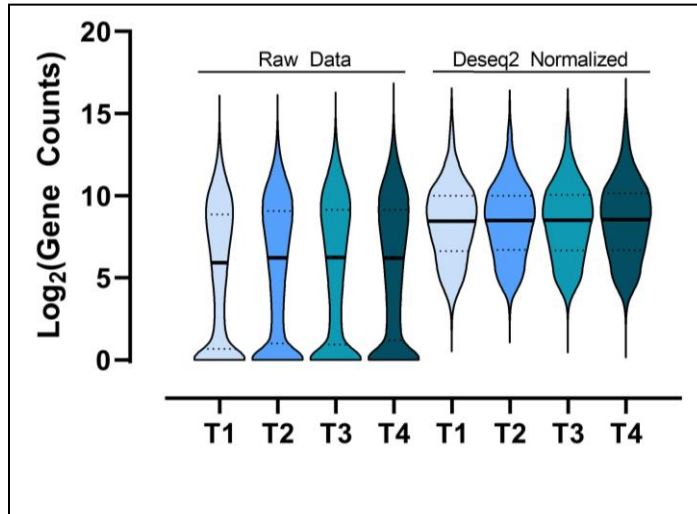
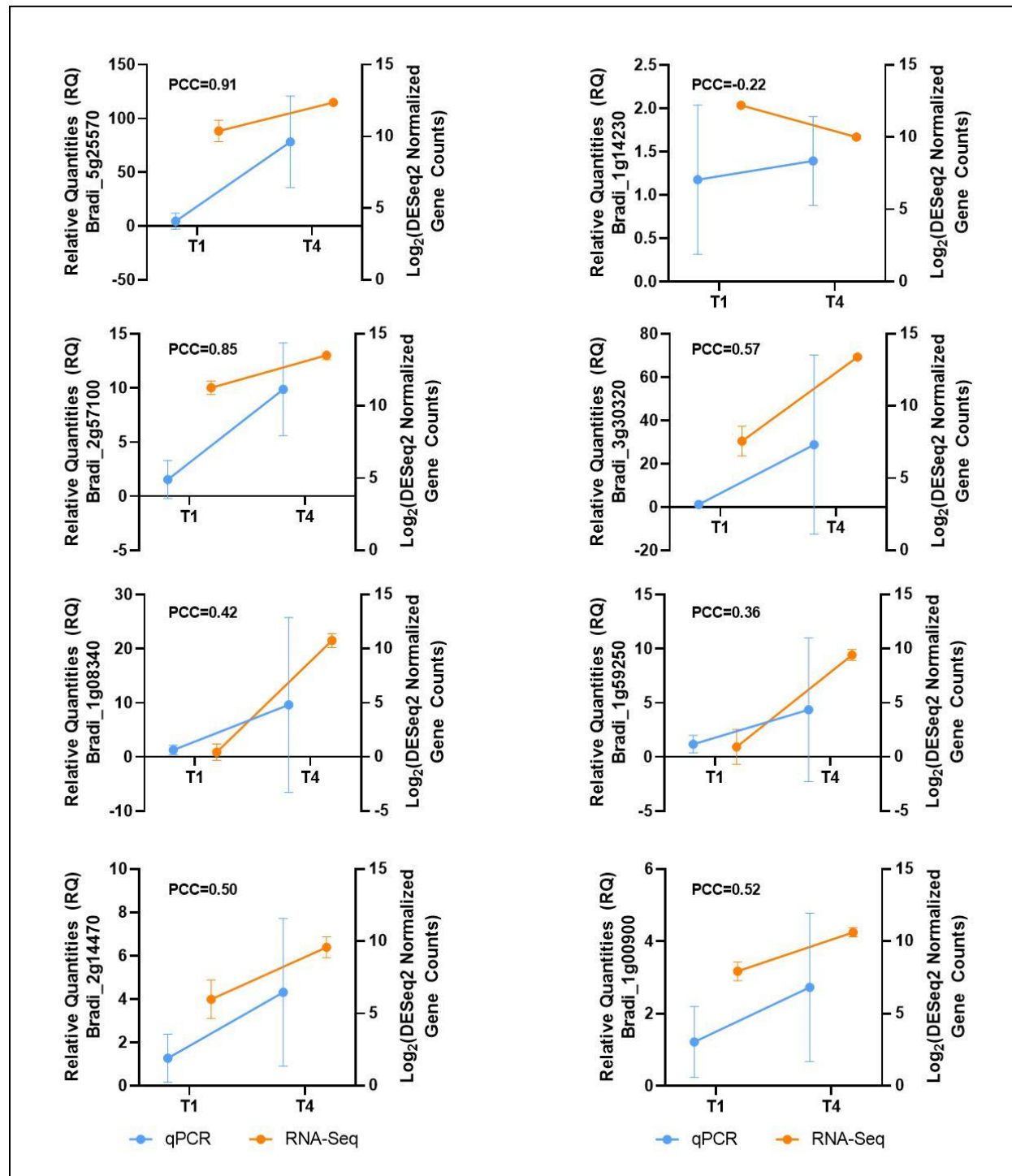


Supp Fig S3



Supplemental Figure S3. Violin plots demonstrating the effectiveness of normalization and pre-filtering procedure. Prior to normalization the raw abundance estimates (“raw data”, left) have large observable differences in total gene counts as well as the distribution of gene counts between samples. DESeq2 normalization resulted in a far more normal distribution in log₂ space (right). Solid and dotted lines correspond to median and quartile values, respectively.

Supp Fig S5

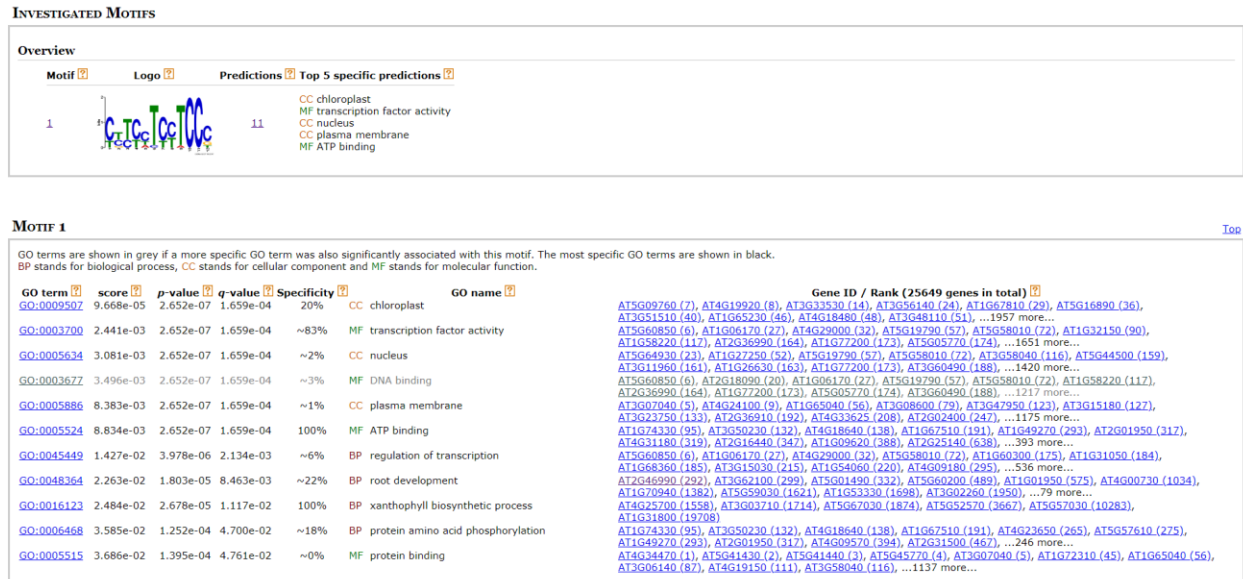


Supplemental Figure S5. RT-qPCR analysis of select genes in comparison with RNA-seq gene count estimations. RT-qPCR was performed in biological triplicate using Bradi_3g14040v3 as an endogenous control. RT-qPCR relative quantities (RQ) values for each gene are shown on the left y-axis in blue, and

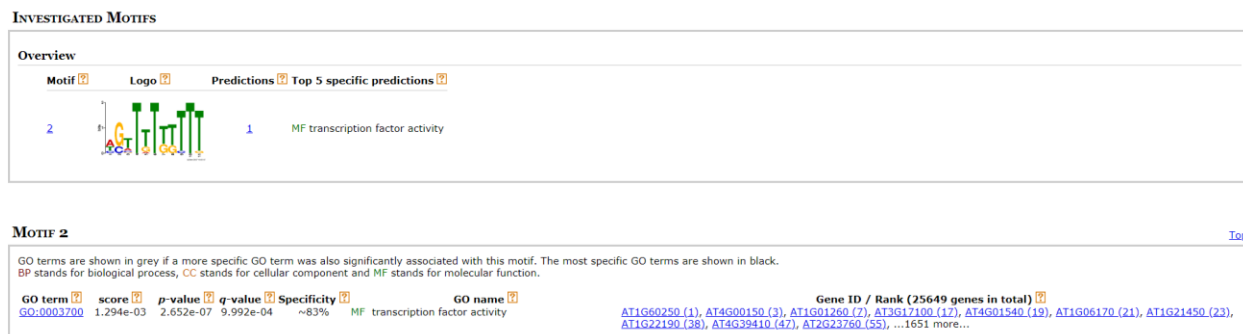
$\log_2$ scaled DESeq2 normalized gene counts are shown on the right y-axis in orange. Error bars represent the propagated standard deviation for qPCR, and standard deviation for $\log_2$ normalized RNA-seq gene counts. PCC, Pearson Correlation Coefficient.

Supplementary figure S8, this set of figures contains the output of the motif analysis performed by GOMo (part of the MEME-suite) using the motifs generated in Table 1 of the manuscript.

Cluster 1-1:



Cluster 1-2:

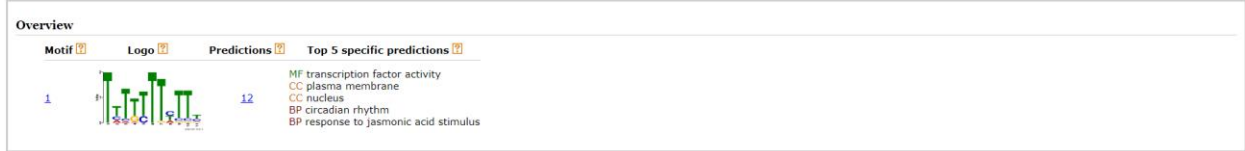


Cluster 2-1:



Cluster 3-1:

INVESTIGATED MOTIFS



MOTIF 1

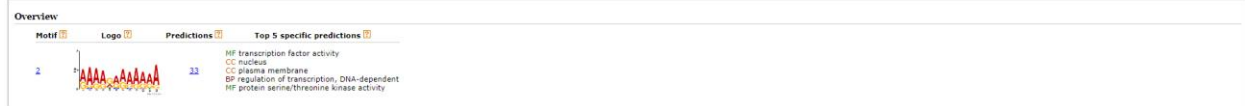
Top

GO terms are shown in grey if a more specific GO term was also significantly associated with this motif. The most specific GO terms are shown in black.
BP stands for biological process, CC stands for cellular component and MF stands for molecular function.

GO term	score	p-value	q-value	Specificity	GO name	Gene ID / Rank (25649 genes in total)
GO:0003700	9.870e-06	2.652e-07	1.661e-04	~83%	MF transcription factor activity	ATG060496 (4), ATG18400 (15), ATG355370 (38), ATG352920 (77), ATG252906 (110), ATG439410 (126), ATG436730 (130), ATG549240 (132), ATG509460 (133), ATG430980 (135), ...1651 more...
GO:0045449	9.662e-04	2.652e-07	1.661e-04	~6%	BP regulation of transcription	ATG18400 (15), ATG25900 (110), ATG509460 (133), ATG430980 (135), ATG412620 (138), ATG57150 (146), ATG41030 (198), ATG21320 (218), ATG607690 (219), ATG565100 (293), ...536 more...
GO:0005886	1.487e-03	2.652e-07	1.661e-04	~1%	CC plasma membrane	ATG59350 (11), ATPD11-3 (30), ATG34480 (44), ATG39350 (63), ATG1664650 (69), ATG128290 (98), ATG01890 (100), ATG323600 (115), ATG40370 (111), ATG435240 (151), ...1175 more...
GO:0016301	3.636e-03	2.652e-07	1.661e-04	~1%	MF kinase activity	ATG05650 (7), ATG20300 (9), ATG59350 (11), ATG16760 (32), ATG51790 (62), ATG501890 (100), ATG164210 (127), ATG23950 (129), ATG545810 (140), ATG51830 (155), ...899 more...
GO:0003677	3.797e-03	2.652e-07	1.661e-04	~3%	MF DNA binding	ATG06490 (4), ATG355370 (38), ATG353920 (77), ATG38810 (91), ATG24850 (95), ATG25900 (110), ATG18900 (118), ATG430980 (135), ATG12620 (138), ATG41020 (141), ...1217 more...
GO:0005634	4.989e-03	2.652e-07	1.661e-04	~2%	CC nucleus	ATG355370 (38), ATG41580 (64), ATG31300 (82), ATG50790 (83), ATG23600 (115), ATG168070 (121), ATG12620 (138), ATG56000 (159), ATG32890 (175), ATG168550 (179), ...1420 more...
GO:0007623	1.522e-02	3.182e-06	1.708e-03	~6%	BP circadian rhythm	ATG08920 (235), ATG436240 (259), ATG159940 (469), ATG424470 (604), ATG10470 (755), ATG241310 (862), ATG44680 (915), ATG168830 (1231), ATG46640 (1324), ATG525830 (1458), ...35 more...
GO:0009753	1.858e-02	7.160e-06	3.363e-03	~45%	BP response to jasmonic acid stimulus	ATG06490 (4), ATG128290 (98), ATG434710 (117), ATG507690 (219), ATG507700 (283), ATG422880 (373), ATG16470 (418), ATG1606160 (421), ATG423100 (465), ATG31180 (531), ...110 more...
GO:0007169	2.072e-02	1.034e-05	4.318e-03	~12%	BP transmembrane receptor protein tyrosine kinase signaling pathway	ATG501890 (100), ATG164210 (127), ATG308880 (223), ATG25790 (254), ATG128440 (321), ATG202780 (331), ATG303770 (396), ATG302880 (731), ATG151830 (1234), ATG302190 (1466), ...120 more...
GO:0007010	2.623e-02	3.182e-05	1.196e-02	~2%	BP cytoskeleton organization	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0006355	2.903e-02	4.747e-05	1.622e-02	~8%	BP regulation of transcription, DNA-dependent	ATG06490 (4), ATG353920 (77), ATG439410 (126), ATG168550 (179), ATG130330 (215), ATG607690 (219), ATG31650 (227), ATG174650 (253), ATG507700 (283), ATG357600 (300), ...622 more...
GO:0004674	3.365e-02	8.433e-05	2.641e-02	~11%	MF protein serine/threonine kinase activity	ATG501890 (100), ATG164210 (127), ATG308880 (223), ATG25790 (254), ATG128440 (321), ATG26980 (330), ATG202780 (331), ATG303770 (396), ATG166750 (538), ATG302880 (731), ...164 more...

Cluster 3-2:

INVESTIGATED MOTIFS



MOTIF 2

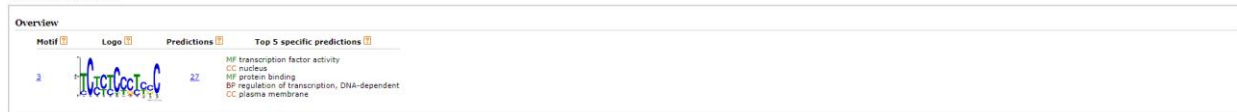
Top

GO terms are shown in grey if a more specific GO term was also significantly associated with this motif. The most specific GO terms are shown in black.
BP stands for biological process, CC stands for cellular component and MF stands for molecular function.

GO term	score	p-value	q-value	Specificity	GO name	Gene ID / Rank (25649 genes in total)
GO:0003700	2.892e-14	2.652e-07	8.555e-05	~83%	MF transcription factor activity	ATG01520 (8), ATG47602 (21), ATG355370 (38), ATG404330 (38), ATG463460 (39), ATG45160 (60), ATG69310 (61), ATG84270 (53), ATG14770 (99), ...1651 more...
GO:0005634	1.390e-08	2.652e-07	8.555e-05	~2%	CC nucleus	ATG05570 (28), ATG24820 (70), ATG13860 (76), ATG46330 (78), ATG463460 (39), ATG13740 (46), ATG19760 (483), ATG463460 (39), ATG463460 (39), ATG463460 (39), ...1420 more...
GO:0003677	1.212e-07	2.652e-07	8.555e-05	~3%	MF DNA binding	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0005886	9.998e-06	2.652e-07	8.555e-05	~1%	CC plasma membrane	ATG463460 (39), ATG463460 (39), ATG463460 (39), ATG463460 (39), ATG463460 (39), ATG463460 (39), ATG463460 (39), ATG463460 (39), ATG463460 (39), ...1175 more...
GO:0006355	4.709e-05	2.652e-07	8.555e-05	~8%	BP regulation of transcription, DNA-dependent	ATG06490 (4), ATG353920 (77), ATG439410 (126), ATG168550 (179), ATG130330 (215), ATG607690 (219), ATG31650 (227), ATG174650 (253), ATG507700 (283), ATG357600 (300), ...622 more...
GO:0004674	2.355e-04	2.652e-07	8.555e-05	~11%	MF protein serine/threonine kinase activity	ATG501890 (100), ATG164210 (127), ATG308880 (223), ATG25790 (254), ATG128440 (321), ATG26980 (330), ATG202780 (331), ATG303770 (396), ATG166750 (538), ATG302880 (731), ...164 more...
GO:0007169	3.328e-04	2.652e-07	8.555e-05	~12%	BP transmembrane receptor protein tyrosine kinase signaling pathway	ATG463460 (39), ATG463460 (39), ATG463460 (39), ATG463460 (39), ATG463460 (39), ATG463460 (39), ATG463460 (39), ATG463460 (39), ATG463460 (39), ...120 more...
GO:0006488	1.278e-03	2.652e-07	8.555e-05	~18%	BP protein amino acid phosphorylation	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0005515	1.341e-03	2.652e-07	8.555e-05	~9%	BP protein binding	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0007623	4.012e-03	2.652e-07	8.555e-05	~6%	BP circadian rhythm	ATG08920 (235), ATG436240 (259), ATG159940 (469), ATG424470 (604), ATG10470 (755), ATG241310 (862), ATG44680 (915), ATG168830 (1231), ATG46640 (1324), ATG525830 (1458), ...35 more...
GO:0009908	9.162e-03	2.652e-07	8.555e-05	~13%	BP flower development	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0048366	9.792e-03	2.652e-07	8.555e-05	40%	BP leaf development	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0005524	1.107e-02	2.652e-07	8.555e-05	100%	MF ATP binding	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0020841	1.432e-02	1.591e-06	3.687e-04	50%	BP response to water deprivation	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0002317	1.937e-02	3.447e-06	7.519e-04	~1%	CC cytoskeleton	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0002236	1.690e-02	3.713e-06	7.647e-04	100%	BP cytokine mediated signaling pathway	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0004722	1.899e-02	5.834e-06	1.138e-03	~94%	BP protein serine/threonine phosphatase activity	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0009948	2.066e-02	1.087e-05	2.016e-03	100%	BP polarity specification of apical/abaxial axis	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0006472	2.871e-02	4.800e-05	7.415e-03	~5%	MF protein kinase activity	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0043565	2.944e-02	5.456e-05	8.062e-03	~12%	MF sequence-specific DNA binding	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0009640	3.012e-02	5.887e-05	8.395e-03	~91%	BP photomorphogenesis	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0009753	3.089e-02	6.470e-05	8.885e-03	~45%	BP response to jasmonic acid stimulus	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0007010	3.264e-02	7.955e-05	1.053e-02	~2%	BP cytoskeleton organization	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0009741	3.306e-02	8.433e-05	1.078e-02	~6%	BP response to brassinosteroid stimulus	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0010051	3.709e-02	1.313e-04	1.622e-02	~55%	BP xylem and phloem pattern formation	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0016563	3.784e-02	1.458e-04	1.744e-02	~29%	MF transcription activator activity	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0006813	4.430e-02	2.829e-04	3.278e-02	~73%	BP potassium ion transport	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...
GO:0010154	4.607e-02	3.363e-04	3.778e-02	~19%	BP fruit development	ATG168060 (84), ATG429350 (379), ATG19760 (483), ATG561980 (565), ATG241740 (1723), ATG29890 (1945), ATG42940 (278), ATG144840 (4678), ATG566600 (5799), ATG353750 (6612), ...11 more...

Cluster 3-3:

INVESTIGATED MOTIFS



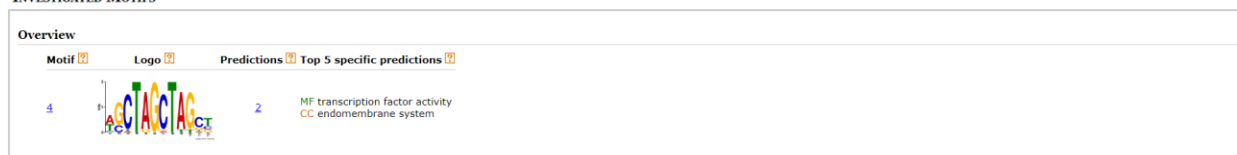
MOTIF 3

GO terms are shown in grey if a more specific GO term was also significantly associated with this motif. The most specific GO terms are shown in black. BP stands for biological process, CC stands for cellular component and MF stands for molecular function.

[illegible]

Cluster 3-4:

INVESTIGATED MOTIFS



MOTIF 4

GO terms are shown in grey if a more specific GO term was also significantly associated with this motif. The most specific GO terms are shown in black. BP stands for biological process, CC stands for cellular component and MF stands for molecular function.

GO term	score	p-value	q-value	Specificity	GO name	Gene ID / Rank (25649 genes in total)
GO:0003700	2.191e-03	2.652e-07	1.000e-03	~83%	MF transcription factor activity	AT4G04890 (7), AT1G13300 (13), AT4G38340 (17), AT4G79840 (41), AT3G19070 (88), AT4G33450 (115), AT5G58850 (132), AT7G76510 (156), AT3G50330 (163), AT6G10270 (170), ...1651 more...
GO:0012505	2.197e-02	1.777e-05	3.350e-02	~2%	CC endomembrane system	AT3G51644 (1), AT2G19893 (10), AT2G23690 (11), AT4G48440 (21), AT3G04170 (39), AT5G14105 (44), AT4G13968 (54), AT1G13290 (58), AT4G28695 (73), AT5G15725 (82), ...2957 more...

Cluster 3-5:

INVESTIGATED MOTIFS

Overview

Motif

Logo

Predictions

Top 5 specific predictions

5

2

MF transcription factor activity

CC endomembrane system

BP response to auxin stimulus

MF polygalacturonase activity

BP oligopeptide transport

Motif 5

GO terms are shown in grey if a more specific GO term was also significantly associated with this motif. The most specific GO terms are shown in black.
BP stands for biological process, CC stands for cellular component and MF stands for molecular function.

GO term	score	p-value	q-value	Specificity	GO name	Gene ID / Rank (25649 genes in total)
GO:0003700	1.982e-08	2.652e-07	1.663e-04	~83%	MF transcription factor activity	AT3G30260 (2), AT1G13300 (3), AT2G36890 (57), AT1G74430 (70), AT1G43160 (76), AT1G73410 (101), AT5G67010 (111), AT2G46970 (118), AT1G71130 (139), AT4G30180 (158), ...1651 more...
GO:0012505	7.573e-06	2.652e-07	1.663e-04	~2%	CC endomembrane system	AT3G48740 (7), AT3G29300 (11), AT2G33175 (17), AT1G06135 (18), AT2G03832 (36), AT1G23350 (43), AT3G47480 (48), AT4G16165 (50), AT3G47630 (58), AT3G28007 (75), ...2957 more...
GO:0045449	1.022e-03	2.652e-07	1.663e-04	~6%	BP regulation of transcription	AT1G13300 (3), AT2G46970 (118), AT4G30180 (158), AT4G37850 (171), AT3G46090 (215), AT5G61620 (231), AT1G20910 (234), AT1G69590 (247), AT2G26580 (266), AT1G46480 (377), ...536 more...
GO:0009733	2.324e-03	2.652e-07	1.663e-04	~43%	BP response to auxin stimulus	AT5G18060 (23), AT5G18050 (22), AT1G72430 (54), AT3G03847 (222), AT3G03850 (255), AT3G28860 (374), AT5G18020 (382), AT4G00880 (400), AT5G57560 (444), AT4G33880 (464), ...244 more...
GO:0003677	4.741e-03	2.652e-07	1.663e-04	~3%	MF DNA binding	AT3G30260 (2), AT1G13300 (3), AT2G36890 (57), AT1G74430 (70), AT1G43160 (76), AT1G73410 (101), AT5G67010 (111), AT1G71130 (139), AT1G12630 (162), AT4G37850 (171), ...1217 more...
GO:0004650	8.602e-03	2.652e-07	1.663e-04	100%	MF polygalacturonase activity	AT4G32380 (98), AT3G07840 (340), AT4G20050 (417), AT5G17200 (500), AT1G70500 (641), AT1G02790 (762), AT1G55710 (965), AT3G14040 (1173), AT4G23820 (1187), AT3G48950 (1496), ...61 more...
GO:0006857	1.913e-02	7.160e-06	3.850e-03	~45%	BP oligopeptide transport	AT5G62680 (15), AT3G47960 (336), AT3G27020 (649), AT1G18880 (862), AT1G72130 (1150), AT1G72140 (1166), AT3G21670 (2169), AT3G45710 (2200), AT5G46050 (2415), AT5G01180 (2507), ...51 more...
GO:0005975	2.259e-02	1.538e-05	7.236e-03	~0%	BP carbohydrate metabolic process	AT4G32380 (98), AT3G07840 (340), AT5G17200 (500), AT5G51820 (568), AT1G70500 (641), AT1G02790 (762), AT1G55710 (965), AT3G14040 (1173), AT4G23820 (1187), AT1G15380 (1204), ...106 more...
GO:0006355	3.032e-02	6.126e-05	2.562e-02	~8%	BP regulation of transcription, DNA-dependent	AT2G36890 (57), AT1G74430 (70), AT1G43160 (76), AT1G73410 (101), AT5G67010 (111), AT1G71130 (139), AT1G12630 (162), AT5G62320 (177), AT2G40750 (183), AT1G35490 (192), ...622 more...

Cluster 4-1:

INVESTIGATED MOTIFS



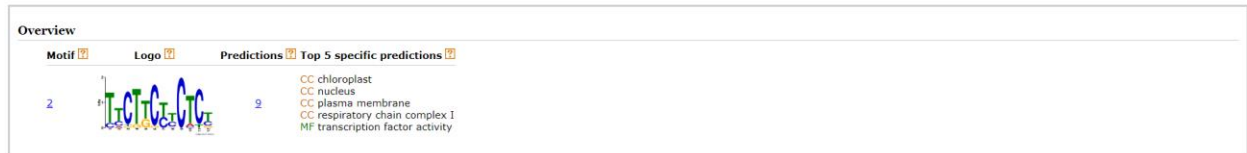
Motif 1

GO terms are shown in grey if a more specific GO term was also significantly associated with this motif. The most specific GO terms are shown in black. BP stands for biological process, CC stands for cellular component and MF stands for molecular function.

GO term	score	p-value	q-value	Specificity	GO name	Gene ID / Rank (25649 genes in total)
GO:0003302	8.936e-13	2.632e-07	8.172e-05	~83%	MF transcription factor activity	AT4601520 (3), AT3047602 (11), AT5060332 (14), AT5032732 (20), AT3010040 (22), AT6060500 (39), AT1047966 (48), AT5017955 (56), AT5028532 (56), ...1651 more...
GO:0005430	1.345e-07	2.632e-07	8.172e-05	~2%	CC nucleus	AT5043330 (14), AT4617950 (14), AT5045080 (28), AT5042500 (42), AT5011962 (54), AT5013180 (66), AT307591 (79), AT5014962 (87), AT5042170 (101), ...1420 more...
GO:0005272	1.032e-06	2.632e-07	8.172e-05	~2%	BP DNA binding	AT5047600 (11), AT5045030 (14), AT5047950 (18), AT5010480 (18), AT5031720 (20), AT5028620 (22), AT5044607 (27), AT5018300 (36), AT5042170 (101), AT5030001 (103), ...1317 more...
GO:0005886	9.339e-05	2.632e-07	8.172e-05	~1%	CC plasma membrane	AT5030740 (1), AT501180 (2), AT5030330 (28), AT5043800 (31), AT5037990 (31), AT5017600 (62), AT5043330 (64), AT5018960 (87), AT5035680 (89), AT5040771 (111), ...1179 more...
GO:0005155	1.515e-04	2.632e-07	8.172e-05	~6%	BP regulation of transcription, DNA-dependent	AT4617950 (14), AT5031720 (20), AT5045080 (28), AT5010480 (18), AT5049400 (17), AT5045030 (18), AT5045030 (18), AT5035798 (117), AT5018300 (131), AT5042170 (101), ...442 more...
GO:0005450	1.721e-04	2.632e-07	8.172e-05	~6%	BP regulation of transcription	AT5047600 (11), AT5045030 (14), AT5042170 (20), AT5010480 (18), AT5048632 (52), AT5042170 (101), AT5030001 (103), AT5045030 (132), AT5045160 (135), AT5040771 (145), ...336 more...
GO:0005625	1.294e-03	2.632e-07	8.172e-05	~11%	BP protein serine/threonine kinase activity	AT5018300 (18), AT5030770 (49), AT5031720 (69), AT5043800 (129), AT5048480 (149), AT5045030 (159), AT5045030 (159), AT5045030 (159), AT5045030 (159), AT5045030 (159), ...164 more...
GO:0005636	1.942e-03	2.632e-07	8.172e-05	~6%	BP cell development	AT5018960 (87), AT5028532 (118), AT5031720 (181), AT5041520 (182), AT5035680 (182), AT5037630 (182), AT5011160 (182), AT5041520 (182), AT5028532 (182), ...77 more...
GO:0005312	2.376e-03	2.632e-07	8.172e-05	~6%	BP protein binding	AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), ...137 more...
GO:0007623	4.745e-03	2.632e-07	8.172e-05	~6%	BP circadian rhythm	AT5048260 (162), AT5057280 (126), AT5045030 (126), AT5048260 (126), AT5048260 (126), AT5048260 (126), AT5048260 (126), AT5048260 (126), AT5048260 (126), AT5048260 (126), ...35 more...
GO:0003772	6.924e-03	2.632e-07	8.172e-05	~8%	BP microtubule motor activity	AT5047600 (11), AT5045030 (14), AT5042170 (20), AT5010480 (18), AT5043800 (31), AT5037990 (31), AT5017600 (62), AT5043330 (64), AT5018960 (87), AT5035680 (89), ...1179 more...
GO:0005444	7.084e-03	2.632e-07	8.172e-05	~8%	BP protein amino acid phosphorylation	AT5030770 (49), AT5031720 (69), AT5043800 (129), AT5048480 (149), AT5045030 (159), AT5045030 (159), AT5045030 (159), AT5045030 (159), AT5045030 (159), AT5045030 (159), ...24 more...
GO:0005461	7.375e-03	5.034e-07	1.401e-04	~29%	BP transcription activator activity	AT5045030 (14), AT5018960 (87), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), ...100 more...
GO:0007242	7.915e-03	5.304e-07	1.401e-04	~12%	BP transmembrane receptor protein tyrosine kinase signaling pathway	AT5030770 (49), AT5018960 (87), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), ...120 more...
GO:0005522	1.137e-02	1.325e-06	3.269e-04	100%	BP ATP binding	AT5027880 (4), AT5009370 (45), AT5046800 (114), AT5046030 (118), AT5001890 (119), AT5046800 (146), AT5032880 (152), AT5031950 (235), AT5045800 (281), AT5043950 (282), ...393 more...
GO:0003942	1.186e-02	1.895e-06	4.299e-04	100%	BP polarity specification of apical/lateral axis	AT5045180 (39), AT5032490 (62), AT5012140 (102), AT5045170 (148), AT5037102 (148), AT5045180 (148), AT5045180 (148), AT5045180 (148), AT5045180 (148), AT5045180 (148), ...6 more...
GO:0005051	1.484e-02	8.351e-06	5.020e-03	~55%	BP vesicle and plasma pattern formation	AT5017950 (12), AT5010310 (62), AT5045550 (62), AT5045180 (74), AT5035080 (74), AT5045060 (104), AT5030030 (118), AT5045060 (121), AT5045060 (121), AT5045060 (121), ...8 more...
GO:0005294	2.087e-02	1.325e-05	2.550e-03	~23%	BP positive regulation of transcription	AT5045060 (12), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), ...24 more...
GO:0005746	2.110e-02	1.379e-05	2.550e-03	~67%	BP response to osmotic stimulus	AT5031720 (69), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), AT5045030 (121), ...14 more...
GO:0005273	2.110e-02	1.379e-05	2.550e-03	~43%	BP response to auxin stimulus	AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), ...24 more...
GO:0004302	2.397e-02	2.380e-05	6.196e-03	~91%	MF kinase activity	AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), ...24 more...
GO:0005653	2.442e-02	2.519e-05	6.239e-03	~86%	BP ovule development	AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), ...24 more...
GO:0021125	2.619e-02	4.877e-05	7.840e-03	~19%	BP root development	AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), ...24 more...
GO:0003962	3.125e-02	8.379e-05	1.080e-03	~13%	BP flower development	AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), ...24 more...
GO:0003963	3.139e-02	9.373e-05	1.168e-03	~10%	BP leaf morphogenesis	AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), ...24 more...
GO:0001141	3.444e-02	1.103e-04	1.560e-02	100%	BP abscisic acid response	AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), ...24 more...
GO:0003732	3.511e-02	1.188e-04	1.627e-03	~1%	CC cytoplasm	AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), ...24 more...
GO:0005652	3.550e-02	1.215e-04	1.630e-03	~9%	BP protein kinase activity	AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), ...24 more...
GO:0003656	4.051e-02	2.118e-04	2.803e-02	~12%	BP sequence-specific DNA binding	AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), ...24 more...
GO:0005274	4.305e-02	2.387e-04	3.347e-02	100%	BP cytokinin mediated signaling pathway	AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), ...24 more...
GO:0004483	4.314e-02	2.405e-04	3.347e-02	100%	BP negative regulation of transcription	AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), ...24 more...
GO:0005121	4.507e-02	3.445e-04	5.981e-02	~22%	CC ubiquitin ligase complex	AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), ...24 more...
GO:0003654	4.646e-02	3.901e-04	4.371e-02	~91%	BP photomorphogenesis	AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), AT5045030 (14), ...24 more...

Cluster 4-2:

INVESTIGATED MOTIFS



Motif 2

GO terms are shown in grey if a more specific GO term was also significantly associated with this motif. The most specific GO terms are shown in black. BP stands for biological process, CC stands for cellular component and MF stands for molecular function.

GO term	score	p-value	q-value	Specificity	GO name	Gene ID / Rank (25649 genes in total)
GO:0005907	8.026e-05	2.652e-07	3.312e-04	20%	CC chloroplast	AT1G11520 (12), AT5G40610 (18), AT5G07020 (41), AT5G30020 (92), AT1G22700 (95), AT1G32900 (105), AT4G33130 (116), AT5G55610 (124), AT5G10920 (131), AT1G35680 (131), ...1957 more...
GO:0005634	5.480e-03	2.652e-07	3.312e-04	~2%	CC nucleus	AT2G38940 (11), AT3G23890 (15), AT3G55320 (24), AT5G64960 (65), AT3G22170 (87), AT5G62660 (88), AT1G14130 (93), AT4G24020 (130), AT2G26990 (142), AT3G23050 (145), ...1420 more...
GO:0005886	6.040e-03	2.652e-07	3.312e-04	~1%	CC plasma membrane	AT4G23460 (5), AT4G27740 (63), AT5G10020 (83), AT1G24300 (84), AT1G24300 (84), AT5G10020 (84), AT5G10020 (84), AT5G10020 (84), AT5G10020 (84), AT5G10020 (84), ...19 more...
GO:0045271	1.456e-02	4.243e-06	3.974e-03	~73%	CC respiratory chain complex I	AT2G31820 (154), AT1G27120 (172), AT1G27120 (172), AT1G27120 (172), AT1G27120 (172), AT1G27120 (172), AT1G27120 (172), AT1G27120 (172), AT1G27120 (172), AT1G27120 (172), ...1175 more...
GO:0003700	2.026e-02	1.034e-05	6.458e-03	~83%	MF transcription factor activity	AT2G02050 (696), AT5G67590 (759), AT5G64070 (1050), AT2G31490 (1069), AT2G02510 (1265), AT2G47690 (1397), AT1G67785 (1640), AT1G47260 (1715), AT1G76200 (2077), AT5G08530 (2341), ...335 more...
GO:0016301	2.048e-02	1.034e-05	6.458e-03	~1%	MF kinase activity	AT5G11180 (20), AT2G02450 (46), AT4G29000 (49), AT1G12860 (59), AT1G29950 (74), AT4G01460 (76), AT3G22170 (87), AT1G26960 (88), AT5G04840 (89), AT5G39700 (103), ...1651 more...
GO:0004674	2.499e-02	2.493e-05	1.334e-02	~11%	MF protein serine/threonine kinase activity	AT5G56040 (43), AT5G64960 (65), AT1G34300 (84), AT1G09600 (102), AT1G51790 (132), AT3G45390 (137), AT5G12480 (146), AT1G48480 (186), AT5G58300 (206), AT2G38910 (219), ...899 more...
GO:0007169	2.927e-02	5.198e-05	2.434e-02	~12%	BP transmembrane receptor protein tyrosine kinase signaling pathway	AT5G56040 (43), AT5G10020 (83), AT2G49670 (122), AT5G45840 (134), AT1G48480 (186), AT5G47760 (202), AT5G58300 (206), AT2G16250 (235), AT1G53730 (317), AT1G52120 (317), AT1G52120 (317), ...164 more...
GO:0003723	3.612e-02	1.199e-04	4.990e-02	~2%	MF RNA binding	AT5G56040 (43), AT5G10020 (83), AT2G49670 (122), AT5G45840 (134), AT1G48480 (186), AT5G47760 (202), AT5G58300 (206), AT2G16250 (235), AT1G53730 (317), AT1G52120 (317), AT1G52120 (317), ...120 more...