

Fold Induction	Gene Identity	Description	adjPVal	B statistic	Odds of differential expression: wild type (min to max)	vfb mutant (min to max)	
10,43	AT4G32280	auxin-responsive AUX/IAA family protein	2.62e-06	11,42	100,00%	94,76 (54,55 to 130,2)	8,632 (7,184 to 10,23)
7,26	AT5G62280	expressed protein	6.25e-07	13,88	100,00%	234,2 (185,9 to 284,9)	31,76 (31,42 to 31,93)
6,47	AT2G42870	expressed protein	1.33e-06	12,66	100,00%	151 (128,7 to 174)	23,73 (17,28 to 29,45)
4,66	AT5G57760	expressed protein	1.33e-06	12,69	100,00%	61,4 (59,79 to 62,37)	13,41 (10,11 to 15,98)
4,64	AT3G04210	disease resistance protein (TIR-NBS class), putative	3.48719e-04	3,84	97,90%	271,4 (204,1 to 376,1)	57,06 (46,12 to 64,41)
4,35	AT5G18060	auxin-responsive protein, putative	1.59213e-04	4,98	99,32%	150,7 (122,9 to 205,8)	33,61 (32 to 34,59)
4,28	AT5G02760	protein phosphatase 2C family protein / PP2C family protein	1.55e-06	12,24	100,00%	447,7 (288,1 to 549,5)	102,2 (79,51 to 119,7)
3,88	AT3G59350	serine/threonine protein kinase, putative	3.66789e-04	3,77	97,75%	469,9 (390 to 549,4)	121,9 (100,7 to 152,6)
3,81	AT1G79700	ovule development protein, putative	1.66454e-04	4,89	99,25%	155,8 (130,1 to 187)	43,18 (24,12 to 59,28)
3,76	AT3G21550	expressed protein	8.25e-05	5,99	99,75%	74,79 (67,68 to 83,85)	20,84 (12,31 to 25,73)
3,51	AT1G28330	dormancy-associated protein, putative (DRM1)	3.35288e-04	3,91	98,04%	1.277 (1.225 to 1.336)	391,3 (224,6 to 580,3)
3,35	AT1G78970	lupeol synthase (LUP1) / 2,3-oxidosqualene-triterpenoid cyclase	8.19e-05	6,01	99,76%	181,3 (167 to 195,4)	54,26 (50,05 to 60,57)
3,29	AT2G34770	fatty acid hydroxylase (FAH1)	1.06901e-04	5,61	99,64%	714,2 (654,9 to 811,2)	219,9 (174,8 to 275)
3,28	AT2G33570	expressed protein	2.3e-05	7,9	99,96%	216,6 (202,7 to 226,6)	66,1 (58,9 to 71,55)
3,27	AT3G15540	auxin-responsive protein / indoleacetic acid-induced protein 19 (I	3.08e-05	7,48	99,94%	109,2 (103,3 to 115,9)	33,6 (27,75 to 37,8)
3,26	AT4G34770	auxin-responsive family protein	1.65e-06	12,14	100,00%	65,48 (56,96 to 77,05)	20,46 (15,62 to 26,81)
3,15	AT3G58120	bZIP transcription factor family protein	3.01686e-04	4,07	98,32%	427,4 (391 to 446)	139,5 (99,5 to 180,7)
3,11	AT5G37990	S-adenosyl-L-methionine	1.51238e-04	5,06	99,37%	313,6 (262,5 to 358,6)	100,4 (92,58 to 114,8)
2,97	AT1G04240	auxin-responsive protein / indoleacetic acid-induced protein 3 (IA	2.1e-05	8,07	99,97%	198,6 (171,9 to 243,3)	66,2 (63,8 to 68,37)
2,92	AT1G43790	expressed protein	1.60411e-04	4,96	99,30%	170 (136 to 203,3)	57,65 (51,53 to 62,64)
2,87	AT5G47370	homeobox-leucine zipper protein 2 (HAT2) / HD-ZIP protein 2	1.33e-06	12,58	100,00%	237,9 (187,9 to 273,2)	82,06 (74,25 to 86,45)
2,86	AT1G64360	expressed protein	7.09e-05	6,25	99,81%	103,3 (84,34 to 122,1)	36,18 (28,5 to 43)
2,83	AT1G03870	fasciclin-like arabinogalactan-protein (FLA9)	4.92e-05	6,85	99,89%	1.494 (1.433 to 1.615)	536 (415,9 to 641,6)
2,81	AT4G35320	expressed protein	2.00253e-04	4,65	99,05%	58,38 (51,32 to 66,12)	20,9 (17,62 to 25,48)
2,71	AT3G03840	auxin-responsive protein, putative	5.75141e-04	3,06	95,52%	37,43 (32,37 to 43,88)	14,02 (10,18 to 17,41)
2,66	AT5G03260	laccase, putative / diphenol oxidase, putative	1.63125e-04	4,92	99,28%	32,17 (28,33 to 38,73)	12,13 (10,68 to 14,85)
2,65	AT1G64640	plastocyanin-like domain-containing protein	9.27e-06	9,49	99,99%	142,9 (131,7 to 159,1)	54,69 (41,86 to 63,17)
2,63	AT1G29430	auxin-responsive family protein	4.65316e-04	3,41	96,80%	212,1 (156,8 to 292)	78,34 (70,26 to 88,68)
2,60	AT4G35350	cysteine endopeptidase, papain-type (XCP1)	2.77381e-04	4,18	98,49%	158,4 (138,6 to 177,5)	60,78 (54,1 to 64,97)
2,55	AT1G19530	expressed protein	3.63e-08	18,02	100,00%	41,97 (31,34 to 53,04)	16,11 (15,5 to 16,44)
2,52	AT1G02640	glycosyl hydrolase family 3 protein	7.34e-06	9,88	99,99%	269,6 (250,4 to 289,7)	109,4 (78,45 to 127,9)
2,49	AT2G42530	cold-responsive protein / cold-regulated protein (cor15b)	4.94e-05	6,83	99,89%	802,6 (705 to 924,7)	332,1 (225,5 to 432,6)
2,48	AT4G03190	F-box family protein (FBL18)	4.58e-05	6,95	99,90%	247,2 (219,1 to 280,2)	99,22 (94,58 to 107,2)
2,48	AT3G63440	FAD-binding domain-containing protein / cytokinin oxidase family	9.27e-06	9,47	99,99%	38,85 (33,89 to 42,3)	15,62 (15,1 to 16,36)
2,47	AT1G14920	gibberellin response modulator (GAI) (RGA2) / gibberellin-respon	3.20353e-04	3,97	98,15%	432,5 (366,1 to 488,6)	176,4 (141,2 to 210,5)
2,45	AT3G01670	expressed protein	3.93251e-04	3,64	97,44%	142,9 (130 to 154,8)	58,48 (51,01 to 65,5)
2,44	AT5G48900	pectate lyase family protein	4.83028e-04	3,35	96,61%	281,9 (244,2 to 301,3)	115,4 (102,7 to 125,4)
2,44	AT3G23030	auxin-responsive protein / indoleacetic acid-induced protein 2 (IA	3.01e-05	7,51	99,95%	1.109 (1.015 to 1.264)	454 (414,2 to 490,5)
2,43	AT5G15160	bHLH family protein	1.1354e-04	5,5	99,59%	106 (87,3 to 121,4)	43,22 (40,07 to 46,33)
2,40	AT5G15580	expressed protein	2.37355e-04	4,4	98,79%	164,6 (139,4 to 179,7)	68,62 (60,23 to 78,22)
2,36	AT1G29500	auxin-responsive protein, putative	5.23e-05	6,75	99,88%	165,1 (146,7 to 201)	69,71 (59,58 to 76,61)
2,34	AT4G16515	expressed protein	5.94e-05	6,54	99,86%	175,7 (166,7 to 190,8)	78,1 (50,77 to 101,5)
2,32	AT4G25260	basic helix-loop-helix (bHLH) family protein	6.57e-05	6,38	99,83%	142,8 (136 to 151,7)	61,67 (57,18 to 67,49)
2,32	AT1G29440	auxin-responsive family protein	2.71175e-04	4,21	98,54%	91,05 (63,75 to 118,8)	38,24 (34,9 to 43,61)
2,32	AT2G06850	xyloglucan	1.06e-05	9,21	99,99%	4.020 (3.945 to 4.058)	1.743 (1.588 to 1.986)
2,25	AT4G30410	expressed protein	2.00453e-04	4,65	99,05%	152,2 (149,9 to 154,5)	67,67 (64,57 to 72,39)
2,25	AT3G57795	auxin-responsive protein / indoleacetic acid-induced protein 6 (IA	1.16859e-04	5,45	99,57%	21,39 (20,44 to 21,96)	9,579 (7,938 to 10,45)

2,23	AT4G14560	auxin-responsive protein / indoleacetic acid-induced protein 1 (IA	1.67e-05	8,47	99,98%	73,78 (62,95 to 83,6)	32,93 (31,08 to 34,74)
2,22	AT2G35880	expressed protein	1.2594e-04	5,32	99,51%	321,9 (291,1 to 350,7)	144,7 (137,5 to 155,6)
2,22	AT1G52190	proton-dependent oligopeptide transport (POT) family protein	1.49136e-04	5,08	99,38%	553,3 (502,7 to 596,7)	249,9 (224,8 to 284,2)
2,21	AT5G44260	zinc finger (CCH-type) family protein	6.25e-07	14,28	100,00%	59,25 (58,37 to 60,92)	27,52 (22,25 to 37,11)
2,19	AT5G19530	spermine/spermidine synthase family protein	2.17015e-04	4,53	98,93%	175,3 (166,5 to 185,6)	80,03 (72,24 to 86,25)
2,19	AT2G15680	calmodulin-related protein, putative	3.52502e-04	3,82	97,85%	84,49 (75,79 to 92,1)	38,53 (37,01 to 40,69)
2,14	AT1G06850	bZIP transcription factor, putative	1.18e-05	9,06	99,99%	36,64 (31,13 to 41,54)	17,05 (15,62 to 19,39)
2,14	AT1G14290	acid phosphatase, putative	4.45e-06	10,83	100,00%	185,8 (179,6 to 194,5)	86,72 (83,5 to 89,27)
2,14	AT5G22500	acyl CoA reductase, putative / male-sterility protein, putative	8.6e-05	5,94	99,74%	152 (145,5 to 162,1)	71,27 (64,88 to 80,22)
2,12	AT3G13980	expressed protein	5.27677e-04	3,21	96,12%	81,51 (74,83 to 88,72)	38,32 (38,06 to 38,68)
2,11	AT1G11545	xyloglucan	9.27e-06	9,48	99,99%	137,3 (116 to 157,7)	64,62 (61,89 to 69,93)
2,11	AT3G20570	pathogenesis-related protein, putative	2.15588e-04	4,54	98,94%	56,34 (46,31 to 73,78)	26,36 (22,48 to 30,26)
2,08	AT2G17880	DNAJ heat shock protein, putative	2.25608e-04	4,48	98,88%	106,6 (94,01 to 131,6)	51,79 (36,62 to 61,91)
2,08	AT1G15580	auxin-responsive protein / indoleacetic acid-induced protein 5 (IA	2.43e-05	7,81	99,96%	16,79 (13,13 to 20,2)	7,967 (7,582 to 8,677)
2,06	AT4G34760	auxin-responsive family protein	2.3e-05	7,9	99,96%	335,1 (310,8 to 352,2)	162,4 (151 to 170,3)
2,05	AT1G14280	phytochrome kinase, putative	3.36059e-04	3,9	98,02%	585,2 (552 to 628,2)	285,2 (268,8 to 307,1)
2,03	AT3G62660	glycosyl transferase family 8 protein	1.48006e-04	5,09	99,39%	183,1 (170,3 to 198,1)	92,14 (71,46 to 119,9)
2,00	AT4G09890	expressed protein	1.73657e-04	4,83	99,21%	162,6 (144,1 to 193)	81,08 (74,82 to 93,11)
1,98	AT1G75500	nodulin MtN21 family protein	3.02456e-04	4,06	98,30%	596,2 (571,1 to 627,7)	301,5 (272,2 to 328,6)
1,98	AT5G02540	short-chain dehydrogenase/reductase (SDR) family protein	6.25e-07	14,32	100,00%	59,55 (45,4 to 71,69)	29,67 (26,96 to 32,1)
1,96	AT2G42040	expressed protein	4.62333e-04	3,42	96,83%	144,8 (115,8 to 175,9)	72,99 (65,89 to 78,11)
1,92	AT2G47930	hydroxyproline-rich glycoprotein family protein	9.43e-05	5,79	99,70%	154,7 (139,7 to 167)	81,12 (71,79 to 98,24)
1,90	AT1G12080	expressed protein	8.09e-06	9,76	99,99%	94,52 (85,73 to 101,5)	50 (45,05 to 58,91)
1,90	AT2G01420	auxin transport protein, putative	4.77277e-04	3,37	96,68%	304,1 (292,4 to 318,9)	160,4 (151 to 176,4)
1,89	AT2G33990	calmodulin-binding family protein	5.69614e-04	3,07	95,56%	104,3 (96,73 to 110,2)	55,51 (47,27 to 65,09)
1,88	AT3G15630	expressed protein	4.78166e-04	3,37	96,68%	784,3 (662,9 to 982)	423,9 (286,2 to 498,9)
1,86	AT4G30650	hydrophobic protein, putative / low temperature and salt responsi	3.06482e-04	4,04	98,27%	1.911 (1.610 to 2.322)	1.032 (787,3 to 1.210)
1,85	AT2G14900	gibberellin-regulated family protein	2.43e-05	7,81	99,96%	290 (286 to 293,6)	156,8 (148,3 to 164,8)
1,85	AT1G70940	auxin transport protein, putative (PIN3)	3.90964e-04	3,64	97,44%	269 (247,5 to 305,5)	145,4 (129,1 to 164,9)
1,85	AT4G01330	protein kinase family protein	8.09e-06	9,75	99,99%	243 (233,4 to 259,9)	131,6 (120,8 to 144,8)
1,85	AT1G74740	calcium-dependent protein kinase, putative / CDPK, putative	4.4085e-04	3,49	97,04%	52,19 (42,8 to 60,86)	28,09 (24,89 to 31,33)
1,85	AT2G15320	leucine-rich repeat family protein	3.88337e-04	3,65	97,47%	56,32 (53,61 to 60,81)	30,65 (26,37 to 34,39)
1,84	AT1G79660	expressed protein	5.92267e-04	3,01	95,30%	190,2 (164 to 237,1)	101,9 (96,89 to 104,7)
1,83	AT2G21050	multi-copper oxidase type I family protein	2.1e-05	8,07	99,97%	180,2 (150,9 to 201,7)	98,84 (82,08 to 117)
1,83	AT5G66920	amino acid permease, putative	7.72e-05	6,11	99,78%	111,6 (107,2 to 117,9)	61,08 (56,28 to 64,78)
1,81	AT3G60260	phagocytosis and cell motility protein ELMO1-related	4.90494e-04	3,32	96,51%	122,1 (109,3 to 136,7)	67,51 (60,21 to 78,57)
1,80	AT1G23080	auxin efflux carrier protein, putative	8.19e-05	6,02	99,76%	189,8 (169,3 to 202,2)	107,5 (87,13 to 141,9)
1,72	AT1G36940	hypothetical protein	6.25e-07	13,95	100,00%	22,29 (19,53 to 24,47)	12,94 (11,6 to 14,53)
1,72	AT3G49220	pectinesterase family protein	2.0067e-04	4,64	99,04%	535,5 (501,7 to 596)	310,7 (296,8 to 329,1)
1,69	AT3G23690	wound-responsive protein-related	4.96017e-04	3,31	96,48%	764,5 (732,7 to 784,3)	452,8 (415,9 to 475,4)
1,68	AT5G19770	tubulin alpha-3/alpha-5 chain (TUA3)	4.8829e-04	3,33	96,54%	2.655 (2.497 to 2.779)	1.585 (1.414 to 1.763)
1,68	AT5G66080	zinc finger (GATA type) family protein	3.38734e-04	3,88	97,98%	19,95 (18,55 to 22,11)	12,2 (9,528 to 16,45)
1,67	AT5G54510	auxin-responsive GH3 protein, putative (DFL-1)	2.02999e-04	4,63	99,03%	476,4 (421,8 to 506)	288,8 (216,6 to 341,1)
1,67	AT1G80280	26.5 kDa class P-related heat shock protein (HSP26.5-P)	1.89723e-04	4,72	99,12%	615,2 (523,9 to 726,1)	366,1 (340,3 to 410,7)
1,67	AT2G46780	hydrolase, alpha/beta fold family protein	1.50209e-04	5,07	99,38%	107,1 (72,49 to 139,9)	62,3 (52,53 to 69,17)
1,67	AT4G21870	RNA recognition motif (RRM)-containing protein	1.22189e-04	5,37	99,54%	20,63 (18,28 to 22,01)	12,31 (11,82 to 12,88)
1,67	AT1G07050	CONSTANS-like protein-related	2.23e-05	7,94	99,96%	180,7 (150,5 to 210,1)	107,4 (107,2 to 107,7)
1,67	AT1G34760	14-3-3 protein GF14 omicron (GRF11)	3.85588e-04	3,67	97,52%	29,36 (26,45 to 31,22)	17,68 (15,29 to 19,69)

1,65	AT1G01620	plasma membrane intrinsic protein 1C (PIP1C) / aquaporin PIP1.	4.21348e-04	3,54	97,18%	1.711 (1.692 to 1.738)	1.043 (917 to 1.154)
1,65	AT5G52900	expressed protein	1.53108e-04	5,04	99,36%	158,3 (103,3 to 189,9)	92,84 (91,14 to 95,79)
1,64	AT2G28080	glycosyltransferase family protein	5.22086e-04	3,23	96,19%	189,7 (166,9 to 217,3)	115,2 (114,8 to 115,5)
1,63	AT1G68810	basic helix-loop-helix (bHLH) family protein	2.62e-06	11,43	100,00%	45,95 (42,49 to 48,97)	28,22 (25,82 to 29,98)
1,62	AT2G26710	cytochrome P450, putative	5.04e-06	10,58	100,00%	41 (39,67 to 43,05)	25,97 (20,18 to 34,69)
1,62	AT1G76090	cysteine protease inhibitor family protein / cystatin family protein	1.99729e-04	4,66	99,06%	717,6 (673,4 to 781,5)	443,1 (427 to 470,5)
1,61	AT5G60860	cysteine proteinase inhibitor-related	4.58e-05	6,95	99,90%	23,1 (20,99 to 25,99)	14,33 (13,03 to 15,8)
1,61	AT3G62110	glycoside hydrolase family 28 protein / polygalacturonase (pectin	2.17015e-04	4,53	98,93%	237,3 (217,5 to 261,2)	148,4 (125,3 to 168,3)
1,60	AT1G05250	peroxidase, putative	8.65e-05	5,92	99,73%	29,72 (24,17 to 35,86)	18,84 (13,19 to 22,38)
1,59	AT5G39320	UDP-glucose 6-dehydrogenase, putative	7.0e-05	6,29	99,81%	223,8 (213,3 to 239,5)	140,7 (129,8 to 149,5)
1,58	AT2G19460	xyloglucan	3.27185e-04	3,94	98,09%	143,1 (118,4 to 167,3)	90,02 (82,75 to 102,7)
1,58	AT3G12710	methyladenine glycosylase family protein	1.96e-05	8,18	99,97%	52,07 (50,45 to 54,7)	33,05 (29,32 to 36,88)
1,58	AT5G21170	5'-AMP-activated protein kinase beta-2 subunit, putative	1.75812e-04	4,82	99,20%	485 (462,8 to 500,1)	324,3 (191 to 426)
1,58	AT3G54430	lateral root primordium (LRP) protein-related	3.49345e-04	3,84	97,90%	49,96 (37,58 to 57,73)	31,22 (29,76 to 33,74)
1,57	AT2G22980	serine carboxypeptidase S10 family protein	3.50878e-04	3,83	97,88%	739,5 (665,5 to 786,5)	472,3 (423,3 to 545,9)
1,56	AT3G25710	nodulin MtN21 family protein	1.13278e-04	5,51	99,60%	17,21 (16,55 to 17,59)	11,2 (8,773 to 12,62)
1,56	AT1G02340	MADS-box family protein	1.96e-05	8,16	99,97%	54,28 (51,82 to 59,09)	35,17 (29,72 to 41,39)
1,55	AT5G60850	protein kinase, putative	1.40156e-04	5,16	99,43%	12,35 (10,72 to 14,24)	8,029 (6,274 to 9,911)
1,55	AT3G10120	phototropic-responsive NPH3 family protein	3.32679e-04	3,92	98,05%	35,86 (33,7 to 39,28)	23,3 (19,05 to 27,27)
1,55	AT5G47800	expressed protein	2.63824e-04	4,25	98,59%	109,8 (98,95 to 117,9)	71,62 (60,28 to 89,01)
1,54	AT5G49170	expressed protein	3.32679e-04	3,92	98,05%	14,39 (11,88 to 16,49)	9,354 (7,467 to 10,83)
1,53	AT5G64410	oligopeptide transporter OPT family protein	4.04447e-04	3,6	97,34%	103,9 (83,24 to 115,7)	67,6 (61,97 to 78,35)
1,51	AT1G06080	delta 9 desaturase (ADS1)	1.4023e-04	5,16	99,43%	83,8 (77,9 to 87,8)	55,8 (49,99 to 61,36)
1,50	AT2G32450	calcium-binding EF hand family protein	3.79464e-04	3,7	97,59%	62,38 (54,41 to 70,99)	41,4 (39,45 to 43,89)

Supplemental Table 4: List of genes repressed in the *vfb* mutants and in the *csn4* mutant seedlings compared to the wild type (Odds of differential expression $\geq 95\%$, fold repression ≥ 1.5). Shown are the fold repression (column A); the AGI code (gene identity; column B); the gene function (Description; column C); the adjusted p-value after Benjamini and Hochberg (adjPval; column D); the B statistic, which estimates the log odds of differential expression for each gene (B statistic; column E); the odds of differential expression determined based on the B statistics (odds of differential expression; column F); raw values (min to max) of wild type (column H) and *vfb* mutant (column J) samples. Genes are ranked by fold repression.