

Table S1- General description of mRNA-sequencing results

mRNA-sequencing reads	In planta
Total read number	810,694,678
Number of total reads after quality trimming	809,938,396
Percentage of total reads after quality trimming	99.91%
Number of mapped reads	724,293,326
Proportion of mapped reads (% of trimmed reads)	89.43%
Number of reads mapped to Endophyte genome	13,360,773
Percentage of mapped fungal reads to total mapped reads	1.84%
Number of reads mapped to Ryegrass genome	710,932,553
Percentage of mapped ryegrass reads to total mapped reads	98.16%

Table S2- DEGs encode proteins involved in RNA metabolism (RNA transcription, regulation of transcription, RNA processing). Fold changes show in bold are statistically significant (FDR≤0.05) changed more than two times. Empty fold change cells are representative of not expressed gene in both compared strains.

Gene ID	Bincode Name	Fold Change					
		S WT-(E-)	S Δ ve1A-(E-)	S Δ ve1A-WT	IP WT-(E-)	IP Δ ve1A-(E-)	IP Δ ve1A-WT
3844 0040294-0.1	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'	-1.44	3.87	5.56			
147 0025650-0.0	'RNA.regulation of transcription.ARR'	1.93	2.47	1.28	-1.71	-1.11	1.54
2364 0012727-0.2	'RNA.regulation of transcription.ARR'	1.27	2.16	1.70	-2.08	-1.08	1.92
9362 0031205-0.0	'RNA.regulation of transcription.ARR'	-1.03	3.69	3.81	-1.09	1.27	1.38
11344 0035200-0.0	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'	-1.79	7.05	12.60	-7.96	-47.80	-6.00
12784 0025142-0.0	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'	-2.01	-7.71	-3.83			
17470 0028125-0.0	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'	-1.17	-1.10	1.07	6.65	11.29	1.70
3713 0000708-0.1	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'	-2.10	1.11	2.34			
3792 0047500-0.0	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'	-1.21	-2.87	-2.38			
4747 0030631-0.1	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'	-2.07	-1.37	1.51	1.88	1.06	-1.76
6305 0035940-0.0	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'	-1.28	-3.22	-2.52	1.75	8.44	4.82
6305 0035940-0.1	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'	-1.37	-3.23	-2.35	2.08	33.65	16.19
6831 0001693-0.0	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'	1.24	2.74	2.21	-2.19	1.11	2.43
8268 0029681-0.0	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'	1.93	3.65	1.90			
8775 0031402-0.0	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'	-2.85	2.52	7.18	-2.18	-6.70	-3.07
1431 0015715-0.3	'RNA.regulation of transcription.bZIP transcription factor family'	1.11	-1.09	-1.20	4.81	-2.00	-9.60
10840 0020844-0.0	'RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family'	-3.76	-1.21	3.12	2.30	3.38	1.47
14292 0002956-0.0	'RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family'	-3.22	-1.36	2.36	1.84	2.15	1.17
2645 0017739-0.0	'RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family'	1.35	-1.51	-2.04	-1.22	-1.12	1.09
4172 0027178-0.1	'RNA.regulation of transcription.C2C2(Zn) CO-	1.99	-1.27	-2.52	-1.09	-1.31	-1.20

	like, Constans-like zinc finger family'						
5346 0024732-0.3	'RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family'	-3.21	-1.18	2.73	1.52	1.60	1.05
12108 0008083-0.1	'RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family'	-3.65	-1.71	2.13	1.42	1.12	-1.27
1517 0023937-0.3	'RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family'	-2.77	-1.09	2.54	1.87	2.31	1.23
20491 0015122-0.0	'RNA.regulation of transcription.C2H2 zinc finger family'	1.39	2.36	1.70	-1.19	1.15	1.37
2402 0024285-0.0	'RNA.regulation of transcription.C2H2 zinc finger family'	1.10	1.11	1.01	2.05	-2.37	-4.86
3255 0017506-0.0	'RNA.regulation of transcription.C2H2 zinc finger family'	2.21	3.33	1.50			
9254 0010925-0.0	'RNA.regulation of transcription.C2H2 zinc finger family'	1.08	-1.06	-1.15	4.31	-1.72	-7.43
1903 0001342-0.3	'RNA.regulation of transcription.Chromatin Remodeling Factors'	1.07	1.44	1.35	-623.32	-2.91	209.35
1937 0031964-0.1	'RNA.regulation of transcription.Chromatin Remodeling Factors'	-1.32	-1.35	-1.03	1511.81	3326.33	2.61
3398 0039790-0.2	'RNA.regulation of transcription.DNA methyltransferases'	1.54	-1.09	-1.68	3.17	-2.83	-8.99
6504 0036370-0.0	'RNA.regulation of transcription.DNA methyltransferases'	1.29	-2.94	-3.78			
3445 0010060-0.0	'RNA.regulation of transcription.G2-like transcription factor family, GARP'	-2.12	-1.44	1.47	1.90	1.20	-1.58
557 0013553-0.0	'RNA.regulation of transcription.G2-like transcription factor family, GARP'	-2.27	-1.08	2.10	-1.02	1.03	1.04
1541 0030919-0.0	'RNA.regulation of transcription.HB,Homeobox transcription factor family'	1.46	1.62	1.11	5.11	1.40	-3.65
3204 0012050-0.1	'RNA.regulation of transcription.HB,Homeobox transcription factor family'	-1.37	-1.23	1.12	2.76	-4.65	-12.88
7825 0043151-0.0	'RNA.regulation of transcription.HB,Homeobox transcription factor family'	1.16	2.12	1.83			
10734 0046517-0.1	'RNA.regulation of transcription.HSF,Heat-shock transcription factor family'	2.23	1.07	-2.09	1.73	-1.09	-1.89
16643 0040016-0.1	'RNA.regulation of transcription.HSF,Heat-shock transcription factor family'	1.94	-1.12	-2.17	1.33	2.80	2.12
2069 0002052-0.2	'RNA.regulation of transcription.MADS box transcription factor family'	-1.27	-1.57	-1.24	4.13	-1.15	-4.74
2923 0025539-0.0	'RNA.regulation of transcription.MADS box transcription factor family'	1.43	3.08	2.15			

7524 0034213-0.0	'RNA.regulation of transcription.MADS box transcription factor family'	1.21	-1.78	-2.16	1.18	-1.20	-1.42
2307 0023751-0.0	'RNA.regulation of transcription.MYB domain transcription factor family'	-1.50	2.42	3.63			
28835 0029238-0.0	'RNA.regulation of transcription.MYB domain transcription factor family'	1.07	1.03	-1.04	-1.55	-8.26	-5.33
405 0021379-0.2	'RNA.regulation of transcription.MYB domain transcription factor family'	1.31	-1.80	-2.36			
5759 0024249-0.0	'RNA.regulation of transcription.MYB domain transcription factor family'	3.12	-1.28	-3.99	1.13	1.36	1.21
5934 0044269-0.0	'RNA.regulation of transcription.MYB domain transcription factor family'	-1.80	1.48	2.65	1.17	-1.83	-2.13
691 0011197-0.3	'RNA.regulation of transcription.MYB domain transcription factor family'	-1.30	1.74	2.25			
15721 0015845-0.0	'RNA.regulation of transcription.MYB-related transcription factor family'	1.09	3.22	2.96			
4082 0025941-0.0	'RNA.regulation of transcription.MYB-related transcription factor family'	-3.71	-1.27	2.92	3.32	4.59	1.38
4972 0039514-0.0	'RNA.regulation of transcription.MYB-related transcription factor family'	1.34	1.17	-1.14	-103.96	-4.47	23.24
7202 0017613-0.0	'RNA.regulation of transcription.MYB-related transcription factor family'	-2.87	-1.32	2.18	2.56	3.54	1.38
873 0029587-0.1	'RNA.regulation of transcription.MYB-related transcription factor family'	1.13	2.56	2.26			
2733 0022591-0.0	'RNA.regulation of transcription.NAC domain transcription factor family'	-1.79	1.18	2.10	-1.43	-1.90	-1.34
3994 0007765-0.1	'RNA.regulation of transcription.NAC domain transcription factor family'	-2.67	-1.39	1.93	5.28	1.01	-5.20
6009 0025573-0.0	'RNA.regulation of transcription.NAC domain transcription factor family'	1.99	-1.04	-2.08	-1.54	-2.48	-1.61
2926 0025544-0.0	'RNA.regulation of transcription.Psdo ARR transcription factor family'	-2.36	-1.54	1.53	1.24	1.16	-1.07
4675 0001294-0.0	'RNA.regulation of transcription.putative transcription regulator'	-1.47	-1.74	-1.18	6.04	-1.78	-10.73
10500 0032179-0.2	'RNA.regulation of transcription.unclassified'	1.40	1.40	-1.00	7.22	3.85	-1.87
14522 0016919-0.2	'RNA.regulation of transcription.unclassified'	-1.29	1.89	2.43	-1.34	-1.39	-1.03
17402 0022797-0.0	'RNA.regulation of transcription.unclassified'	-1.57	-1.25	1.26	195.64	512.61	2.74
316 0002700-0.0	'RNA.regulation of transcription.unclassified'	-1.73	1.23	2.13	-1.11	-6.47	-5.83
3647 0041486-0.1	'RNA.regulation of transcription.unclassified'	-1.58	1.44	2.28	-1.39	-1.95	-1.40
917 0038170-0.6	'RNA.regulation of transcription.unclassified'	-1.26	1.12	1.41	-1.27	4.36	5.56
9201 0005498-0.1	'RNA.regulation of transcription.unclassified'	-1.19	1.52	1.81	-6.51	-4.40	1.48

11930 0014594-0.0	'RNA.regulation of transcription.WRKY domain transcription factor family'	-1.07	2.05	2.21	-1.55	-1.84	-1.19
224 0023185-0.1	'RNA.regulation of transcription.WRKY domain transcription factor family'	1.50	3.34	2.22	1.27	2.03	1.60
3427 0047537-0.1	'RNA.regulation of transcription.WRKY domain transcription factor family'	1.15	2.86	2.50			
3946 0006688-0.0	'RNA.regulation of transcription.WRKY domain transcription factor family'	-1.31	1.82	2.38	1.20	1.54	1.29
5265 0022303-0.1	'RNA.regulation of transcription.WRKY domain transcription factor family'	1.37	2.95	2.15	-1.07	2.22	2.38
637 0045345-0.0	'RNA.regulation of transcription.WRKY domain transcription factor family'	-1.46	1.53	2.23	-1.31	-2.10	-1.61
6432 0018061-0.0	'RNA.regulation of transcription.WRKY domain transcription factor family'	-1.96	1.36	2.66			
7925 0032956-0.0	'RNA.regulation of transcription.WRKY domain transcription factor family'	-1.04	3.82	3.98	-2.50	-2.71	-1.08
9874 0038606-0.0	'RNA.regulation of transcription.WRKY domain transcription factor family'	-2.50	1.48	3.68	-6.12	-6.54	-1.07
4193 0041308-0.0	'RNA.RNA binding'	1.22	1.26	1.03	2.54	-569.81	-1581.76
1189 0015287-0.3	'RNA.transcription'	-1.12	-1.05	1.06	14.01	19.44	1.39
15129 0001576-0.0	'RNA.processing.RNA helicase'	-1.18	1.25	1.47	260.84	105.58	-2.42

Table S3- DEGs encode proteins involved in nucleotide metabolism (Synthesis, degradation and salvage). Fold changes show in bold are statistically significant (FDR≤0.05) changed more than two times.

Gene ID	Bincode Name	Fold Change					
		S WT-(E-)	S Δ veIA-(E-)	S Δ veIA-WT	IP WT-(E-)	IP Δ veIA-(E-)	IP Δ veIA-WT
18772 0007075-0.0	'nucleotide metabolism.salvage.phosphoribosyltransferases.aprt'	-1.65	1.30	2.15	1.18	1.18	-1.01
2374 0043192-0.1	'nucleotide metabolism.degradation.pyrimidine.beta-ureidopropionase'	1.31	1.12	-1.16	-8.39	-2.21	3.79
2441 0047435-0.0	'nucleotide metabolism.deoxynucleotide metabolism.pseudouridine synthase'	-2.43	-1.36	1.79	5.55	1.09	-5.08
4196 0041311-0.2	'nucleotide metabolism.salvage.phosphoribosyltransferases.aprt'	1.55	2.46	1.59	-1.58	-1.26	1.26
6732 0019325-0.0	'nucleotide metabolism.degradation.purine'	-3.36	-1.34	2.50	-1.04	-3.94	-3.79
8947 0012172-0.0	'nucleotide metabolism.synthesis.pyrimidine.orotate phosphoribosyltransferase'	1.41	1.86	1.32	-1.49	3.57	5.33
18772 0007075-0.0	'nucleotide metabolism.salvage.phosphoribosyltransferases.aprt'	-1.65	1.30	2.15	1.18	1.18	-1.01
2374 0043192-0.1	'nucleotide metabolism.degradation.pyrimidine.beta-ureidopropionase'	1.31	1.12	-1.16	-8.39	-2.21	3.79

Table S4- DEGs predicted to encode enzymes engaged in sugar metabolism. Fold changes show in bold are statistically significant (FDR≤0.05) changed more than two times. Empty fold change cells are representative of not expressed gene in both compared strains.

Gene ID	Bincode Name	Best annotation	Fold Change					
			S WT- (E-)	S Δ _{ve} A- (E-)	S Δ _{ve} A/ WT	IP WT- (E-)	IP Δ _{ve} A/ (E-)	IP Δ _{ve} A/ WT
8128 ref0015167-0.0	'major CHO metabolism synthesis sucrose (SPS)'	Sucrose phosphate synthase 1 [<i>Arabidopsis thaliana</i>]				-8.72	-1.56	5.57
5904 ref0034294-0.1	'major CHO metabolism synthesis sucrose (SPS)'	Sucrose-6-phosphate phosphohydrolase [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	1.17	2.17	1.85	-2.05	1.10	2.26
12649 ref0035145-0.0	'major CHO metabolism degradation sucrose hexokinase'	hexokinase-7 [<i>Brachypodium distachyon</i>]	-2.02	1.29	2.62	1.13	-1.37	-1.55
5327 ref0035434-0.0	'major CHO metabolism degradation sucrose invertases cell wall'	fructan exohydrolase [<i>Phleum pratense</i>]	-1.77	-1.03	1.72	6.61	-1.10	-7.30
731 ref0019652-0.3	'major CHO metabolism degradation sucrose invertases cell wall'	fructan exohydrolase [<i>Phleum pratense</i>]	-1.70	1.26	2.14			
406 ref0021378-0.3	'major CHO metabolism degradation sucrose invertases cell wall'	cell wall invertase [<i>Lolium perenne</i>]	-1.29	1.56	2.01	-2.38	1.15	2.73
9463 ref0034934-0.0	'major CHO metabolism degradation sucrose invertases cell wall'	cell wall invertase [<i>Triticum aestivum</i>]	1.27	2.44	1.93	-1.99	-1.03	1.94
1673 ref0036117-0.0	'major CHO metabolism degradation sucrose invertases vacuolar'	fructosyltransferase- like protein [Lolium <i>perenne</i>]	-1.95	-1.62	1.21	-9.06	-17.12	-1.89
671 ref0020303-0.0	'major CHO metabolism degradation sucrose invertases vacuolar'	putative fructosyltransferase1 [<i>Lolium perenne</i>]	1.74	-1.02	-1.76	-2.13	2.75	5.88
6955 ref0011933-0.0	'transport sugars sucrose'	Sucrose transport protein SUT5 [<i>Triticum urartu</i>]	2.27	-1.08	-2.47	1.04	-1.16	-1.21
13424 ref0032032-0.0	'transport.sugars'	PREDICTED: sugar transport protein 13 [<i>Setaria italica</i>]	1.04	1.10	1.06	1.97	5.62	2.85
245 ref0012158-1.0	'transport.sugars'	hexose transporter [<i>Oryza sativa</i> Japonica Group]	-1.16	-1.01	1.15	16.68	14.04	-1.18
13641 ref0014757-0.0	'transport.sugars'	Sugar carrier protein C [Triticum urartu]	-1.00	2.04	2.05	1.65	1.06	-1.55
18487 ref0015440-0.0	'transport.sugars'	sugar transport protein 5-like isoform X1 [Brachypodium <i>distachyon</i>]	-2.30	-1.03	2.24	1.40	4.58	3.27
5190 ref0021123-0.3	'transport.sugars'	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	-2.02	1.54	3.12	-3.15	-2.02	1.56
6199 ref0042523-0.0	'transport.sugars'	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	-2.02	1.26	2.54	-1.93	1.07	2.07
8121 ref0015158-0.0	'transport.sugars'	sugar transport protein 14 [Brachypodium <i>distachyon</i>]	-1.81	1.34	2.42	-1.60	-1.19	1.34
8522 ref0019595-0.1	'transport.sugars'	Sugar transport protein 13 [Aegilops <i>tauschii</i>]	-1.76	1.18	2.08	-2.26	-1.06	2.13
8701 ref0036885-0.0	'transport.sugars'	MFS transporter [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	-1.36	1.84	2.51	-2.38	-1.55	1.54

Table S5- DEGs predicted to encode enzymes engaged in photosynthesis. Fold changes show in bold are statistically significant (FDR≤0.05) changed more than two times. Empty fold change cells are representative of not expressed gene in both compared strains.

Gene ID	Bincode Name	Best annotation	Fold Change					
			S WT- (E-)	S Δ <i>veIA</i> - (E-)	S Δ <i>veIA</i> - WT	IP WT- (E-)	IP Δ <i>veIA</i> - (E-)	IP Δ <i>veIA</i> - WT
3163 0009846-0.1	'PS light reaction photosystem I LHC-I'	photosystem I light harvesting complex gene 2	-1.93	1.04	2.01	2.00	1.05	-1.90
7424 0044379-0.1	'PS light reaction photosystem I LHC-I'	photosystem I light harvesting complex gene 2	-2.28	-1.35	1.68	1.38	1.03	-1.34
1452 0003114-0.3	'PS light reaction photosystem II LHC-II'	Chlorophyll a-b binding protein 1B, chloroplastic [Aegilops tauschii]	-3.74	-1.22	3.07	2.43	1.59	-1.53
1452 0003114-0.5	'PS light reaction photosystem II LHC-II'	Chlorophyll a-b binding protein 1B, chloroplastic [Aegilops tauschii]	-2.55	1.18	3.01	22.27	5.37	-4.14
1998 0021188-0.0	'PS light reaction photosystem II LHC-II'	chlorophyll a-b binding protein, chloroplastic [Brachypodium distachyon]	-2.16	-1.20	1.80	1.52	1.25	-1.22
228 0023193-1.3	'PS light reaction photosystem II LHC-II'	chlorophyll a-b binding protein of LHCII type 1 [Brachypodium distachyon]	-1.98	1.12	2.23	2.27	1.74	-1.31
399 0000946-0.5	'PS light reaction photosystem II LHC-II'	Chlorophyll a-b binding protein CP26, chloroplastic [Aegilops tauschii]	-2.22	-1.21	1.83	1.64	1.25	-1.32
7637 0001662-0.1	'PS light reaction photosystem II PSII polypeptide subunits'	Photosystem II 1 kDa polypeptide, chloroplast [Salmo salar]	-1.70	-1.46	1.17	1.78	-5.60	-9.95
7637 0001662-0.2	'PS light reaction photosystem II PSII polypeptide subunits'	Photosystem II 1 kDa polypeptide, chloroplastic [Aegilops tauschii]	-1.92	-1.32	1.46	5.46	-4.65	-25.44
21159 0002244-0.0	'PS light reaction state transition'	unnamed protein product [Triticum aestivum]				-1.00	-8.87	-8.83
22186 0033836-0.0	'PS light reaction state transition'	putative vesicle associated membrane protein [Triticum aestivum]	2.97	2.29	-1.30	-2.87	-1.96	1.47
4713 0037794-0.0	'PS light reaction state transition'	myosin-15-like isoform X1 [Brachypodium distachyon]	1.21	1.05	-1.15	-18.29	-27.73	-1.52

Table S6- DEGs predicted to encode enzymes associated in plant and fungal cell wall. Fold changes show in bold are statistically significant (FDR≤0.05) changed more than two times. Empty fold change cells are representative of not expressed gene in both compared strains.

Gene ID	Bincode Name	Best annotation	Fold change					
			S WT-(E-)	S Δ ^{velA} -(E-)	S Δ ^{velA} -WT	IP WT-(E-)	IP Δ ^{velA} -(E-)	IP Δ ^{velA} -WT
10004 0012901-0.0	'cell wall.cellulose synthesis.cellulose synthase'	cellulose synthase-like D3 [Arabidopsis thaliana]				-12.18	-2.43	5.05
12401 0030411-0.0	'cell wall.cellulose synthesis.cellulose synthase'	cellulose synthase-like D3 [Arabidopsis thaliana]	1.25	1.46	1.15	-1.63	-12.32	-7.67
1704 0031283-0.0	'cell wall.cellulose synthesis.cellulose synthase'	cellulose synthase like G2 [Arabidopsis thaliana]	-1.48	-4.18	-2.73			
2515 0039698-0.1	'cell wall.cellulose synthesis.COBRA'	predicted protein [Hordeum vulgare subsp. vulgare]	1.59	3.46	2.05	-1.83	1.10	2.04
246 0012161-0.1	'cell wall.cellulose synthesis'	hypothetical protein F775_1266 [Aegilops tauschii]	-2.54	-4.38	-1.74			
6792 0008466-0.0	'cell wall.hemicellulose synthesis.glucuronoxylan'	hypothetical protein F775_1266 [Aegilops tauschii]	2.44	4.00	1.81	-1.34	-1.23	1.03
2462 0011551-0.0	'cell wall.degradation.mannan-xylose-arabinose-fucose'	predicted protein [Hordeum vulgare subsp. vulgare]	2.62	2.49	-1			
5328 0035447-0.0	'cell wall.degradation.mannan-xylose-arabinose-fucose'	xyloglucan xyloglucosyl transferase [Hordeum vulgare]	-1.64	-1.07	1.54	5.24	11.63	2.23
5359 0042439-0.0	'cell wall.degradation.mannan-xylose-arabinose-fucose'	mannan endo-1,4-beta-mannosidase 1 [Brachypodium distachyon]	1.53	-1.29	-1.97	-14.22	1.42	20.39
634 0045342-0.5	'cell wall.degradation.pectate lyases and polygalacturonases'	hypothetical protein ZEAMMB73_269375 [Zea mays]	2.01	2.46	1.2			
16353 0013246-0.0	'cell wall.modification'	expansin B4 [Arabidopsis thaliana]	1.85	-1.18	-2.17	-2.22	-10.25	-4.98
10034 0030944-0.0	'cell wall.modification'	expansin A15 [Arabidopsis thaliana]	-1.07	-2.65	-2.48			
5014 0044908-0.1	'cell wall.modification'	expansin A1 [Arabidopsis thaliana]	1.48	2.19	1.47			
1899 0018801-0.0	'cell wall.modification'	expansin-A21-like [Brachypodium distachyon]	2.11	1.15	-1.84			
1776 0013307-0.1	'cell wall.modification'	xyloglucan endotransglucosylase [Arabidopsis thaliana]	1.62	1.13	-1.43	1.92	-3.11	-5.84
2451 0017008-0.0	'cell wall.modification'	xyloglucan endotransglucosylase [Hordeum vulgare]	-1.35	1.82	2.47	2.24	-2.22	-4.93
4019 0041942-0.5	'cell wall.pectin*esterases.acetyl esterase'	Pectinacetyl esterase family protein [Arabidopsis thaliana]	-2.39	1.34	3.19	1.24	1.74	1.42

Table S7- DEGs encode proteins involved in secondary metabolites biosynthesis. Fold changes show in bold are statistically significant (FDR≤0.05) changed more than two times. Empty fold change cells are representative of not expressed gene in both compared strains.

Gene ID	Bincode Name	Best annotation	Fold Change					
			S WT-(E-)	S Δ veIA-(E-)	S Δ veIA-WT	IP WT-(E-)	IP Δ veIA-(E-)	IP Δ veIA-WT
1716 0000676-0.6	secondary metabolism.phenylpropanoids.lignin biosynthesis.4CL'	OPC-8:0 CoA ligase1	2.25	3.36	1.49	1.07	1.81	1.69
0 0040988-3.1	'secondary metabolism.phenylpropanoids.lignin biosynthesis.C4H'	cytochrome P450, family 98, subfamily A, polypeptide 3	-1.38	-2.33	-1.69			
2479 0029533-0.1	'secondary metabolism.phenylpropanoids.lignin biosynthesis.C4H'	cytochrome P450, family 98, subfamily A, polypeptide 3	10.55	51.80	4.93			
2324 0036197-0.0	'secondary metabolism.phenylpropanoids.lignin biosynthesis.CCR1'	cinnamoyl coa reductase	1.80	1.07	-1.68	2.24	205.67	463.97
4219 0035898-0.0	secondary metabolism.phenylpropanoids.lignin biosynthesis.CCR1'	NAD(P)-binding Rossmann-fold superfamily protein	-3.89	-1.11	3.52	2.84	2.66	-1.07
4368 0002962-0.0	'secondary metabolism.phenylpropanoids.lignin biosynthesis.F5H'	cytochrome P450, family 71, subfamily B, polypeptide 34	2.55	4.82	1.89	-1.70	1.51	2.57
529 0042161-0.3	secondary metabolism.phenylpropanoids.lignin biosynthesis.F5H'	Cytochrome P450 superfamily protein	-2.29	-1.05	2.18	-1.28	4.49	5.73
5292 0013391-0.0	'secondary metabolism.phenylpropanoids.lignin biosynthesis.F5H'	cytochrome P450, family 71, subfamily B, polypeptide 34	1.52	2.74	1.80	-1.35	1.37	1.86
4885 0034746-0.0	secondary metabolism.phenylpropanoids.lignin biosynthesis.HCT'	HXXXD-type acyl-transferase family protein	2.02	2.59	1.28			
7436 0026562-0.0	'secondary metabolism.phenylpropanoids.lignin biosynthesis.HCT'	HXXXD-type acyl-transferase family protein	-1.19	3.41	4.04			

3264 0023028-0.0	'secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL'	phenylalanine ammonia-lyase 2	1.10	2.58	2.35	-6.60	-2.50	2.64
3264 0023028-0.1	'secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL'	phenylalanine ammonia-lyase 2	2.34	2.76	1.18	-4.97	-2.84	1.75
1105 0016983-0.7	'secondary metabolism.isoprenoids.terpenoids'	Terpenoid cyclases/Protein prenyltransferases superfamily protein	1.02	-2.62	-2.66			
15392 0002671- 0.0	'secondary metabolism.isoprenoids.terpenoids'	terpene synthase-like sequence-1,8-cineole				13.51	7.34	-1.84
2163 0015757-0.0	'secondary metabolism.isoprenoids.terpenoids'	Terpenoid cyclases/Protein prenyltransferases superfamily protein	1.64	2.14	1.30			
3397 0039783-0.5	'secondary metabolism.isoprenoids.terpenoids'	terpene synthase-like sequence-1,8-cineole				-2.94	-5.83	-1.98
408 0021371-0.2	'secondary metabolism.isoprenoids.terpenoids'	Terpenoid cyclases/Protein prenyltransferases superfamily protein	-1.83	1.51	2.76	-5.37	-2.06	2.61
529 0042161-0.1	'secondary metabolism.isoprenoids.terpenoids'	terpene synthase-like sequence-1,8-cineole	-1.84	15.05	27.66	-1.31	-88.26	-67.71
15239 0044829- 0.0	secondary metabolism.flavonoids.anthocyanins.anthocy anidin reductase'	dihydroflavonol 4-reductase	2.34	2.52	1.08	-1.93	-1.74	1.11
2994 0021678-0.1	'secondary metabolism.flavonoids.anthocyanins.anthocy anidin reductase'	dihydroflavonol 4-reductase	-1.72	1.03	1.77	1.46	-7.80	-11.39
5717 0000643-0.0	'secondary metabolism.flavonoids.anthocyanins'	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	-1.13	3.58	4.06	-2.55	-5.23	-2.05
16995 0020958- 0.0	'secondary metabolism.flavonoids.chalcones.naringenin- chalcone synthase'	Chalcone and stilbene synthase family protein	1.17	-1.51	-1.77	-4.84	2.13	10.29
2884 0002567-0.0	'secondary metabolism.flavonoids.chalcones'	Chalcone and stilbene synthase family protein	1.85	38.23	20.71			
8997 0019391-0.0	'secondary metabolism.flavonoids.dihydroflavonols.dihyd roflavonol 4-reductase'	NAD(P)-binding Rossmann-fold superfamily protein	-1.68	-4.28	-2.55			
10510 0001618- 0.0	'secondary metabolism.flavonoids.dihydroflavonols.flavon oid 3''-monooxygenase'	cytochrome P450, family 71, subfamily A, polypeptide 15	-2.55	1.02	2.61	1.15	-1.36	-1.56
11445 0015996- 0.0	secondary metabolism.flavonoids.dihydroflavonols.flavon oid 3''-monooxygenase'	cytochrome P450, family 71 subfamily B, polypeptide 7	-1.66	-2.12	-1.28	-1.12	1.53	1.72

11649 0038902-0.1	'secondary metabolism.flavonoids.dihydroflavonols.flavonoid 3''-monooxygenase'	cytochrome P450, family 706, subfamily A, polypeptide 6	-2.23	-1.38	1.62	1.59	1.50	-1.06
15453 0008137-0.1	'secondary metabolism.flavonoids.dihydroflavonols.flavonoid 3''-monooxygenase'	cytochrome P450, family 71, subfamily B, polypeptide 35	1.18	-2.37	-2.80	7.02	17.80	2.54
4211 0043078-0.0	'secondary metabolism.flavonoids.dihydroflavonols.flavonoid 3''-monooxygenase'	cytochrome P450, family 706, subfamily A, polypeptide 6	1.27	-2.26	-2.86			
4396 0019374-0.0	'secondary metabolism.flavonoids.dihydroflavonols.flavonoid 3''-monooxygenase'	cytochrome P450, family 706, subfamily A, polypeptide 6	1.53	5.65	3.68	-3.73	-1.80	2.07
4481 0040498-0.1	'secondary metabolism.flavonoids.dihydroflavonols.flavonoid 3''-monooxygenase'	cytochrome P450, family 706, subfamily A, polypeptide 6	1.15	6.19	5.37	-5.74	-2.10	2.73
4481 0040498-0.3	'secondary metabolism.flavonoids.dihydroflavonols.flavonoid 3''-monooxygenase'	cytochrome P450, family 706, subfamily A, polypeptide 6	1.46	5.27	3.62	-3.45	-1.20	2.89
6356 0041246-0.0	'secondary metabolism.flavonoids.dihydroflavonols.flavonoid 3''-monooxygenase'	cytochrome P450, family 71, subfamily B, polypeptide 35	-1.34	-1.91	-1.42	3.84	12.61	3.28
6412 0039669-0.0	'secondary metabolism.flavonoids.dihydroflavonols.flavonoid 3''-monooxygenase'	cytochrome P450, family 712, subfamily A, polypeptide 1	1.56	-1.63	-2.54	-2.36	-1.40	1.69
6509 0006070-0.0	'secondary metabolism.flavonoids.dihydroflavonols.flavonoid 3''-monooxygenase'	cytochrome P450, family 706, subfamily A, polypeptide 6	-2.13	-1.95	1.09	1.29	2.07	1.60
8705 0036889-0.0	'secondary metabolism.flavonoids.dihydroflavonols.flavonoid 3''-monooxygenase'	cytochrome P450, family 71, subfamily B, polypeptide 37	1.10	-1.25	-1.38	-13.21	-4.81	2.74
185 0000330-1.0	'secondary metabolism.flavonoids.dihydroflavonols'	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	1.89	6.05	3.19	-3.51	1.34	4.69
185 0000330-1.1	'secondary metabolism.flavonoids.dihydroflavonols'	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	-1.92	1.33	2.55	-5.54	-11.61	-2.10
2542 0011927-0.0	'secondary metabolism.flavonoids.dihydroflavonols'	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	-1.18	2.53	3.00	-1.23	-1.35	-1.09
18564 0016146-0.0	'secondary metabolism.flavonoids.flavonols'	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	1.06	1.24	1.16	-4.21	1.20	5.07
4527 0038439-0.0	'secondary metabolism.flavonoids.flavonols'	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	1.89	2.80	1.48	-1.98	1.01	2.01

14366 0045001-0.0	'secondary metabolism.flavonoids.isoflavones.isoflavone reductase'	NmrA-like negative transcriptional regulator family protein	-1.98	1.04	2.06				
12006 0041597-0.0	'secondary metabolism.isoprenoids.carotenoids.carotenoid beta ring hydroxylase'	beta-carotene hydroxylase 2	1.19	1.28	1.07	1.07	5.75	5.40	
6708 0024836-0.0	'secondary metabolism.isoprenoids.non-mevalonate pathway.DXS'	1-deoxy-D-xylulose 5-phosphate synthase 1	2.40	4.49	1.87	-2.22	1.03	2.29	
snap_4308 0038962-0.15	'secondary metabolism.N misc.alkaloid-like'	FAD-binding Berberine family protein	1.33	1.57	1.18	-5.29	1.49	7.88	
snap_4308 0038962-0.8	'secondary metabolism.N misc.alkaloid-like'	FAD-binding Berberine family protein	1.59	3.13	1.97				
133 0020071-1.2	'secondary metabolism.phenylpropanoids'	O-methyltransferase family protein	1.24	2.28	1.83				
160 0012850-0.0	'secondary metabolism.phenylpropanoids'	HXXXD-type acyl-transferase family protein	1.25	-1.93	-2.41				
1770 0013301-0.0	'secondary metabolism.simple phenols'	laccase 12	-2.61	-6.04	-2.31				
1770 0013301-0.1	'secondary metabolism.simple phenols'	laccase 12	-1.65	-2.29	-1.39				
5878 0040205-0.0	'secondary metabolism.sulfur-containing.glucosinolates.degradation.myrosinase'	beta glucosidase 15	1.50	-1.46	-2.20				
8235 0022638-0.0	'secondary metabolism.sulfur-containing.glucosinolates.synthesis.shared.CYP83B1 phenylacetaldoxime monooxygenase'	cytochrome P450, family 71, subfamily B, polypeptide 20	1.99	2.99	1.51	-1.94	-1.08	1.80	
4851 0029305-0.4	'secondary metabolism.wax'	beta-ketoacyl reductase 2	1.81	2.94	1.62				
6296 0018632-0.0	'secondary metabolism.wax'	Fatty acid hydroxylase superfamily	-1.57	1.54	2.43	-1.16	2.16	2.50	
7855 0036148-0.1	'secondary metabolism.wax'	beta-ketoacyl reductase 1	1.14	-3.01	-3.43				

Table S8- DEGs encode proteins involved in abiotic stresses. Fold changes show in bold are statistically significant (FDR≤0.05) changed more than two times. Empty fold change cells are representative of not expressed gene in both compared strains.

Gene ID	Bincode Name	Best annotation	Fold Change					
			S WT-(E-)	S Δ veIA-(E-)	S Δ veIA-WT	IP WT-(E-)	IP Δ veIA-(E-)	IP Δ veIA-WT
16888 0036561-0.0	'stress.abiotic.cold'	Peroxidase superfamily protein	-1.02	1.17	1.20	1.70	-5.08	-8.62
27094 0033264-0.0	'stress.abiotic.cold'	Peroxidase superfamily protein	-2.45	-516.21	-221.92			
3783 0029599-0.2	'stress.abiotic.cold'	Peroxidase superfamily protein	1.09	-5.11	-5.58			
7468 0021099-0.0	'stress.abiotic.drought/salt'	ERD (early-responsive to dehydration stress) family protein	1.35	1.21	-1.11	-2.29	12.34	28.26
11003 0019732-0.0	'stress.abiotic.heat'	HSP20-like chaperones superfamily protein	2.05	-1.07	-2.20			
15044 0029114-0.0	'stress.abiotic.heat'	Chaperone DnaJ-domain superfamily protein	2.33	-1.04	-2.43	-1.46	-1.85	-1.27
1856 0042057-0.0	'stress.abiotic.heat'	DNAJ heat shock N-terminal domain-containing protein	1.33	-1.03	-1.36	1.59	6.10	3.85
4444 0017402-0.2	'stress.abiotic.heat'	DNAJ heat shock N-terminal domain-containing protein	-2.62	-1.41	1.86	2.08	2.55	1.23
5674 0034274-0.1	'stress.abiotic.heat'	heat shock transcription factor A2	-1.57	-2.30	-1.46	4.32	6.18	1.43
6225 0038301-0.0	'stress.abiotic.heat'	Chaperone DnaJ-domain superfamily protein	-3.34	-2.31	1.45	3.88	-3.80	-14.74
679 0020295-0.0	'stress.abiotic.heat'	winged-helix DNA-binding transcription factor family protein	1.03	2.16	2.09	-1.71	-1.06	1.61
1235 0015297-0.2	'stress.abiotic.touch/wounding'	Wound-responsive family protein	-1.71	2.10	3.34	1.20	-1.63	-1.96
10578 0037683-0.0	'stress.abiotic.unspecified'	RmlC-like cupins superfamily protein	2.25	4.04	1.80	-1.16	-2.13	-1.84
13475 0026757-0.1	'stress.abiotic.unspecified'	unknown protein	-16.04	1.07	17.06			
1655 0023677-0.0	'stress.abiotic.unspecified'	RmlC-like cupins superfamily protein	2.27	2.37	1.05			
2106 0029322-0.1	'stress.abiotic.unspecified'	RmlC-like cupins superfamily protein	1.11	-1.11	-1.23	10.38	6.16	-1.69

557 0013553-0.2	'stress.abiotic.unspecified'	RmlC-like cupins superfamily protein	1.46	2.40	1.64			
557 0013553-0.5	'stress.abiotic.unspecified'	RmlC-like cupins superfamily protein	1.54	2.73	1.77			
6807 0019838-0.4	'stress.abiotic.unspecified'	RmlC-like cupins superfamily protein	-1.21	1.86	2.26			
10085 0011254-0.0	'stress.abiotic'	SPX domain gene 1	1.23	-1.67	-2.06	-1.39	1.07	1.49

Table S9- DEGs encode proteins involved in biotic stresses. Fold changes show in bold are statistically significant (FDR≤0.05) changed more than two times. Empty fold change cells are representative of not expressed gene in both compared strains.

Gene ID	Bincode Name	Best annotation	Fold Change					
			S WT-(E-)	S Δ veIA-(E-)	S Δ veIA-WT	IP WT-(E-)	IP Δ veIA-(E-)	IP Δ veIA-WT
13893 0007097-0.0	'not assigned.unknown'	Pathogenesis-related protein Bet v	1.07	1.20	1.12	-2.89	-8.95	-3.10
snap_1310 0005233-0.18	'stress.biotic'	basic pathogenesis-related protein 1	-1.04	2.29	2.38			
snap_367 0009954-0.1	'stress.biotic'	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein	1.51	3.14	2.08			
snap_18280 0002333-0.0	'stress.biotic'	basic pathogenesis-related protein 1	2.44	5.02	2.06	2.53	1.03	-2.47
snap_27036 0021856-0.0	'stress.biotic'	basic pathogenesis-related protein 1	1.39	2.21	1.58	1.57	-1.15	-1.81
snap_10431 0035258-0.6	'stress.biotic'	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein	1.73	2.92	1.69	-2.03	-1.57	1.29
537 0024475-0.2	'not assigned.unknown'	Pathogenesis-related protein Bet v	1.57	2.19	1.39	-1.57	1.11	1.74
2380 0021883-0.0	'not assigned.unknown'	START-like domain Bet v	1.89	2.39	1.27			
8639 0033693-0.0	'not assigned.unknown'	START-like domain Bet v	1.68	2.32	1.38			
8639 0033693-0.1	'not assigned.unknown'	Pathogenesis-related protein Bet v	1.48	2.16	1.46	-2.07	-1.96	1.06
snap_17168 0014271-0.1	'stress.abiotic'	Pathogenesis-related thaumatin superfamily protein	2.30	2.23	-1.03	-1.13	1.01	1.14
snap_19370 0001080-0.0	'stress.abiotic'	Pathogenesis-related thaumatin superfamily protein	1.30	2.48	1.92	-1.31	-2.52	-1.92
snap_376 0040308-0.21	'stress.abiotic'	Pathogenesis-related thaumatin superfamily protein	2.01	3.38	1.68	-7.13	-2.22	3.21
509 0006343-0.3	'stress.biotic.PR-proteins'	receptor like protein 12				5.86	7.09	1.21
1247 0044125-0.3	'stress.biotic.respiratory burst'	NADPH/respiratory burst oxidase protein D	-1.23	2.31	2.84			
783 0026874-0.6	'stress.biotic.signalling.MLO-like'	Seven transmembrane MLO family protein	2.11	5.35	2.53	-2.29	-1.44	1.59
10465 0029861-0.0	'stress.biotic'	HXXXD-type acyl-transferase family protein	1.75	7.07	4.05	-7.62	-2.75	2.77

12352 0024047-0.0	'stress.biotic'	HXXXD-type acyl-transferase family protein	-1.29	1.05	1.35	3.56	9.25	2.60
17121 0039368-0.0	'stress.biotic'	Plant basic secretory protein (BSP) family protein	2.39	4.43	1.86	-1.61	1.55	2.50
11164 0016212-0.0	'stress.biotic'	Chitinase family protein	1.98	3.15	1.59	-7.11	-1.77	4.03
13325 0046918-0.0	'stress.biotic'	Chitinase family protein	2.32	7.06	3.04	-4.63	-4.33	1.07
1983 0003140-0.1	'stress.biotic'	Chitinase family protein	4.55	11.80	2.60	-3.25	1.12	3.65
21371 0046601-0.0	'stress.biotic'	Chitinase family protein	-1.19	2.00	2.36	-1.92	-1.12	1.72
25915 0013866-0.0	'stress.biotic'	Chitinase family protein	1.66	3.14	1.89	-2.28	-2.32	-1.02
5518 0030549-0.0	'stress.biotic'	LRR and NB-ARC domains-containing disease resistance protein	1.16	-1.16	-1.35	3.01	9.09	3.02
274 0017642-1.2	'stress.biotic'	LRR and NB-ARC domains-containing disease resistance protein	-1.11	1.08	1.20	9.79	4.11	-2.38
476 0026821-0.2	'stress.biotic'	LRR and NB-ARC domains-containing disease resistance protein	-1.35	1.50	2.02	-1.15	-1.00	1.15
10643 0016359-0.0	'stress.biotic'	NB-ARC domain-containing disease resistance protein	1.16	1.06	-1.09	1.43	-4.98	-7.13
11308 0010204-0.1	'stress.biotic'	Disease resistance protein (CC-NBS-LRR class) family	1.33	4.66	3.50			
31175 0012032-0.0	'stress.biotic'	NB-ARC domain-containing disease resistance protein	1.34	-1.67	-2.23	2.62	1.89	-1.38
3297 0040849-0.0	'stress.biotic'	RPS5-like 1	-1.18	-1.23	-1.05	-25.74	1.97	50.73
1595 0025675-0.2	'stress.biotic'	LRR and NB-ARC domains-containing disease resistance protein	-1.28	1.73	2.21	-1.30	2.81	3.64
4245 0027234-0.0	'stress.biotic'	Disease resistance protein (CC-NBS-LRR class) family				1.68	-6.90	-11.59
4364 0002974-0.2	'stress.biotic'	Disease resistance protein (CC-NBS-LRR class) family	1.40	2.46	1.76			
545 0031512-0.1	'stress.biotic'	LRR and NB-ARC domains-containing disease resistance protein	-2.32	-1.19	1.95	1.08	2.37	2.19
5593 0028879-0.1	'stress.biotic'	Disease resistance protein (CC-NBS-LRR class) family	-1.63	-1.50	1.09	-192.8	1.39	266.3
6532 0046890-0.2	'stress.biotic'	Disease resistance protein (CC-NBS-LRR class) family				-2.93	-1623.0	-606.3

695 0011193-0.3	'stress.biotic'	NB-ARC domain-containing disease resistance protein	1.21	1.05	-1.15	-1.30	5.75	7.46
7128 0030119-0.0	'stress.biotic'	Disease resistance protein (CC-NBS-LRR class) family	-1.10	-1.26	-1.14	-7.19	1.13	8.12
7492 0015655-0.0	'stress.biotic'	NB-ARC domain-containing disease resistance protein	1.63	2.20	1.35			
888 0020833-0.4	'stress.biotic'	basic chitinase	2.61	4.82	1.85	-2.07	-1.84	1.13
101 0001927-0.2	'not assigned.unknown'	Putative disease resistance protein RGA1	-2.04	1.22	2.49	2.11	-1.15	-2.44
10403 0017285-0.2	'not assigned.unknown'	Disease resistance protein RGA2	-1.38	1.34	1.84	-31.41	-2.86	10.95
14642 0039966-0.0	'not assigned.unknown'	unknown protein	-1.04	-2.16	-2.08			
19048 0042926-0.0	'not assigned.no ontology'	Leucine-rich repeat (LRR) family protein	-1.27	1.81	2.30	-2.18	-2.76	-1.27
6 0040996-1.2	'not assigned.unknown'	unknown protein	1.01	-1.40	-1.41	-6.07	-1.54	3.95
903 0007606-0.3	'stress.biotic'	NB-ARC domain-containing disease resistance protein	-2.18	1.16	2.53	-2.71	-2.05	1.32
12002 0041593-0.0	'stress'	cysteine-rich RLK (RECEPTOR-like protein kinase) 8	-2.03	1.21	2.47	-1.02	-2.48	-2.42
13207 0000774-0.0	'stress'	cysteine-rich RLK (RECEPTOR-like protein kinase) 10	-1.70	1.43	2.43	-1.28	-1.07	1.20
13207 0000774-0.1	'stress'	cysteine-rich RLK (RECEPTOR-like protein kinase) 10	-1.93	1.96	3.79	-2.28	-1.41	1.62
14476 0031662-0.0	'stress'	cysteine-rich RLK (RECEPTOR-like protein kinase) 4	-1.27	1.57	2.00	6.03	2.00	-3.01
15194 0021387-0.0	'stress'	cysteine-rich RLK (RECEPTOR-like protein kinase) 8	1.25	2.48	1.98	-1.58	-2.39	-1.52
1737 0036758-0.0	'stress'	S-locus lectin protein kinase family protein	-1.01	1.24	1.26	-1.10	-99.74	-91.58
2057 0007590-0.1	'stress'	cysteine-rich RLK (RECEPTOR-like protein kinase) 8	1.10	1.39	1.26	-145.9	-1.69	86.31
2891 0020639-0.1	'stress'	cysteine-rich RLK (RECEPTOR-like protein kinase) 8	-2.11	1.19	2.50	-1.02	-1.73	-1.69
3862 0004424-0.0	'stress'	cysteine-rich RLK (RECEPTOR-like protein kinase) 8	1.30	2.41	1.85	-2.02	-1.18	1.71
4226 0017958-0.2	'stress'	cysteine-rich RLK (RECEPTOR-like protein kinase) 4	-1.06	2.58	2.74	-1.31	-1.16	1.13
6395 0016207-0.0	'stress'	cysteine-rich RLK (RECEPTOR-like protein kinase) 19	1.47	1.74	1.18	-3.78	2.55	9.64

Table S10- DEGs encode proteins involved in ROS production and detoxification. Fold changes show in bold are statistically significant (FDR≤0.05) changed more than two times. Empty fold change cells are representative of not expressed gene in both compared strains.

Gene ID	Bincode Name	Best annotation	Fold Change					
			S WT-(E-)	S Δ velA-(E-)	S Δ velA-WT	IP WT-(E-)	IP Δ velA-(E-)	IP Δ velA-WT
11920 0032529-0.0	'misc.peroxidases'	Peroxidase superfamily protein	-1.42	1.43	2.02			
13363 0021942-0.0	'misc.peroxidases'	Peroxidase superfamily protein	1.50	-1.48	-2.21			
191 0030881-1.2	'misc.peroxidases'	Peroxidase superfamily protein	1.22	2.30	1.89	-1.36	1.32	1.80
29 0012215-0.0	'misc.peroxidases'	Peroxidase family protein	-1.35	1.57	2.12	1.06	1.01	-1.05
13400 0019582-0.0	'misc.peroxidases'	Peroxidase superfamily protein	1.34	2.15	1.61			
3020 0043251-0.1	'misc.peroxidases'	Peroxidase superfamily protein	-1.06	2.50	2.66			
21563 0025807-0.0	'misc.peroxidases'	Peroxidase superfamily protein	-1.34	-2.65	-1.97			
2254 0004379-0.3	'misc.peroxidases'	Peroxidase superfamily protein	-1.71	-7.17	-4.20			
8229 0004594-0.0	'misc.peroxidases'	Peroxidase superfamily protein	1.48	2.66	1.80			
3783 0029599-0.2	'stress.abiotic.cold'	Peroxidase superfamily protein	1.09	-5.11	-5.58			
27094 0033264-0.0	'stress.abiotic.cold'	Peroxidase superfamily protein	-2.45	-516.21	-221.92			
16888 0036561-0.0	'stress.abiotic.cold'	Peroxidase superfamily protein	-1.02	1.17	1.20	1.70	-5.08	-8.62
8786 0035014-0.2	'redox.ascorbate and glutathione.glutathione'	glutathione peroxidase 7	-3.73	-1.18	3.16	3.75	4.30	1.15
30 0030220-2.0	'misc.glutathione S transferases'	glutathione S-transferase tau 7	-2.26	1.20	2.71	-2.31	-3.35	-1.45
1335 0041028-0.3	'misc.glutathione S transferases'	glutathione S-transferase tau 4	1.28	3.09	2.42	-2.67	1.06	2.82
4704 0007237-0.2	'misc.glutathione S transferases'	glutathione S-transferase 6	-1.87	1.11	2.07	1.68	1.91	1.14
4704 0007237-0.3	'misc.glutathione S transferases'	glutathione S-transferase 6	-1.99	1.11	2.21	1.27	-1.08	-1.37
17715 0008450-0.0	'misc.glutathione S transferases'	Glutathione S-transferase family protein	-2.67	-2.84	-1.07			
1565 0043379-0.0	'misc.glutathione S transferases'	Glutathione S-transferase family protein	1.35	-1.57	-2.13	-1.13	-2.94	-2.61
4382 0037315-0.0	'misc.glutathione S transferases'	glutathione S-transferase 6	2.57	7.37	2.87	-3.17	1.23	3.89
5539 0043047-0.0	'misc.glutathione S transferases'	Peroxidase superfamily protein	2.48	21.58	8.70	-3.01	-2.11	1.43
5539 0043047-0.1	'misc.glutathione S transferases'	Peroxidase superfamily protein	1.07	4.52	4.21	-3.94	-2.99	1.32

3511 0019559-0.2	'misc.glutathione S transferases'	glutathione S-transferase TAU 18	-1.23	-2.49	-2.03			
11527 0037060-0.0	'misc.glutathione S transferases'	glutathione S-transferase tau 4	-1.19	2.36	2.80	-2.30	-1.10	2.09
2254 0004379-0.5	'misc.glutathione S transferases'	glutathione S-transferase TAU 18	-1.53	1.01	1.55	-8.07	-4.22	1.91
869 0011605-0.1	'misc.glutathione S transferases'	Peroxidase superfamily protein	1.76	2.68	1.53			
28602 0004008-0.0	'misc.glutathione S transferases'	Glutathione S-transferase family protein	1.44	-1.61	-2.31	-1.12	1.00	1.12
8786 0035014-0.2	'redox.ascorbate and glutathione.glutathione'	glutathione peroxidase 7	-3.73	-1.18	3.16	3.75	4.30	1.15
5890 0031114-0.6	redox.thioredoxin'	tetratricopeptide-repeat thioredoxin-like 2	1.16	1.31	1.13	1.70	-3.72	-6.34
7843 0005643-0.1	'redox.thioredoxin'	thioredoxin F-type 1	-2.24	-1.52	1.48	1.69	2.13	1.27
20777 0001419-0.0	'redox.ascorbate and glutathione'	cytochrome B5 isoform B	2.67	5.55	2.08			
3042 0007389-0.0	'redox.ascorbate and glutathione.ascorbate'	Plant L-ascorbate oxidase	1.09	2.71	2.48	1.62	-1.20	-1.94
542 0031513-0.2	'redox.heme'	haemoglobin 2	1.44	15.83	11.07			

Table S11- DEGs encode proteins involved in hormone metabolism. Fold changes show in bold are statistically significant (FDR≤0.05) changed more than two times. Empty fold change cells are representative of not expressed gene in both compared strains.

Gene ID	Bincode Name	Best annotation	Fold Change					
			S WT- (E-)	S Δ veIA- (E-)	S Δ veIA- WT	IP WT- (E-)	IP Δ veIA- (E-)	IP Δ veIA- WT
Brassinosteroid (BR)								
12035 0036245-0.0	'hormone metabolism.brassinosteroid.synthesis- degradation.sterols.CYP51'	cytochrome P450, family 707, subfamily A, polypeptide 4	2.98	4.20	1.41			
529 0042161-0.4	'hormone metabolism.brassinosteroid.synthesis- degradation.sterols.CYP51'	cytochrome P450, family 707, subfamily A, polypeptide 4	-2.65	-4.45	-1.68	1.18	-1.24	-1.46
6857 0012593-0.0	'hormone metabolism.brassinosteroid.synthesis- degradation.sterols.CYP51'	cytochrome P450, family 707, subfamily A, polypeptide 4	2.54	2.21	-1.15	-1.60	1.18	1.88
11890 0002733-0.0	'hormone metabolism.brassinosteroid.synthesis- degradation.sterols.CYP51'	cytochrome P450, family 707, subfamily A, polypeptide 4	-1.37	-107.83	-79.88			
Jasmonic acid (JA)								
3901 0030125-0.0	hormone metabolism.jasmonate.synthesis- degradation.12-Oxo-PDA-reductase'	12-oxophytodienoate reductase 1	-1.12	1.58	1.77	-6.39	-1.59	4.02
15130 0032139-0.0	'hormone metabolism.jasmonate.synthesis- degradation.12-Oxo-PDA-reductase'	12-oxophytodienoate reductase 2	1.33	2.17	1.63	-1.34	-2.56	-1.91
9293 0011514-0.0	'hormone metabolism.jasmonate.synthesis- degradation.jasmonate-O- methyltransferase'	S-adenosyl-L-methionine- dependent methyltransferases superfamily protein	1.45	-1.55	-2.25	1.55	1.03	-1.50
3223 0047938-0.2	'hormone metabolism.jasmonate.synthesis- degradation.jasmonate-O- methyltransferase'	S-adenosyl-L-methionine- dependent methyltransferases superfamily protein	-1.97	-1.38	1.42	1.46	4.94	3.38
1134 0047379-0.0	'hormone metabolism.jasmonate.synthesis- degradation.jasmonate-O- methyltransferase'	S-adenosyl-L-methionine- dependent methyltransferases superfamily protein	1.29	2.27	1.76	1.42	-1.49	-2.11

3877 0034879-0.1	'hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase'	PLAT/LH2 domain-containing lipoxygenase family protein	-1.39	1.49	2.07	-2.92	-2.49	1.18
786 0026877-0.0	'hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase'	PLAT/LH2 domain-containing lipoxygenase family protein	-1.30	8.75	11.41	-6.92	-210.46	-30.41
14669 0004090-0.0	'hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase'	PLAT/LH2 domain-containing lipoxygenase family protein	1.05	2.01	1.92	-1.68	-1.88	-1.13
12318 0000453-0.2	'hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase'	PLAT/LH2 domain-containing lipoxygenase family protein	-1.88	-1.30	1.45	-15.85	-24.25	-1.53
7715 0034244-0.1	'hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase'	PLAT/LH2 domain-containing lipoxygenase family protein	1.21	1.66	1.37	-5.02	-29.79	-5.93
10098 0041679-0.1	'hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase'	PLAT/LH2 domain-containing lipoxygenase family protein	-1.88	1.37	2.58	-1.16	-1.48	-1.28
Salicylic acid (SA)								
4452 0035376-0.1	'hormone metabolism.salicylic acid.synthesis-degradation'	UDP-glycosyltransferase 74 F1	-1.43	1.69	2.42	-1.41	1.42	2.01
Abscisic acid (ABA)								
812 0040415-0.2	'hormone metabolism.abscisic acid.signal transduction'	highly ABA-induced PP2C gene 2	-1.15	1.21	1.39	1.60	6.27	3.92
5258 0040140-0.0	'hormone metabolism.abscisic acid.synthesis-degradation'	aldehyde oxidase 2	1.08	-1.06	-1.15	-9.09	-2.31	3.94
7065 0030538-0.3	'hormone metabolism.abscisic acid.synthesis-degradation'	aldehyde oxidase 2	-1.14	1.20	1.37	5.10	2.08	-2.45
767 0012406-0.0	'hormone metabolism.abscisic acid.synthesis-degradation.degradation.8-hydroxylase'	cytochrome P450, family 707, subfamily A, polypeptide 3	-1.61	1.41	2.27	5.78	-1.17	-6.76
3566 0012299-0.0	'hormone metabolism.abscisic acid.synthesis-degradation.synthesis.short chain alcohol dehydrogenase (ABA2)'	NAD	1.68	3.45	2.05			
658 0032726-0.3	'hormone metabolism.abscisic acid.synthesis-degradation.synthesis.zeaxanthin epoxidase'	FAD/NAD	-3.50	-1.26	2.77	2.74	3.02	1.10
Auxin								
2098 0032594-0.0	'hormone metabolism.auxin'	methyl esterase 18	-1.91	1.18	2.25	-1.10	1.87	2.06

765 0012408-0.2	'hormone metabolism.auxin.induced-regulated-responsive-activated'	Auxin-responsive GH3 family protein				-1.91	-5.16	-2.70
1613 0046846-0.1	'hormone metabolism.auxin.induced-regulated-responsive-activated'	NAD	1.39	-1.56	-2.16	-1.69	-1.76	-1.04
1566 0043380-0.0	'hormone metabolism.auxin.induced-regulated-responsive-activated'	NAD	-1.94	-1.58	1.23	5.71	2.66	-2.15
3065 0019997-0.0	'hormone metabolism.auxin.induced-regulated-responsive-activated'	NAD	-3.46	1.12	3.88	-1.14	-1.25	-1.09
3870 0034872-0.1	'hormone metabolism.auxin.induced-regulated-responsive-activated'	AUX/IAA transcriptional regulator family protein	-1.11	2.07	2.31			
7380 0034159-0.0	'hormone metabolism.auxin.induced-regulated-responsive-activated'	Auxin-responsive GH3 family protein	-1.16	2.82	3.28	-1.39	1.60	2.22
446 0044598-0.2	'hormone metabolism.auxin.induced-regulated-responsive-activated'	NAD	1.48	-1.58	-2.34			
16122 0031619-0.0	'hormone metabolism.auxin.induced-regulated-responsive-activated'	Auxin-responsive family protein	-1.43	1.41	2.02	-1.42	-2.14	-1.51
549 0031519-0.5	'hormone metabolism.auxin.signal transduction'	Auxin efflux carrier family protein	1.45	-1.50	-2.17	1.22	-1.43	-1.74
549 0031519-0.6	'hormone metabolism.auxin.signal transduction'	Auxin efflux carrier family protein	1.40	-1.61	-2.27	1.23	-2.02	-2.48
Cytokinin (CK)								
4523 0038435-snap-gene-0.14	'hormone metabolism.cytokinin.synthesis-degradation'	cytokinin oxidase/dehydrogenase 6	-1.98	1.56	3.09			
237 0040978-1.0	'hormone metabolism.cytokinin.synthesis-degradation'	UDP-glucosyl transferase 85A2	2.04	7.70	3.78	-2.37	1.43	3.39
12802 0010595-0.1	'hormone metabolism.cytokinin.synthesis-degradation'	cytokinin oxidase/dehydrogenase 6	1.76	3.50	1.99	1.25	1.20	-1.05
1477 0040490-0.2	'hormone metabolism.cytokinin.synthesis-degradation'	cytokinin oxidase/dehydrogenase 1	-1.56	1.64	2.56	-2.12	-2.04	1.04
21174 0004587-0.0	'hormone metabolism.cytokinin.synthesis-degradation'	UDP-glucosyl transferase 85A3	-2.16	1.01	2.17	4.27	-1.60	-6.83
569 0019014-0.3	'misc.cytochrome P450'	cytochrome P450, family 735, subfamily A, polypeptide 2	1.18	1.17	-1.01	13.45	-127.43	-1871.42
Ethylene								
19592 0025930-0.0	'hormone metabolism.ethylene.induced-regulated-responsive-activated'	Adenine nucleotide alpha hydrolases-like superfamily protein	-2.72	2.95	8.03			
730 0019653-0.3	'hormone metabolism.ethylene.signal transduction'	Integrase-type DNA-binding superfamily protein	-1.14	2.65	3.03			

14174 0020942-0.0	'hormone metabolism.ethylene.synthesis-degradation.1-aminocyclopropane-1-carboxylate oxidase'	2-oxoglutarate	2.16	13.19	6.10			
21938 0036377-0.0	'hormone metabolism.ethylene.synthesis-degradation.1-aminocyclopropane-1-carboxylate synthase'	ACC synthase 1	1.30	2.46	1.90			
Gibberellic acid (GA)								
2519 0039696-0.0	'hormone metabolism.gibberelin.synthesis-degradation.ent-kaurene oxidase'	Cytochrome P450 superfamily protein	1.40	2.19	1.57	1.03	1.12	1.09
4368 0002962-0.1	'hormone metabolism.gibberelin.synthesis-degradation.ent-kaurene synthase'	terpene synthase 04	2.06	3.89	1.89	-3.37	1.19	4.01
7191 0025967-0.1	'hormone metabolism.gibberelin.synthesis-degradation.GA2 oxidase'	gibberellin 2-oxidase	-1.64	1.36	2.22			
5374 0030002-0.0	'hormone metabolism.gibberelin.synthesis-degradation.GA2 oxidase'	gibberellin 2-oxidase 3	1.97	1.12	-1.76	3.69	-2.73	-10.06
3140 0022390-0.2	'hormone metabolism.gibberelin.synthesis-degradation.GA20 oxidase'	gibberellin 20 oxidase 2	-1.60	1.78	2.84			
Not defined								
2664 0005249-0.1	'hormone metabolism'	acetone-cyanohydrin lyase	2.42	4.44	1.84	-23.36	-2.42	9.65
2664 0005249-0.2	'hormone metabolism'	acetone-cyanohydrin lyase	3.79	4.51	1.19			