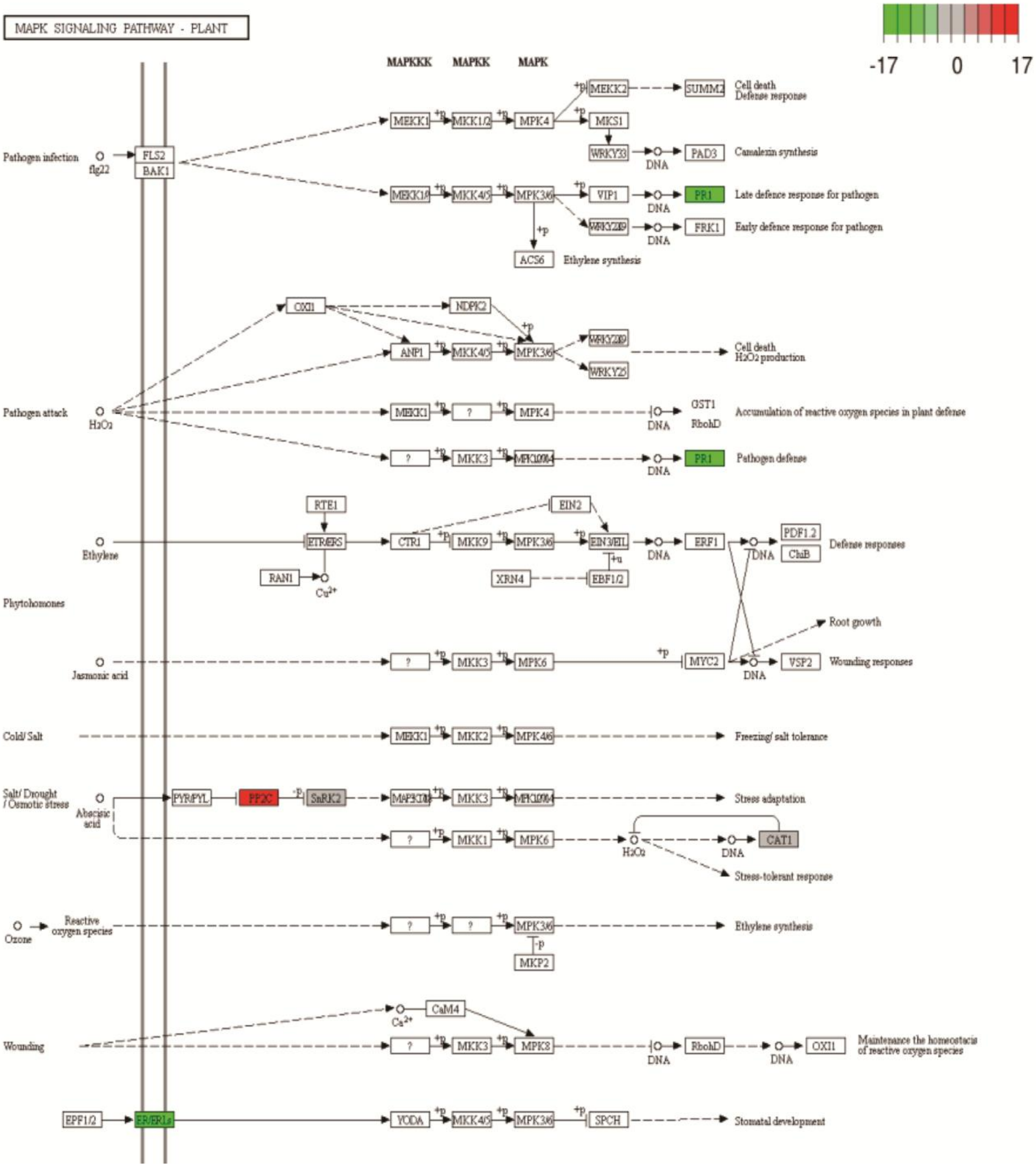
Suppl. Table S10 — Effect of salinity level on dry weight of root and shoot for different rice genotypes at different salt concentrations *in vivo*

Genotypes	Dry weight at different salt concentration							
	control	EC2	EC4	EC6	EC8	EC10	EC12	EC14
IRLON GSR 9	0.5 (100.00)	0.7 (140.00)	0.6 (120.00)	0.5 (100.00)	0.7 (140.00)	0.5 (100.00)	0.4 (80.00)	0.3 (60.00)
IRLON GSR 5	0.8 (100.00)	0.1 (125.00)	0.9 (112.50)	0.8 (100.00)	0.1 (12.50)	0.9 (112.50)	0.7 (87.50)	0.6 (75.00)
CSR 2016 IR 18 18	0.7 (100.00)	0.9 (128.57)	0.8 (114.29)	0.7 (100.00)	0.9 (128.57)	0.8 (114.29)	0.6 (85.71)	0.5 (71.43)
CR 3878-245-2-4-1	1.4 (100.00)	1.4 (94.44)	1.4 (88.89)	1.1 (83.33)	1.2 (77.78)	1.2 (72.22)	1.1 (72.22)	0.9 (66.67)
CSR-11-143	1.1 (100.00)	1.2 (100.00)	1.1 (100.00)	0.1 (78.57)	0.9 (85.71)	1.1 (85.71)	0.9 (78.57)	0.8 (64.75)
CARIDHAN 7	1.8 (100.00)	1.7 (100.00)	1.6 (93.75)	1.5 (75.00)	1.4 (81.25)	1.3 (75.00)	0.13 (75.00)	0.12 (68.75)
CSR 2748-44-195	1.6 (100.00)	1.6 (109.09)	1.5 (100.00)	1.2 (90.91)	1.3 (81.82)	1.2 (100.00)	1.2 (81.82)	1.1 (72.73)
CR 3437-1*200 83	0.6 (100.00)	0.8 (133.33)	0.7 (116.67)	0.6 (100.00)	0.8 (133.33)	0.7 (116.67)	0.5 (83.33)	0.4 (66.67)
JK-58	0.9 (100.00)	1.1 (122.22)	0.1 (111.11)	0.9 (100.00)	1.1 (122.22)	0.1 (111.11)	0.8 (88.89)	0.7 (77.78)
NDRK 11-20	0.4 (100.00)	0.6 (150.00)	0.5 (125.00)	0.4 (100.00)	0.6 (150.00)	0.9 (225.00)	0.3 (75.00)	0.2 (50.00)
CV	4.54	4.86	4.72	4.37	4.94	5.23	5.68	5.72
SE(D)	1.94	1.67	1.54	1.43	1.17	0.98	0.76	0.55
CD 5%	2.62	2.52	2.41	2.36	2.18	1.97	1.67	1.54
CD1%	3.79	3.66	3.54	3.26	3.12	2.92	2.76	2.49

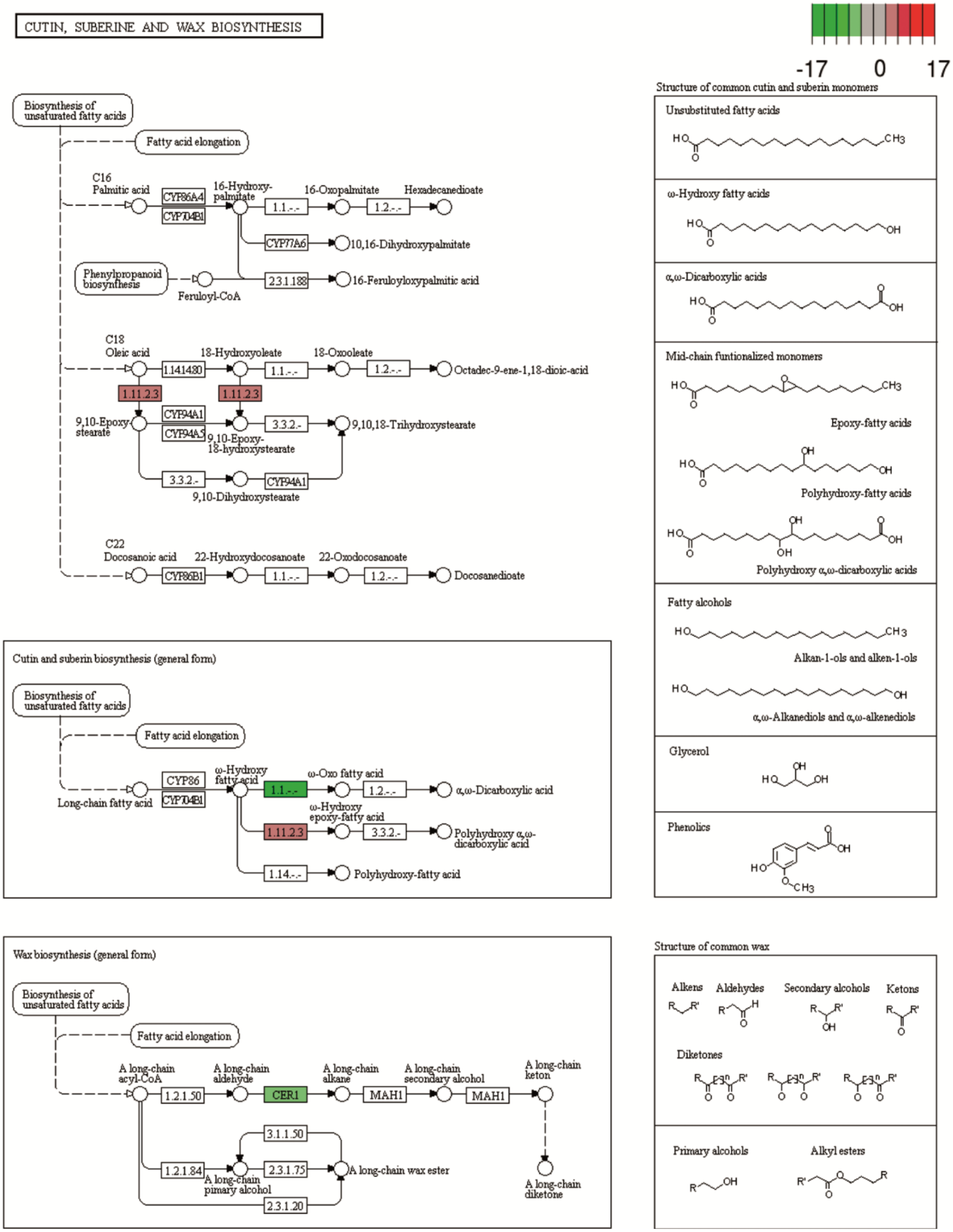
[Figures in parentheses indicate percentage over control]

Suppl. Table S11 — Gene ontology of significantly expressed genes

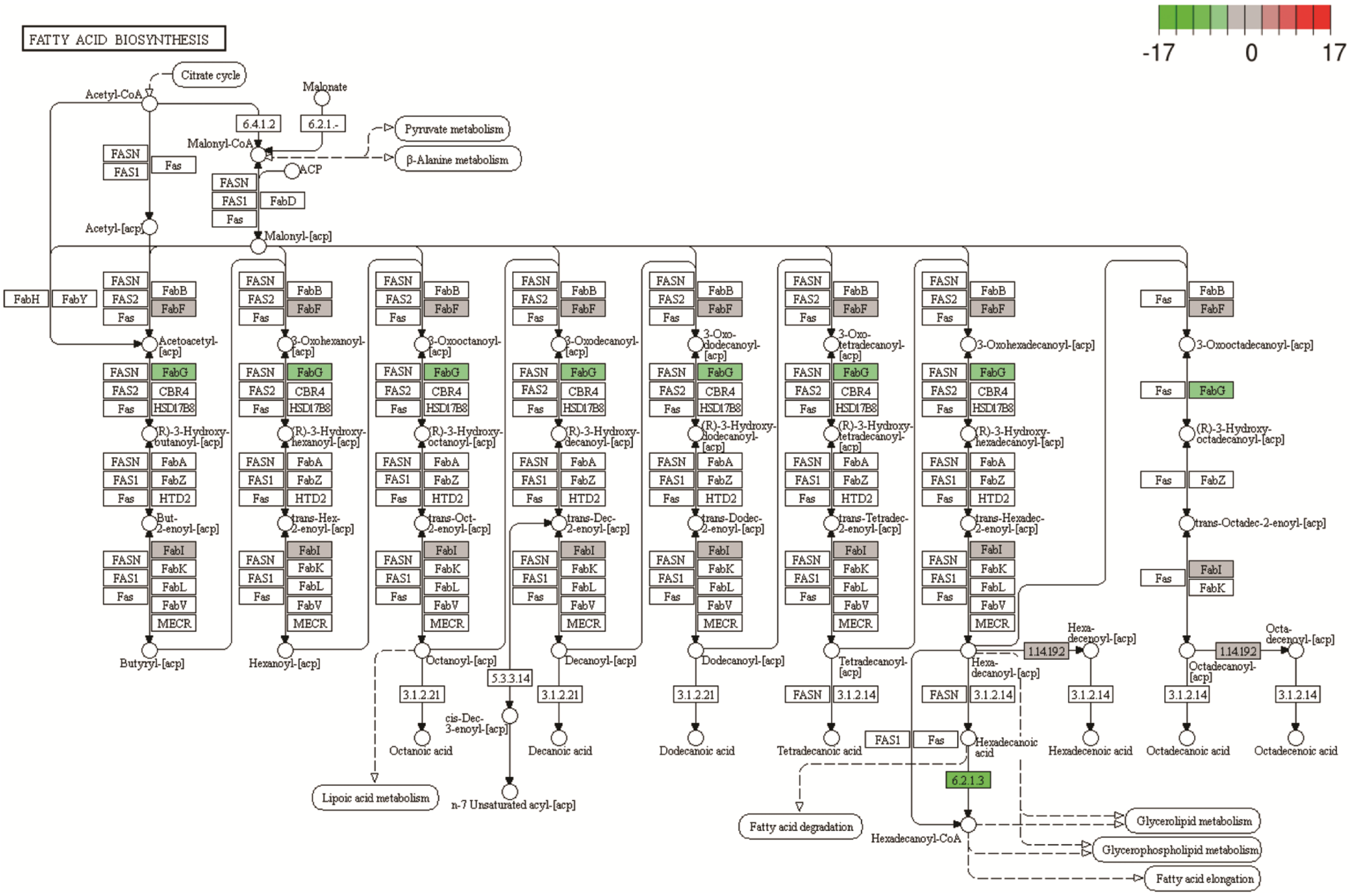
Category	ID	Description	Query item	Query total	Bg item	Bg total	P value	FDR
BP	GO:0006950	response to stress	55	757	611	23155	1.00E-10	1.60E-07
BP	GO:0006629	lipid metabolic process	47	757	516	23155	1.80E-09	1.30E-06
BP	GO:0050896	response to stimulus	67	757	917	23155	3.50E-09	1.80E-06
BP	GO:0055114	oxidation reduction	47	757	543	23155	7.80E-09	3.00E-06
BP	GO:0051501	diterpene phytoalexin metabolic process	9	757	17	23155	5.90E-08	1.50E-05
BP	GO:0052314	phytoalexin metabolic process	9	757	17	23155	5.90E-08	1.50E-05
BP	GO:0016101	diterpenoid metabolic process	11	757	43	23155	8.20E-07	0.00018
BP	GO:0006952	defense response	17	757	125	23155	2.70E-06	0.00049
BP	GO:0006721	terpenoid metabolic process	12	757	61	23155	2.90E-06	0.00049
BP	GO:0051502	diterpene phytoalexin biosynthetic process	6	757	9	23155	3.90E-06	0.00054
BP	GO:0052315	phytoalexin biosynthetic process	6	757	9	23155	3.90E-06	0.00054
BP	GO:0008610	lipid biosynthetic process	21	757	191	23155	4.20E-06	0.00054
BP	GO:0044255	cellular lipid metabolic process	26	757	279	23155	5.30E-06	0.00062
BP	GO:0006720	isoprenoid metabolic process	13	757	79	23155	6.50E-06	0.00071
BP	GO:0032787	monocarboxylic acid metabolic process	19	757	175	23155	1.40E-05	0.0014
BP	GO:0006633	fatty acid biosynthetic process	13	757	92	23155	2.80E-05	0.0027
BP	GO:0006631	fatty acid metabolic process	13	757	104	23155	8.70E-05	0.0078
BP	GO:0051504	diterpene phytoalexin precursor biosynthetic process pathway	4	757	7	23155	0.00028	0.023
BP	GO:0009415	response to water	6	757	24	23155	0.00031	0.023
BP	GO:0019748	secondary metabolic process	14	757	136	23155	0.0003	0.023
BP	GO:0006869	lipid transport	10	757	76	23155	0.00039	0.027
BP	GO:0042221	response to chemical stimulus	30	757	452	23155	0.00037	0.027
BP	GO:0046246	terpene biosynthetic process	4	757	9	23155	0.00057	0.038
BP	GO:0043436	oxoacid metabolic process	31	757	492	23155	0.00068	0.041
BP	GO:0006082	organic acid metabolic process	31	757	493	23155	0.0007	0.041
BP	GO:0019752	carboxylic acid metabolic process	31	757	492	23155	0.00068	0.041
BP	GO:0042214	terpene metabolic process	4	757	10	23155	0.00077	0.044
MF	GO:0016491	oxidoreductase activity	101	757	1387	23155	2.70E-13	3.10E-10
MF	GO:0009055	electron carrier activity	57	757	667	23155	2.90E-10	1.70E-07
MF	GO:0005506	iron ion binding	53	757	616	23155	1.00E-09	3.90E-07
MF	GO:0020037	heme binding	41	757	472	23155	6.50E-08	1.40E-05
MF	GO:0046906	tetrapyrrole binding	41	757	476	23155	8.00E-08	1.40E-05
MF	GO:0043167	ion binding	147	757	2900	23155	8.50E-08	1.40E-05
MF	GO:0043169	cation binding	147	757	2899	23155	8.30E-08	1.40E-05
MF	GO:0046872	metal ion binding	136	757	2709	23155	4.90E-07	7.10E-05
MF	GO:0046914	transition metal ion binding	114	757	2220	23155	1.80E-06	0.00023
MF	GO:0004497	monooxygenase activity	29	757	326	23155	3.60E-06	0.00041
MF	GO:0003824	catalytic activity	316	757	7902	23155	1.10E-05	0.0011
MF	GO:0003993	acid phosphatase activity	8	757	34	23155	4.40E-05	0.0042
MF	GO:0005507	copper ion binding	12	757	100	23155	0.00023	0.019
MF	GO:0030145	manganese ion binding	13	757	115	23155	0.00022	0.019
MF	GO:0000287	magnesium ion binding	15	757	162	23155	0.00053	0.041
MF	GO:0016160	amylase activity	5	757	21	23155	0.0012	0.085
CC	GO:0016023	cytoplasmic membrane-bounded vesicle	238	757	4736	23155	2.00E-12	1.40E-10
CC	GO:0031988	membrane-bounded vesicle	238	757	4736	23155	2.00E-12	1.40E-10
CC	GO:0031982	Vesicle	238	757	4738	23155	2.10E-12	1.40E-10
CC	GO:0031410	cytoplasmic vesicle	238	757	4738	23155	2.10E-12	1.40E-10
CC	GO:0005576	extracellular region	23	757	261	23155	4.10E-05	0.0022
CC	GO:0048046	Apoplast	13	757	110	23155	0.00014	0.0066
CC	GO:0043227	membrane-bounded organelle	533	757	15274	23155	0.0058	0.18
CC	GO:0043231	intracellular membrane-bounded organelle	533	757	15273	23155	0.0057	0.18
CC	GO:0005737	Cytoplasm	511	757	14583	23155	0.0059	0.18
CC	GO:0044444	cytoplasmic part	500	757	14318	23155	0.01	0.28



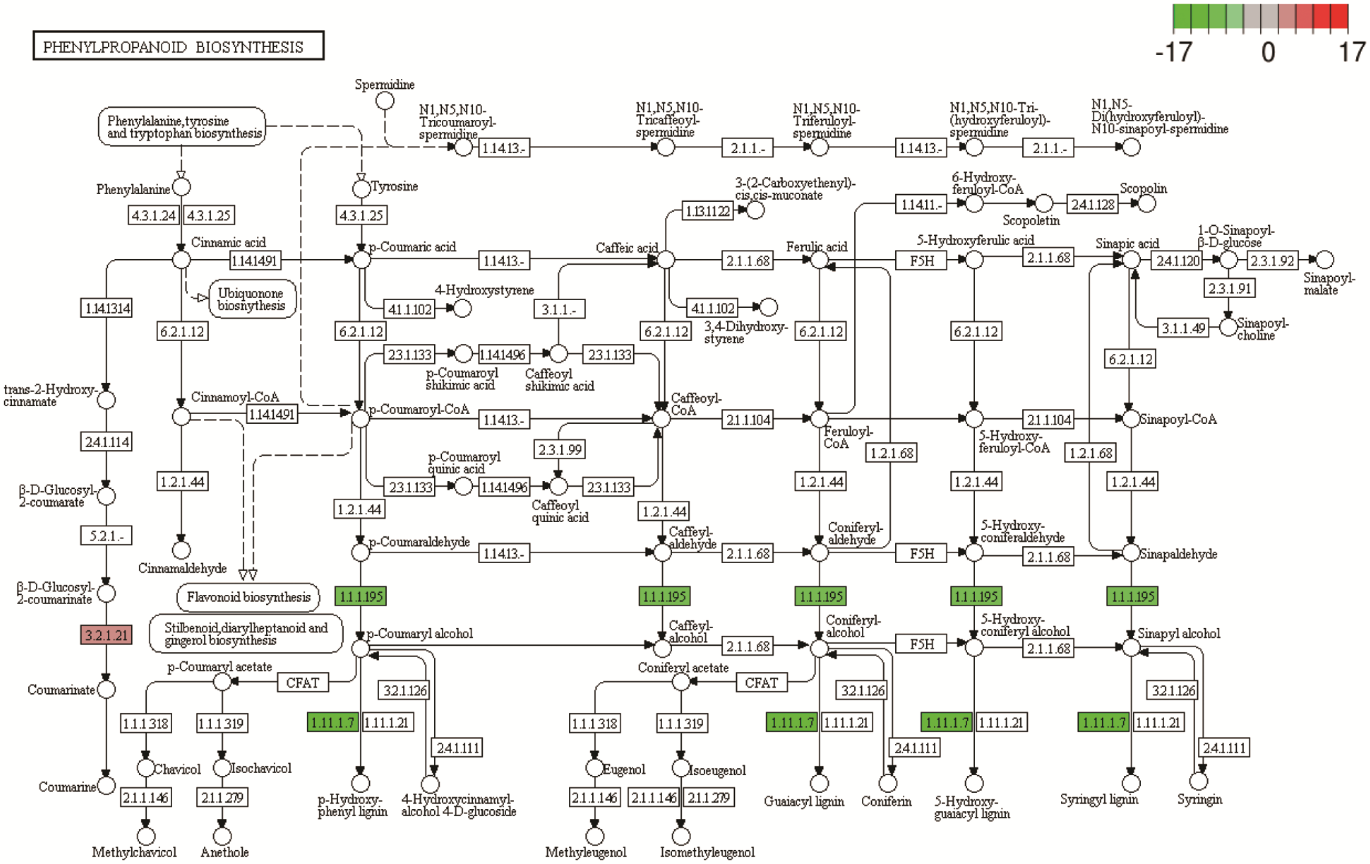
Suppl. Fig. 1S — Significant pathways describing the up- and down-regulation of genes involved in various pathways. (A) MAPK Signalling Pathway



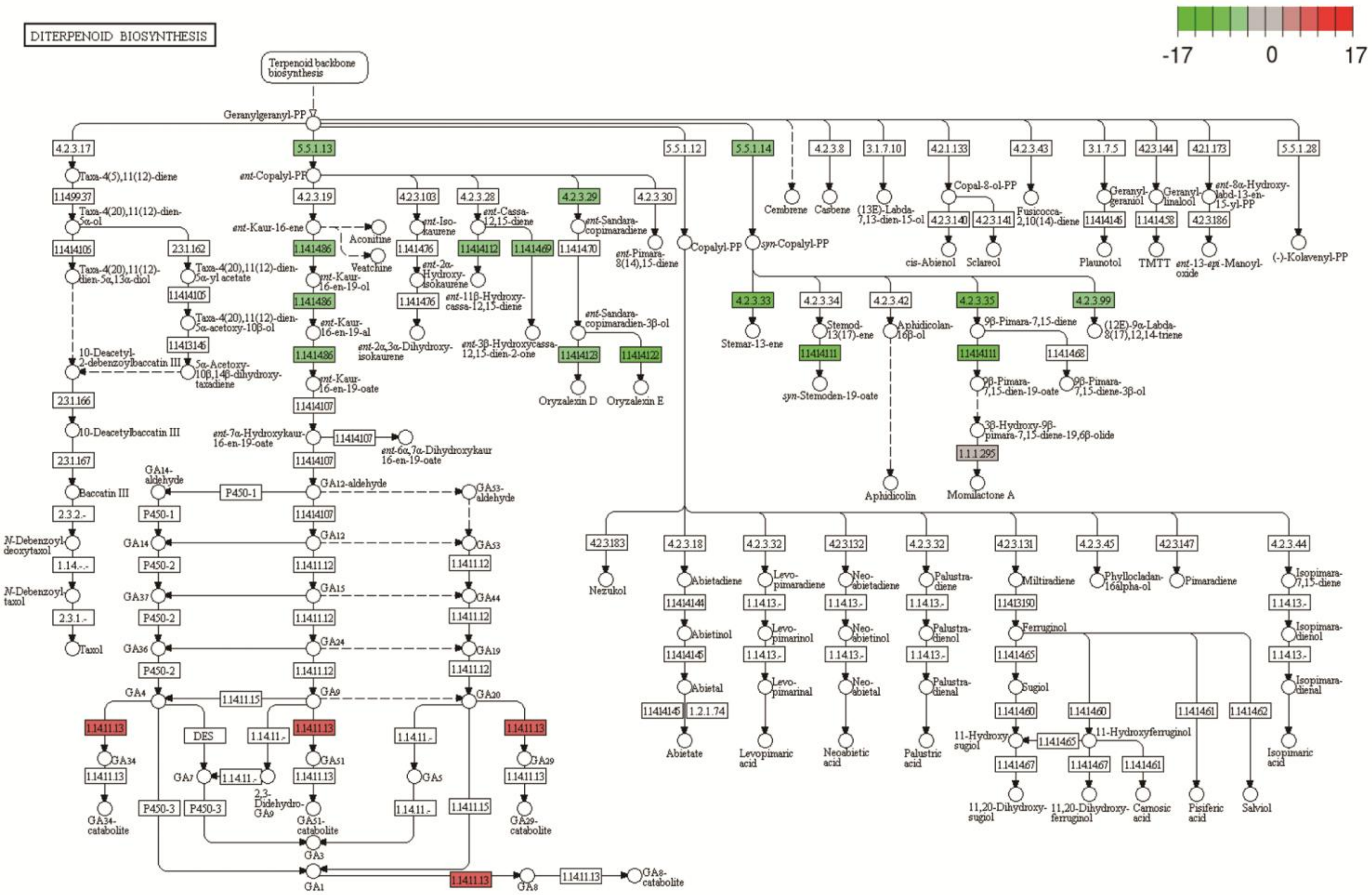
Suppl. Fig. 1S — Significant pathways describing the up- and down-regulation of genes involved in various pathways. (B) Cutin, suberine and wax biosynthesis



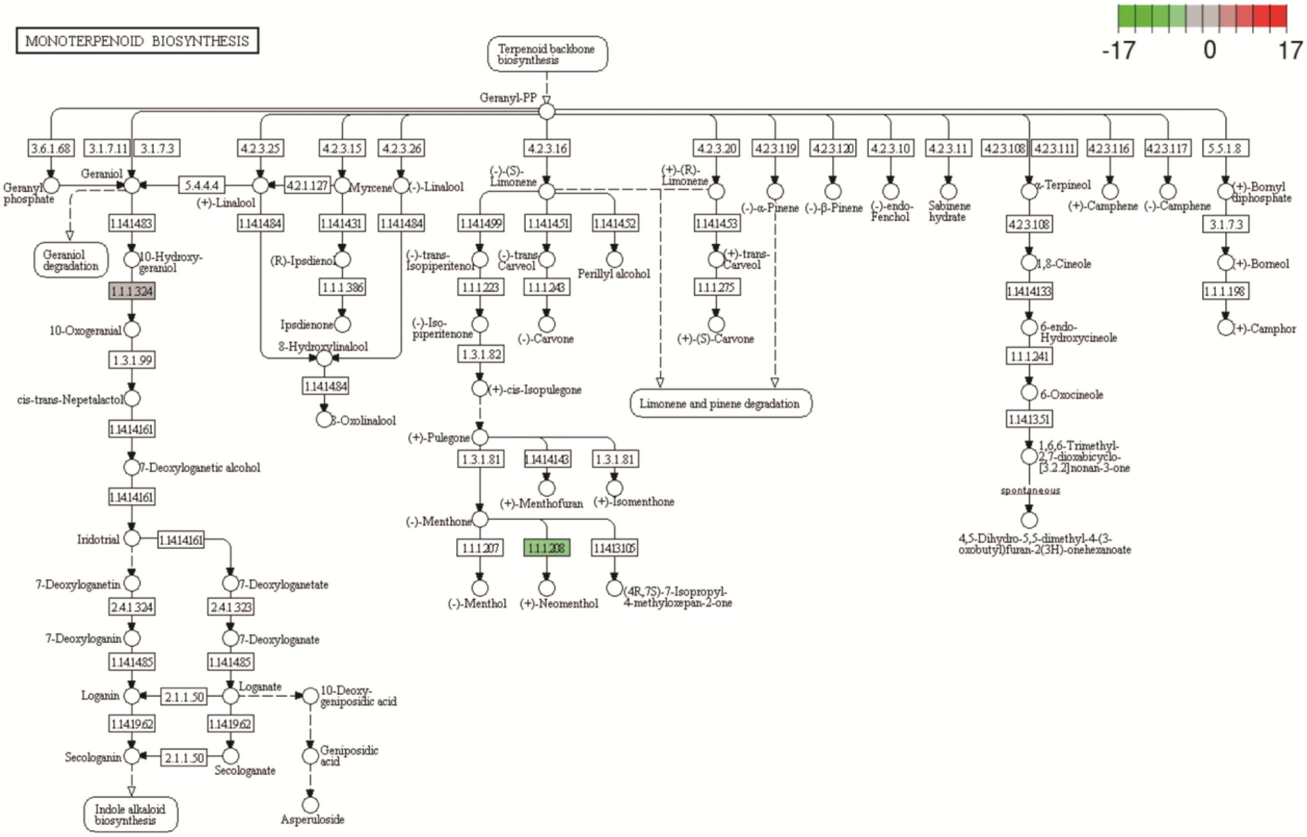
Suppl. Fig. 1S — Significant pathways describing the up- and down-regulation of genes involved in various pathways. (C) Fatty acid biosynthesis



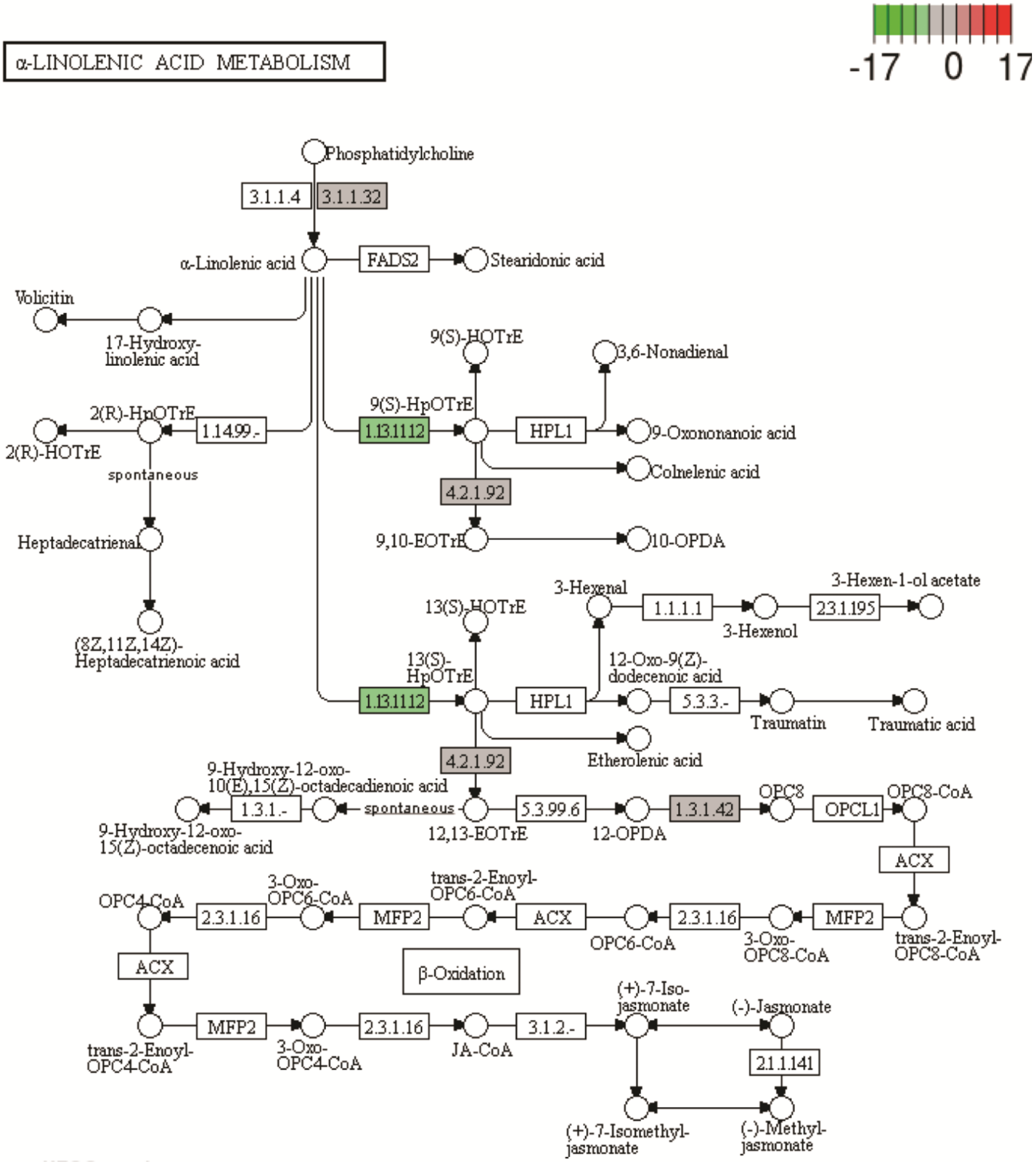
Suppl. Fig. 1S — Significant pathways describing the up- and down-regulation of genes involved in various pathways. (D) Phenylpropanoid biosynthesis



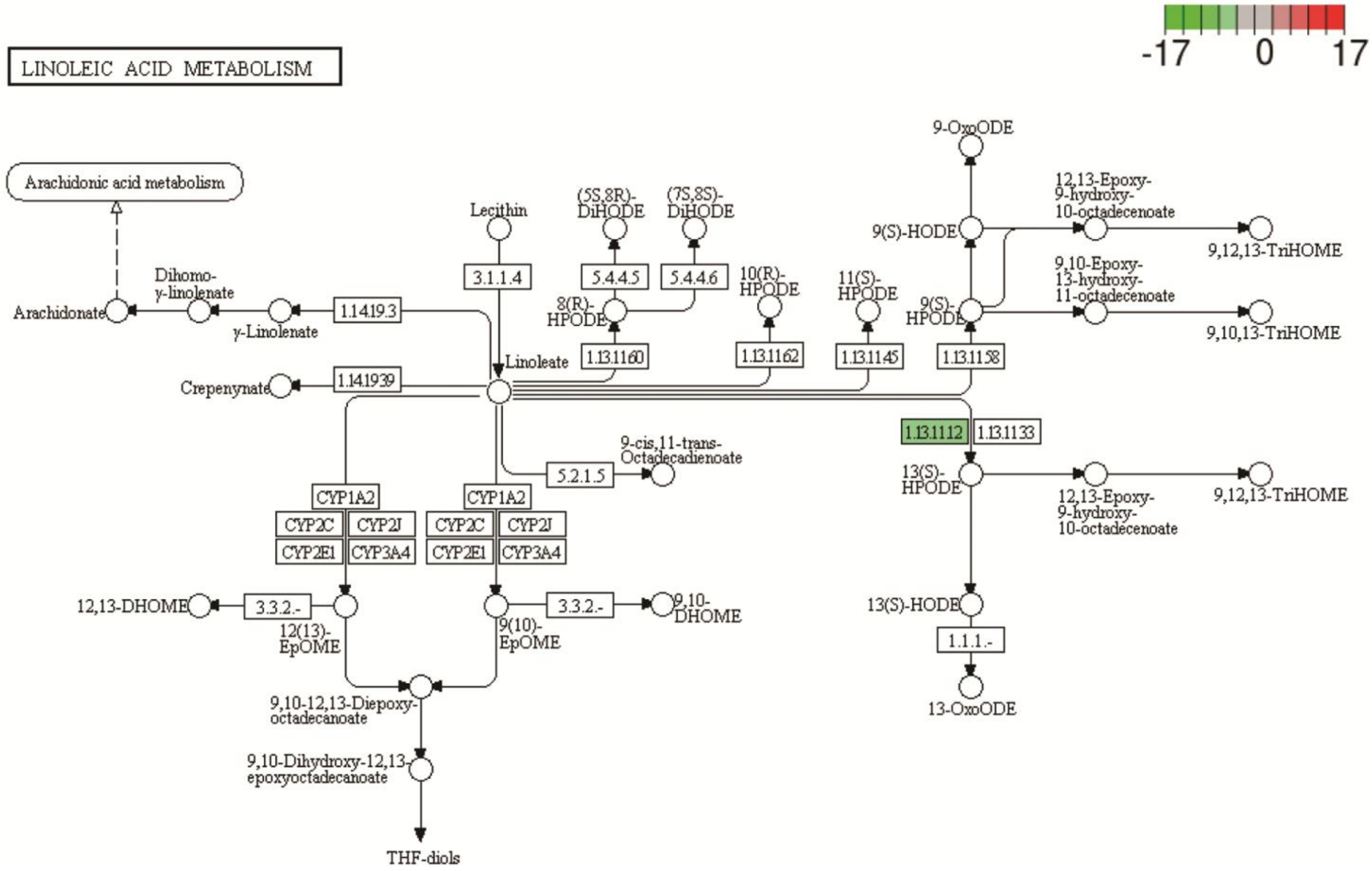
Suppl. Fig. 1S — Significant pathways describing the up- and down-regulation of genes involved in various pathways. (E) Diterpenoid biosynthesis



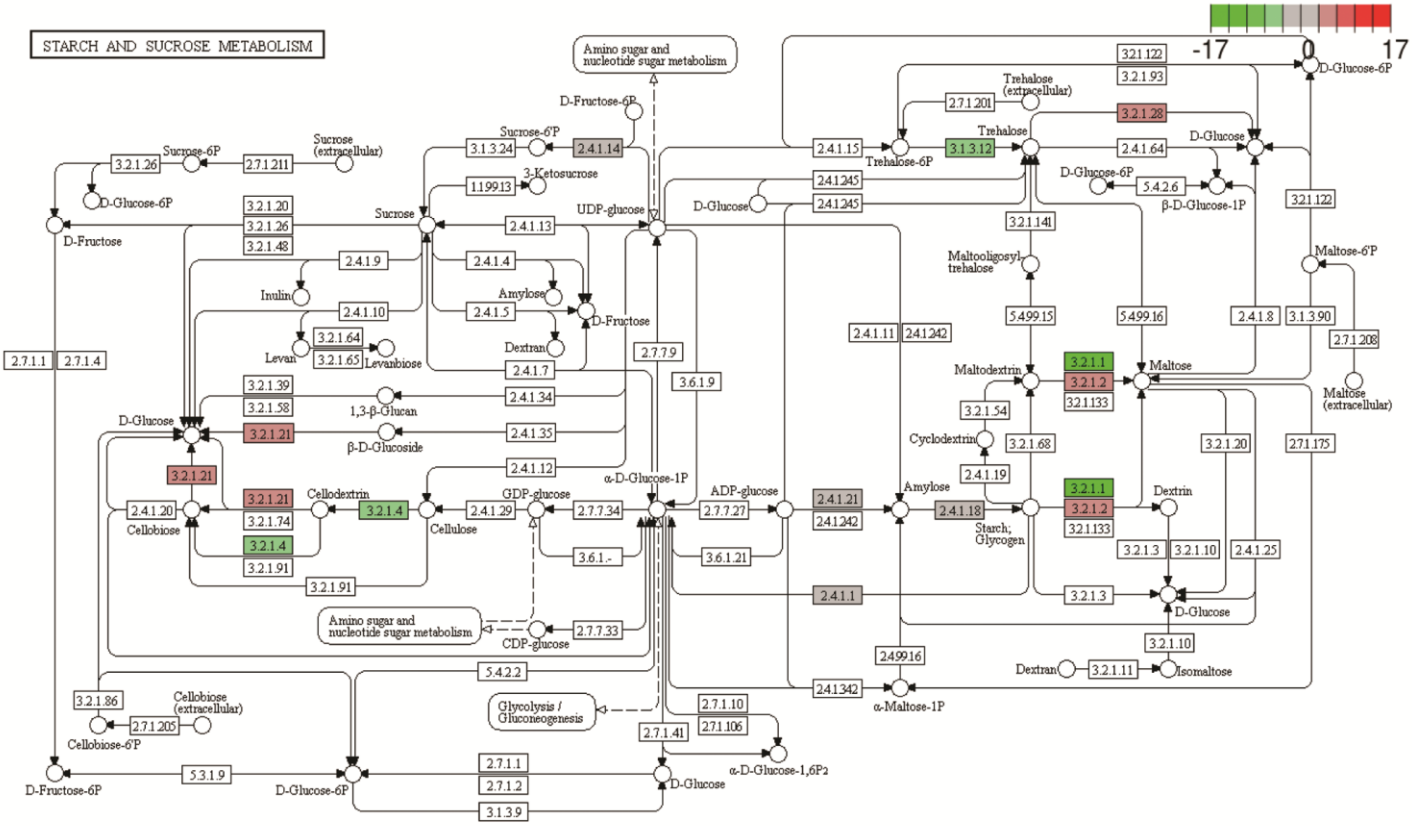
Suppl. Fig. 1S — Significant pathways describing the up- and down-regulation of genes involved in various pathways. (F) Monoterpenoid biosynthesis



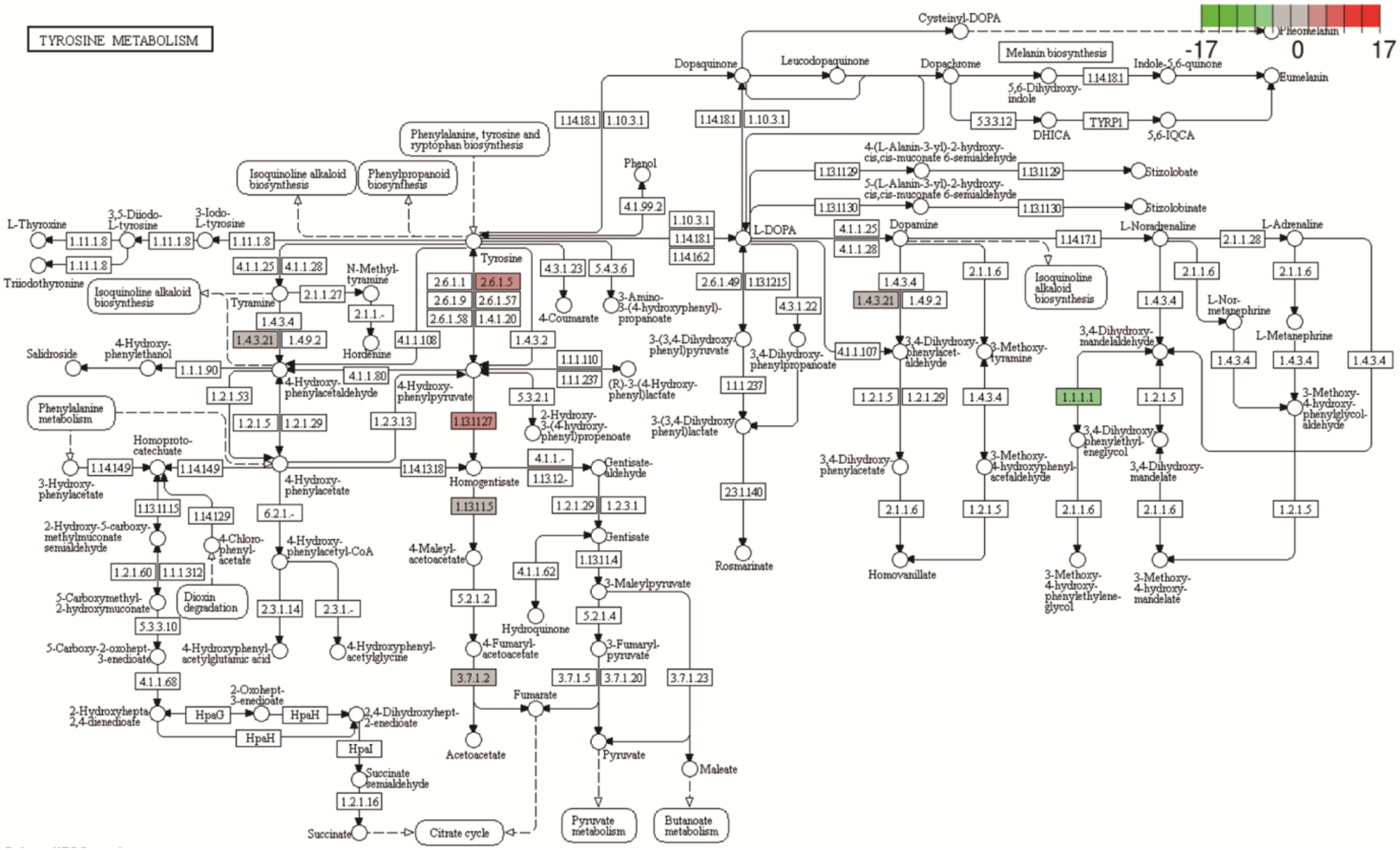
Suppl. Fig. 1S — Significant pathways describing the up- and down-regulation of genes involved in various pathways. (G) α-linolenic acid metabolism



Suppl. Fig. 1S — Significant pathways describing the up- and down-regulation of genes involved in various pathways. (H) Linoleic acid metabolism



Suppl. Fig. 1S — Significant pathways describing the up- and down-regulation of genes involved in various pathways. (I) Starch and sucrose metabolism



Suppl. Fig. 1S — Significant pathways describing the up- and down-regulation of genes involved in various pathways. (J) Tyrosine metabolism