Supplemental Table 1. Summary of BLASTn analysis with contig sequences deconstructed to overlapping 1 kb segments

CONTIG A

Start	Stop	Score	Gene model	Description	Classification
0	1000	E=7.0e-55	At5g47710.1	MCA23.3, C2 domain-containing protein, GO:0005554 [molecular_function unknown]	Additional collinear gene fragment
500	1500	E=2.7e-68	At5g47710.1	MCA23.3, C2 domain-containing protein, GO:0005554 [molecular_function unknown]	Additional collinear gene fragment
1000	2000	E=7.5e-16	At5g47710.1	MCA23.3, C2 domain-containing protein, GO:0005554 [molecular_function unknown]	Additional collinear gene fragment
2500	3500	E=2.7e-15	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
3000	4000	E=9.8e-35	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
3500	4500	E=3.2e-24	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
4000	5000	E=2.4e-18	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
4500	5500	E=1.3e-90	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
5000	6000	E=9.2e-105	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
5500	6500	E=2.4e-71	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
6000	7000	E=6.9e-78	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
6500	7500	E=2.9e-43	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
7000	8000	E=4.6e-42	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
7500	8500	E=1.9e-47	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
8000	9000	E=2.3e-68	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
8500	9500	E=9.7e-54	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
9000	10000	E=6.4e-	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function	Conserved

		46		unknown]	collinear gene
9500	10500	E=2.8e-98	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
10000	11000	E=1.1e-82	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
10500	11500	E=1.4e-32	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
11000	12000	E=2.1e-09	At5g47690.1	MNJ7.28, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
11500	12500	E=9.1e-23	At5g47680.1	MNJ7.27, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
12000	13000	E=9.1e-23	At5g47680.1	MNJ7.27, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
19000	20000	E=9.7e-31	At5g47670.1	MNJ7.26, CCAAT-box binding transcription factor family protein / leafy cotyledon 1-related (L1L), GO:0003700 [transcription factor activity]	Conserved collinear gene
19500	20500	E=2.2e-89	At5g47670.1	MNJ7.26, CCAAT-box binding transcription factor family protein / leafy cotyledon 1-related (L1L), GO:0003700 [transcription factor activity]	Conserved collinear gene
20000	21000	E=8.4e-66	At5g47670.1	MNJ7.26, CCAAT-box binding transcription factor family protein / leafy cotyledon 1-related (L1L), GO:0003700 [transcription factor activity]	Conserved collinear gene
20500	21500	E=1.7e-41	At5g47660.1	MNJ7.25, DNA-binding protein-related, GO:0003700 [transcription factor activity]	Conserved collinear gene
21000	22000	E=2.4e-55	At5g47660.1	MNJ7.25, DNA-binding protein-related, GO:0003700 [transcription factor activity]	Conserved collinear gene
21500	22500	E=1.3e-22	At5g47660.1	MNJ7.25, DNA-binding protein-related, GO:0003700 [transcription factor activity]	Conserved collinear gene
22000	23000	E=4.4e-34	At5g47660.1	MNJ7.25, DNA-binding protein-related, GO:0003700 [transcription factor activity]	Conserved collinear gene
22500	23500	E=2.8e-23	At5g47660.1	MNJ7.25, DNA-binding protein-related, GO:0003700 [transcription factor activity]	Conserved collinear gene
23000	24000	E=5.5e-21	At5g47650.1	MNJ7.24, MutT/nudix family protein, GO:0016787 [hydrolase activity]	Conserved collinear gene
23500	24500	E=6.4e-53	At5g47650.1	MNJ7.24, MutT/nudix family protein, GO:0016787 [hydrolase activity]	Conserved collinear gene
24000	25000	E=2.2e-83	At5g47650.1	MNJ7.24, MutT/nudix family protein, GO:0016787 [hydrolase activity]	Conserved collinear gene
24500	25500	E=1.8e-55	At5g47650.1	MNJ7.24, MutT/nudix family protein, GO:0016787 [hydrolase activity]	Conserved collinear gene
25000	26000	E=2.5e-91	At5g47640.1	MNJ7.23, CCAAT-box binding transcription factor subunit B (NF-YB) (HAP3) (AHAP3) family (Hap3b), GO:0003700 [transcription factor activity]	Conserved collinear gene
25500	26500	E=7.9e-	At5g47640.1	MNJ7.23, CCAAT-box binding transcription factor subunit B (NF-YB)	Conserved

		75		(HAP3) (AHAP3) family (Hap3b), GO:0003700 [transcription factor activity]	collinear gene
27000	28000	E=2.6e-12	At2g40113.1	F27I1.6, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
27500	28500	E=1.5e-33	At5g47630.1	MNJ7.22, acyl carrier family protein / ACP family protein, GO:0006633 [fatty acid biosynthesis] GO:0000036 [acyl carrier activity]	Conserved collinear gene
28000	29000	E=8.7e-42	At5g47630.1	MNJ7.22, acyl carrier family protein / ACP family protein, GO:0006633 [fatty acid biosynthesis] GO:0000036 [acyl carrier activity]	Conserved collinear gene
28500	29500	E=7.2e-10	At5g47630.1	MNJ7.22, acyl carrier family protein / ACP family protein, GO:0006633 [fatty acid biosynthesis] GO:0000036 [acyl carrier activity]	Conserved collinear gene
36000	37000	E=1.1e-09	At5g49590.1	K6M13.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
38000	39000	E=3.8e-15	At1g02230.1	T7I23.19, no apical meristem (NAM) family protein, GO:0007275 [development] GO:0005554 [molecular_function unknown] GO:0003700 [transcription factor activity]	Inserted fragment within model
38500	39500	E=7.4e-07	At5g35805.1	MIK22.10, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
40000	41000	E=1.1e-08	At1g28410.1	F3M18.15, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
42000	43000	E=1.2e-33	At5g47620.2	MNJ7.21, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative, GO:0003723 [RNA binding]	Conserved collinear gene
42500	43500	E=9.2e-101	At5g47620.2	MNJ7.21, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative, GO:0003723 [RNA binding]	Conserved collinear gene
43000	44000	E=4.7e-141	At5g47620.2	MNJ7.21, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative, GO:0003723 [RNA binding]	Conserved collinear gene
43500	44500	E=7.7e-98	At5g47620.2	MNJ7.21, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative, GO:0003723 [RNA binding]	Conserved collinear gene
44000	45000	E=9.8e-24	At5g47620.3	MNJ7.21, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative, GO:0003723 [RNA binding]	Conserved collinear gene
44500	45500	E=4.9e-66	At5g47610.1	MNJ7.20, zinc finger (C3HC4-type RING finger) family protein, GO:0005515 [protein binding] GO:0008270 [zinc ion binding]	Conserved collinear gene
45000	46000	E=9.7e-49	At5g47610.1	MNJ7.20, zinc finger (C3HC4-type RING finger) family protein, GO:0005515 [protein binding] GO:0008270 [zinc ion binding]	Conserved collinear gene
45500	46500	E=7.0e-	At5g47570.1	MNJ7.16, expressed protein, GO:0005554 [molecular_function	Conserved

		22		unknown]	collinear gene
46000	47000	E=3.3e-37	At5g47570.1	MNJ7.16, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
46500	47500	E=7.1e-13	At5g47570.1	MNJ7.16, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
49500	50500	E=2.1e-52	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	Conserved collinear gene
50000	51000	E=5.3e-74	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	Conserved collinear gene
50500	51500	E=4.7e-14	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	Conserved collinear gene
51000	52000	E=4.6e-12	At1g45165.1	F27F5.24, Expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
51500	52500	E=1.7e-22	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	Conserved collinear gene
52000	53000	E=4.2e-86	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	Conserved collinear gene
52500	53500	E=7.7e-164	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	Conserved collinear gene
53000	54000	E=9.4e-78	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	Conserved collinear gene
56000	57000	E=4.3e-29	At5g47550.1	MNJ7.14, cysteine protease inhibitor, putative / cystatin, putative, GO:0004869 [cysteine protease inhibitor activity]	Conserved collinear gene
56500	57500	E=4.3e-29	At5g47550.1	MNJ7.14, cysteine protease inhibitor, putative / cystatin, putative, GO:0004869 [cysteine protease inhibitor activity]	Conserved collinear gene
60500	61500	E=4.2e-24	At2g22710.1	T9I22.15, myb family protein, GO:0003677 [DNA binding]	Inserted fragment within model
61000	62000	E=4.6e-36	At2g22710.1	T9I22.15, myb family protein, GO:0003677 [DNA binding]	Inserted fragment within model
61500	62500	E=1.7e-07	At4g08270.1	T12G13.110, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model

62000	63000	E=2.4e-09	At1g62760.1	F23N19.12, invertase/pectin methylesterase inhibitor family protein, GO:0046910 [pectinesterase inhibitor activity]	Inserted fragment within model
62500	63500	E=9.7e-76	At3g15310.1	K7L4.11, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
63000	64000	E=3.2e-92	At3g15310.1	K7L4.11, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
63500	64500	E=1.3e-31	At5g34838.1	F11P10.11, hypothetical protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
65500	66500	E=4.0e-14	At5g47540.1	MNJ7.13, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
66000	67000	E=7.9e-46	At5g47540.1	MNJ7.13, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
66500	67500	E=6.7e-52	At5g47540.1	MNJ7.13, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
67000	68000	E=1.2e-37	At5g47540.1	MNJ7.13, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
67500	68500	E=4.9e-29	At5g47540.1	MNJ7.13, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
68000	69000	E=4.0e-34	At5g47530.1	MNJ7.12, auxin-responsive protein, putative, GO:0016020 [membrane] GO:0007275 [development] GO:0005554 [molecular_function unknown]	Conserved collinear gene
68500	69500	E=2.2e-86	At5g47530.1	MNJ7.12, auxin-responsive protein, putative, GO:0016020 [membrane] GO:0007275 [development] GO:0005554 [molecular_function unknown]	Conserved collinear gene
69000	70000	E=2.8e-95	At5g47530.1	MNJ7.12, auxin-responsive protein, putative, GO:0016020 [membrane] GO:0007275 [development] GO:0005554 [molecular_function unknown]	Conserved collinear gene
69500	70500	E=3.6e-97	At5g47530.1	MNJ7.12, auxin-responsive protein, putative, GO:0016020 [membrane] GO:0007275 [development] GO:0005554 [molecular_function unknown]	Conserved collinear gene
70000	71000	E=2.3e-39	At5g47530.1	MNJ7.12, auxin-responsive protein, putative, GO:0016020 [membrane] GO:0007275 [development] GO:0005554 [molecular_function unknown]	Conserved collinear gene
75000	76000	E=1.3e-51	At5g47520.1	MNJ7.11, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
75500	76500	E=2.2e-60	At5g47520.1	MNJ7.11, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
76000	77000	E=1.8e-58	At5g47520.1	MNJ7.11, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
77000	78000	E=4.1e-11	At5g47510.1	MNJ7.10, SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, GO:0006810 [transport] GO:0008372 [cellular_component unknown] GO:0005215 [transporter activity]	Conserved collinear gene

77500	78500	E=2.8e-12	At5g47510.1	MNJ7.10, SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, GO:0006810 [transport] GO:0008372 [cellular_component unknown] GO:0005215 [transporter activity]	Conserved collinear gene
80000	81000	E=7.4e-07	At1g65440.1	T8F5.22, glycine-rich protein, GO:0006333 [chromatin assembly/disassembly] GO:0006352 [transcription initiation]	Inserted fragment within model
80500	81500	E=7.4e-07	At1g65440.1	T8F5.22, glycine-rich protein, GO:0006333 [chromatin assembly/disassembly] GO:0006352 [transcription initiation]	Inserted fragment within model
88000	89000	E=1.0e-42	At5g47500.1	MNJ7.9, pectinesterase family protein, GO:0030599 [pectinesterase activity] GO:0009505 [cell wall (sensu Magnoliophyta)]	Conserved collinear gene
88500	89500	E=2.3e-103	At5g47500.1	MNJ7.9, pectinesterase family protein, GO:0030599 [pectinesterase activity] GO:0009505 [cell wall (sensu Magnoliophyta)]	Conserved collinear gene
89000	90000	E=1.4e-78	At5g47500.1	MNJ7.9, pectinesterase family protein, GO:0030599 [pectinesterase activity] GO:0009505 [cell wall (sensu Magnoliophyta)]	Conserved collinear gene
89500	90500	E=2.3e-68	At5g47500.1	MNJ7.9, pectinesterase family protein, GO:0030599 [pectinesterase activity] GO:0009505 [cell wall (sensu Magnoliophyta)]	Conserved collinear gene
90000	91000	E=6.9e-15	At5g47500.1	MNJ7.9, pectinesterase family protein, GO:0030599 [pectinesterase activity] GO:0009505 [cell wall (sensu Magnoliophyta)]	Conserved collinear gene
91000	92000	E=1.4e-40	At5g47470.1	MNJ7.6, nodulin MtN21 family protein, GO:0016020 [membrane] GO:0005554 [molecular_function unknown]	Conserved collinear gene
91500	92500	E=6.3e-79	At5g47470.1	MNJ7.6, nodulin MtN21 family protein, GO:0016020 [membrane] GO:0005554 [molecular_function unknown]	Conserved collinear gene
92000	93000	E=1.9e-77	At5g47470.1	MNJ7.6, nodulin MtN21 family protein, GO:0016020 [membrane] GO:0005554 [molecular_function unknown]	Conserved collinear gene
92500	93500	E=1.7e-42	At5g47470.1	MNJ7.6, nodulin MtN21 family protein, GO:0016020 [membrane] GO:0005554 [molecular_function unknown]	Conserved collinear gene
93000	94000	E=6.7e-80	At5g47460.1	MNJ7.5, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
93500	94500	E=4.9e-159	At5g47460.1	MNJ7.5, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
94000	95000	E=3.8e-170	At5g47460.1	MNJ7.5, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
94500	95500	E=5.1e-104	At5g47460.1	MNJ7.5, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372	Conserved collinear gene

				[cellular_component unknown] GO:0005554 [molecular_function unknown]	
95000	96000	E=3.6e-14	At5g47460.1	MNJ7.5, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
95500	96500	E=1.7e-21	At5g47455.5	MNJ7.31, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
96000	97000	E=1.5e-42	At5g47455.5	MNJ7.31, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
96500	97500	E=1.2e-17	At5g47455.4	MNJ7.31, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
99500	100500	E=6.4e-27	At5g47450.1	MQL5.31, major intrinsic family protein / MIP family protein, GO:0016020 [membrane] GO:0006810 [transport] GO:0015250 [water channel activity]	Conserved collinear gene
100000	101000	E=3.3e-61	At5g47450.1	MQL5.31, major intrinsic family protein / MIP family protein, GO:0016020 [membrane] GO:0006810 [transport] GO:0015250 [water channel activity]	Conserved collinear gene
100500	101500	E=3.7e-61	At4g17340.1	FCAALL.412, major intrinsic family protein / MIP family protein, GO:0016020 [membrane] GO:0006810 [transport] GO:0015250 [water channel activity]	Conserved collinear gene
101000	102000	E=1.8e-61	At5g47450.1	MQL5.31, major intrinsic family protein / MIP family protein, GO:0016020 [membrane] GO:0006810 [transport] GO:0015250 [water channel activity]	Conserved collinear gene
101500	102500	E=1.2e-20	At5g47450.1	MQL5.31, major intrinsic family protein / MIP family protein, GO:0016020 [membrane] GO:0006810 [transport] GO:0015250 [water channel activity]	Conserved collinear gene
103000	104000	E=5.5e-08	At1g77930.2	F28K19.14, DNAJ heat shock N-terminal domain-containing protein, GO:0006457 [protein folding] GO:0003754 [chaperone activity] GO:0008372 [cellular_component unknown]	Inserted fragment outside gene models
103500	104500	E=5.5e-08	At1g77930.2	F28K19.14, DNAJ heat shock N-terminal domain-containing protein, GO:0006457 [protein folding] GO:0003754 [chaperone activity] GO:0008372 [cellular_component unknown]	Inserted fragment outside gene models
118000	119000	E=1.7e-13	At2g11830.1	F7E22.2, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
118500	119500	E=1.7e-13	At2g11830.1	F7E22.2, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
119500	120500	E=1.2e-60	At4g34880.1	F11I11.120, amidase family protein, GO:0004040 [amidase activity]	Largely intact relocated

					gene
120000	121000	E=7.8e-77	At4g34880.1	F11I11.120, amidase family protein, GO:0004040 [amidase activity]	Largely intact relocated gene
120500	121500	E=3.1e-52	At4g34880.1	F11I11.120, amidase family protein, GO:0004040 [amidase activity]	Largely intact relocated gene
121000	122000	E=8.1e-90	At4g34880.1	F11I11.120, amidase family protein, GO:0004040 [amidase activity]	Largely intact relocated gene
121500	122500	E=8.8e-74	At4g34880.1	F11I11.120, amidase family protein, GO:0004040 [amidase activity]	Largely intact relocated gene
122000	123000	E=1.4e-53	At5g47420.1	MQL5.28, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
122500	123500	E=1.3e-58	At5g47420.1	MQL5.28, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
123000	124000	E=7.4e-42	At5g47420.1	MQL5.28, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
123500	124500	E=6.4e-36	At5g47420.1	MQL5.28, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
124000	125000	E=1.9e-07	At5g47410.1	MQL5.27, hypothetical protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
124500	125500	E=7.9e-51	At5g47390.1	MQL5.25, myb family transcription factor, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
125000	126000	E=3.3e-68	At5g47390.1	MQL5.25, myb family transcription factor, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
125500	126500	E=1.8e-99	At5g47390.1	MQL5.25, myb family transcription factor, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
126000	127000	E=1.5e-50	At5g47390.1	MQL5.25, myb family transcription factor, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
130000	131000	E=4.7e-07	At2g31700.1	T9H9.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
130500	131500	E=4.7e-07	At2g31700.1	T9H9.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment

					outside gene models
132000	133000	E=3.6e-07	At5g47160.1	K14A3.1, YDG/SRA domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
134500	135500	E=4.2e-08	At5g47380.1	MQL5.24, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Additional collinear gene fragment
135000	136000	E=4.2e-08	At5g47380.1	MQL5.24, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Additional collinear gene fragment
137000	138000	E=1.6e-11	At1g33710.1	F14M2.21, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
142500	143500	E=1.6e-40	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Predicted transposon
143000	144000	E=2.0e-33	At5g33303.1	F19N2.6, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
145500	146500	E=1.3e-20	At5g47370.1	MQL5.23, homeobox-leucine zipper protein 2 (HAT2) / HD-ZIP protein 2, GO:0009826 [cell elongation] GO:0009733 [response to auxin stimulus] GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0009734 [auxin mediated si	Additional collinear gene fragment
146000	147000	E=1.3e-20	At5g47370.1	MQL5.23, homeobox-leucine zipper protein 2 (HAT2) / HD-ZIP protein 2, GO:0009826 [cell elongation] GO:0009733 [response to auxin stimulus] GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0009734 [auxin mediated si	Additional collinear gene fragment
148500	149500	E=4.5e-21	At1g70910.1	F15H11.25, zinc finger (C3HC4-type RING finger) family protein, GO:0005515 [protein binding] GO:0008270 [zinc ion binding]	Inserted fragment within model
149000	150000	E=2.6e-12	At1g57730.1	T8L23.19, zinc finger (C3HC4-type RING finger) family protein, GO:0005515 [protein binding] GO:0008270 [zinc ion binding]	Inserted fragment within model
149500	150500	E=1.1e-08	At5g47150.1	K14A3.10, YDG/SRA domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
151000	152000	E=7.3e-15	At5g53620.2	MNC6.16, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model

151500	152500	E=9.3e-14	At5g53620.2	MNC6.16, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
153500	154500	E=1.7e-11	At5g47150.1	K14A3.10, YDG/SRA domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
166000	167000	E=5.4e-12	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
166500	167500	E=1.3e-11	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
169000	170000	E=4.8e-37	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
169500	170500	E=1.5e-62	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
170000	171000	E=1.9e-55	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
170500	171500	E=1.6e-21	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
198000	199000	E=9.7e-06	At1g36550.1	F28J9.18, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
198500	199500	E=1.5e-06	At1g36550.1	F28J9.18, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
201500	202500	E=6.6e-28	At5g47220.1	MQL5.7, ethylene-responsive element-binding factor 2 (ERF2), GO:0003677 [DNA binding] GO:0045941 [positive regulation of transcription] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0008372 [cellular_	annotation error
202000	203000	E=7.0e-50	At4g17500.1	FCAALL.123, ethylene-responsive element-binding protein 1 (ERF1) / EREBP-2 protein, GO:0005643 [nuclear pore] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0003700 [transcription factor activity]	Conserved collinear gene
202500	203500	E=3.6e-40	At4g17500.1	FCAALL.123, ethylene-responsive element-binding protein 1 (ERF1) / EREBP-2 protein, GO:0005643 [nuclear pore] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0003700 [transcription factor activity]	Conserved collinear gene
204500	205500	E=3.7e-08	At5g47210.1	MQL5.6, nuclear RNA-binding protein, putative, GO:0003723 [RNA binding]	Conserved collinear gene
205000	206000	E=7.0e-	At5g47210.1	MQL5.6, nuclear RNA-binding protein, putative, GO:0003723 [RNA	Conserved

		13		binding]	collinear gene
205500	206500	E=4.8e-11	At5g47210.1	MQL5.6, nuclear RNA-binding protein, putative, GO:0003723 [RNA binding]	Conserved collinear gene
206000	207000	E=2.2e-64	At5g47210.1	MQL5.6, nuclear RNA-binding protein, putative, GO:0003723 [RNA binding]	Conserved collinear gene
206500	207500	E=1.0e-66	At5g47210.1	MQL5.6, nuclear RNA-binding protein, putative, GO:0003723 [RNA binding]	Conserved collinear gene
207000	208000	E=1.2e-18	At5g47210.1	MQL5.6, nuclear RNA-binding protein, putative, GO:0003723 [RNA binding]	Conserved collinear gene
207500	208500	E=1.6e-39	At5g47200.1	MQL5.5, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
208000	209000	E=1.2e-58	At5g47200.1	MQL5.5, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
208500	209500	E=8.5e-13	At5g47200.1	MQL5.5, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
216000	217000	E=2.2e-09	At5g47190.1	MQL5.4, ribosomal protein L19 family protein, GO:0005840 [ribosome] GO:0007046 [ribosome biogenesis] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Additional collinear gene fragment
216500	217500	E=6.1e-18	At5g47190.1	MQL5.4, ribosomal protein L19 family protein, GO:0005840 [ribosome] GO:0007046 [ribosome biogenesis] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Additional collinear gene fragment
217000	218000	E=1.2e-17	At5g47190.1	MQL5.4, ribosomal protein L19 family protein, GO:0005840 [ribosome] GO:0007046 [ribosome biogenesis] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Additional collinear gene fragment
217500	218500	E=3.1e-13	At5g47190.1	MQL5.4, ribosomal protein L19 family protein, GO:0005840 [ribosome] GO:0007046 [ribosome biogenesis] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Additional collinear gene fragment
218500	219500	E=1.7e-24	At5g47180.2	MQL5.3, vesicle-associated membrane family protein / VAMP family protein, GO:0005198 [structural molecule activity]	Conserved collinear gene
219000	220000	E=7.5e-56	At5g47180.2	MQL5.3, vesicle-associated membrane family protein / VAMP family protein, GO:0005198 [structural molecule activity]	Conserved collinear gene
219500	220500	E=3.0e-56	At5g47180.2	MQL5.3, vesicle-associated membrane family protein / VAMP family protein, GO:0005198 [structural molecule activity]	Conserved collinear gene
220000	221000	E=6.0e-30	At5g47180.2	MQL5.3, vesicle-associated membrane family protein / VAMP family protein, GO:0005198 [structural molecule activity]	Conserved collinear gene
220500	221500	E=6.5e-17	At5g47180.2	MQL5.3, vesicle-associated membrane family protein / VAMP family protein, GO:0005198 [structural molecule activity]	Conserved collinear gene
222000	223000	E=3.8e-32	At5g47150.1	K14A3.10, YDG/SRA domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
222500	223500	E=7.4e-	At5g47150.1	K14A3.10, YDG/SRA domain-containing protein, GO:0000004	Conserved

		84		[biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	collinear gene
223000	224000	E=2.8e-47	At5g47150.1	K14A3.10, YDG/SRA domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
228000	229000	E=3.2e-16	At5g47150.1	K14A3.10, YDG/SRA domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	annotation error
228500	229500	E=7.6e-86	At5g47150.1	K14A3.10, YDG/SRA domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	annotation error
229000	230000	E=1.1e-78	At5g47150.1	K14A3.10, YDG/SRA domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	annotation error
229500	230500	E=4.6e-06	At5g47150.1	K14A3.10, YDG/SRA domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	annotation error
232500	233500	E=3.1e-45	At5g47140.1	K14A3.9, zinc finger (GATA type) family protein, GO:0003700 [transcription factor activity]	Conserved collinear gene
233000	234000	E=7.0e-53	At5g47140.1	K14A3.9, zinc finger (GATA type) family protein, GO:0003700 [transcription factor activity]	Conserved collinear gene
233500	234500	E=3.1e-67	At5g47140.1	K14A3.9, zinc finger (GATA type) family protein, GO:0003700 [transcription factor activity]	Conserved collinear gene
234000	235000	E=7.0e-85	At5g47140.1	K14A3.9, zinc finger (GATA type) family protein, GO:0003700 [transcription factor activity]	Conserved collinear gene
234500	235500	E=8.3e-33	At5g47140.1	K14A3.9, zinc finger (GATA type) family protein, GO:0003700 [transcription factor activity]	Conserved collinear gene
243500	244500	E=3.8e-14	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
249500	250500	E=2.5e-62	At5g47120.1	K14A3.7, Bax inhibitor-1 putative / BI-1 putative, GO:0005783 [endoplasmic reticulum] GO:0006916 [anti-apoptosis] GO:0005635 [nuclear membrane] GO:0006915 [apoptosis] GO:0016329 [apoptosis regulator activity] GO:0008189 [apoptosis inhibitor activity]	Conserved collinear gene
250000	251000	E=6.4e-52	At5g47120.1	K14A3.7, Bax inhibitor-1 putative / BI-1 putative, GO:0005783 [endoplasmic reticulum] GO:0006916 [anti-apoptosis] GO:0005635 [nuclear membrane] GO:0006915 [apoptosis] GO:0016329 [apoptosis regulator activity] GO:0008189 [apoptosis inhibitor activity]	Conserved collinear gene
250500	251500	E=1.2e-39	At5g47120.1	K14A3.7, Bax inhibitor-1 putative / BI-1 putative, GO:0005783 [endoplasmic reticulum] GO:0006916 [anti-apoptosis] GO:0005635 [nuclear membrane] GO:0006915 [apoptosis] GO:0016329 [apoptosis regulator activity] GO:0008189 [apoptosis inhibitor activity]	Conserved collinear gene

251000	252000	E=9.2e-17	At5g47120.1	K14A3.7, Bax inhibitor-1 putative / BI-1 putative, GO:0005783 [endoplasmic reticulum] GO:0006916 [anti-apoptosis] GO:0005635 [nuclear membrane] GO:0006915 [apoptosis] GO:0016329 [apoptosis regulator activity] GO:0008189 [apoptosis inhibitor activity]	Conserved collinear gene
263000	264000	E=1.1e-29	At1g11420.1	T23J18.9, agenet domain-containing protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
263500	264500	E=5.5e-12	At1g26540.1	T1K7.9, agenet domain-containing protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
265500	266500	E=2.5e-09	At3g32900.1	T7B9.14, Ulp1 protease family protein, GO:0008234 [cysteine-type peptidase activity] GO:0006508 [proteolysis and peptidolysis]	Inserted fragment within model
266000	267000	E=2.5e-09	At3g32900.1	T7B9.14, Ulp1 protease family protein, GO:0008234 [cysteine-type peptidase activity] GO:0006508 [proteolysis and peptidolysis]	Inserted fragment within model
266500	267500	E=5.3e-07	At1g74250.1	F1O17.8, DNAJ heat shock N-terminal domain-containing protein, GO:0006457 [protein folding] GO:0003754 [chaperone activity] GO:0008372 [cellular_component unknown]	Inserted fragment within model
267000	268000	E=3.4e-06	At1g56660.1	F25P12.91, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
270000	271000	E=7.9e-37	At5g47110.1	K14A3.6, lil3 protein, putative, GO:0009765 [photosynthesis light harvesting] GO:0005554 [molecular_function unknown]	Conserved collinear gene
270500	271500	E=3.4e-78	At5g47110.1	K14A3.6, lil3 protein, putative, GO:0009765 [photosynthesis light harvesting] GO:0005554 [molecular_function unknown]	Conserved collinear gene
271000	272000	E=4.1e-42	At5g47110.1	K14A3.6, lil3 protein, putative, GO:0009765 [photosynthesis light harvesting] GO:0005554 [molecular_function unknown]	Conserved collinear gene
271500	272500	E=2.6e-64	At3g01910.1	F28J7.38, sulfite oxidase, putative, GO:0006790 [sulfur metabolism] GO:0008482 [sulfite oxidase activity]	Largely intact relocated gene
272000	273000	E=1.4e-86	At3g01910.1	F28J7.38, sulfite oxidase, putative, GO:0006790 [sulfur metabolism] GO:0008482 [sulfite oxidase activity]	Largely intact relocated gene
272500	273500	E=1.6e-61	At3g01910.1	F28J7.38, sulfite oxidase, putative, GO:0006790 [sulfur metabolism] GO:0008482 [sulfite oxidase activity]	Largely intact relocated gene
273000	274000	E=6.2e-49	At3g01910.1	F28J7.38, sulfite oxidase, putative, GO:0006790 [sulfur metabolism] GO:0008482 [sulfite oxidase activity]	Largely intact relocated gene
273500	274500	E=3.3e-	At3g01910.1	F28J7.38, sulfite oxidase, putative, GO:0006790 [sulfur metabolism]	Largely intact

		18		GO:0008482 [sulfite oxidase activity]	relocated gene
276000	277000	E=2.8e-16	At5g16180.1	T21H19.100, hypothetical protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
276500	277500	E=2.8e-16	At5g16180.1	T21H19.100, hypothetical protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
281500	282500	E=6.2e-07	At5g37120.1	MJG14.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
287500	288500	E=6.2e-09	At5g47100.1	K14A3.5, calcineurin B-like protein 9 (CBL9), GO:0006950 [response to stress] GO:0008287 [protein serine/threonine phosphatase complex] GO:0005509 [calcium ion binding]	Conserved collinear gene
288000	289000	E=1.3e-44	At4g17615.1	FCAALL.122, calcineurin B-like protein 1 (CBL1), GO:0006970 [response to osmotic stress] GO:0019722 [calcium-mediated signaling] GO:0005509 [calcium ion binding] GO:0005886 [plasma membrane]	Conserved collinear gene
288500	289500	E=8.3e-63	At5g47100.1	K14A3.5, calcineurin B-like protein 9 (CBL9), GO:0006950 [response to stress] GO:0008287 [protein serine/threonine phosphatase complex] GO:0005509 [calcium ion binding]	Conserved collinear gene
289000	290000	E=1.9e-42	At5g47100.1	K14A3.5, calcineurin B-like protein 9 (CBL9), GO:0006950 [response to stress] GO:0008287 [protein serine/threonine phosphatase complex] GO:0005509 [calcium ion binding]	Conserved collinear gene
294000	295000	E=1.4e-50	At5g47080.1	MQD22.23, casein kinase II beta chain, putative, GO:0005956 [protein kinase CK2 complex] GO:0008605 [protein kinase CK2 regulator activity]	Conserved collinear gene
294500	295500	E=1.8e-74	At4g17640.1	FCAALL.14, casein kinase II beta chain, putative, GO:0005956 [protein kinase CK2 complex] GO:0008605 [protein kinase CK2 regulator activity]	Conserved collinear gene
295000	296000	E=7.8e-39	At5g47080.1	MQD22.23, casein kinase II beta chain, putative, GO:0005956 [protein kinase CK2 complex] GO:0008605 [protein kinase CK2 regulator activity]	Conserved collinear gene
295500	296500	E=2.0e-16	At5g47080.2	MQD22.23, casein kinase II beta chain, putative, GO:0005956 [protein kinase CK2 complex] GO:0008605 [protein kinase CK2 regulator activity]	Conserved collinear gene
296000	297000	E=3.0e-06	At5g62750.1	MQB2.7, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models

296500	297500	E=3.6e-07	At3g28770.1	T19N8.6, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
297500	298500	E=5.6e-30	At1g54430.1	F20D21.25, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
298000	299000	E=3.1e-54	At1g54430.1	F20D21.25, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
298500	299500	E=3.5e-17	At1g54430.1	F20D21.25, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
308500	309500	E=2.2e-11	At3g44713.1	T18B22.3, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
309000	310000	E=3.6e-10	At3g44713.1	T18B22.3, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
309500	310500	E=3.7e-46	At1g74310.1	F1O17.2, heat shock protein 101 (HSP101), GO:0005524 [ATP binding] GO:0009408 [response to heat] GO:0016887 [ATPase activity] GO:0003773 [heat shock protein activity]	Inserted fragment within model
310000	311000	E=3.7e-46	At1g74310.1	F1O17.2, heat shock protein 101 (HSP101), GO:0005524 [ATP binding] GO:0009408 [response to heat] GO:0016887 [ATPase activity] GO:0003773 [heat shock protein activity]	Inserted fragment within model
310500	311500	E=2.2e-09	At5g54440.1	F24B18.6, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
313500	314500	E=1.7e-22	At5g47090.1	K14A3.4, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
314000	315000	E=4.1e-84	At5g47090.1	K14A3.4, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
314500	315500	E=1.7e-108	At5g47090.1	K14A3.4, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
315000	316000	E=3.2e-53	At5g47090.1	K14A3.4, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
315500	316500	E=1.6e-20	At2g36310.1	F2H17.8, inosine-uridine preferring nucleoside hydrolase family protein, GO:0016787 [hydrolase activity]	Inserted fragment outside gene models
316000	317000	E=3.4e-	At2g36310.1	F2H17.8, inosine-uridine preferring nucleoside hydrolase family protein,	Inserted

		35		GO:0016787 [hydrolase activity]	fragment outside gene models
316500	317500	E=2.1e-20	At2g36310.1	F2H17.8, inosine-uridine preferring nucleoside hydrolase family protein, GO:0016787 [hydrolase activity]	Inserted fragment outside gene models
326500	327500	E=2.9e-15	At5g47070.1	MQD22.21, protein kinase, putative, GO:0016301 [kinase activity]	annotation error
327000	328000	E=2.9e-15	At5g47070.1	MQD22.21, protein kinase, putative, GO:0016301 [kinase activity]	annotation error
333500	334500	E=7.3e-27	At5g47070.1	MQD22.21, protein kinase, putative, GO:0016301 [kinase activity]	Conserved collinear gene
334000	335000	E=1.3e-87	At5g47070.1	MQD22.21, protein kinase, putative, GO:0016301 [kinase activity]	Conserved collinear gene
334500	335500	E=1.8e-40	At5g47070.1	MQD22.21, protein kinase, putative, GO:0016301 [kinase activity]	Conserved collinear gene
335000	336000	E=3.9e-89	At5g47070.1	MQD22.21, protein kinase, putative, GO:0016301 [kinase activity]	Conserved collinear gene
335500	336500	E=1.0e-64	At5g47070.1	MQD22.21, protein kinase, putative, GO:0016301 [kinase activity]	Conserved collinear gene
336000	337000	E=6.4e-25	At4g17670.1	FCAALL.414, senescence-associated protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
336500	337500	E=1.5e-54	At4g17670.1	FCAALL.414, senescence-associated protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
337000	338000	E=1.9e-28	At5g47060.1	MQD22.20, senescence-associated protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
342000	343000	E=9.3e-24	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Inserted fragment outside gene models
342500	343500	E=3.0e-24	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Inserted fragment outside gene models
343500	344500	E=1.3e-30	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Inserted fragment outside gene models
344000	345000	E=2.4e-30	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Inserted fragment

					outside gene models
345500	346500	E=8.1e-06	At5g45570.1	MFC19.3, Ulp1 protease family protein, GO:0008233 [peptidase activity]	Inserted fragment within model
346000	347000	E=8.1e-06	At5g45570.1	MFC19.3, Ulp1 protease family protein, GO:0008233 [peptidase activity]	Inserted fragment within model
348500	349500	E=8.9e-06	At4g08880.1	T3H13.8, Ulp1 protease family protein, GO:0008234 [cysteine-type peptidase activity] GO:0006508 [proteolysis and peptidolysis]	Inserted fragment within model
349000	350000	E=8.9e-06	At4g08880.1	T3H13.8, Ulp1 protease family protein, GO:0008234 [cysteine-type peptidase activity] GO:0006508 [proteolysis and peptidolysis]	Inserted fragment within model
351000	352000	E=7.1e-07	At1g62760.1	F23N19.12, invertase/pectin methylesterase inhibitor family protein, GO:0046910 [pectinesterase inhibitor activity]	Predicted transposon
351500	352500	E=7.5e-08	At1g62760.1	F23N19.12, invertase/pectin methylesterase inhibitor family protein, GO:0046910 [pectinesterase inhibitor activity]	Predicted transposon

CONTIG B

Start	**Stop**	**Score**	**BLASTn hit**	**Description**	**Classification**
3500	4500	E=2.3e-41	At5g47620.2	MNJ7.21, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative, GO:0003723 [RNA binding]	Conserved collinear gene
4000	5000	E=1.1e-125	At5g47620.2	MNJ7.21, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative, GO:0003723 [RNA binding]	Conserved collinear gene
4500	5500	E=1.1e-93	At5g47620.2	MNJ7.21, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative, GO:0003723 [RNA binding]	Conserved collinear gene
5000	6000	E=3.2e-59	At5g47620.2	MNJ7.21, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative, GO:0003723 [RNA binding]	Conserved collinear gene
6500	7500	E=1.2e-20	At5g47570.1	MNJ7.16, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
7000	8000	E=2.1e-35	At5g47570.1	MNJ7.16, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
7500	8500	E=2.0e-18	At5g47570.1	MNJ7.16, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
9500	10500	E=9.0e-29	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	Conserved collinear gene
10000	11000	E=2.7e-71	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic	Conserved collinear gene

				acid transport] GO:0006814 [sodium ion transport]	
10500	11500	E=1.6e-63	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	Conserved collinear gene
11000	12000	E=9.8e-109	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	Conserved collinear gene
11500	12500	E=2.6e-169	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	Conserved collinear gene
12000	13000	E=1.1e-87	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	Conserved collinear gene
20000	21000	E=5.1e-20	At5g47550.1	MNJ7.14, cysteine protease inhibitor, putative / cystatin, putative, GO:0004869 [cysteine protease inhibitor activity]	Conserved collinear gene
20500	21500	E=7.4e-24	At5g47550.1	MNJ7.14, cysteine protease inhibitor, putative / cystatin, putative, GO:0004869 [cysteine protease inhibitor activity]	Conserved collinear gene
27000	28000	E=3.9e-39	At2g15520.1	F9O13.7, zinc finger protein, putative, GO:0005554 [molecular_function unknown]	Predicted transposon
27500	28500	E=4.2e-36	At2g15520.1	F9O13.7, zinc finger protein, putative, GO:0005554 [molecular_function unknown]	Predicted transposon
32500	33500	E=4.1e-09	At5g47540.1	MNJ7.13, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
33000	34000	E=2.7e-59	At5g47540.1	MNJ7.13, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
33500	34500	E=3.3e-71	At5g47540.1	MNJ7.13, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
34000	35000	E=2.0e-35	At5g47540.1	MNJ7.13, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
34500	35500	E=4.5e-35	At5g47540.1	MNJ7.13, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
35000	36000	E=7.6e-70	At5g47530.1	MNJ7.12, auxin-responsive protein, putative, GO:0016020 [membrane] GO:0007275 [development] GO:0005554 [molecular_function unknown]	Conserved collinear gene
35500	36500	E=2.1e-106	At5g47530.1	MNJ7.12, auxin-responsive protein, putative, GO:0016020 [membrane] GO:0007275 [development] GO:0005554 [molecular_function unknown]	Conserved collinear gene
36000	37000	E=1.4e-32	At5g47530.1	MNJ7.12, auxin-responsive protein, putative, GO:0016020 [membrane] GO:0007275 [development] GO:0005554 [molecular_function unknown]	Conserved collinear gene
38500	39500	E=3.5e-17	At5g14700.1	T15N1.190, cinnamoyl-CoA reductase-related, GO:0016621 [cinnamoyl-CoA reductase activity] GO:0009809 [lignin biosynthesis]	Inserted fragment outside gene models

39000	40000	E=3.5e-17	At5g14700.1	T15N1.190, cinnamoyl-CoA reductase-related, GO:0016621 [cinnamoyl-CoA reductase activity] GO:0009809 [lignin biosynthesis]	Inserted fragment outside gene models
40000	41000	E=7.7e-18	At1g70490.3	F24J13.6, ADP-ribosylation factor, putative, GO:0003926 [ARF small monomeric GTPase activity]	Inserted fragment within model
40500	41500	E=1.0e-34	At2g47170.1	T8I13.1, ADP-ribosylation factor 1 (ARF1), GO:0003926 [ARF small monomeric GTPase activity] GO:0005798 [Golgi vesicle]	Inserted fragment within model
41000	42000	E=2.3e-48	At3g16380.1	T2O4.4, polyadenylate-binding protein, putative / PABP, putative, GO:0003723 [RNA binding] GO:0003743 [translation initiation factor activity]	Inserted fragment within model
41500	42500	E=1.5e-48	At3g16380.1	T2O4.4, polyadenylate-binding protein, putative / PABP, putative, GO:0003723 [RNA binding] GO:0003743 [translation initiation factor activity]	Inserted fragment within model
45500	46500	E=7.4e-06	At3g28770.1	T19N8.6, expressed protein, GO:0005554 [molecular_function unknown]	Predicted transposon
46000	47000	E=1.2e-06	At3g28770.1	T19N8.6, expressed protein, GO:0005554 [molecular_function unknown]	Predicted transposon
49000	50000	E=4.7e-73	At5g47520.1	MNJ7.11, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
49500	50500	E=7.5e-108	At5g47520.1	MNJ7.11, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
50000	51000	E=2.8e-34	At5g47520.1	MNJ7.11, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
52000	53000	E=9.2e-45	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
52500	53500	E=4.4e-73	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
53000	54000	E=3.4e-65	At5g47480.1	MNJ7.7, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
53500	54500	E=6.3e-68	At5g47480.1	MNJ7.7, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
54000	55000	E=2.1e-51	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
54500	55500	E=2.7e-46	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
55000	56000	E=1.2e-59	At5g47480.1	MNJ7.7, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
55500	56500	E=4.1e-	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved

		102			collinear gene
56000	57000	E=3.1e-106	At5g47480.1	MNJ7.7, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
56500	57500	E=1.0e-132	At5g47480.1	MNJ7.7, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
57000	58000	E=1.8e-87	At5g47480.1	MNJ7.7, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
57500	58500	E=2.9e-46	At5g47480.1	MNJ7.7, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
58000	59000	E=3.0e-13	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
60500	61500	E=9.5e-45	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	fragments only
61000	62000	E=8.2e-65	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	fragments only
61500	62500	E=2.3e-68	At5g47480.1	MNJ7.7, expressed protein, GO:0005554 [molecular_function unknown]	fragments only
62000	63000	E=4.4e-86	At5g47480.1	MNJ7.7, expressed protein, GO:0005554 [molecular_function unknown]	fragments only
62500	63500	E=1.2e-67	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	fragments only
63000	64000	E=2.7e-44	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	fragments only
63500	64500	E=3.1e-32	At5g47480.1	MNJ7.7, expressed protein, GO:0005554 [molecular_function unknown]	fragments only
64000	65000	E=5.8e-44	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	fragments only
64500	65500	E=3.4e-70	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	fragments only
65000	66000	E=1.1e-130	At5g47480.1	MNJ7.7, expressed protein, GO:0005554 [molecular_function unknown]	fragments only
65500	66500	E=5.6e-148	At5g47480.1	MNJ7.7, expressed protein, GO:0005554 [molecular_function unknown]	fragments only
66000	67000	E=2.3e-81	At5g47480.1	MNJ7.7, expressed protein, GO:0005554 [molecular_function unknown]	fragments only
66500	67500	E=1.9e-44	At5g47480.1	MNJ7.7, expressed protein, GO:0005554 [molecular_function unknown]	fragments only
67000	68000	E=2.8e-36	At1g43590.1	T10P12.13, hypothetical protein, GO:0005554 [molecular_function unknown] GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown]	Inserted fragment within model
67500	68500	E=1.6e-	At3g15310.1	K7L4.11, expressed protein, GO:0000004 [biological_process	Largely intact

		104		unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	relocated gene
68000	69000	E=1.0e-107	At3g15310.1	K7L4.11, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Largely intact relocated gene
68500	69500	E=2.6e-37	At3g15310.1	K7L4.11, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Largely intact relocated gene
69500	70500	E=4.8e-38	At2g16140.1	F7H1.16, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
70000	71000	E=5.2e-28	At2g16140.1	F7H1.16, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
71000	72000	E=2.3e-07	At2g18540.1	F24H14.11, cupin family protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
74500	75500	E=1.3e-09	At2g07240.1	T13E11.1, Ulp1 protease family protein, GO:0008234 [cysteine-type peptidase activity] GO:0006508 [proteolysis and peptidolysis]	Inserted fragment within model
77000	78000	E=4.4e-08	At5g28250.1	T8M17.20, Ulp1 protease family protein, GO:0008234 [cysteine-type peptidase activity] GO:0006508 [proteolysis and peptidolysis]	Inserted fragment within model
77500	78500	E=6.0e-30	At5g28250.1	T8M17.20, Ulp1 protease family protein, GO:0008234 [cysteine-type peptidase activity] GO:0006508 [proteolysis and peptidolysis]	Inserted fragment within model
82000	83000	E=7.0e-07	At3g52410.1	F22O6.210, hypothetical protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
83500	84500	E=9.7e-12	At5g47430.1	MQL5.29, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
84000	85000	E=2.0e-29	At5g47430.1	MQL5.29, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
84500	85500	E=5.7e-28	At5g47430.1	MQL5.29, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
85000	86000	E=1.1e-58	At5g47430.1	MQL5.29, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
85500	86500	E=9.9e-83	At5g47430.1	MQL5.29, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
86000	87000	E=7.3e-	At5g47430.1	MQL5.29, expressed protein, GO:0005554 [molecular_function	Conserved

		70		unknown]	collinear gene
86500	87500	E=1.9e-67	At5g47430.1	MQL5.29, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
87000	88000	E=5.5e-64	At5g47430.1	MQL5.29, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
87500	88500	E=1.2e-62	At5g47430.1	MQL5.29, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
88000	89000	E=2.8e-64	At5g47430.1	MQL5.29, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
88500	89500	E=1.8e-48	At5g47430.1	MQL5.29, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
89000	90000	E=9.0e-27	At5g47430.1	MQL5.29, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
89500	90500	E=7.3e-41	At5g47390.1	MQL5.25, myb family transcription factor, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
90000	91000	E=3.3e-74	At5g47390.1	MQL5.25, myb family transcription factor, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
90500	91500	E=6.1e-67	At5g47390.1	MQL5.25, myb family transcription factor, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
91000	92000	E=5.0e-35	At5g47390.1	MQL5.25, myb family transcription factor, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
96500	97500	E=4.3e-25	At5g47380.1	MQL5.24, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
97000	98000	E=1.7e-83	At5g47380.1	MQL5.24, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
97500	98500	E=5.0e-99	At5g47380.1	MQL5.24, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
98000	99000	E=7.7e-58	At5g47380.1	MQL5.24, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
98500	99500	E=4.6e-68	At5g47380.1	MQL5.24, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
99000	100000	E=1.6e-51	At5g47380.1	MQL5.24, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
99500	100500	E=6.5e-16	At2g37560.1	F13M22.6, origin recognition complex subunit 2 (ORC2), GO:0003688 [DNA replication origin binding] GO:0006260 [DNA replication]	Inserted fragment

				GO:0000808 [origin of replication recognition complex]	outside gene models
104000	105000	E=1.1e-12	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Inserted fragment within model
104500	105500	E=2.9e-30	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Inserted fragment within model
117000	118000	E=7.3e-40	At5g47370.1	MQL5.23, homeobox-leucine zipper protein 2 (HAT2) / HD-ZIP protein 2, GO:0009826 [cell elongation] GO:0009733 [response to auxin stimulus] GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0009734 [auxin mediated si	Conserved collinear gene
117500	118500	E=7.9e-81	At5g47370.1	MQL5.23, homeobox-leucine zipper protein 2 (HAT2) / HD-ZIP protein 2, GO:0009826 [cell elongation] GO:0009733 [response to auxin stimulus] GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0009734 [auxin mediated si	Conserved collinear gene
118000	119000	E=3.6e-47	At5g47370.1	MQL5.23, homeobox-leucine zipper protein 2 (HAT2) / HD-ZIP protein 2, GO:0009826 [cell elongation] GO:0009733 [response to auxin stimulus] GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0009734 [auxin mediated si	Conserved collinear gene
121500	122500	E=5.3e-09	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
122000	123000	E=2.0e-08	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
122500	123500	E=1.6e-07	At4g03940.1	T24M8.7, expressed protein, GO:0005554 [molecular_function unknown]	Predicted transposon
125000	126000	E=3.5e-38	At5g47360.1	MQL5.22, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Additional collinear gene fragment
125500	126500	E=4.3e-47	At5g47360.1	MQL5.22, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Additional collinear gene fragment
126000	127000	E=8.5e-34	At5g47360.1	MQL5.22, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Additional collinear gene fragment

126500	127500	E=1.3e-38	At5g47330.1	MQL5.19, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
127000	128000	E=6.9e-62	At5g47330.1	MQL5.19, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
127500	128500	E=1.1e-16	At5g47340.1	MQL5.20, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
132000	133000	E=5.4e-09	At5g47330.1	MQL5.19, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
132500	133500	E=5.2e-49	At5g47330.1	MQL5.19, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
133000	134000	E=2.4e-31	At5g47350.1	MQL5.21, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
133500	134500	E=3.9e-08	At1g43170.2	F1I21.1, 60S ribosomal protein L3 (RPL3A), GO:0005840 [ribosome] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Inserted fragment within model
134000	135000	E=3.9e-08	At1g43170.2	F1I21.1, 60S ribosomal protein L3 (RPL3A), GO:0005840 [ribosome] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Inserted fragment within model
135500	136500	E=3.6e-10	At3g52680.1	F3C22.80, F-box family protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
136000	137000	E=2.7e-30	At5g47240.1	MQL5.10, MutT/nudix family protein, GO:0016787 [hydrolase activity]	Conserved collinear gene
136500	137500	E=1.7e-60	At5g47240.1	MQL5.10, MutT/nudix family protein, GO:0016787 [hydrolase activity]	Conserved collinear gene
137000	138000	E=3.0e-24	At5g47240.1	MQL5.10, MutT/nudix family protein, GO:0016787 [hydrolase activity]	Conserved collinear gene
137500	138500	E=6.6e-32	At5g47240.1	MQL5.10, MutT/nudix family protein, GO:0016787 [hydrolase activity]	Conserved collinear gene
138500	139500	E=2.1e-15	At4g13340.1	T9E8.80, leucine-rich repeat family protein / extensin family protein, GO:0000004 [biological_process unknown] GO:0005554 [molecular_function unknown]	Predicted transposon
139000	140000	E=2.5e-18	At4g13340.1	T9E8.80, leucine-rich repeat family protein / extensin family protein, GO:0000004 [biological_process unknown] GO:0005554 [molecular_function unknown]	Predicted transposon
144000	145000	E=5.9e-46	At1g19260.1	T29M8.13, hAT dimerisation domain-containing protein, GO:0005554 [molecular_function unknown]	Predicted transposon
144500	145500	E=2.4e-107	At1g19260.1	T29M8.13, hAT dimerisation domain-containing protein, GO:0005554 [molecular_function unknown]	Predicted transposon
145000	146000	E=3.4e-	At1g19260.1	T29M8.13, hAT dimerisation domain-containing protein, GO:0005554	Predicted

		111		[molecular_function unknown]	transposon
145500	146500	E=2.4e-86	At1g41920.1	F5A13.9, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
146000	147000	E=5.5e-33	At1g19260.1	T29M8.13, hAT dimerisation domain-containing protein, GO:0005554 [molecular_function unknown]	Predicted transposon
147500	148500	E=6.3e-32	At5g47230.1	MQL5.9, ethylene-responsive element-binding factor 5 (ERF5), GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0003700 [transcription factor activity]	Conserved collinear gene
148000	149000	E=2.5e-97	At5g47230.1	MQL5.9, ethylene-responsive element-binding factor 5 (ERF5), GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0003700 [transcription factor activity]	Conserved collinear gene
148500	149500	E=4.3e-62	At5g47230.1	MQL5.9, ethylene-responsive element-binding factor 5 (ERF5), GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0003700 [transcription factor activity]	Conserved collinear gene
149000	150000	E=2.0e-12	At5g47230.1	MQL5.9, ethylene-responsive element-binding factor 5 (ERF5), GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0003700 [transcription factor activity]	Conserved collinear gene
152000	153000	E=1.4e-07	At5g47225.1	MQL5.8, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
156000	157000	E=5.3e-07	At5g47225.1	MQL5.8, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
156500	157500	E=5.3e-07	At5g47225.1	MQL5.8, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
176500	177500	E=1.0e-15	At3g01750.1	F28J7.8, ankyrin repeat family protein, GO:0005515 [protein binding]	Inserted fragment outside gene models
177000	178000	E=1.8e-15	At3g01750.1	F28J7.8, ankyrin repeat family protein, GO:0005515 [protein binding]	Inserted fragment outside gene models

181500	182500	E=9.0e-08	At1g12725.1	T12C24.25, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
182000	183000	E=9.0e-08	At1g12725.1	T12C24.25, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
183000	184000	E=1.9e-22	At5g47220.1	MQL5.7, ethylene-responsive element-binding factor 2 (ERF2), GO:0003677 [DNA binding] GO:0045941 [positive regulation of transcription] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0008372 [cellular_	Conserved collinear gene
183500	184500	E=4.1e-68	At5g47220.1	MQL5.7, ethylene-responsive element-binding factor 2 (ERF2), GO:0003677 [DNA binding] GO:0045941 [positive regulation of transcription] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0008372 [cellular_	Conserved collinear gene
184000	185000	E=1.4e-47	At4g17500.1	FCAALL.123, ethylene-responsive element-binding protein 1 (ERF1) / EREBP-2 protein, GO:0005643 [nuclear pore] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0003700 [transcription factor activity]	Conserved collinear gene
195500	196500	E=1.3e-25	At2g15620.1	F9O13.17, ferredoxin--nitrite reductase, putative, GO:0006118 [electron transport] GO:0050421 [nitrite reductase (NO-forming) activity] GO:0047889 [ferredoxin-nitrate reductase activity]	Inserted fragment within model
196000	197000	E=1.1e-25	At2g15620.1	F9O13.17, ferredoxin--nitrite reductase, putative, GO:0006118 [electron transport] GO:0050421 [nitrite reductase (NO-forming) activity] GO:0047889 [ferredoxin-nitrate reductase activity]	Inserted fragment within model
201000	202000	E=1.5e-06	At3g28770.1	T19N8.6, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
213500	214500	E=4.8e-37	At2g12905.1	T19K21.20, expressed protein, GO:0005554 [molecular_function unknown]	.
214000	215000	E=4.8e-37	At2g12905.1	T19K21.20, expressed protein, GO:0005554 [molecular_function unknown]	.
220500	221500	E=8.3e-18	At5g47210.1	MQL5.6, nuclear RNA-binding protein, putative, GO:0003723 [RNA binding]	Conserved collinear gene
221000	222000	E=6.9e-43	At5g47210.1	MQL5.6, nuclear RNA-binding protein, putative, GO:0003723 [RNA binding]	Conserved collinear gene
221500	222500	E=1.4e-63	At5g47210.1	MQL5.6, nuclear RNA-binding protein, putative, GO:0003723 [RNA binding]	Conserved collinear gene
222000	223000	E=4.9e-62	At5g47210.1	MQL5.6, nuclear RNA-binding protein, putative, GO:0003723 [RNA binding]	Conserved collinear gene

222500	223500	E=3.9e-12	At5g47200.1	MQL5.5, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
223000	224000	E=9.2e-61	At5g47200.1	MQL5.5, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
223500	224500	E=1.0e-68	At5g47200.1	MQL5.5, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
224000	225000	E=2.2e-26	At5g47200.1	MQL5.5, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
224500	225500	E=9.2e-06	At5g47200.1	MQL5.5, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
239000	240000	E=4.3e-22	At4g17560.1	FCAALL.39, ribosomal protein L19 family protein, GO:0005840 [ribosome] GO:0007046 [ribosome biogenesis] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Conserved collinear gene
239500	240500	E=4.5e-48	At5g47190.1	MQL5.4, ribosomal protein L19 family protein, GO:0005840 [ribosome] GO:0007046 [ribosome biogenesis] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Conserved collinear gene
240000	241000	E=1.0e-41	At5g47190.1	MQL5.4, ribosomal protein L19 family protein, GO:0005840 [ribosome] GO:0007046 [ribosome biogenesis] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Conserved collinear gene
240500	241500	E=2.5e-17	At4g17560.1	FCAALL.39, ribosomal protein L19 family protein, GO:0005840 [ribosome] GO:0007046 [ribosome biogenesis] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Conserved collinear gene
245500	246500	E=4.5e-22	At5g47180.2	MQL5.3, vesicle-associated membrane family protein / VAMP family protein, GO:0005198 [structural molecule activity]	Conserved collinear gene
246000	247000	E=5.2e-51	At5g47180.2	MQL5.3, vesicle-associated membrane family protein / VAMP family protein, GO:0005198 [structural molecule activity]	Conserved collinear gene
246500	247500	E=5.5e-50	At5g47180.2	MQL5.3, vesicle-associated membrane family protein / VAMP family protein, GO:0005198 [structural molecule activity]	Conserved collinear gene
247000	248000	E=1.5e-16	At5g47180.2	MQL5.3, vesicle-associated membrane family protein / VAMP family protein, GO:0005198 [structural molecule activity]	Conserved collinear gene
247500	248500	E=3.6e-16	At5g47180.2	MQL5.3, vesicle-associated membrane family protein / VAMP family protein, GO:0005198 [structural molecule activity]	Conserved collinear gene
248000	249000	E=2.7e-23	At5g47140.1	K14A3.9, zinc finger (GATA type) family protein, GO:0003700 [transcription factor activity]	Conserved collinear gene
248500	249500	E=3.8e-52	At5g47140.1	K14A3.9, zinc finger (GATA type) family protein, GO:0003700 [transcription factor activity]	Conserved collinear gene
249000	250000	E=1.0e-81	At5g47140.1	K14A3.9, zinc finger (GATA type) family protein, GO:0003700 [transcription factor activity]	Conserved collinear gene
249500	250500	E=7.3e-83	At5g47140.1	K14A3.9, zinc finger (GATA type) family protein, GO:0003700 [transcription factor activity]	Conserved collinear gene
250000	251000	E=1.8e-	At5g47140.1	K14A3.9, zinc finger (GATA type) family protein, GO:0003700	Conserved

		09		[transcription factor activity]	collinear gene
254000	255000	E=4.7e-07	At5g20920.1	F22D1.90, eukaryotic translation initiation factor 2 subunit 2, putative / eIF-2-beta, putative, GO:0006413 [translational initiation] GO:0003743 [translation initiation factor activity]	Inserted fragment outside gene models
254500	255500	E=1.0e-15	At5g20920.1	F22D1.90, eukaryotic translation initiation factor 2 subunit 2, putative / eIF-2-beta, putative, GO:0006413 [translational initiation] GO:0003743 [translation initiation factor activity]	Inserted fragment outside gene models
255000	256000	E=2.0e-10	At2g32430.1	T32F6.5, galactosyltransferase family protein, GO:0016758 [transferase activity, transferring hexosyl groups] GO:0016757 [transferase activity, transferring glycosyl groups]	Inserted fragment outside gene models
255500	256500	E=4.8e-30	At2g32430.1	T32F6.5, galactosyltransferase family protein, GO:0016758 [transferase activity, transferring hexosyl groups] GO:0016757 [transferase activity, transferring glycosyl groups]	Inserted fragment outside gene models
256000	257000	E=2.1e-23	At2g32430.1	T32F6.5, galactosyltransferase family protein, GO:0016758 [transferase activity, transferring hexosyl groups] GO:0016757 [transferase activity, transferring glycosyl groups]	Inserted fragment outside gene models
257000	258000	E=5.8e-34	At5g47120.1	K14A3.7, Bax inhibitor-1 putative / BI-1 putative, GO:0005783 [endoplasmic reticulum] GO:0006916 [anti-apoptosis] GO:0005635 [nuclear membrane] GO:0006915 [apoptosis] GO:0016329 [apoptosis regulator activity] GO:0008189 [apoptosis inhibitor activity]	Conserved collinear gene
257500	258500	E=2.3e-55	At5g47120.1	K14A3.7, Bax inhibitor-1 putative / BI-1 putative, GO:0005783 [endoplasmic reticulum] GO:0006916 [anti-apoptosis] GO:0005635 [nuclear membrane] GO:0006915 [apoptosis] GO:0016329 [apoptosis regulator activity] GO:0008189 [apoptosis inhibitor activity]	Conserved collinear gene
258000	259000	E=6.0e-53	At5g47120.1	K14A3.7, Bax inhibitor-1 putative / BI-1 putative, GO:0005783 [endoplasmic reticulum] GO:0006916 [anti-apoptosis] GO:0005635 [nuclear membrane] GO:0006915 [apoptosis] GO:0016329 [apoptosis regulator activity] GO:0008189 [apoptosis inhibitor activity]	Conserved collinear gene
258500	259500	E=1.5e-14	At5g47120.1	K14A3.7, Bax inhibitor-1 putative / BI-1 putative, GO:0005783 [endoplasmic reticulum] GO:0006916 [anti-apoptosis] GO:0005635 [nuclear membrane] GO:0006915 [apoptosis] GO:0016329 [apoptosis regulator activity] GO:0008189 [apoptosis inhibitor activity]	Conserved collinear gene
259000	260000	E=4.6e-21	At5g47110.1	K14A3.6, lil3 protein, putative, GO:0009765 [photosynthesis light harvesting] GO:0005554 [molecular_function unknown]	Conserved collinear gene
259500	260500	E=6.5e-47	At5g47110.1	K14A3.6, lil3 protein, putative, GO:0009765 [photosynthesis light harvesting] GO:0005554 [molecular_function unknown]	Conserved collinear gene

260000	261000	E=6.6e-68	At5g47110.1	K14A3.6, lil3 protein, putative, GO:0009765 [photosynthesis light harvesting] GO:0005554 [molecular_function unknown]	Conserved collinear gene
260500	261500	E=6.5e-38	At5g47110.1	K14A3.6, lil3 protein, putative, GO:0009765 [photosynthesis light harvesting] GO:0005554 [molecular_function unknown]	Conserved collinear gene
267000	268000	E=2.2e-29	At3g23690.1	MYM9.3, basic helix-loop-helix (bHLH) family protein, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Inserted fragment within model
267500	268500	E=1.2e-57	At3g23690.1	MYM9.3, basic helix-loop-helix (bHLH) family protein, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Inserted fragment within model
268000	269000	E=4.0e-20	At3g23690.1	MYM9.3, basic helix-loop-helix (bHLH) family protein, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Inserted fragment within model
269000	270000	E=1.6e-23	At4g11710.1	T5C23.140, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
269500	270500	E=1.7e-26	At4g11710.1	T5C23.140, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
270000	271000	E=3.7e-12	At1g35570.1	F15O4.34, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
271500	272500	E=2.4e-11	At5g47100.1	K14A3.5, calcineurin B-like protein 9 (CBL9), GO:0006950 [response to stress] GO:0008287 [protein serine/threonine phosphatase complex] GO:0005509 [calcium ion binding]	Conserved collinear gene
272000	273000	E=7.7e-27	At4g17615.2	FCAALL.122, calcineurin B-like protein 1 (CBL1), GO:0006970 [response to osmotic stress] GO:0019722 [calcium-mediated signaling] GO:0005509 [calcium ion binding] GO:0005886 [plasma membrane]	Conserved collinear gene
272500	273500	E=2.5e-43	At5g47100.1	K14A3.5, calcineurin B-like protein 9 (CBL9), GO:0006950 [response to stress] GO:0008287 [protein serine/threonine phosphatase complex] GO:0005509 [calcium ion binding]	Conserved collinear gene
273000	274000	E=7.2e-41	At5g47100.1	K14A3.5, calcineurin B-like protein 9 (CBL9), GO:0006950 [response to stress] GO:0008287 [protein serine/threonine phosphatase complex] GO:0005509 [calcium ion binding]	Conserved collinear gene
273500	274500	E=1.6e-31	At5g47080.1	MQD22.23, casein kinase II beta chain, putative, GO:0005956 [protein kinase CK2 complex] GO:0008605 [protein kinase CK2 regulator activity]	Additional collinear gene fragment
274000	275000	E=1.6e-31	At5g47080.1	MQD22.23, casein kinase II beta chain, putative, GO:0005956 [protein kinase CK2 complex] GO:0008605 [protein kinase CK2 regulator activity]	Additional collinear gene fragment
275500	276500	E=6.3e-44	At2g45730.1	F4I18.29, eukaryotic initiation factor 3 gamma subunit family protein, GO:0006446 [regulation of translational initiation] GO:0003743 [translation initiation factor activity]	Inserted fragment within model
276000	277000	E=5.5e-	At2g45730.1	F4I18.29, eukaryotic initiation factor 3 gamma subunit family protein,	Inserted

		70		GO:0006446 [regulation of translational initiation] GO:0003743 [translation initiation factor activity]	fragment within model
276500	277500	E=6.1e-18	At2g45730.1	F4I18.29, eukaryotic initiation factor 3 gamma subunit family protein, GO:0006446 [regulation of translational initiation] GO:0003743 [translation initiation factor activity]	Inserted fragment within model
279000	280000	E=1.3e-18	At3g25860.1	MPE11.6, dihydrolipoamide S-acetyltransferase (LTA2), GO:0004742 [dihydrolipoyllysine-residue acetyltransferase activity] GO:0008152 [metabolism]	Inserted fragment outside gene models
279500	280500	E=4.1e-41	At3g57800.1	T10K17.10, basic helix-loop-helix (bHLH) family protein, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Inserted fragment outside gene models
280000	281000	E=4.1e-41	At3g57800.1	T10K17.10, basic helix-loop-helix (bHLH) family protein, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Inserted fragment outside gene models
280500	281500	E=2.1e-19	At4g17660.1	FCAALL.77, protein kinase, putative, GO:0016301 [kinase activity]	Conserved collinear gene
281000	282000	E=1.5e-21	At4g17660.1	FCAALL.77, protein kinase, putative, GO:0016301 [kinase activity]	Conserved collinear gene

CONTIG C

Start	**Stop**	**Score**	**BLASTn hit**	**Description**	**Classification**
0	1000	E=1.1e-09	At3g43770.1	T28A8.60, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
500	1500	E=1.9e-14	At5g13540.1	T6I14.70, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
1000	2000	E=1.5e-34	At5g65770.1	MPA24.12, nuclear matrix constituent protein-related, GO:0005554 [molecular_function unknown]	Inserted fragment within model
1500	2500	E=1.5e-34	At5g65770.1	MPA24.12, nuclear matrix constituent protein-related, GO:0005554 [molecular_function unknown]	Inserted fragment within model
2000	3000	E=4.8e-58	At1g14610.1	T5E21.11, valyl-tRNA synthetase / valine--tRNA ligase (VALRS), GO:0005524 [ATP binding] GO:0006418 [tRNA aminoacylation for protein translation] GO:0004812 [tRNA ligase activity]	Inserted fragment within model
2500	3500	E=5.9e-	At1g14610.1	T5E21.11, valyl-tRNA synthetase / valine--tRNA ligase (VALRS),	Inserted

		47		GO:0005524 [ATP binding] GO:0006418 [tRNA aminoacylation for protein translation] GO:0004812 [tRNA ligase activity]	fragment within model
3000	4000	E=3.4e-38	At5g54480.1	F24B18.10, hypothetical protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
3500	4500	E=1.5e-08	At5g54480.1	F24B18.10, hypothetical protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
5000	6000	E=2.4e-17	At5g47620.2	MNJ7.21, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative, GO:0003723 [RNA binding]	Conserved collinear gene
5500	6500	E=1.2e-55	At5g47620.2	MNJ7.21, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative, GO:0003723 [RNA binding]	Conserved collinear gene
6000	7000	E=2.7e-104	At5g47620.2	MNJ7.21, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative, GO:0003723 [RNA binding]	Conserved collinear gene
6500	7500	E=1.4e-142	At5g47620.2	MNJ7.21, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative, GO:0003723 [RNA binding]	Conserved collinear gene
7000	8000	E=3.5e-65	At5g47620.2	MNJ7.21, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative, GO:0003723 [RNA binding]	Conserved collinear gene
7500	8500	E=4.2e-42	At5g47610.1	MNJ7.20, zinc finger (C3HC4-type RING finger) family protein, GO:0005515 [protein binding] GO:0008270 [zinc ion binding]	Conserved collinear gene
8000	9000	E=7.4e-66	At5g47610.1	MNJ7.20, zinc finger (C3HC4-type RING finger) family protein, GO:0005515 [protein binding] GO:0008270 [zinc ion binding]	Conserved collinear gene
8500	9500	E=6.7e-19	At5g47610.1	MNJ7.20, zinc finger (C3HC4-type RING finger) family protein, GO:0005515 [protein binding] GO:0008270 [zinc ion binding]	Conserved collinear gene
11000	12000	E=1.3e-20	At5g47590.1	MNJ7.18, heat shock protein-related, GO:0005554 [molecular_function unknown]	fragments only
11500	12500	E=1.6e-43	At5g47590.1	MNJ7.18, heat shock protein-related, GO:0005554 [molecular_function unknown]	fragments only
12000	13000	E=4.6e-22	At5g47590.1	MNJ7.18, heat shock protein-related, GO:0005554 [molecular_function unknown]	fragments only
12500	13500	E=3.6e-08	At2g26310.1	T1D16.5, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
13000	14000	E=2.8e-08	At5g47600.1	MNJ7.19, heat shock protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
13500	14500	E=2.7e-38	At5g47600.1	MNJ7.19, heat shock protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
14000	15000	E=1.6e-24	At5g47600.1	MNJ7.19, heat shock protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
15500	16500	E=1.6e-09	At5g47590.1	MNJ7.18, heat shock protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene

16000	17000	E=5.7e-57	At5g47590.1	MNJ7.18, heat shock protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
16500	17500	E=9.5e-50	At5g47590.1	MNJ7.18, heat shock protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
17000	18000	E=1.1e-06	At2g26310.1	T1D16.5, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
17500	18500	E=1.0e-36	At5g47570.1	MNJ7.16, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
18000	19000	E=5.9e-52	At5g47570.1	MNJ7.16, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
18500	19500	E=5.6e-11	At5g47570.1	MNJ7.16, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
29000	30000	E=4.3e-12	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
29500	30500	E=4.3e-12	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
31000	32000	E=2.2e-29	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	Conserved collinear gene
31500	32500	E=8.8e-73	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	Conserved collinear gene
32000	33000	E=4.8e-39	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	Conserved collinear gene
34500	35500	E=2.2e-11	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	annotation error
35000	36000	E=2.5e-95	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	annotation error
35500	36500	E=2.3e-160	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	annotation error
36000	37000	E=2.8e-91	At5g47560.1	MNJ7.15, sodium/dicarboxylate cotransporter, putative, GO:0017153 [sodium:dicarboxylate symporter activity] GO:0006835 [dicarboxylic acid transport] GO:0006814 [sodium ion transport]	annotation error
38000	39000	E=9.0e-	At5g47550.1	MNJ7.14, cysteine protease inhibitor, putative / cystatin, putative,	Conserved

		12		GO:0004869 [cysteine protease inhibitor activity]	collinear gene
38500	39500	E=2.5e-29	At5g47550.1	MNJ7.14, cysteine protease inhibitor, putative / cystatin, putative, GO:0004869 [cysteine protease inhibitor activity]	Conserved collinear gene
39000	40000	E=3.0e-11	At5g47550.1	MNJ7.14, cysteine protease inhibitor, putative / cystatin, putative, GO:0004869 [cysteine protease inhibitor activity]	Conserved collinear gene
40500	41500	E=6.2e-50	At3g29265.1	MMF24.1, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
41000	42000	E=5.6e-29	At3g29265.1	MMF24.1, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
44500	45500	E=1.0e-06	At4g07666.1	F10A2.6, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
45000	46000	E=1.0e-06	At4g07666.1	F10A2.6, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
46500	47500	E=2.7e-07	At5g47540.1	MNJ7.13, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
47000	48000	E=3.3e-59	At5g47540.1	MNJ7.13, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
47500	48500	E=1.0e-66	At5g47540.1	MNJ7.13, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
48000	49000	E=7.0e-37	At5g47540.1	MNJ7.13, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
48500	49500	E=1.8e-30	At5g47540.1	MNJ7.13, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
49000	50000	E=5.7e-16	At5g47540.1	MNJ7.13, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
51000	52000	E=3.7e-59	At5g47520.1	MNJ7.11, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
51500	52500	E=1.4e-113	At5g47520.1	MNJ7.11, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
52000	53000	E=6.2e-52	At5g47520.1	MNJ7.11, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
52500	53500	E=2.1e-09	At5g47510.1	MNJ7.10, SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, GO:0006810 [transport] GO:0008372 [cellular_component unknown] GO:0005215 [transporter activity]	Conserved collinear gene
53000	54000	E=8.2e-40	At5g47510.1	MNJ7.10, SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, GO:0006810 [transport] GO:0008372 [cellular_component unknown] GO:0005215 [transporter activity]	Conserved collinear gene
53500	54500	E=8.6e-77	At5g47510.1	MNJ7.10, SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, GO:0006810 [transport] GO:0008372 [cellular_component unknown] GO:0005215 [transporter activity]	Conserved collinear gene
54000	55000	E=8.8e-	At5g47510.1	MNJ7.10, SEC14 cytosolic factor family protein / phosphoglyceride	Conserved

		59		transfer family protein, GO:0006810 [transport] GO:0008372 [cellular_component unknown] GO:0005215 [transporter activity]	collinear gene
54500	55500	E=1.8e-20	At5g47510.1	MNJ7.10, SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, GO:0006810 [transport] GO:0008372 [cellular_component unknown] GO:0005215 [transporter activity]	Conserved collinear gene
55500	56500	E=3.8e-16	At1g33710.1	F14M2.21, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
56000	57000	E=1.1e-30	At1g33710.1	F14M2.21, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
56500	57500	E=2.9e-12	At5g52065.1	MSG15.16, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
57000	58000	E=2.9e-12	At5g52065.1	MSG15.16, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
65500	66500	E=3.6e-34	At3g29265.1	MMF24.1, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
66000	67000	E=2.9e-47	At3g29265.1	MMF24.1, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
69500	70500	E=7.9e-31	At5g47500.1	MNJ7.9, pectinesterase family protein, GO:0030599 [pectinesterase activity] GO:0009505 [cell wall (sensu Magnoliophyta)]	Conserved collinear gene
70000	71000	E=2.5e-72	At5g47500.1	MNJ7.9, pectinesterase family protein, GO:0030599 [pectinesterase activity] GO:0009505 [cell wall (sensu Magnoliophyta)]	Conserved collinear gene
70500	71500	E=2.8e-121	At5g47500.1	MNJ7.9, pectinesterase family protein, GO:0030599 [pectinesterase activity] GO:0009505 [cell wall (sensu Magnoliophyta)]	Conserved collinear gene
71000	72000	E=6.9e-71	At5g47500.1	MNJ7.9, pectinesterase family protein, GO:0030599 [pectinesterase activity] GO:0009505 [cell wall (sensu Magnoliophyta)]	Conserved collinear gene
73000	74000	E=1.9e-07	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
76000	77000	E=1.2e-32	At5g33303.1	F19N2.6, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
76500	77500	E=1.4e-17	At2g04135.1	F3L12.19, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
81000	82000	E=9.2e-45	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Predicted transposon
81500	82500	E=2.9e-37	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Predicted transposon
86500	87500	E=2.5e-12	At3g21865.1	MSD21.24, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment

					outside gene models
87000	88000	E=3.9e-06	At3g21865.1	MSD21.24, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
88500	89500	E=1.2e-23	At5g47070.1	MQD22.21, protein kinase, putative, GO:0016301 [kinase activity]	Inserted fragment within model
89000	90000	E=1.7e-25	At5g47070.1	MQD22.21, protein kinase, putative, GO:0016301 [kinase activity]	Inserted fragment within model
89500	90500	E=2.6e-07	At5g47070.1	MQD22.21, protein kinase, putative, GO:0016301 [kinase activity]	Inserted fragment within model
90500	91500	E=7.9e-20	At4g01200.1	F2N1.36, C2 domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
91000	92000	E=7.9e-20	At4g01200.1	F2N1.36, C2 domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
91500	92500	E=7.0e-69	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
92000	93000	E=8.8e-119	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
92500	93500	E=1.1e-81	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
93000	94000	E=2.6e-80	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
93500	94500	E=1.1e-59	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
94000	95000	E=1.3e-61	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
94500	95500	E=6.9e-59	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
95000	96000	E=1.7e-78	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
95500	96500	E=3.3e-121	At5g47480.1	MNJ7.7, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
96000	97000	E=2.7e-135	At5g47480.1	MNJ7.7, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene

96500	97500	E=5.9e-93	At5g47480.1	MNJ7.7, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
97000	98000	E=4.5e-52	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
97500	98500	E=3.1e-09	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
98000	99000	E=9.4e-47	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
98500	99500	E=1.4e-54	At5g47490.1	MNJ7.8, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
100000	101000	E=3.8e-24	At5g47470.1	MNJ7.6, nodulin MtN21 family protein, GO:0016020 [membrane] GO:0005554 [molecular_function unknown]	Conserved collinear gene
100500	101500	E=8.9e-80	At5g47470.1	MNJ7.6, nodulin MtN21 family protein, GO:0016020 [membrane] GO:0005554 [molecular_function unknown]	Conserved collinear gene
101000	102000	E=1.4e-75	At5g47470.1	MNJ7.6, nodulin MtN21 family protein, GO:0016020 [membrane] GO:0005554 [molecular_function unknown]	Conserved collinear gene
101500	102500	E=1.6e-60	At5g47470.1	MNJ7.6, nodulin MtN21 family protein, GO:0016020 [membrane] GO:0005554 [molecular_function unknown]	Conserved collinear gene
102000	103000	E=3.3e-17	At5g47470.1	MNJ7.6, nodulin MtN21 family protein, GO:0016020 [membrane] GO:0005554 [molecular_function unknown]	Conserved collinear gene
107500	108500	E=8.6e-32	At5g47460.1	MNJ7.5, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
108000	109000	E=8.6e-32	At5g47460.1	MNJ7.5, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
110000	111000	E=2.6e-79	At5g47460.1	MNJ7.5, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
110500	111500	E=1.8e-154	At5g47460.1	MNJ7.5, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
111000	112000	E=4.1e-125	At5g47460.1	MNJ7.5, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
111500	112500	E=1.7e-	At5g47460.1	MNJ7.5, pentatricopeptide (PPR) repeat-containing protein,	Conserved

		95		GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	collinear gene
112500	113500	E=2.8e-29	At5g47455.5	MNJ7.31, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
113000	114000	E=7.5e-44	At5g47455.5	MNJ7.31, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
113500	114500	E=1.3e-10	At5g47455.4	MNJ7.31, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
115000	116000	E=1.0e-13	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
115500	116500	E=8.4e-13	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
121500	122500	E=1.6e-48	At5g47450.1	MQL5.31, major intrinsic family protein / MIP family protein, GO:0016020 [membrane] GO:0006810 [transport] GO:0015250 [water channel activity]	Conserved collinear gene
122000	123000	E=3.9e-57	At5g47450.1	MQL5.31, major intrinsic family protein / MIP family protein, GO:0016020 [membrane] GO:0006810 [transport] GO:0015250 [water channel activity]	Conserved collinear gene
123000	124000	E=8.6e-62	At5g47450.1	MQL5.31, major intrinsic family protein / MIP family protein, GO:0016020 [membrane] GO:0006810 [transport] GO:0015250 [water channel activity]	Conserved collinear gene
123500	124500	E=8.6e-62	At5g47450.1	MQL5.31, major intrinsic family protein / MIP family protein, GO:0016020 [membrane] GO:0006810 [transport] GO:0015250 [water channel activity]	Conserved collinear gene
127500	128500	E=4.1e-23	At5g47440.1	MNJ7.2, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
128000	129000	E=2.9e-94	At5g47440.1	MNJ7.2, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
128500	129500	E=4.3e-116	At5g47440.1	MNJ7.2, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
129000	130000	E=1.9e-89	At5g47440.1	MNJ7.2, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
129500	130500	E=3.6e-53	At5g47435.2	MNJ7.1, formyltetrahydrofolate deformylase, putative, GO:0009152 [purine ribonucleotide biosynthesis] GO:0008864 [formyltetrahydrofolate deformylase activity] GO:0009058 [biosynthesis] GO:0016742 [hydroxymethyl-, formyl- and related transferase activity]	Conserved collinear gene
130000	131000	E=1.6e-87	At5g47435.2	MNJ7.1, formyltetrahydrofolate deformylase, putative, GO:0009152 [purine ribonucleotide biosynthesis] GO:0008864	Conserved collinear gene

				[formyltetrahydrofolate deformylase activity] GO:0009058 [biosynthesis] GO:0016742 [hydroxymethyl-, formyl- and related transferase activity]	
130500	131500	E=2.2e-62	At5g47435.2	MNJ7.1, formyltetrahydrofolate deformylase, putative, GO:0009152 [purine ribonucleotide biosynthesis] GO:0008864 [formyltetrahydrofolate deformylase activity] GO:0009058 [biosynthesis] GO:0016742 [hydroxymethyl-, formyl- and related transferase activity]	Conserved collinear gene
131000	132000	E=2.6e-64	At5g47435.2	MNJ7.1, formyltetrahydrofolate deformylase, putative, GO:0009152 [purine ribonucleotide biosynthesis] GO:0008864 [formyltetrahydrofolate deformylase activity] GO:0009058 [biosynthesis] GO:0016742 [hydroxymethyl-, formyl- and related transferase activity]	Conserved collinear gene
131500	132500	E=3.0e-07	At2g31700.1	T9H9.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
132000	133000	E=3.0e-07	At2g31700.1	T9H9.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
132500	133500	E=2.2e-18	At5g36200.1	MAB16.1, F-box family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
133000	134000	E=5.5e-17	At5g36200.1	MAB16.1, F-box family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
133500	134500	E=2.8e-51	At5g47420.1	MQL5.28, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
134000	135000	E=1.3e-56	At5g47420.1	MQL5.28, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
134500	135500	E=3.2e-46	At4g17420.1	FCAALL.389, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
135000	136000	E=2.5e-40	At5g47420.1	MQL5.28, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
135500	136500	E=5.3e-37	At5g47410.1	MQL5.27, hypothetical protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
136000	137000	E=1.6e-54	At5g47410.1	MQL5.27, hypothetical protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
136500	137500	E=3.5e-20	At5g47400.1	MQL5.26, hypothetical protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
137000	138000	E=1.6e-	At5g47400.1	MQL5.26, hypothetical protein, GO:0005554 [molecular_function	Conserved

		68		unknown]	collinear gene
137500	138500	E=8.5e-142	At5g47400.1	MQL5.26, hypothetical protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
138000	139000	E=7.5e-174	At5g47400.1	MQL5.26, hypothetical protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
138500	139500	E=2.5e-122	At5g47400.1	MQL5.26, hypothetical protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
139000	140000	E=1.6e-40	At5g47400.1	MQL5.26, hypothetical protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
151000	152000	E=3.5e-41	At5g47370.1	MQL5.23, homeobox-leucine zipper protein 2 (HAT2) / HD-ZIP protein 2, GO:0009826 [cell elongation] GO:0009733 [response to auxin stimulus] GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0009734 [auxin mediated si	Conserved collinear gene
151500	152500	E=1.1e-87	At5g47370.1	MQL5.23, homeobox-leucine zipper protein 2 (HAT2) / HD-ZIP protein 2, GO:0009826 [cell elongation] GO:0009733 [response to auxin stimulus] GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0009734 [auxin mediated si	Conserved collinear gene
152000	153000	E=1.7e-78	At5g47370.1	MQL5.23, homeobox-leucine zipper protein 2 (HAT2) / HD-ZIP protein 2, GO:0009826 [cell elongation] GO:0009733 [response to auxin stimulus] GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0009734 [auxin mediated si	Conserved collinear gene
152500	153500	E=1.4e-22	At5g47370.1	MQL5.23, homeobox-leucine zipper protein 2 (HAT2) / HD-ZIP protein 2, GO:0009826 [cell elongation] GO:0009733 [response to auxin stimulus] GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0009734 [auxin mediated si	Conserved collinear gene
153000	154000	E=2.3e-08	At5g20920.1	F22D1.90, eukaryotic translation initiation factor 2 subunit 2, putative / eIF-2-beta, putative, GO:0006413 [translational initiation] GO:0003743 [translation initiation factor activity]	Inserted fragment outside gene models
153500	154500	E=3.8e-12	At5g20920.1	F22D1.90, eukaryotic translation initiation factor 2 subunit 2, putative / eIF-2-beta, putative, GO:0006413 [translational initiation] GO:0003743 [translation initiation factor activity]	Inserted fragment outside gene models
161000	162000	E=8.6e-63	At5g47360.1	MQL5.22, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene

161500	162500	E=1.0e-146	At5g47360.1	MQL5.22, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
162000	163000	E=4.7e-165	At5g47360.1	MQL5.22, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
162500	163500	E=2.6e-81	At5g47360.1	MQL5.22, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
163500	164500	E=1.0e-10	At2g01560.1	F2I9.18, hypothetical protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
165000	166000	E=2.5e-06	At1g67020.1	F1O19.7, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
165500	166500	E=1.3e-06	At1g67020.1	F1O19.7, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
170500	171500	E=1.7e-29	At5g47330.1	MQL5.19, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	annotation error
171000	172000	E=1.1e-57	At5g47350.1	MQL5.21, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
171500	172500	E=8.6e-32	At5g47340.1	MQL5.20, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
172000	173000	E=4.1e-62	At5g47330.1	MQL5.19, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
172500	173500	E=2.9e-41	At5g47330.1	MQL5.19, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
177500	178500	E=2.3e-27	At5g47310.1	MQL5.17, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
178000	179000	E=1.2e-79	At5g47310.1	MQL5.17, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
178500	179500	E=2.1e-80	At5g47310.1	MQL5.17, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
179000	180000	E=8.6e-25	At5g47310.1	MQL5.17, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
183000	184000	E=1.7e-09	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
183500	184500	E=3.9e-13	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon

189500	190500	E=1.6e-08	At2g24780.1	F27C12.30, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
190000	191000	E=1.6e-08	At2g24780.1	F27C12.30, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
196500	197500	E=1.3e-11	At2g38255.1	F16M14.24, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Predicted transposon
197000	198000	E=9.4e-12	At2g38255.1	F16M14.24, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Predicted transposon
198500	199500	E=5.7e-09	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Inserted fragment within model
199000	200000	E=9.8e-49	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Predicted transposon
199500	200500	E=2.9e-38	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Predicted transposon
204000	205000	E=9.6e-25	At2g38255.1	F16M14.24, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Predicted transposon
204500	205500	E=9.6e-25	At2g38255.1	F16M14.24, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Predicted transposon
205500	206500	E=6.9e-09	At2g38255.1	F16M14.24, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Predicted transposon
206000	207000	E=1.3e-24	At2g27320.1	F12K2.10, hypothetical protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
206500	207500	E=5.3e-40	At2g27320.1	F12K2.10, hypothetical protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
207000	208000	E=4.4e-43	At2g38255.1	F16M14.24, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
207500	208500	E=2.8e-	At2g38255.1	F16M14.24, expressed protein, GO:0000004 [biological_process	Inserted

		26		unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	fragment outside gene models
208500	209500	E=4.1e-50	At3g51770.1	ATEM1.2, tetratricopeptide repeat (TPR)-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
209000	210000	E=9.7e-101	At3g51770.1	ATEM1.2, tetratricopeptide repeat (TPR)-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
209500	210500	E=9.5e-57	At3g51770.1	ATEM1.2, tetratricopeptide repeat (TPR)-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
212000	213000	E=2.6e-07	At2g04600.1	F7D11.4, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
212500	213500	E=1.3e-07	At3g29450.1	MUO10.19, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
213000	214000	E=1.3e-07	At3g29450.1	MUO10.19, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
219500	220500	E=2.5e-14	At1g02230.1	T7I23.19, no apical meristem (NAM) family protein, GO:0007275 [development] GO:0005554 [molecular_function unknown] GO:0003700 [transcription factor activity]	Predicted transposon
220000	221000	E=5.9e-20	At5g47225.1	MQL5.8, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
220500	221500	E=4.9e-09	At4g29090.1	F25O24.5, reverse transcriptase, putative / RNA-dependent DNA polymerase, putative, GO:0003723 [RNA binding] GO:0003964 [RNA-directed DNA polymerase activity] GO:0006278 [RNA dependent DNA replication]	Predicted transposon
221000	222000	E=1.1e-11	At4g29090.1	F25O24.5, reverse transcriptase, putative / RNA-dependent DNA polymerase, putative, GO:0003723 [RNA binding] GO:0003964 [RNA-directed DNA polymerase activity] GO:0006278 [RNA dependent DNA replication]	Predicted transposon
231500	232500	E=3.4e-11	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
232000	233000	E=3.4e-	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function	Predicted

		11		unknown]	transposon
241000	242000	E=1.0e-17	At3g52680.1	F3C22.80, F-box family protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
241500	242500	E=1.0e-17	At3g52680.1	F3C22.80, F-box family protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
242000	243000	E=1.1e-35	At5g47240.1	MQL5.10, MutT/nudix family protein, GO:0016787 [hydrolase activity]	Conserved collinear gene
242500	243500	E=4.9e-63	At5g47240.1	MQL5.10, MutT/nudix family protein, GO:0016787 [hydrolase activity]	Conserved collinear gene
243000	244000	E=1.3e-83	At5g47240.1	MQL5.10, MutT/nudix family protein, GO:0016787 [hydrolase activity]	Conserved collinear gene
243500	244500	E=2.3e-44	At5g47240.1	MQL5.10, MutT/nudix family protein, GO:0016787 [hydrolase activity]	Conserved collinear gene
244000	245000	E=1.8e-13	At5g47240.1	MQL5.10, MutT/nudix family protein, GO:0016787 [hydrolase activity]	Conserved collinear gene
250500	251500	E=6.0e-47	At3g29265.1	MMF24.1, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
251000	252000	E=1.9e-33	At3g29265.1	MMF24.1, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
255500	256500	E=4.8e-08	At1g31150.1	F28K20.8, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
257500	258500	E=2.3e-06	At5g10430.1	F12B17.220, arabinogalactan-protein (AGP4), GO:0005554 [molecular_function unknown]	Inserted fragment within model
258000	259000	E=2.3e-06	At5g10430.1	F12B17.220, arabinogalactan-protein (AGP4), GO:0005554 [molecular_function unknown]	Inserted fragment within model
260500	261500	E=3.4e-06	At5g07570.1	T2I1.280, glycine/proline-rich protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
261000	262000	E=9.6e-09	At1g62760.1	F23N19.12, invertase/pectin methylesterase inhibitor family protein, GO:0046910 [pectinesterase inhibitor activity]	Inserted fragment outside gene models
262500	263500	E=5.8e-34	At2g07320.1	T13E11.9, SWIM zinc finger family protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
269500	270500	E=1.3e-	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676	Predicted

		40		[nucleic acid binding]	transposon
270000	271000	E=3.4e-32	At5g33303.1	F19N2.6, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
276000	277000	E=7.4e-11	At5g47230.1	MQL5.9, ethylene-responsive element-binding factor 5 (ERF5), GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0003700 [transcription factor activity]	Conserved collinear gene
276500	277500	E=1.9e-10	At5g47230.1	MQL5.9, ethylene-responsive element-binding factor 5 (ERF5), GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0003700 [transcription factor activity]	Conserved collinear gene
278000	279000	E=1.6e-06	At4g37570.1	F19F18.60, hypothetical protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
278500	279500	E=2.0e-14	At5g07570.1	T2I1.280, glycine/proline-rich protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
279000	280000	E=1.8e-15	At4g17490.1	FCAALL.120, ethylene-responsive element-binding protein, putative, GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
279500	280500	E=7.0e-53	At5g47230.1	MQL5.9, ethylene-responsive element-binding factor 5 (ERF5), GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0003700 [transcription factor activity]	Conserved collinear gene
280000	281000	E=1.7e-41	At5g47230.1	MQL5.9, ethylene-responsive element-binding factor 5 (ERF5), GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0003700 [transcription factor activity]	Conserved collinear gene
280500	281500	E=5.6e-09	At5g47230.1	MQL5.9, ethylene-responsive element-binding factor 5 (ERF5), GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0003700 [transcription factor activity]	Conserved collinear gene
284000	285000	E=8.8e-	At4g23570.2	F9D16.40, phosphatase-related, GO:0000004 [biological_process	Inserted

		11		unknown] GO:0019005 [SCF ubiquitin ligase complex] GO:0008372 [cellular_component unknown] GO:0006511 [ubiquitin-dependent protein catabolism] GO:0005554 [molecular_func	fragment within model
284500	285500	E=1.2e-55	At4g23570.2	F9D16.40, phosphatase-related, GO:0000004 [biological_process unknown] GO:0019005 [SCF ubiquitin ligase complex] GO:0008372 [cellular_component unknown] GO:0006511 [ubiquitin-dependent protein catabolism] GO:0005554 [molecular_func	Inserted fragment within model
285000	286000	E=1.2e-38	At4g23570.2	F9D16.40, phosphatase-related, GO:0000004 [biological_process unknown] GO:0019005 [SCF ubiquitin ligase complex] GO:0008372 [cellular_component unknown] GO:0006511 [ubiquitin-dependent protein catabolism] GO:0005554 [molecular_func	Inserted fragment within model

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Start	**Stop**	**Score**	**BLASTn hit**	**Description**	**Classification**
2000	3000	E=7.5e-08	At1g62760.1	F23N19.12, invertase/pectin methylesterase inhibitor family protein, GO:0046910 [pectinesterase inhibitor activity]	Predicted transposon
4500	5500	E=6.9e-06	At1g25886.1	F14G11.4, Ulp1 protease family protein, GO:0008234 [cysteine-type peptidase activity] GO:0006508 [proteolysis and peptidolysis]	Inserted fragment within model
5000	6000	E=6.9e-06	At1g25886.1	F14G11.4, Ulp1 protease family protein, GO:0008234 [cysteine-type peptidase activity] GO:0006508 [proteolysis and peptidolysis]	Inserted fragment within model
12000	13000	E=2.4e-26	At4g17170.1	FCAALL.365, Rab2-like GTP-binding protein (RAB2), GO:0003924 [GTPase activity] GO:0005525 [GTP binding]	Conserved collinear gene
12500	13500	E=1.7e-81	At4g17170.1	FCAALL.365, Rab2-like GTP-binding protein (RAB2), GO:0003924 [GTPase activity] GO:0005525 [GTP binding]	Conserved collinear gene
13000	14000	E=3.2e-69	At4g17170.1	FCAALL.365, Rab2-like GTP-binding protein (RAB2), GO:0003924 [GTPase activity] GO:0005525 [GTP binding]	Conserved collinear gene
13500	14500	E=2.5e-30	At4g17170.1	FCAALL.365, Rab2-like GTP-binding protein (RAB2), GO:0003924 [GTPase activity] GO:0005525 [GTP binding]	Conserved collinear gene
15500	16500	E=2.9e-73	At4g17210.1	FCAALL.382, myosin heavy chain-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
16000	17000	E=2.1e-144	At4g17210.1	FCAALL.382, myosin heavy chain-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
16500	17500	E=2.3e-130	At4g17210.1	FCAALL.382, myosin heavy chain-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
17000	18000	E=2.6e-87	At4g17210.1	FCAALL.382, myosin heavy chain-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
17500	18500	E=4.4e-25	At4g17210.1	FCAALL.382, myosin heavy chain-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene

18000	19000	E=5.7e-32	At4g06599.1	T11G11.4, ubiquitin family protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
19500	20500	E=1.1e-62	At4g17215.1	FCAALL.231, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
20000	21000	E=6.9e-55	At4g17215.1	FCAALL.231, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
20500	21500	E=3.0e-43	At4g17220.1	FCAALL.385, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
21000	22000	E=2.7e-97	At4g17220.1	FCAALL.385, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
21500	22500	E=1.0e-107	At4g17220.1	FCAALL.385, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
22000	23000	E=1.2e-87	At4g17220.1	FCAALL.385, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
22500	23500	E=7.6e-33	At4g17220.1	FCAALL.385, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
24500	25500	E=2.2e-47	At4g17250.1	FCAALL.204, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
25000	26000	E=2.9e-123	At4g17250.1	FCAALL.204, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
25500	26500	E=2.9e-123	At4g17250.1	FCAALL.204, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
26000	27000	E=3.7e-104	At5g47580.1	MNJ7.17, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
26500	27500	E=6.7e-91	At5g47580.1	MNJ7.17, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
27000	28000	E=3.0e-26	At5g47580.1	MNJ7.17, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
28000	29000	E=2.1e-73	At4g17260.1	FCAALL.172, L-lactate dehydrogenase, putative, GO:0004457 [lactate dehydrogenase activity]	Conserved collinear gene
28500	29500	E=2.4e-90	At4g17260.1	FCAALL.172, L-lactate dehydrogenase, putative, GO:0004457 [lactate dehydrogenase activity]	Conserved collinear gene
29000	30000	E=1.1e-73	At4g17260.1	FCAALL.172, L-lactate dehydrogenase, putative, GO:0004457 [lactate dehydrogenase activity]	Conserved collinear gene
29500	30500	E=3.9e-12	At4g17260.1	FCAALL.172, L-lactate dehydrogenase, putative, GO:0004457 [lactate dehydrogenase activity]	Conserved collinear gene
32000	33000	E=1.7e-33	At4g17270.1	FCAALL.22, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
32500	33500	E=1.2e-	At4g17270.1	FCAALL.22, Mo25 family protein, GO:0005554 [molecular_function	Conserved

		52		unknown]	collinear gene
33000	34000	E=1.4e-33	At4g17270.1	FCAALL.22, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
33500	34500	E=7.0e-27	At4g17270.1	FCAALL.22, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
34000	35000	E=6.2e-13	At4g17270.1	FCAALL.22, Mo25 family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
35500	36500	E=2.3e-45	At4g17350.1	FCAALL.415, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
36000	37000	E=1.7e-77	At5g47440.1	MNJ7.2, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
36500	37500	E=1.2e-82	At5g47440.1	MNJ7.2, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
37000	38000	E=4.2e-51	At4g17350.1	FCAALL.415, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
37500	38500	E=4.9e-82	At4g17370.1	FCAALL.420, oxidoreductase family protein, GO:0008152 [metabolism] GO:0006118 [electron transport] GO:0016491 [oxidoreductase activity]	Conserved collinear gene
38000	39000	E=2.6e-104	At4g17370.1	FCAALL.420, oxidoreductase family protein, GO:0008152 [metabolism] GO:0006118 [electron transport] GO:0016491 [oxidoreductase activity]	Conserved collinear gene
38500	39500	E=1.5e-57	At4g17370.1	FCAALL.420, oxidoreductase family protein, GO:0008152 [metabolism] GO:0006118 [electron transport] GO:0016491 [oxidoreductase activity]	Conserved collinear gene
39000	40000	E=1.1e-31	At4g17370.1	FCAALL.420, oxidoreductase family protein, GO:0008152 [metabolism] GO:0006118 [electron transport] GO:0016491 [oxidoreductase activity]	Conserved collinear gene
40000	41000	E=2.6e-44	At4g17390.1	FCAALL.32, 60S ribosomal protein L15 (RPL15B), GO:0005840 [ribosome] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Conserved collinear gene
40500	41500	E=8.2e-83	At4g17390.1	FCAALL.32, 60S ribosomal protein L15 (RPL15B), GO:0005840 [ribosome] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Conserved collinear gene
41000	42000	E=3.5e-53	At4g17390.1	FCAALL.32, 60S ribosomal protein L15 (RPL15B), GO:0005840 [ribosome] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Conserved collinear gene
41500	42500	E=2.3e-29	At4g17390.1	FCAALL.32, 60S ribosomal protein L15 (RPL15B), GO:0005840 [ribosome] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Conserved collinear gene
43500	44500	E=2.0e-08	At3g44790.1	T32N15.4, meprin and TRAF homology domain-containing protein / MATH domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
44000	45000	E=5.2e-19	At1g31370.1	T19E23.22, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment

					within model
44500	45500	E=6.5e-57	At3g58410.1	F9D24.320, meprin and TRAF homology domain-containing protein / MATH domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
45000	46000	E=1.3e-50	At4g17430.1	FCAALL.1, expressed protein, GO:0005554 [molecular_function unknown]	Additional collinear gene fragment
45500	46500	E=6.6e-49	At4g17430.1	FCAALL.1, expressed protein, GO:0005554 [molecular_function unknown]	Additional collinear gene fragment
46500	47500	E=2.0e-36	At5g47390.1	MQL5.25, myb family transcription factor, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
47000	48000	E=4.0e-92	At5g47390.1	MQL5.25, myb family transcription factor, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
47500	48500	E=1.9e-59	At5g47390.1	MQL5.25, myb family transcription factor, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
57500	58500	E=2.8e-24	At4g17440.1	FCAALL.6, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
58000	59000	E=2.8e-24	At4g17440.1	FCAALL.6, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
59000	60000	E=1.4e-15	At3g52110.1	F4F15.220, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
59500	60500	E=1.4e-15	At3g52110.1	F4F15.220, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
60500	61500	E=1.4e-07	At1g18900.2	F14D16.2, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
61000	62000	E=1.4e-07	At1g18900.2	F14D16.2, pentatricopeptide (PPR) repeat-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
68500	69500	E=3.0e-41	At4g17460.1	FCAALL.65, homeobox-leucine zipper protein 1 (HAT1) / HD-ZIP protein 1, GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene

69000	70000	E=1.3e-94	At4g17460.1	FCAALL.65, homeobox-leucine zipper protein 1 (HAT1) / HD-ZIP protein 1, GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
69500	70500	E=1.2e-65	At4g17460.1	FCAALL.65, homeobox-leucine zipper protein 1 (HAT1) / HD-ZIP protein 1, GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
70000	71000	E=1.1e-08	At4g17460.1	FCAALL.65, homeobox-leucine zipper protein 1 (HAT1) / HD-ZIP protein 1, GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
70500	71500	E=1.6e-13	At4g17483.1	FCAALL.16, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
71000	72000	E=3.7e-32	At4g17483.1	FCAALL.16, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
71500	72500	E=1.2e-63	At4g17483.1	FCAALL.16, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
72000	73000	E=2.8e-42	At4g17483.1	FCAALL.16, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
72500	73500	E=2.8e-09	At4g17483.1	FCAALL.16, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
74500	75500	E=2.2e-45	At4g17486.1	FCAALL.234, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
75000	76000	E=5.8e-75	At4g17486.1	FCAALL.234, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
75500	76500	E=1.2e-33	At5g47310.1	MQL5.17, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
76000	77000	E=7.3e-08	At4g17510.1	FCAALL.31, ubiquitin carboxyl-terminal hydrolase, putative / ubiquitin thiolesterase, putative, GO:0005622 [intracellular] GO:0004221 [ubiquitin thiolesterase activity] GO:0006511 [ubiquitin-dependent protein catabolism]	Conserved collinear gene
76500	77500	E=4.1e-38	At4g17510.1	FCAALL.31, ubiquitin carboxyl-terminal hydrolase, putative / ubiquitin thiolesterase, putative, GO:0005622 [intracellular] GO:0004221 [ubiquitin thiolesterase activity] GO:0006511 [ubiquitin-dependent protein catabolism]	Conserved collinear gene
77000	78000	E=2.6e-60	At4g17510.1	FCAALL.31, ubiquitin carboxyl-terminal hydrolase, putative / ubiquitin thiolesterase, putative, GO:0005622 [intracellular] GO:0004221 [ubiquitin thiolesterase activity] GO:0006511 [ubiquitin-dependent protein catabolism]	Conserved collinear gene
77500	78500	E=1.5e-	At4g17510.1	FCAALL.31, ubiquitin carboxyl-terminal hydrolase, putative / ubiquitin	Conserved

		47		thiolesterase, putative, GO:0005622 [intracellular] GO:0004221 [ubiquitin thiolesterase activity] GO:0006511 [ubiquitin-dependent protein catabolism]	collinear gene
78000	79000	E=3.2e-14	At4g17520.1	FCAALL.142, nuclear RNA-binding protein, putative, GO:0003723 [RNA binding]	Conserved collinear gene
78500	79500	E=5.7e-47	At4g17520.1	FCAALL.142, nuclear RNA-binding protein, putative, GO:0003723 [RNA binding]	Conserved collinear gene
79000	80000	E=6.8e-51	At4g17520.1	FCAALL.142, nuclear RNA-binding protein, putative, GO:0003723 [RNA binding]	Conserved collinear gene
79500	80500	E=6.5e-58	At4g17520.1	FCAALL.142, nuclear RNA-binding protein, putative, GO:0003723 [RNA binding]	Conserved collinear gene
80000	81000	E=1.9e-31	At4g17520.1	FCAALL.142, nuclear RNA-binding protein, putative, GO:0003723 [RNA binding]	Conserved collinear gene
80500	81500	E=2.4e-41	At4g17530.1	FCAALL.87, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
81000	82000	E=1.4e-59	At4g17530.1	FCAALL.87, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
81500	82500	E=1.9e-24	At4g17530.1	FCAALL.87, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
84500	85500	E=8.3e-29	At4g17550.1	FCAALL.41, transporter-related, GO:0005351 [sugar porter activity] GO:0008643 [carbohydrate transport]	Conserved collinear gene
85000	86000	E=1.6e-104	At4g17550.1	FCAALL.41, transporter-related, GO:0005351 [sugar porter activity] GO:0008643 [carbohydrate transport]	Conserved collinear gene
85500	86500	E=1.7e-134	At4g17550.1	FCAALL.41, transporter-related, GO:0005351 [sugar porter activity] GO:0008643 [carbohydrate transport]	Conserved collinear gene
86000	87000	E=4.1e-107	At4g17550.1	FCAALL.41, transporter-related, GO:0005351 [sugar porter activity] GO:0008643 [carbohydrate transport]	Conserved collinear gene
86500	87500	E=1.2e-34	At4g17550.1	FCAALL.41, transporter-related, GO:0005351 [sugar porter activity] GO:0008643 [carbohydrate transport]	Conserved collinear gene
92500	93500	E=7.3e-37	At5g47110.1	K14A3.6, lil3 protein, putative, GO:0009765 [photosynthesis light harvesting] GO:0005554 [molecular_function unknown]	Conserved collinear gene
93000	94000	E=6.1e-72	At5g47110.1	K14A3.6, lil3 protein, putative, GO:0009765 [photosynthesis light harvesting] GO:0005554 [molecular_function unknown]	Conserved collinear gene
93500	94500	E=1.7e-34	At4g17600.1	FCAALL.30, lil3 protein, GO:0005554 [molecular_function unknown] GO:0003700 [transcription factor activity]	Conserved collinear gene
94000	95000	E=4.5e-10	At1g45165.1	F27F5.24, Expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
98000	99000	E=4.3e-21	At4g17615.1	FCAALL.122, calcineurin B-like protein 1 (CBL1), GO:0006970 [response to osmotic stress] GO:0019722 [calcium-mediated signaling]	Conserved collinear gene

				GO:0005509 [calcium ion binding] GO:0005886 [plasma membrane]	
98500	99500	E=2.3e-19	At4g17615.1	FCAALL.122, calcineurin B-like protein 1 (CBL1), GO:0006970 [response to osmotic stress] GO:0019722 [calcium-mediated signaling] GO:0005509 [calcium ion binding] GO:0005886 [plasma membrane]	Conserved collinear gene
99000	100000	E=4.1e-41	At4g17615.2	FCAALL.122, calcineurin B-like protein 1 (CBL1), GO:0006970 [response to osmotic stress] GO:0019722 [calcium-mediated signaling] GO:0005509 [calcium ion binding] GO:0005886 [plasma membrane]	Conserved collinear gene
99500	100500	E=1.4e-50	At4g17615.1	FCAALL.122, calcineurin B-like protein 1 (CBL1), GO:0006970 [response to osmotic stress] GO:0019722 [calcium-mediated signaling] GO:0005509 [calcium ion binding] GO:0005886 [plasma membrane]	Conserved collinear gene
100000	101000	E=1.7e-17	At4g17615.1	FCAALL.122, calcineurin B-like protein 1 (CBL1), GO:0006970 [response to osmotic stress] GO:0019722 [calcium-mediated signaling] GO:0005509 [calcium ion binding] GO:0005886 [plasma membrane]	Conserved collinear gene
102500	103500	E=6.2e-11	At4g17620.1	FCAALL.74, glycine-rich protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
103000	104000	E=6.3e-22	At4g17620.1	FCAALL.74, glycine-rich protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
103500	104500	E=2.9e-52	At4g17620.1	FCAALL.74, glycine-rich protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
104000	105000	E=9.3e-46	At4g17620.1	FCAALL.74, glycine-rich protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
104500	105500	E=1.1e-57	At4g17620.1	FCAALL.74, glycine-rich protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
105000	106000	E=1.6e-46	At4g17620.1	FCAALL.74, glycine-rich protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
105500	106500	E=2.3e-47	At4g17620.1	FCAALL.74, glycine-rich protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
106000	107000	E=2.6e-25	At4g17640.1	FCAALL.14, casein kinase II beta chain, putative, GO:0005956 [protein kinase CK2 complex] GO:0008605 [protein kinase CK2 regulator activity]	Conserved collinear gene
106500	107500	E=1.7e-68	At4g17640.1	FCAALL.14, casein kinase II beta chain, putative, GO:0005956 [protein kinase CK2 complex] GO:0008605 [protein kinase CK2 regulator activity]	Conserved collinear gene
107000	108000	E=2.3e-71	At4g17640.1	FCAALL.14, casein kinase II beta chain, putative, GO:0005956 [protein kinase CK2 complex] GO:0008605 [protein kinase CK2 regulator activity]	Conserved collinear gene
107500	108500	E=1.3e-43	At5g47080.1	MQD22.23, casein kinase II beta chain, putative, GO:0005956 [protein kinase CK2 complex] GO:0008605 [protein kinase CK2 regulator activity]	Conserved collinear gene
108000	109000	E=2.2e-32	At4g17660.1	FCAALL.77, protein kinase, putative, GO:0016301 [kinase activity]	Additional collinear gene

					fragment
108500	109500	E=3.2e-54	At4g17660.1	FCAALL.77, protein kinase, putative, GO:0016301 [kinase activity]	Additional collinear gene fragment
109000	110000	E=3.0e-16	At4g17660.1	FCAALL.77, protein kinase, putative, GO:0016301 [kinase activity]	Additional collinear gene fragment
110000	111000	E=2.9e-17	At4g17660.1	FCAALL.77, protein kinase, putative, GO:0016301 [kinase activity]	Additional collinear gene fragment
110500	111500	E=5.6e-17	At4g17660.1	FCAALL.77, protein kinase, putative, GO:0016301 [kinase activity]	Additional collinear gene fragment
111000	112000	E=8.4e-29	At4g17670.1	FCAALL.414, senescence-associated protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
111500	112500	E=8.8e-69	At4g17670.1	FCAALL.414, senescence-associated protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
112000	113000	E=4.0e-31	At4g17670.1	FCAALL.414, senescence-associated protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
126500	127500	E=1.2e-11	At2g31700.1	T9H9.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
127000	128000	E=1.4e-07	At2g31700.1	T9H9.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
131000	132000	E=5.1e-41	At4g17680.1	FCAALL.78, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
131500	132500	E=2.7e-82	At4g17680.1	FCAALL.78, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
132000	133000	E=1.3e-34	At4g17680.1	FCAALL.78, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
138500	139500	E=4.0e-63	At4g17690.1	FCAALL.96, peroxidase, putative, GO:0004601 [peroxidase activity]	Conserved collinear gene
139000	140000	E=7.9e-138	At4g17690.1	FCAALL.96, peroxidase, putative, GO:0004601 [peroxidase activity]	Conserved collinear gene
139500	140500	E=1.7e-84	At4g17690.1	FCAALL.96, peroxidase, putative, GO:0004601 [peroxidase activity]	Conserved collinear gene
140000	141000	E=2.6e-06	At4g17690.1	FCAALL.96, peroxidase, putative, GO:0004601 [peroxidase activity]	Conserved collinear gene

145500	146500	E=1.0e-11	At2g31700.1	T9H9.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
146000	147000	E=1.0e-11	At2g31700.1	T9H9.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
146500	147500	E=6.1e-06	At2g31700.1	T9H9.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
163500	164500	E=1.5e-40	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Predicted transposon
164000	165000	E=2.6e-43	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Predicted transposon
173000	174000	E=1.3e-07	At3g28770.1	T19N8.6, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
180000	181000	E=1.1e-41	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	fragment only
180500	181500	E=5.3e-94	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	fragment only
181000	182000	E=7.7e-48	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	fragment only
187000	188000	E=2.8e-43	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	fragment only
187500	188500	E=2.8e-43	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	fragment only
188000	189000	E=2.8e-43	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	fragment only
194000	195000	E=1.6e-68	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	fragment only
194500	195500	E=5.3e-94	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	fragment only
195000	196000	E=3.4e-21	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	fragment only
199000	200000	E=3.3e-08	At3g28770.1	T19N8.6, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
209500	210500	E=1.1e-	At3g28770.1	T19N8.6, expressed protein, GO:0005554 [molecular_function	Inserted

		07		unknown]	fragment within model
217500	218500	E=1.2e-29	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	fragment only
218000	219000	E=5.3e-94	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	fragment only
218500	219500	E=6.7e-60	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	fragment only
224500	225500	E=2.8e-43	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	Conserved collinear gene
225000	226000	E=1.1e-60	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	Conserved collinear gene
225500	226500	E=3.7e-41	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	Conserved collinear gene
226000	227000	E=2.4e-10	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	Conserved collinear gene
232000	233000	E=2.4e-60	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	fragment only
232500	233500	E=7.8e-116	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	fragment only
233000	234000	E=1.5e-53	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	fragment only
233500	234500	E=3.5e-12	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	fragment only
234500	235500	E=1.5e-27	At5g46860.1	MSD23.9, syntaxin 22 (SYP22) (VAM3), GO:0030140 [trans-Golgi network transport vesicle] GO:0005770 [late endosome] GO:0006944 [membrane fusion] GO:0009705 [vacuolar membrane (sensu Magnoliophyta)] GO:0006886 [intracellular protein transp	Conserved collinear gene
235000	236000	E=9.9e-54	At5g46860.1	MSD23.9, syntaxin 22 (SYP22) (VAM3), GO:0030140 [trans-Golgi network transport vesicle] GO:0005770 [late endosome] GO:0006944 [membrane fusion] GO:0009705 [vacuolar membrane (sensu Magnoliophyta)] GO:0006886 [intracellular protein transp	Conserved collinear gene
235500	236500	E=2.6e-41	At4g17730.1	FCAALL.117, syntaxin 23 (SYP23) / PEP12-like protein, GO:0006944 [membrane fusion] GO:0006886 [intracellular protein transport] GO:0005486 [t-SNARE activity]	Conserved collinear gene
236000	237000	E=6.7e-33	At4g17740.2	FCAALL.169, C-terminal processing protease, putative, GO:0009543 [thylakoid lumen (sensu Viridiplantae)] GO:0007242 [intracellular signaling cascade]	Conserved collinear gene
236500	237500	E=2.0e-53	At4g17740.2	FCAALL.169, C-terminal processing protease, putative, GO:0009543 [thylakoid lumen (sensu Viridiplantae)] GO:0007242 [intracellular signaling cascade]	Conserved collinear gene

237000	238000	E=2.2e-48	At4g17740.2	FCAALL.169, C-terminal processing protease, putative, GO:0009543 [thylakoid lumen (sensu Viridiplantae)] GO:0007242 [intracellular signaling cascade]	Conserved collinear gene
237500	238500	E=5.9e-85	At4g17740.1	FCAALL.169, C-terminal processing protease, putative, GO:0009543 [thylakoid lumen (sensu Viridiplantae)] GO:0007242 [intracellular signaling cascade]	Conserved collinear gene
238000	239000	E=1.8e-81	At4g17740.2	FCAALL.169, C-terminal processing protease, putative, GO:0009543 [thylakoid lumen (sensu Viridiplantae)] GO:0007242 [intracellular signaling cascade]	Conserved collinear gene
238500	239500	E=9.2e-50	At4g17740.1	FCAALL.169, C-terminal processing protease, putative, GO:0009543 [thylakoid lumen (sensu Viridiplantae)] GO:0007242 [intracellular signaling cascade]	Conserved collinear gene
239000	240000	E=1.3e-06	At4g17740.1	FCAALL.169, C-terminal processing protease, putative, GO:0009543 [thylakoid lumen (sensu Viridiplantae)] GO:0007242 [intracellular signaling cascade]	Conserved collinear gene
240000	241000	E=1.1e-38	At5g10240.1	F18D22.10, asparagine synthetase 3 (ASN3), GO:0006529 [asparagine biosynthesis] GO:0004066 [asparagine synthase (glutamine-hydrolyzing) activity]	Inserted fragment within model
240500	241500	E=1.6e-40	At5g10240.1	F18D22.10, asparagine synthetase 3 (ASN3), GO:0006529 [asparagine biosynthesis] GO:0004066 [asparagine synthase (glutamine-hydrolyzing) activity]	Inserted fragment within model
242500	243500	E=1.6e-08	At3g43460.1	T18D12.30, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
243000	244000	E=1.5e-15	At3g43460.1	T18D12.30, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
246000	247000	E=2.9e-08	At3g42690.1	T12K4.140, Ulp1 protease family protein, GO:0008234 [cysteine-type peptidase activity] GO:0006508 [proteolysis and peptidolysis]	Inserted fragment within model
254500	255500	E=1.2e-12	At4g17760.1	FCAALL.108, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
255000	256000	E=2.2e-44	At4g17760.1	FCAALL.108, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
255500	256500	E=2.9e-70	At4g17760.1	FCAALL.108, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
256000	257000	E=3.5e-72	At4g17760.1	FCAALL.108, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
256500	257500	E=2.6e-20	At4g17760.1	FCAALL.108, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
274500	275500	E=9.7e-	At4g17770.1	FCAALL.9, glycosyl transferase family 20 protein / trehalose-	Conserved

		42		phosphatase family protein, GO:0005992 [trehalose biosynthesis] GO:0004805 [trehalose-phosphatase activity] GO:0016757 [transferase activity, transferring glycosyl groups] GO:0003825 [alpha,alpha-trehalose-phosphate synthase (UD	collinear gene
275000	276000	E=1.7e-119	At4g17770.1	FCAALL.9, glycosyl transferase family 20 protein / trehalose-phosphatase family protein, GO:0005992 [trehalose biosynthesis] GO:0004805 [trehalose-phosphatase activity] GO:0016757 [transferase activity, transferring glycosyl groups] GO:0003825 [alpha,alpha-trehalose-phosphate synthase (UD	Conserved collinear gene
275500	276500	E=9.3e-152	At4g17770.1	FCAALL.9, glycosyl transferase family 20 protein / trehalose-phosphatase family protein, GO:0005992 [trehalose biosynthesis] GO:0004805 [trehalose-phosphatase activity] GO:0016757 [transferase activity, transferring glycosyl groups] GO:0003825 [alpha,alpha-trehalose-phosphate synthase (UD	Conserved collinear gene
276000	277000	E=5.5e-159	At4g17770.1	FCAALL.9, glycosyl transferase family 20 protein / trehalose-phosphatase family protein, GO:0005992 [trehalose biosynthesis] GO:0004805 [trehalose-phosphatase activity] GO:0016757 [transferase activity, transferring glycosyl groups] GO:0003825 [alpha,alpha-trehalose-phosphate synthase (UD	Conserved collinear gene
276500	277500	E=6.0e-108	At4g17770.1	FCAALL.9, glycosyl transferase family 20 protein / trehalose-phosphatase family protein, GO:0005992 [trehalose biosynthesis] GO:0004805 [trehalose-phosphatase activity] GO:0016757 [transferase activity, transferring glycosyl groups] GO:0003825 [alpha,alpha-trehalose-phosphate synthase (UD	Conserved collinear gene
277000	278000	E=3.5e-74	At4g17770.1	FCAALL.9, glycosyl transferase family 20 protein / trehalose-phosphatase family protein, GO:0005992 [trehalose biosynthesis] GO:0004805 [trehalose-phosphatase activity] GO:0016757 [transferase activity, transferring glycosyl groups] GO:0003825 [alpha,alpha-trehalose-phosphate synthase (UD	Conserved collinear gene
277500	278500	E=2.0e-97	At4g17770.1	FCAALL.9, glycosyl transferase family 20 protein / trehalose-phosphatase family protein, GO:0005992 [trehalose biosynthesis] GO:0004805 [trehalose-phosphatase activity] GO:0016757 [transferase activity, transferring glycosyl groups] GO:0003825 [alpha,alpha-trehalose-phosphate synthase (UD	Conserved collinear gene
278000	279000	E=2.2e-46	At2g43440.1	T1O24.18, F-box family protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
278500	279500	E=4.8e-86	At2g43260.1	F14B2.20, F-box family protein / S locus-related, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
279000	280000	E=5.6e-	At4g17780.1	FCAALL.161, F-box family protein, GO:0005554 [molecular_function	Conserved

		62		unknown]	collinear gene
279500	280500	E=6.7e-14	At4g17785.1	FCAALL.109, myb family transcription factor (MYB39), GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
280000	281000	E=7.0e-83	At4g17785.1	FCAALL.109, myb family transcription factor (MYB39), GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
280500	281500	E=2.1e-85	At4g17785.1	FCAALL.109, myb family transcription factor (MYB39), GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
281000	282000	E=4.0e-66	At4g17785.1	FCAALL.109, myb family transcription factor (MYB39), GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
281500	282500	E=1.6e-44	At4g17785.1	FCAALL.109, myb family transcription factor (MYB39), GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
290500	291500	E=9.5e-10	At2g07070.1	T25N22.2, AT hook motif-containing protein, GO:0003677 [DNA binding]	Inserted fragment within model
291000	292000	E=9.5e-10	At2g07070.1	T25N22.2, AT hook motif-containing protein, GO:0003677 [DNA binding]	Inserted fragment within model
292000	293000	E=2.0e-22	At2g06820.1	T14A4.2, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
292500	293500	E=4.4e-27	At2g06820.1	T14A4.2, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
300500	301500	E=8.9e-32	At4g17790.1	FCAALL.62, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
301000	302000	E=2.8e-52	At4g17790.1	FCAALL.62, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
301500	302500	E=1.5e-14	At4g17790.1	FCAALL.62, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
305000	306000	E=2.7e-09	At3g29220.1	MXO21.7, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
305500	306500	E=5.4e-07	At3g29220.1	MXO21.7, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene

					models
307500	308500	E=4.6e-30	At4g17790.1	FCAALL.62, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
308000	309000	E=4.6e-30	At4g17790.1	FCAALL.62, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
312000	313000	E=5.9e-96	At4g17800.1	FCAALL.129, DNA-binding protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
312500	313500	E=4.2e-158	At4g17800.1	FCAALL.129, DNA-binding protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
313000	314000	E=4.8e-61	At4g17800.1	FCAALL.129, DNA-binding protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
325500	326500	E=2.2e-07	At2g31700.1	T9H9.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
326000	327000	E=2.2e-07	At2g31700.1	T9H9.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
328500	329500	E=3.1e-54	At5g32621.1	F15I15.2, expressed protein, GO:0005554 [molecular_function unknown] GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown]	Inserted fragment within model
329000	330000	E=6.9e-103	At3g15310.1	K7L4.11, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
329500	330500	E=6.4e-48	At3g15310.1	K7L4.11, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
331000	332000	E=3.9e-18	At3g15320.1	K7L4.12, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
331500	332500	E=1.4e-23	At3g15320.1	K7L4.12, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
334000	335000	E=3.6e-59	At4g17810.1	FCAALL.130, zinc finger (C2H2 type) family protein, GO:0003676 [nucleic acid binding] GO:0008270 [zinc ion binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
334500	335500	E=3.9e-82	At4g17810.1	FCAALL.130, zinc finger (C2H2 type) family protein, GO:0003676 [nucleic acid binding] GO:0008270 [zinc ion binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
335000	336000	E=3.1e-	At4g17810.1	FCAALL.130, zinc finger (C2H2 type) family protein, GO:0003676	Conserved

		20		[nucleic acid binding] GO:0008270 [zinc ion binding] GO:0003700 [transcription factor activity]	collinear gene
343500	344500	E=4.9e-48	At4g17830.1	FCAALL.133, peptidase M20/M25/M40 family protein, GO:0008237 [metallopeptidase activity] GO:0006508 [proteolysis and peptidolysis]	Conserved collinear gene
344000	345000	E=2.3e-109	At4g17830.1	FCAALL.133, peptidase M20/M25/M40 family protein, GO:0008237 [metallopeptidase activity] GO:0006508 [proteolysis and peptidolysis]	Conserved collinear gene
344500	345500	E=1.5e-79	At4g17830.1	FCAALL.133, peptidase M20/M25/M40 family protein, GO:0008237 [metallopeptidase activity] GO:0006508 [proteolysis and peptidolysis]	Conserved collinear gene
345000	346000	E=1.8e-84	At4g17830.1	FCAALL.133, peptidase M20/M25/M40 family protein, GO:0008237 [metallopeptidase activity] GO:0006508 [proteolysis and peptidolysis]	Conserved collinear gene
345500	346500	E=3.7e-60	At4g17830.1	FCAALL.133, peptidase M20/M25/M40 family protein, GO:0008237 [metallopeptidase activity] GO:0006508 [proteolysis and peptidolysis]	Conserved collinear gene
346000	347000	E=2.2e-53	At4g17840.1	T6K21.20, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
346500	347500	E=1.2e-68	At4g17840.1	T6K21.20, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
347000	348000	E=1.3e-79	At4g17840.1	T6K21.20, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
347500	348500	E=1.7e-26	At4g17840.1	T6K21.20, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
348000	349000	E=6.1e-63	At4g17870.1	T6K21.50, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
348500	349500	E=5.7e-86	At4g17870.1	T6K21.50, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
349000	350000	E=4.0e-18	At4g17870.1	T6K21.50, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene

CONTIG E

Start	**Stop**	**Score**	**BLASTn hit**	**Description**	**Classification**
0	1000	E=4.5e-73	At4g17380.1	FCAALL.423, DNA mismatch repair MutS family protein, GO:0005524 [ATP binding] GO:0006298 [mismatch repair] GO:0003684 [damaged DNA binding]	fragment only
500	1500	E=1.3e-33	At4g17380.1	FCAALL.423, DNA mismatch repair MutS family protein, GO:0005524 [ATP binding] GO:0006298 [mismatch repair] GO:0003684 [damaged DNA binding]	fragment only
1000	2000	E=4.5e-72	At4g17390.1	FCAALL.32, 60S ribosomal protein L15 (RPL15B), GO:0005840 [ribosome] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Additional collinear gene fragment
1500	2500	E=6.3e-104	At4g17390.1	FCAALL.32, 60S ribosomal protein L15 (RPL15B), GO:0005840 [ribosome] GO:0006412 [protein biosynthesis] GO:0003735 [structural	Additional collinear gene

				constituent of ribosome]	fragment
2000	3000	E=3.5e-40	At4g17390.1	FCAALL.32, 60S ribosomal protein L15 (RPL15B), GO:0005840 [ribosome] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Additional collinear gene fragment
6000	7000	E=3.2e-19	At1g02230.1	T7I23.19, no apical meristem (NAM) family protein, GO:0007275 [development] GO:0005554 [molecular_function unknown] GO:0003700 [transcription factor activity]	Inserted fragment outside gene models
6500	7500	E=2.9e-26	At1g26860.1	T2P11.5, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
7000	8000	E=6.2e-11	At1g26860.1	T2P11.5, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
23000	24000	E=1.5e-42	At4g17380.1	FCAALL.423, DNA mismatch repair MutS family protein, GO:0005524 [ATP binding] GO:0006298 [mismatch repair] GO:0003684 [damaged DNA binding]	Conserved collinear gene
23500	24500	E=2.6e-64	At4g17380.1	FCAALL.423, DNA mismatch repair MutS family protein, GO:0005524 [ATP binding] GO:0006298 [mismatch repair] GO:0003684 [damaged DNA binding]	Conserved collinear gene
24000	25000	E=5.9e-13	At4g17380.1	FCAALL.423, DNA mismatch repair MutS family protein, GO:0005524 [ATP binding] GO:0006298 [mismatch repair] GO:0003684 [damaged DNA binding]	Conserved collinear gene
34500	35500	E=2.4e-38	At3g29785.1	T26G12.25, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
35000	36000	E=2.4e-38	At3g29785.1	T26G12.25, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
37000	38000	E=3.8e-10	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
37500	38500	E=3.8e-10	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
40000	41000	E=1.8e-16	At1g55790.1	F14J16.3, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
40500	41500	E=6.8e-14	At1g05160.1	YUP8H12.23, ent-kaurenoic acid hydroxylase (KAO1) / cytochrome P450 88A3, putative (CYP88A3), GO:0015034 [cytochrome P450 activity] GO:0019825 [oxygen binding]	Inserted fragment outside gene models
41000	42000	E=3.5e-13	At1g05160.1	YUP8H12.23, ent-kaurenoic acid hydroxylase (KAO1) / cytochrome P450 88A3, putative (CYP88A3), GO:0015034 [cytochrome P450	Inserted fragment

				activity] GO:0019825 [oxygen binding]	outside gene models
48500	49500	E=4.5e-23	At2g27780.1	F15K20.12, expressed protein, GO:0005554 [molecular_function unknown]	Predicted transposon
49000	50000	E=3.6e-40	At2g27780.1	F15K20.12, expressed protein, GO:0005554 [molecular_function unknown]	Predicted transposon
49500	50500	E=1.1e-19	At2g13640.1	T10F5.18, Golgi GDP mannose transporter (GONST1), GO:0005554 [molecular_function unknown]	Inserted fragment within model
50500	51500	E=9.6e-12	At1g14750.1	F10B6.15, cyclin, putative (SDS), GO:0000074 [regulation of cell cycle] GO:0004693 [cyclin-dependent protein kinase activity]	Inserted fragment outside gene models
51000	52000	E=9.6e-12	At1g14750.1	F10B6.15, cyclin, putative (SDS), GO:0000074 [regulation of cell cycle] GO:0004693 [cyclin-dependent protein kinase activity]	Inserted fragment outside gene models
52500	53500	E=4.7e-15	At5g63740.1	MBK5.22, zinc finger protein-related, GO:0005554 [molecular_function unknown]	Predicted transposon
53000	54000	E=2.2e-14	At5g63740.1	MBK5.22, zinc finger protein-related, GO:0005554 [molecular_function unknown]	Predicted transposon
61500	62500	E=1.6e-23	At2g27780.1	F15K20.12, expressed protein, GO:0005554 [molecular_function unknown]	Predicted transposon
62000	63000	E=8.1e-43	At2g27780.1	F15K20.12, expressed protein, GO:0005554 [molecular_function unknown]	Predicted transposon
62500	63500	E=1.5e-18	At2g13640.1	T10F5.18, Golgi GDP mannose transporter (GONST1), GO:0005554 [molecular_function unknown]	Inserted fragment within model
63500	64500	E=9.6e-12	At1g14750.1	F10B6.15, cyclin, putative (SDS), GO:0000074 [regulation of cell cycle] GO:0004693 [cyclin-dependent protein kinase activity]	Inserted fragment outside gene models
64000	65000	E=2.5e-09	At1g14750.1	F10B6.15, cyclin, putative (SDS), GO:0000074 [regulation of cell cycle] GO:0004693 [cyclin-dependent protein kinase activity]	Inserted fragment outside gene models
65500	66500	E=2.7e-08	At1g48400.1	F11A17.5, F-box family protein, GO:0005554 [molecular_function unknown]	Predicted transposon
66000	67000	E=6.9e-16	At5g63740.1	MBK5.22, zinc finger protein-related, GO:0005554 [molecular_function unknown]	Predicted transposon
73000	74000	E=3.1e-	At5g63740.1	MBK5.22, zinc finger protein-related, GO:0005554 [molecular_function	Inserted

		14		unknown]	fragment within model
73500	74500	E=6.9e-08	At5g63740.1	MBK5.22, zinc finger protein-related, GO:0005554 [molecular_function unknown]	Inserted fragment within model
86500	87500	E=1.7e-12	At5g47225.1	MQL5.8, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
87000	88000	E=4.7e-13	At5g47225.1	MQL5.8, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
90000	91000	E=3.7e-16	At3g30240.1	MIL15.14, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
90500	91500	E=1.6e-11	At3g30240.1	MIL15.14, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
98000	99000	E=5.7e-23	At2g07190.1	T25N22.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
101000	102000	E=9.1e-16	At3g43770.1	T28A8.60, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
101500	102500	E=2.6e-16	At3g43770.1	T28A8.60, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
106500	107500	E=1.1e-23	At1g21330.1	F24J8.25, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
107000	108000	E=2.4e-33	At3g24255.1	K13K6.3, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
107500	108500	E=8.5e-12	At3g24255.1	K13K6.3, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
110500	111500	E=6.8e-09	At5g33200.1	T29A4.10, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
111000	112000	E=6.8e-09	At5g33200.1	T29A4.10, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
116500	117500	E=3.8e-	At1g41860.1	F5A13.6, hypothetical protein, GO:0005554 [molecular_function	Predicted

		10		unknown]	transposon
135500	136500	E=9.3e-22	At4g31130.1	F6E21.50, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
136000	137000	E=5.4e-15	At4g31130.1	F6E21.50, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
143000	144000	E=3.9e-12	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
143500	144500	E=3.9e-12	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
145000	146000	E=4.2e-13	At2g20595.1	F23N11.19, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
145500	146500	E=4.2e-13	At2g20595.1	F23N11.19, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
146000	147000	E=3.4e-12	At3g43770.1	T28A8.60, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
146500	147500	E=1.6e-18	At3g43770.1	T28A8.60, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
147000	148000	E=9.4e-18	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
147500	148500	E=2.1e-27	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
148000	149000	E=1.8e-15	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
151500	152500	E=6.2e-09	At4g17483.1	FCAALL.16, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
152000	153000	E=2.0e-33	At4g17483.1	FCAALL.16, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
152500	153500	E=2.8e-66	At4g17470.1	FCAALL.11, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
153000	154000	E=2.9e-60	At4g17483.1	FCAALL.16, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
153500	154500	E=2.0e-08	At4g17483.1	FCAALL.16, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene

154000	155000	E=1.0e-37	At4g17486.1	FCAALL.234, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
154500	155500	E=5.6e-91	At4g17486.1	FCAALL.234, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
155000	156000	E=2.1e-50	At4g17486.1	FCAALL.234, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
155500	156500	E=4.4e-22	At4g17486.1	FCAALL.234, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
157000	158000	E=9.3e-19	At4g17490.1	FCAALL.120, ethylene-responsive element-binding protein, putative, GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
157500	158500	E=1.0e-55	At5g47230.1	MQL5.9, ethylene-responsive element-binding factor 5 (ERF5), GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0003700 [transcription factor activity]	Conserved collinear gene
158000	159000	E=5.5e-46	At4g17490.1	FCAALL.120, ethylene-responsive element-binding protein, putative, GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
158500	159500	E=6.8e-08	At4g17490.1	FCAALL.120, ethylene-responsive element-binding protein, putative, GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
165000	166000	E=2.9e-07	At4g11710.1	T5C23.140, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
165500	166500	E=3.9e-08	At4g11710.1	T5C23.140, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
166000	167000	E=5.4e-12	At1g43730.1	F2J6.21, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
166500	167500	E=6.5e-10	At1g43730.1	F2J6.21, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
183500	184500	E=2.1e-09	At4g17500.1	FCAALL.123, ethylene-responsive element-binding protein 1 (ERF1) / EREBP-2 protein, GO:0005643 [nuclear pore] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0003700 [transcription factor activity]	Conserved collinear gene
184000	185000	E=3.2e-63	At5g47220.1	MQL5.7, ethylene-responsive element-binding factor 2 (ERF2), GO:0003677 [DNA binding] GO:0045941 [positive regulation of transcription] GO:0006355 [regulation of transcription, DNA-dependent]	Conserved collinear gene

184500	185500	E=9.7e-51	At4g17500.1	GO:0016563 [transcriptional activator activity] GO:0008372 [cellular_ FCAALL.123, ethylene-responsive element-binding protein 1 (ERF1) / EREBP-2 protein, GO:0005643 [nuclear pore] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0016563 [transcriptional activator activity] GO:0003700 [transcription factor activity]	Conserved collinear gene
185500	186500	E=4.8e-06	At1g56660.1	F25P12.91, expressed protein, GO:0005554 [molecular_function unknown]	Predicted transposon
186500	187500	E=1.9e-24	At2g14570.1	T13P21.5, SWIM zinc finger family protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Predicted transposon
187000	188000	E=1.5e-11	At1g48290.1	F11A17.26, expressed protein, GO:0005554 [molecular_function unknown]	Predicted transposon
190000	191000	E=1.4e-11	At3g26660.1	MLJ15.5, LOB domain protein, putative / lateral organ boundaries domain protein, putative (LBD24), GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
190500	191500	E=1.4e-11	At3g26660.1	MLJ15.5, LOB domain protein, putative / lateral organ boundaries domain protein, putative (LBD24), GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
192000	193000	E=5.9e-45	At1g35940.1	F10O5.11, AT hook motif-containing protein-related, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
192500	193500	E=3.6e-62	At3g13250.1	MDC11.18, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
193000	194000	E=2.0e-71	At1g52960.1	F14G24.23, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
193500	194500	E=2.7e-46	At1g52960.1	F14G24.23, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
195000	196000	E=7.1e-33	At3g42100.1	F4M19.60, AT hook motif-containing protein-related, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
195500	196500	E=1.5e-54	At3g42100.1	F4M19.60, AT hook motif-containing protein-related, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
196000	197000	E=1.1e-50	At3g30560.1	MQP15.20, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment

					within model
196500	197500	E=5.5e-41	At3g30560.1	MQP15.20, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
197000	198000	E=4.0e-22	At5g37110.1	MJG14.16, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
209000	210000	E=1.3e-12	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Predicted transposon
209500	210500	E=6.6e-11	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Predicted transposon
212000	213000	E=8.2e-09	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
212500	213500	E=8.2e-09	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
215500	216500	E=1.6e-06	At5g56040.1	MDA7.8, leucine-rich repeat protein kinase, putative, GO:0005524 [ATP binding] GO:0016301 [kinase activity] GO:0006468 [protein amino acid phosphorylation] GO:0008372 [cellular_component unknown] GO:0007169 [transmembrane receptor protein tyrosine kinase	Inserted fragment outside gene models
216000	217000	E=1.6e-06	At5g56040.1	MDA7.8, leucine-rich repeat protein kinase, putative, GO:0005524 [ATP binding] GO:0016301 [kinase activity] GO:0006468 [protein amino acid phosphorylation] GO:0008372 [cellular_component unknown] GO:0007169 [transmembrane receptor protein tyrosine kinase	Inserted fragment outside gene models
216500	217500	E=8.8e-20	At5g19850.1	T29J13.270, hydrolase, alpha/beta fold family protein, GO:0016787 [hydrolase activity]	Inserted fragment within model
217000	218000	E=2.3e-16	At5g19850.1	T29J13.270, hydrolase, alpha/beta fold family protein, GO:0016787 [hydrolase activity]	Inserted fragment within model
218000	219000	E=3.6e-09	At1g50430.1	F11F12.21, 7-dehydrocholesterol reductase / 7-DHC reductase / sterol delta-7-reductase (ST7R) / dwarf5 protein, GO:0016126 [sterol biosynthesis] GO:0030176 [integral to endoplasmic reticulum membrane] GO:0016132 [brassinosteroid biosynthesis] GO:0009918 [sterol delta7 reductase activity]	Inserted fragment outside gene models
223500	224500	E=4.8e-16	At4g17520.1	FCAALL.142, nuclear RNA-binding protein, putative, GO:0003723 [RNA binding]	Conserved collinear gene
224000	225000	E=1.3e-57	At4g17520.1	FCAALL.142, nuclear RNA-binding protein, putative, GO:0003723 [RNA binding]	Conserved collinear gene
224500	225500	E=2.2e-80	At4g17520.1	FCAALL.142, nuclear RNA-binding protein, putative, GO:0003723 [RNA binding]	Conserved collinear gene
225000	226000	E=3.3e-	At4g17520.1	FCAALL.142, nuclear RNA-binding protein, putative, GO:0003723	Conserved

		57		[RNA binding]	collinear gene
225500	226500	E=2.3e-13	At4g17530.1	FCAALL.87, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
226000	227000	E=1.7e-55	At5g47200.1	MQL5.5, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
226500	227500	E=7.4e-76	At5g47200.1	MQL5.5, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
227000	228000	E=7.2e-23	At5g47200.1	MQL5.5, Ras-related GTP-binding protein, putative, GO:0005525 [GTP binding]	Conserved collinear gene
228000	229000	E=9.8e-34	At4g17550.1	FCAALL.41, transporter-related, GO:0005351 [sugar porter activity] GO:0008643 [carbohydrate transport]	Conserved collinear gene
228500	229500	E=9.9e-89	At4g17550.1	FCAALL.41, transporter-related, GO:0005351 [sugar porter activity] GO:0008643 [carbohydrate transport]	Conserved collinear gene
229000	230000	E=1.2e-128	At4g17550.1	FCAALL.41, transporter-related, GO:0005351 [sugar porter activity] GO:0008643 [carbohydrate transport]	Conserved collinear gene
229500	230500	E=3.3e-141	At4g17550.1	FCAALL.41, transporter-related, GO:0005351 [sugar porter activity] GO:0008643 [carbohydrate transport]	Conserved collinear gene
230000	231000	E=9.0e-61	At4g17550.1	FCAALL.41, transporter-related, GO:0005351 [sugar porter activity] GO:0008643 [carbohydrate transport]	Conserved collinear gene
230500	231500	E=5.7e-26	At4g17560.1	FCAALL.39, ribosomal protein L19 family protein, GO:0005840 [ribosome] GO:0007046 [ribosome biogenesis] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Conserved collinear gene
231000	232000	E=3.8e-55	At4g17560.1	FCAALL.39, ribosomal protein L19 family protein, GO:0005840 [ribosome] GO:0007046 [ribosome biogenesis] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Conserved collinear gene
231500	232500	E=3.8e-50	At5g47190.1	MQL5.4, ribosomal protein L19 family protein, GO:0005840 [ribosome] GO:0007046 [ribosome biogenesis] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Conserved collinear gene
232000	233000	E=6.2e-18	At4g17560.1	FCAALL.39, ribosomal protein L19 family protein, GO:0005840 [ribosome] GO:0007046 [ribosome biogenesis] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Conserved collinear gene
233000	234000	E=6.6e-29	At4g17570.1	FCAALL.45, zinc finger (GATA type) family protein, GO:0003700 [transcription factor activity]	Conserved collinear gene
233500	234500	E=7.5e-77	At4g17570.1	FCAALL.45, zinc finger (GATA type) family protein, GO:0003700 [transcription factor activity]	Conserved collinear gene
234000	235000	E=2.8e-45	At4g17570.1	FCAALL.45, zinc finger (GATA type) family protein, GO:0003700 [transcription factor activity]	Conserved collinear gene
234500	235500	E=9.0e-112	At4g17570.1	FCAALL.45, zinc finger (GATA type) family protein, GO:0003700 [transcription factor activity]	Conserved collinear gene
235000	236000	E=9.4e-67	At4g17570.1	FCAALL.45, zinc finger (GATA type) family protein, GO:0003700 [transcription factor activity]	Conserved collinear gene

241500	242500	E=1.2e-08	At4g29090.1	F25O24.5, reverse transcriptase, putative / RNA-dependent DNA polymerase, putative, GO:0003723 [RNA binding] GO:0003964 [RNA-directed DNA polymerase activity] GO:0006278 [RNA dependent DNA replication]	Predicted transposon
242000	243000	E=7.8e-07	At4g29090.1	F25O24.5, reverse transcriptase, putative / RNA-dependent DNA polymerase, putative, GO:0003723 [RNA binding] GO:0003964 [RNA-directed DNA polymerase activity] GO:0006278 [RNA dependent DNA replication]	Predicted transposon
242500	243500	E=1.5e-10	At5g35805.1	MIK22.10, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
243000	244000	E=1.5e-10	At5g35805.1	MIK22.10, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
250000	251000	E=6.1e-10	At5g47580.1	MNJ7.17, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
250500	251500	E=1.0e-22	At5g47580.1	MNJ7.17, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
251000	252000	E=7.0e-09	At5g47580.1	MNJ7.17, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
255000	256000	E=9.2e-21	At4g17280.1	FCAALL.393, auxin-responsive family protein, GO:0016020 [membrane] GO:0007275 [development] GO:0005554 [molecular_function unknown]	Inserted fragment within model
255500	256500	E=3.2e-17	At4g17280.1	FCAALL.393, auxin-responsive family protein, GO:0016020 [membrane] GO:0007275 [development] GO:0005554 [molecular_function unknown]	Inserted fragment within model
262500	263500	E=6.8e-09	At2g11910.2	F23M2.7, expressed protein, GO:0005554 [molecular_function unknown]	Predicted transposon
263000	264000	E=5.5e-09	At2g18540.1	F24H14.11, cupin family protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Predicted transposon
291500	292500	E=2.7e-17	At3g30240.1	MIL15.14, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
292000	293000	E=2.7e-17	At3g30240.1	MIL15.14, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model

296500	297500	E=5.1e-16	At2g46470.1	F11C10.16, OXA1 protein, putative, GO:0005554 [molecular_function unknown] GO:0005739 [mitochondrion] GO:0045039 [mitochondrial inner membrane protein import]	Inserted fragment within model
297000	298000	E=5.1e-16	At2g46470.1	F11C10.16, OXA1 protein, putative, GO:0005554 [molecular_function unknown] GO:0005739 [mitochondrion] GO:0045039 [mitochondrial inner membrane protein import]	Inserted fragment within model
297500	298500	E=1.1e-13	At2g46470.1	F11C10.16, OXA1 protein, putative, GO:0005554 [molecular_function unknown] GO:0005739 [mitochondrion] GO:0045039 [mitochondrial inner membrane protein import]	Inserted fragment within model
318500	319500	E=1.4e-19	At4g17650.1	FCAALL.381, aromatic-rich family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
319000	320000	E=1.4e-19	At4g17650.1	FCAALL.381, aromatic-rich family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
319500	320500	E=9.8e-30	At4g17650.1	FCAALL.381, aromatic-rich family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
320000	321000	E=4.9e-51	At4g17650.1	FCAALL.381, aromatic-rich family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
320500	321500	E=2.4e-18	At4g17650.1	FCAALL.381, aromatic-rich family protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
322000	323000	E=3.2e-06	At5g47225.1	MQL5.8, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
322500	323500	E=1.4e-23	At5g47225.1	MQL5.8, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
323000	324000	E=8.5e-13	At5g47225.1	MQL5.8, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
326000	327000	E=7.2e-51	At4g17660.1	FCAALL.77, protein kinase, putative, GO:0016301 [kinase activity]	Conserved collinear gene
326500	327500	E=1.4e-95	At4g17660.1	FCAALL.77, protein kinase, putative, GO:0016301 [kinase activity]	Conserved collinear gene
327000	328000	E=1.4e-88	At4g17660.1	FCAALL.77, protein kinase, putative, GO:0016301 [kinase activity]	Conserved collinear gene
327500	328500	E=3.0e-66	At4g17660.1	FCAALL.77, protein kinase, putative, GO:0016301 [kinase activity]	Conserved collinear gene
328500	329500	E=2.1e-19	At4g05145.1	C17L7.18, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
329000	330000	E=1.1e-18	At1g43570.1	T10P12.5, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment

					within model
343000	344000	E=3.4e-15	At4g17695.1	FCAALL.94, myb family transcription factor (KAN3), GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	annotation error
343500	344500	E=3.2e-26	At4g17695.1	FCAALL.94, myb family transcription factor (KAN3), GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	annotation error
344000	345000	E=2.5e-12	At4g17695.1	FCAALL.94, myb family transcription factor (KAN3), GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	annotation error
344500	345500	E=2.0e-08	At4g17695.1	FCAALL.94, myb family transcription factor (KAN3), GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
345000	346000	E=2.8e-63	At4g17695.1	FCAALL.94, myb family transcription factor (KAN3), GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
345500	346500	E=3.7e-53	At4g17695.1	FCAALL.94, myb family transcription factor (KAN3), GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
346000	347000	E=1.8e-06	At4g17695.1	FCAALL.94, myb family transcription factor (KAN3), GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
356500	357500	E=1.4e-14	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
359000	360000	E=2.4e-09	At5g47225.1	MQL5.8, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
359500	360500	E=1.2e-09	At5g47225.1	MQL5.8, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
361500	362500	E=2.1e-07	At2g06908.1	T4E14.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
362000	363000	E=2.1e-07	At2g06908.1	T4E14.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
371500	372500	E=7.7e-43	At4g17710.1	FCAALL.102, homeobox-leucine zipper family protein / lipid-binding START domain-containing protein, GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
372000	373000	E=5.2e-72	At4g17710.1	FCAALL.102, homeobox-leucine zipper family protein / lipid-binding START domain-containing protein, GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
372500	373500	E=3.1e-23	At4g17710.1	FCAALL.102, homeobox-leucine zipper family protein / lipid-binding START domain-containing protein, GO:0005634 [nucleus] GO:0003677	Conserved collinear gene

				[DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	
376500	377500	E=2.1e-11	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
377000	378000	E=6.4e-07	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon

CONTIG F

Start	**Stop**	**Score**	**BLASTn hit**	**Description**	**Classification**
2500	3500	E=4.4e-06	At5g63740.1	MBK5.22, zinc finger protein-related, GO:0005554 [molecular_function unknown]	Predicted transposon
3000	4000	E=3.1e-14	At5g63740.1	MBK5.22, zinc finger protein-related, GO:0005554 [molecular_function unknown]	Predicted transposon
5000	6000	E=1.9e-45	At4g17180.1	FCAALL.368, glycosyl hydrolase family 17 protein, GO:0004553 [hydrolase activity, hydrolyzing O-glycosyl compounds]	Conserved collinear gene
5500	6500	E=1.3e-85	At4g17180.1	FCAALL.368, glycosyl hydrolase family 17 protein, GO:0004553 [hydrolase activity, hydrolyzing O-glycosyl compounds]	Conserved collinear gene
6000	7000	E=1.0e-168	At4g17180.1	FCAALL.368, glycosyl hydrolase family 17 protein, GO:0004553 [hydrolase activity, hydrolyzing O-glycosyl compounds]	Conserved collinear gene
6500	7500	E=6.6e-95	At4g17180.1	FCAALL.368, glycosyl hydrolase family 17 protein, GO:0004553 [hydrolase activity, hydrolyzing O-glycosyl compounds]	Conserved collinear gene
7000	8000	E=9.7e-107	At4g17210.1	FCAALL.382, myosin heavy chain-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
7500	8500	E=1.5e-149	At4g17210.1	FCAALL.382, myosin heavy chain-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
8000	9000	E=1.1e-126	At4g17210.1	FCAALL.382, myosin heavy chain-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
8500	9500	E=5.5e-31	At4g17210.1	FCAALL.382, myosin heavy chain-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
9000	10000	E=1.2e-58	At4g06599.1	T11G11.4, ubiquitin family protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
9500	10500	E=3.1e-27	At4g06599.1	T11G11.4, ubiquitin family protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
10000	11000	E=1.7e-50	At4g06599.1	T11G11.4, ubiquitin family protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene

					models
10500	11500	E=2.0e-42	At4g06599.1	T11G11.4, ubiquitin family protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
26000	27000	E=2.8e-11	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
30500	31500	E=2.3e-06	At2g07360.1	T13E11.13, SH3 domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
31000	32000	E=2.2e-26	At3g22750.1	MWI23.12, protein kinase, putative, GO:0016301 [kinase activity]	Inserted fragment within model
31500	32500	E=2.0e-26	At3g22750.1	MWI23.12, protein kinase, putative, GO:0016301 [kinase activity]	Inserted fragment within model
34000	35000	E=1.9e-20	At5g47635.1	MNJ7.29, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
34500	35500	E=4.8e-40	At5g47635.1	MNJ7.29, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
35000	36000	E=4.6e-25	At4g17220.1	FCAALL.385, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
35500	36500	E=4.8e-70	At4g17220.1	FCAALL.385, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
36000	37000	E=1.9e-117	At4g17220.1	FCAALL.385, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
36500	37500	E=2.8e-85	At4g17220.1	FCAALL.385, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
37000	38000	E=1.9e-29	At4g17220.1	FCAALL.385, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
37500	38500	E=4.7e-18	At4g17220.1	FCAALL.385, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
39000	40000	E=2.8e-22	At4g17230.1	FCAALL.225, scarecrow-like transcription factor 13 (SCL13), GO:0003700 [transcription factor activity]	Conserved collinear gene
39500	40500	E=4.4e-104	At4g17230.1	FCAALL.225, scarecrow-like transcription factor 13 (SCL13), GO:0003700 [transcription factor activity]	Conserved collinear gene
40000	41000	E=2.4e-111	At4g17230.1	FCAALL.225, scarecrow-like transcription factor 13 (SCL13), GO:0003700 [transcription factor activity]	Conserved collinear gene
40500	41500	E=9.8e-30	At4g17230.1	FCAALL.225, scarecrow-like transcription factor 13 (SCL13), GO:0003700 [transcription factor activity]	Conserved collinear gene

50500	51500	E=2.3e-17	At4g17240.1	FCAALL.387, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
51000	52000	E=5.9e-43	At4g17240.1	FCAALL.387, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
51500	52500	E=4.4e-22	At4g17240.1	FCAALL.387, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
52000	53000	E=2.9e-23	At4g17240.1	FCAALL.387, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
52500	53500	E=5.2e-21	At4g17240.1	FCAALL.387, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
55000	56000	E=1.1e-27	At2g16140.1	F7H1.16, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
55500	56500	E=2.8e-25	At2g16140.1	F7H1.16, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
56500	57500	E=7.8e-33	At3g15310.1	K7L4.11, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
57000	58000	E=7.7e-53	At3g15310.1	K7L4.11, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
57500	58500	E=7.8e-55	At3g15310.1	K7L4.11, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
58000	59000	E=2.0e-48	At3g15310.1	K7L4.11, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
58500	59500	E=7.5e-08	At1g43590.1	T10P12.13, hypothetical protein, GO:0005554 [molecular_function unknown] GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown]	Inserted fragment outside gene models
62000	63000	E=3.2e-12	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
62500	63500	E=4.3e-12	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
76000	77000	E=5.0e-07	At1g42190.1	F19C17.40, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
76500	77500	E=5.0e-07	At1g42190.1	F19C17.40, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
80500	81500	E=6.0e-	At4g17245.1	FCAALL.189, zinc finger (C3HC4-type RING finger) family protein,	Predicted

		31		GO:0005515 [protein binding] GO:0008270 [zinc ion binding]	transposon
81000	82000	E=7.7e-41	At4g17245.1	FCAALL.189, zinc finger (C3HC4-type RING finger) family protein, GO:0005515 [protein binding] GO:0008270 [zinc ion binding]	Predicted transposon
81500	82500	E=5.4e-43	At2g31290.1	F16D14.13, expressed protein, GO:0005554 [molecular_function unknown]	Largely intact relocated gene
82000	83000	E=7.1e-126	At2g31290.1	F16D14.13, expressed protein, GO:0005554 [molecular_function unknown]	Largely intact relocated gene
82500	83500	E=7.9e-148	At2g31290.1	F16D14.13, expressed protein, GO:0005554 [molecular_function unknown]	Largely intact relocated gene
83000	84000	E=2.6e-65	At2g31290.1	F16D14.13, expressed protein, GO:0005554 [molecular_function unknown]	Largely intact relocated gene
83500	84500	E=3.0e-36	At5g47580.1 (+4g17250)	MNJ7.17, expressed protein, GO:0005554 [molecular_function unknown]	Predicted transposon
84000	85000	E=1.2e-22	At5g47580.1 (+4g17250)	MNJ7.17, expressed protein, GO:0005554 [molecular_function unknown]	Predicted transposon
90000	91000	E=4.7e-37	At4g17260.1	FCAALL.172, L-lactate dehydrogenase, putative, GO:0004457 [lactate dehydrogenase activity]	Conserved collinear gene
90500	91500	E=1.6e-92	At4g17260.1	FCAALL.172, L-lactate dehydrogenase, putative, GO:0004457 [lactate dehydrogenase activity]	Conserved collinear gene
91000	92000	E=1.3e-62	At4g17260.1	FCAALL.172, L-lactate dehydrogenase, putative, GO:0004457 [lactate dehydrogenase activity]	Conserved collinear gene
91500	92500	E=3.8e-73	At4g17260.1	FCAALL.172, L-lactate dehydrogenase, putative, GO:0004457 [lactate dehydrogenase activity]	Conserved collinear gene
92000	93000	E=5.3e-60	At4g17260.1	FCAALL.172, L-lactate dehydrogenase, putative, GO:0004457 [lactate dehydrogenase activity]	Conserved collinear gene
92500	93500	E=3.7e-07	At4g17270.1	FCAALL.22, Mo25 family protein, GO:0005554 [molecular_function unknown]	Additional collinear gene fragment
93000	94000	E=8.9e-13	At4g17270.1	FCAALL.22, Mo25 family protein, GO:0005554 [molecular_function unknown]	Additional collinear gene fragment
93500	94500	E=9.1e-07	At4g17270.1	FCAALL.22, Mo25 family protein, GO:0005554 [molecular_function unknown]	Additional collinear gene fragment
100000	101000	E=1.4e-07	At4g17270.1	FCAALL.22, Mo25 family protein, GO:0005554 [molecular_function unknown]	Additional collinear gene fragment

100500	101500	E=1.5e-17	At5g47540.1	MNJ7.13, Mo25 family protein, GO:0005554 [molecular_function unknown]	Additional collinear gene fragment
101000	102000	E=2.4e-35	At5g47530.1	MNJ7.12, auxin-responsive protein, putative, GO:0016020 [membrane] GO:0007275 [development] GO:0005554 [molecular_function unknown]	Conserved collinear gene
101500	102500	E=7.4e-107	At5g47530.1	MNJ7.12, auxin-responsive protein, putative, GO:0016020 [membrane] GO:0007275 [development] GO:0005554 [molecular_function unknown]	Conserved collinear gene
102000	103000	E=1.4e-143	At4g17280.1	FCAALL.393, auxin-responsive family protein, GO:0016020 [membrane] GO:0007275 [development] GO:0005554 [molecular_function unknown]	Conserved collinear gene
102500	103500	E=1.6e-66	At4g17280.1	FCAALL.393, auxin-responsive family protein, GO:0016020 [membrane] GO:0007275 [development] GO:0005554 [molecular_function unknown]	Conserved collinear gene
103500	104500	E=4.1e-18	At4g17300.1	FCAALL.396, asparaginyl-tRNA synthetase, chloroplast, mitochondrial / asparagine-tRNA ligase / AsnRS (SYNO), GO:0006421 [asparaginyl-tRNA aminoacylation] GO:0006412 [protein biosynthesis] GO:0004816 [asparagine-tRNA ligase activity] GO:0005739 [mitochondrion] GO:0009507 [chloroplast]	Conserved collinear gene
104000	105000	E=5.1e-77	At4g17300.1	FCAALL.396, asparaginyl-tRNA synthetase, chloroplast, mitochondrial / asparagine-tRNA ligase / AsnRS (SYNO), GO:0006421 [asparaginyl-tRNA aminoacylation] GO:0006412 [protein biosynthesis] GO:0004816 [asparagine-tRNA ligase activity] GO:0005739 [mitochondrion] GO:0009507 [chloroplast]	Conserved collinear gene
104500	105500	E=1.7e-65	At4g17300.1	FCAALL.396, asparaginyl-tRNA synthetase, chloroplast, mitochondrial / asparagine-tRNA ligase / AsnRS (SYNO), GO:0006421 [asparaginyl-tRNA aminoacylation] GO:0006412 [protein biosynthesis] GO:0004816 [asparagine-tRNA ligase activity] GO:0005739 [mitochondrion] GO:0009507 [chloroplast]	Conserved collinear gene
105000	106000	E=9.3e-51	At4g17300.1	FCAALL.396, asparaginyl-tRNA synthetase, chloroplast, mitochondrial / asparagine-tRNA ligase / AsnRS (SYNO), GO:0006421 [asparaginyl-tRNA aminoacylation] GO:0006412 [protein biosynthesis] GO:0004816 [asparagine-tRNA ligase activity] GO:0005739 [mitochondrion] GO:0009507 [chloroplast]	Conserved collinear gene
105500	106500	E=2.3e-48	At4g17300.1	FCAALL.396, asparaginyl-tRNA synthetase, chloroplast, mitochondrial / asparagine-tRNA ligase / AsnRS (SYNO), GO:0006421 [asparaginyl-tRNA aminoacylation] GO:0006412 [protein biosynthesis] GO:0004816 [asparagine-tRNA ligase activity] GO:0005739 [mitochondrion] GO:0009507 [chloroplast]	Conserved collinear gene
106000	107000	E=4.1e-67	At4g17300.1	FCAALL.396, asparaginyl-tRNA synthetase, chloroplast, mitochondrial / asparagine-tRNA ligase / AsnRS (SYNO), GO:0006421 [asparaginyl-tRNA aminoacylation] GO:0006412 [protein biosynthesis] GO:0004816	Conserved collinear gene

				[asparagine-tRNA ligase activity] GO:0005739 [mitochondrion] GO:0009507 [chloroplast]	
106500	107500	E=5.0e-33	At4g17300.1	FCAALL.396, asparaginyl-tRNA synthetase, chloroplast, mitochondrial / asparagine-tRNA ligase / AsnRS (SYNO), GO:0006421 [asparaginyl-tRNA aminoacylation] GO:0006412 [protein biosynthesis] GO:0004816 [asparagine-tRNA ligase activity] GO:0005739 [mitochondrion] GO:0009507 [chloroplast]	Conserved collinear gene
107000	108000	E=1.2e-14	At4g17300.1	FCAALL.396, asparaginyl-tRNA synthetase, chloroplast, mitochondrial / asparagine-tRNA ligase / AsnRS (SYNO), GO:0006421 [asparaginyl-tRNA aminoacylation] GO:0006412 [protein biosynthesis] GO:0004816 [asparagine-tRNA ligase activity] GO:0005739 [mitochondrion] GO:0009507 [chloroplast]	Conserved collinear gene
107500	108500	E=4.2e-65	At4g17300.1	FCAALL.396, asparaginyl-tRNA synthetase, chloroplast, mitochondrial / asparagine-tRNA ligase / AsnRS (SYNO), GO:0006421 [asparaginyl-tRNA aminoacylation] GO:0006412 [protein biosynthesis] GO:0004816 [asparagine-tRNA ligase activity] GO:0005739 [mitochondrion] GO:0009507 [chloroplast]	Conserved collinear gene
108000	109000	E=2.0e-39	At4g17300.1	FCAALL.396, asparaginyl-tRNA synthetase, chloroplast, mitochondrial / asparagine-tRNA ligase / AsnRS (SYNO), GO:0006421 [asparaginyl-tRNA aminoacylation] GO:0006412 [protein biosynthesis] GO:0004816 [asparagine-tRNA ligase activity] GO:0005739 [mitochondrion] GO:0009507 [chloroplast]	Conserved collinear gene
118000	119000	E=7.4e-34	At3g53240.1	T4D2.170, leucine-rich repeat family protein, GO:0007165 [signal transduction] GO:0005515 [protein binding]	Inserted fragment within model
118500	119500	E=1.7e-60	At3g53240.1	T4D2.170, leucine-rich repeat family protein, GO:0007165 [signal transduction] GO:0005515 [protein binding]	Inserted fragment within model
119000	120000	E=1.9e-38	At1g74180.1	F9E11.6, leucine-rich repeat family protein, GO:0007165 [signal transduction] GO:0005515 [protein binding]	Inserted fragment within model
127500	128500	E=4.2e-27	At3g13250.1	MDC11.18, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
128000	129000	E=9.8e-56	At3g51700.1	T18N14.80, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
128500	129500	E=1.3e-61	At3g13250.1	MDC11.18, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
129000	130000	E=8.9e-	At1g52960.1	F14G24.23, hypothetical protein, GO:0005554 [molecular_function	Inserted

		73		unknown]	fragment within model
129500	130500	E=3.8e-35	At3g13250.1	MDC11.18, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
130000	131000	E=1.2e-28	At3g13250.1	MDC11.18, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
130500	131500	E=2.6e-46	At1g35940.1	F10O5.11, AT hook motif-containing protein-related, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
131000	132000	E=1.5e-66	At1g35940.1	F10O5.11, AT hook motif-containing protein-related, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
131500	132500	E=1.9e-50	At2g05080.1	F1O13.21, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
132000	133000	E=5.3e-51	At5g37110.1	MJG14.16, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
132500	133500	E=1.8e-28	At5g37110.1	MJG14.16, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
137000	138000	E=7.8e-10	At4g17330.1	FCAALL.411, agenet domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Additional collinear gene fragment
137500	138500	E=1.9e-47	At4g17330.1	FCAALL.411, agenet domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Additional collinear gene fragment
138000	139000	E=8.1e-33	At4g17330.1	FCAALL.411, agenet domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Additional collinear gene fragment
143500	144500	E=5.0e-35	At1g50920.1	F8A12.14, GTP-binding protein-related, GO:0000166 [nucleotide binding]	Inserted fragment within model
144000	145000	E=5.0e-35	At1g50920.1	F8A12.14, GTP-binding protein-related, GO:0000166 [nucleotide binding]	Inserted fragment within model
145000	146000	E=6.2e-50	At3g31980.1	F8N14.16, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model

145500	146500	E=7.6e-85	At3g31980.1	F8N14.16, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
146000	147000	E=4.0e-90	At3g31980.1	F8N14.16, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
146500	147500	E=8.2e-74	At2g05080.1	F1O13.21, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
147000	148000	E=1.4e-24	At2g05080.1	F1O13.21, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
147500	148500	E=3.3e-17	At5g37110.1	MJG14.16, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
153000	154000	E=6.7e-38	At4g17340.1	FCAALL.412, major intrinsic family protein / MIP family protein, GO:0016020 [membrane] GO:0006810 [transport] GO:0015250 [water channel activity]	Conserved collinear gene
153500	154500	E=1.2e-88	At5g47450.1	MQL5.31, major intrinsic family protein / MIP family protein, GO:0016020 [membrane] GO:0006810 [transport] GO:0015250 [water channel activity]	Conserved collinear gene
154000	155000	E=6.1e-72	At5g47450.1	MQL5.31, major intrinsic family protein / MIP family protein, GO:0016020 [membrane] GO:0006810 [transport] GO:0015250 [water channel activity]	Conserved collinear gene
154500	155500	E=4.0e-23	At4g17340.1	FCAALL.412, major intrinsic family protein / MIP family protein, GO:0016020 [membrane] GO:0006810 [transport] GO:0015250 [water channel activity]	Conserved collinear gene
155500	156500	E=4.4e-40	At4g17350.1	FCAALL.415, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
156000	157000	E=4.1e-87	At4g17350.1	FCAALL.415, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
156500	157500	E=4.1e-99	At4g17350.1	FCAALL.415, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
157000	158000	E=1.6e-95	At4g17350.1	FCAALL.415, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
157500	158500	E=1.9e-46	At4g17350.1	FCAALL.415, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
158000	159000	E=4.0e-49	At5g47435.2	MNJ7.1, formyltetrahydrofolate deformylase, putative, GO:0009152 [purine ribonucleotide biosynthesis] GO:0008864 [formyltetrahydrofolate deformylase activity] GO:0009058 [biosynthesis] GO:0016742 [hydroxymethyl-, formyl- and related transferase activity]	Conserved collinear gene

158500	159500	E=4.8e-84	At4g17360.1	FCAALL.417, formyltetrahydrofolate deformylase, putative, GO:0009152 [purine ribonucleotide biosynthesis] GO:0008864 [formyltetrahydrofolate deformylase activity] GO:0009058 [biosynthesis] GO:0016742 [hydroxymethyl-, formyl- and related transferase activity]	Conserved collinear gene
159000	160000	E=3.0e-68	At4g17360.1	FCAALL.417, formyltetrahydrofolate deformylase, putative, GO:0009152 [purine ribonucleotide biosynthesis] GO:0008864 [formyltetrahydrofolate deformylase activity] GO:0009058 [biosynthesis] GO:0016742 [hydroxymethyl-, formyl- and related transferase activity]	Conserved collinear gene
159500	160500	E=6.3e-23	At4g17360.1	FCAALL.417, formyltetrahydrofolate deformylase, putative, GO:0009152 [purine ribonucleotide biosynthesis] GO:0008864 [formyltetrahydrofolate deformylase activity] GO:0009058 [biosynthesis] GO:0016742 [hydroxymethyl-, formyl- and related transferase activity]	Conserved collinear gene
160500	161500	E=2.4e-39	At4g17390.1	FCAALL.32, 60S ribosomal protein L15 (RPL15B), GO:0005840 [ribosome] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Conserved collinear gene
161000	162000	E=5.4e-75	At4g17390.1	FCAALL.32, 60S ribosomal protein L15 (RPL15B), GO:0005840 [ribosome] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Conserved collinear gene
161500	162500	E=1.4e-60	At4g17390.1	FCAALL.32, 60S ribosomal protein L15 (RPL15B), GO:0005840 [ribosome] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Conserved collinear gene
162000	163000	E=8.9e-29	At4g17390.1	FCAALL.32, 60S ribosomal protein L15 (RPL15B), GO:0005840 [ribosome] GO:0006412 [protein biosynthesis] GO:0003735 [structural constituent of ribosome]	Conserved collinear gene
163000	164000	E=1.4e-23	At3g15310.1	K7L4.11, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
163500	164500	E=3.6e-86	At5g32621.1	F15I15.2, expressed protein, GO:0005554 [molecular_function unknown] GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown]	Inserted fragment within model
164000	165000	E=2.2e-82	At5g32621.1	F15I15.2, expressed protein, GO:0005554 [molecular_function unknown] GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown]	Inserted fragment within model
164500	165500	E=4.1e-16	At5g32621.1	F15I15.2, expressed protein, GO:0005554 [molecular_function unknown] GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown]	Inserted fragment within model
165500	166500	E=1.5e-26	At5g47430.1	MQL5.29, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
166000	167000	E=1.3e-43	At5g47430.1	MQL5.29, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
166500	167500	E=2.5e-	At5g47430.1	MQL5.29, expressed protein, GO:0005554 [molecular_function	Conserved

		43		unknown]	collinear gene
167000	168000	E=3.7e-63	At4g17410.1	FCAALL.426, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
167500	168500	E=5.1e-101	At4g17410.1	FCAALL.426, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
168000	169000	E=8.4e-84	At4g17410.1	FCAALL.426, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
168500	169500	E=1.8e-59	At4g17410.1	FCAALL.426, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
169000	170000	E=4.1e-30	At4g17410.1	FCAALL.426, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
169500	170500	E=2.0e-44	At4g17410.1	FCAALL.426, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
170000	171000	E=4.8e-50	At4g17410.1	FCAALL.426, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
181000	182000	E=3.9e-10	At4g08410.1	T28D5.100, proline-rich extensin-like family protein, GO:0000004 [biological_process unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
181500	182500	E=6.5e-47	At5g35190.1	T25C13.70, proline-rich extensin-like family protein, GO:0000004 [biological_process unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
182000	183000	E=9.3e-94	At2g24980.1	F27C12.10, proline-rich extensin-like family protein, GO:0000004 [biological_process unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
182500	183500	E=1.6e-111	At4g13390.1	T9E8.130, proline-rich extensin-like family protein, GO:0000004 [biological_process unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
183000	184000	E=8.7e-57	At4g13390.1	T9E8.130, proline-rich extensin-like family protein, GO:0000004 [biological_process unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
186000	187000	E=2.7e-22	At5g35190.1	T25C13.70, proline-rich extensin-like family protein, GO:0000004 [biological_process unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
186500	187500	E=2.3e-72	At4g13390.1	T9E8.130, proline-rich extensin-like family protein, GO:0000004 [biological_process unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
187000	188000	E=8.6e-120	At4g13390.1	T9E8.130, proline-rich extensin-like family protein, GO:0000004 [biological_process unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
187500	188500	E=8.0e-58	At4g13390.1	T9E8.130, proline-rich extensin-like family protein, GO:0000004 [biological_process unknown] GO:0005554 [molecular_function	Inserted fragment

				unknown]	within model
189500	190500	E=9.4e-13	At2g31700.1	T9H9.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
191000	192000	E=1.2e-11	At5g35190.1	T25C13.70, proline-rich extensin-like family protein, GO:0000004 [biological_process unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
191500	192500	E=2.6e-87	At4g13390.1	T9E8.130, proline-rich extensin-like family protein, GO:0000004 [biological_process unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
192000	193000	E=4.5e-112	At4g13390.1	T9E8.130, proline-rich extensin-like family protein, GO:0000004 [biological_process unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
192500	193500	E=3.0e-111	At4g13390.1	T9E8.130, proline-rich extensin-like family protein, GO:0000004 [biological_process unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
193000	194000	E=9.8e-65	At4g13390.1	T9E8.130, proline-rich extensin-like family protein, GO:0000004 [biological_process unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
193500	194500	E=1.8e-16	At1g02230.1	T7I23.19, no apical meristem (NAM) family protein, GO:0007275 [development] GO:0005554 [molecular_function unknown] GO:0003700 [transcription factor activity]	Inserted fragment within model
194000	195000	E=5.7e-06	At3g09510.1	F11F8.9, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
208500	209500	E=1.5e-07	At1g48720.1	F11I4.11, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
209000	210000	E=6.5e-42	At1g48720.1	F11I4.11, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
209500	210500	E=8.7e-29	At3g42250.1	F26B15.50, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
225500	226500	E=1.6e-14	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
226000	227000	E=1.4e-14	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
239000	240000	E=9.1e-15	At5g63740.1	MBK5.22, zinc finger protein-related, GO:0005554 [molecular_function unknown]	Predicted transposon
239500	240500	E=2.0e-14	At5g63740.1	MBK5.22, zinc finger protein-related, GO:0005554 [molecular_function unknown]	Predicted transposon
240500	241500	E=2.0e-	At4g17420.1	FCAALL.389, expressed protein, GO:0000004 [biological_process	Conserved

		13		unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	collinear gene
241000	242000	E=1.1e-56	At4g17420.1	FCAALL.389, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
241500	242500	E=3.3e-62	At4g17420.1	FCAALL.389, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
242000	243000	E=5.1e-60	At4g17420.1	FCAALL.389, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
242500	243500	E=2.7e-34	At4g17420.1	FCAALL.389, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Conserved collinear gene
243000	244000	E=1.2e-52	At4g17430.1	FCAALL.1, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
243500	244500	E=2.1e-126	At4g17430.1	FCAALL.1, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
244000	245000	E=1.5e-147	At4g17430.1	FCAALL.1, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
244500	245500	E=3.2e-99	At4g17430.1	FCAALL.1, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
245000	246000	E=1.3e-21	At4g17430.1	FCAALL.1, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
249000	250000	E=9.1e-16	At4g13780.1	F18A5.170, methionine--tRNA ligase, putative / methionyl-tRNA synthetase, putative / MetRS, putative, GO:0004825 [methionine-tRNA ligase activity] GO:0006431 [methionyl-tRNA aminoacylation]	Inserted fragment within model
249500	250500	E=3.5e-25	At4g13780.1	F18A5.170, methionine--tRNA ligase, putative / methionyl-tRNA synthetase, putative / MetRS, putative, GO:0004825 [methionine-tRNA ligase activity] GO:0006431 [methionyl-tRNA aminoacylation]	Inserted fragment within model
250000	251000	E=1.4e-19	At4g13780.1	F18A5.170, methionine--tRNA ligase, putative / methionyl-tRNA synthetase, putative / MetRS, putative, GO:0004825 [methionine-tRNA ligase activity] GO:0006431 [methionyl-tRNA aminoacylation]	Inserted fragment within model
250500	251500	E=1.1e-28	At4g13780.1	F18A5.170, methionine--tRNA ligase, putative / methionyl-tRNA synthetase, putative / MetRS, putative, GO:0004825 [methionine-tRNA ligase activity] GO:0006431 [methionyl-tRNA aminoacylation]	Inserted fragment within model
251000	252000	E=1.4e-09	At4g13780.1	F18A5.170, methionine--tRNA ligase, putative / methionyl-tRNA synthetase, putative / MetRS, putative, GO:0004825 [methionine-tRNA ligase activity] GO:0006431 [methionyl-tRNA aminoacylation]	Inserted fragment within model
254500	255500	E=2.7e-07	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon

255000	256000	E=1.1e-08	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
256500	257500	E=6.3e-10	At2g10050.1	F7B19.19, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Predicted transposon
257000	258000	E=2.4e-16	At2g10090.1	F7B19.23, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
257500	258500	E=1.1e-16	At2g10090.1	F7B19.23, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
261000	262000	E=5.7e-19	At2g19960.1	F6F22.1, hAT dimerisation domain-containing protein / transposase-related, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
265500	266500	E=4.7e-10	At2g16005.1	F7H1.26, MD-2-related lipid recognition domain-containing protein / ML domain-containing protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
266000	267000	E=3.7e-16	At3g43770.1	T28A8.60, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
266500	267500	E=3.7e-16	At3g43770.1	T28A8.60, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
276000	277000	E=1.9e-13	At5g04260.1	F21E1.180, thioredoxin family protein, GO:0030508 [thiol-disulfide exchange intermediate activity]	Inserted fragment outside gene models
276500	277500	E=1.9e-13	At5g04260.1	F21E1.180, thioredoxin family protein, GO:0030508 [thiol-disulfide exchange intermediate activity]	Inserted fragment outside gene models
277000	278000	E=2.0e-06	At3g07790.1	MLP3.24, DGCR14-related, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
277500	278500	E=1.3e-37	At5g47390.1	MQL5.25, myb family transcription factor, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
278000	279000	E=1.5e-73	At5g47390.1	MQL5.25, myb family transcription factor, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
278500	279500	E=4.3e-77	At5g47390.1	MQL5.25, myb family transcription factor, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
279000	280000	E=3.5e-41	At5g47390.1	MQL5.25, myb family transcription factor, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
285000	286000	E=2.6e-	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676	Predicted

		22		[nucleic acid binding]	transposon
285500	286500	E=1.6e-51	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Predicted transposon
286000	287000	E=3.1e-27	At5g32482.1	T15F17.6, zinc knuckle (CCHC-type) family protein, GO:0003676 [nucleic acid binding]	Predicted transposon
290500	291500	E=7.0e-11	At1g70410.3	F17O7.5, carbonic anhydrase, putative / carbonate dehydratase, putative, GO:0015976 [carbon utilization] GO:0008270 [zinc ion binding] GO:0004089 [carbonate dehydratase activity]	Inserted fragment outside gene models
291000	292000	E=2.6e-14	At4g17440.1	FCAALL.6, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
291500	292500	E=2.1e-57	At4g17440.1	FCAALL.6, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
292000	293000	E=1.3e-44	At4g17440.1	FCAALL.6, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
294000	295000	E=2.7e-17	At5g47225.1	MQL5.8, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
294500	295500	E=1.4e-10	At5g47225.1	MQL5.8, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
295000	296000	E=9.8e-15	At4g29090.1	F25O24.5, reverse transcriptase, putative / RNA-dependent DNA polymerase, putative, GO:0003723 [RNA binding] GO:0003964 [RNA-directed DNA polymerase activity] GO:0006278 [RNA dependent DNA replication]	Predicted transposon
295500	296500	E=3.6e-08	At4g29090.1	F25O24.5, reverse transcriptase, putative / RNA-dependent DNA polymerase, putative, GO:0003723 [RNA binding] GO:0003964 [RNA-directed DNA polymerase activity] GO:0006278 [RNA dependent DNA replication]	Predicted transposon
298500	299500	E=2.5e-19	At2g15550.1	F9O13.10, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
299000	300000	E=3.6e-13	At2g15550.1	F9O13.10, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
300500	301500	E=4.8e-12	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
301000	302000	E=4.3e-12	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
309000	310000	E=3.9e-12	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
314500	315500	E=7.5e-08	At2g31700.1	T9H9.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models

315000	316000	E=7.5e-08	At2g31700.1	T9H9.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
321500	322500	E=1.2e-21	At4g17460.1	FCAALL.65, homeobox-leucine zipper protein 1 (HAT1) / HD-ZIP protein 1, GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
322000	323000	E=1.5e-64	At4g17460.1	FCAALL.65, homeobox-leucine zipper protein 1 (HAT1) / HD-ZIP protein 1, GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
322500	323500	E=2.7e-111	At4g17460.1	FCAALL.65, homeobox-leucine zipper protein 1 (HAT1) / HD-ZIP protein 1, GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
323000	324000	E=8.8e-43	At4g17460.1	FCAALL.65, homeobox-leucine zipper protein 1 (HAT1) / HD-ZIP protein 1, GO:0005634 [nucleus] GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
324000	325000	E=8.0e-08	At5g53740.1	MGN6.10, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
325000	326000	E=5.4e-35	At4g17480.1	FCAALL.380, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
325500	326500	E=9.9e-47	At4g17480.1	FCAALL.380, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
326000	327000	E=1.3e-60	At4g17480.1	FCAALL.380, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
326500	327500	E=1.8e-44	At4g17480.1	FCAALL.380, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
329000	330000	E=1.7e-29	At4g02920.1	T5J8.24, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
329500	330500	E=5.3e-28	At4g02920.1	T5J8.24, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
333000	334000	E=8.2e-38	At4g17480.1	FCAALL.380, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
333500	334500	E=3.0e-	At4g17480.1	FCAALL.380, palmitoyl protein thioesterase family protein, GO:0008474	Conserved

		52		[palmitoyl-(protein) hydrolase activity]	collinear gene
334000	335000	E=3.2e-60	At4g17480.1	FCAALL.380, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene
334500	335500	E=2.0e-33	At4g17480.1	FCAALL.380, palmitoyl protein thioesterase family protein, GO:0008474 [palmitoyl-(protein) hydrolase activity]	Conserved collinear gene

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Start	**Stop**	**Score**	**BLASTn hit**	**Description**	**Classification**
3000	4000	E=5.4e-20	At1g33980.1	F12G12.20, Smg-4/UPF3 family protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
3500	4500	E=6.2e-26	At1g33980.1	F12G12.20, Smg-4/UPF3 family protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
6000	7000	E=2.5e-10	At5g03710.1	F17C15.130, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
6500	7500	E=5.8e-12	At3g30190.1	MIL15.1, hypothetical protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
15500	16500	E=4.9e-27	At2g40680.1	T7D17.14, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
16000	17000	E=4.0e-39	At1g43570.1	T10P12.5, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
16500	17500	E=1.8e-18	At1g43570.1	T10P12.5, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
17000	18000	E=5.6e-13	At5g05980.1	K18J17.17, dihydrofolate synthetase/folylpolyglutamate synthetase (DHFS/FPGS2), GO:0006730 [one-carbon compound metabolism] GO:0004326 [tetrahydrofolylpolyglutamate synthase activity] GO:0009570 [chloroplast stroma]	Inserted fragment within model
17500	18500	E=4.4e-31	At5g05980.1	K18J17.17, dihydrofolate synthetase/folylpolyglutamate synthetase (DHFS/FPGS2), GO:0006730 [one-carbon compound metabolism] GO:0004326 [tetrahydrofolylpolyglutamate synthase activity] GO:0009570 [chloroplast stroma]	Inserted fragment within model
18000	19000	E=3.6e-44	At5g05980.1	K18J17.17, dihydrofolate synthetase/folylpolyglutamate synthetase (DHFS/FPGS2), GO:0006730 [one-carbon compound metabolism] GO:0004326 [tetrahydrofolylpolyglutamate synthase activity]	Inserted fragment within model

				GO:0009570 [chloroplast stroma]	
18500	19500	E=5.0e-21	At5g05980.1	K18J17.17, dihydrofolate synthetase/folylpolyglutamate synthetase (DHFS/FPGS2), GO:0006730 [one-carbon compound metabolism] GO:0004326 [tetrahydrofolylpolyglutamate synthase activity] GO:0009570 [chloroplast stroma]	Inserted fragment within model
19500	20500	E=3.2e-33	At4g17690.1	FCAALL.96, peroxidase, putative, GO:0004601 [peroxidase activity]	Conserved collinear gene
20000	21000	E=1.7e-99	At4g17690.1	FCAALL.96, peroxidase, putative, GO:0004601 [peroxidase activity]	Conserved collinear gene
20500	21500	E=2.7e-101	At4g17690.1	FCAALL.96, peroxidase, putative, GO:0004601 [peroxidase activity]	Conserved collinear gene
21000	22000	E=7.5e-35	At4g17690.1	FCAALL.96, peroxidase, putative, GO:0004601 [peroxidase activity]	Conserved collinear gene
22000	23000	E=4.7e-16	At4g17695.1	FCAALL.94, myb family transcription factor (KAN3), GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
22500	23500	E=4.7e-16	At4g17695.1	FCAALL.94, myb family transcription factor (KAN3), GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
23000	24000	E=9.8e-11	At4g17695.1	FCAALL.94, myb family transcription factor (KAN3), GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
23500	24500	E=2.1e-10	At4g17695.1	FCAALL.94, myb family transcription factor (KAN3), GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
24000	25000	E=6.2e-56	At4g17695.1	FCAALL.94, myb family transcription factor (KAN3), GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
24500	25500	E=4.5e-56	At4g17695.1	FCAALL.94, myb family transcription factor (KAN3), GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
25000	26000	E=7.2e-09	At4g17695.1	FCAALL.94, myb family transcription factor (KAN3), GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
39000	40000	E=1.1e-06	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
39500	40500	E=7.5e-14	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
44500	45500	E=8.8e-99	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	Conserved collinear gene
45000	46000	E=8.1e-119	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	Conserved collinear gene
45500	46500	E=4.8e-44	At4g17720.1	FCAALL.73, RNA recognition motif (RRM)-containing protein, GO:0003676 [nucleic acid binding]	Conserved collinear gene
46500	47500	E=8.7e-21	At4g17730.1	FCAALL.117, syntaxin 23 (SYP23) / PEP12-like protein, GO:0006944 [membrane fusion] GO:0006886 [intracellular protein transport] GO:0005486 [t-SNARE activity]	Conserved collinear gene
47000	48000	E=6.8e-	At4g17730.1	FCAALL.117, syntaxin 23 (SYP23) / PEP12-like protein, GO:0006944	Conserved

		69		[membrane fusion] GO:0006886 [intracellular protein transport] GO:0005486 [t-SNARE activity]	collinear gene
47500	48500	E=1.8e-69	At4g17730.1	FCAALL.117, syntaxin 23 (SYP23) / PEP12-like protein, GO:0006944 [membrane fusion] GO:0006886 [intracellular protein transport] GO:0005486 [t-SNARE activity]	Conserved collinear gene
48000	49000	E=6.7e-32	At5g46860.1	MSD23.9, syntaxin 22 (SYP22) (VAM3), GO:0030140 [trans-Golgi network transport vesicle] GO:0005770 [late endosome] GO:0006944 [membrane fusion] GO:0009705 [vacuolar membrane (sensu Magnoliophyta)] GO:0006886 [intracellular protein transp	Conserved collinear gene
48500	49500	E=1.6e-41	At4g17750.1	FCAALL.107, heat shock factor protein 1 (HSF1) / heat shock transcription factor 1 (HSTF1), GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0009408 [response to heat] GO:0008372 [cellular_component unknown] GO:0005515 [protein binding] GO:0003700 [transcri	Conserved collinear gene
49000	50000	E=2.6e-49	At4g17750.1	FCAALL.107, heat shock factor protein 1 (HSF1) / heat shock transcription factor 1 (HSTF1), GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0009408 [response to heat] GO:0008372 [cellular_component unknown] GO:0005515 [protein binding] GO:0003700 [transcri	Conserved collinear gene
49500	50500	E=7.5e-78	At4g17750.1	FCAALL.107, heat shock factor protein 1 (HSF1) / heat shock transcription factor 1 (HSTF1), GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0009408 [response to heat] GO:0008372 [cellular_component unknown] GO:0005515 [protein binding] GO:0003700 [transcri	Conserved collinear gene
50000	51000	E=7.1e-68	At4g17750.1	FCAALL.107, heat shock factor protein 1 (HSF1) / heat shock transcription factor 1 (HSTF1), GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0009408 [response to heat] GO:0008372 [cellular_component unknown] GO:0005515 [protein binding] GO:0003700 [transcri	Conserved collinear gene
50500	51500	E=4.3e-13	At4g17750.1	FCAALL.107, heat shock factor protein 1 (HSF1) / heat shock transcription factor 1 (HSTF1), GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0009408 [response to heat] GO:0008372 [cellular_component unknown] GO:0005515 [protein binding] GO:0003700 [transcri	Conserved collinear gene
52500	53500	E=2.5e-06	At3g25270.1	MJL12.23, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
53000	54000	E=1.1e-17	At2g02650.1	T8K22.5, reverse transcriptase-related, GO:0005554 [molecular_function unknown]	Predicted transposon
53500	54500	E=7.8e-07	At2g02650.1	T8K22.5, reverse transcriptase-related, GO:0005554 [molecular_function unknown]	Predicted transposon
54000	55000	E=1.6e-	At4g17760.1	FCAALL.108, expressed protein, GO:0005554 [molecular_function	Predicted

		09		unknown]	transposon
54500	55500	E=2.6e-45	At4g16015.1	FCAALL.263, DC1 domain-containing protein, GO:0005554 [molecular_function unknown]	Predicted transposon
55000	56000	E=3.9e-110	At4g16015.1	FCAALL.263, DC1 domain-containing protein, GO:0005554 [molecular_function unknown]	Predicted transposon
55500	56500	E=3.4e-136	At4g16015.1	FCAALL.263, DC1 domain-containing protein, GO:0005554 [molecular_function unknown]	Predicted transposon
56000	57000	E=9.5e-99	At4g16015.1	FCAALL.263, DC1 domain-containing protein, GO:0005554 [molecular_function unknown]	Predicted transposon
56500	57500	E=1.3e-21	At4g16015.1	FCAALL.263, DC1 domain-containing protein, GO:0005554 [molecular_function unknown]	Predicted transposon
62000	63000	E=1.0e-11	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
62500	63500	E=1.0e-11	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
71000	72000	E=2.1e-14	At1g36670.1	T15P17.10, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
71500	72500	E=9.4e-28	At1g36670.1	T15P17.10, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
74500	75500	E=1.5e-42	At5g49790.1	K2I5.16, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
75000	76000	E=1.5e-42	At5g49790.1	K2I5.16, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
75500	76500	E=9.2e-31	At4g17770.1	FCAALL.9, glycosyl transferase family 20 protein / trehalose-phosphatase family protein, GO:0005992 [trehalose biosynthesis] GO:0004805 [trehalose-phosphatase activity] GO:0016757 [transferase activity, transferring glycosyl groups] GO:0003825 [alpha,alpha-trehalose-phosphate synthase (UD	Conserved collinear gene
76000	77000	E=6.8e-75	At4g17770.1	FCAALL.9, glycosyl transferase family 20 protein / trehalose-phosphatase family protein, GO:0005992 [trehalose biosynthesis] GO:0004805 [trehalose-phosphatase activity] GO:0016757 [transferase activity, transferring glycosyl groups] GO:0003825 [alpha,alpha-trehalose-phosphate synthase (UD	Conserved collinear gene
76500	77500	E=1.8e-109	At4g17770.1	FCAALL.9, glycosyl transferase family 20 protein / trehalose-phosphatase family protein, GO:0005992 [trehalose biosynthesis] GO:0004805 [trehalose-phosphatase activity] GO:0016757 [transferase activity, transferring glycosyl groups] GO:0003825 [alpha,alpha-	Conserved collinear gene

				trehalose-phosphate synthase (UD	
77000	78000	E=2.0e-52	At4g17770.1	FCAALL.9, glycosyl transferase family 20 protein / trehalose-phosphatase family protein, GO:0005992 [trehalose biosynthesis] GO:0004805 [trehalose-phosphatase activity] GO:0016757 [transferase activity, transferring glycosyl groups] GO:0003825 [alpha,alpha-trehalose-phosphate synthase (UD	Conserved collinear gene
77500	78500	E=3.0e-29	At4g17785.1	FCAALL.109, myb family transcription factor (MYB39), GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
78000	79000	E=2.0e-99	At4g17785.1	FCAALL.109, myb family transcription factor (MYB39), GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
78500	79500	E=1.5e-96	At4g17785.1	FCAALL.109, myb family transcription factor (MYB39), GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
79000	80000	E=8.3e-49	At4g17785.1	FCAALL.109, myb family transcription factor (MYB39), GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
79500	80500	E=2.2e-15	At4g17785.1	FCAALL.109, myb family transcription factor (MYB39), GO:0003677 [DNA binding] GO:0006355 [regulation of transcription, DNA-dependent] GO:0003700 [transcription factor activity]	Conserved collinear gene
93000	94000	E=8.4e-15	At4g05145.1	C17L7.18, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
93500	94500	E=1.4e-07	At4g05145.1	C17L7.18, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
101000	102000	E=1.4e-13	At3g29785.1	T26G12.25, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
101500	102500	E=7.5e-39	At3g29785.1	T26G12.25, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
102000	103000	E=9.6e-20	At3g29785.1	T26G12.25, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
104000	105000	E=5.9e-10	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
105000	106000	E=6.6e-09	At4g23160.1	F21P8.50, protein kinase family protein, GO:0016301 [kinase activity]	Predicted transposon
107000	108000	E=1.2e-06	At5g03710.1	F17C15.130, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models

109500	110500	E=2.1e-34	At4g17790.1	FCAALL.62, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
110000	111000	E=2.8e-81	At4g17790.1	FCAALL.62, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
110500	111500	E=2.4e-42	At4g17790.1	FCAALL.62, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
114000	115000	E=1.3e-86	At4g17800.1	FCAALL.129, DNA-binding protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
114500	115500	E=3.7e-157	At4g17800.1	FCAALL.129, DNA-binding protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
115000	116000	E=4.7e-66	At4g17800.1	FCAALL.129, DNA-binding protein-related, GO:0005554 [molecular_function unknown]	Conserved collinear gene
151000	152000	E=1.0e-10	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
151500	152500	E=2.1e-09	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
157500	158500	E=4.2e-06	At5g07570.1	T2I1.280, glycine/proline-rich protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
158000	159000	E=4.9e-19	At4g01980.1	T7B11.25, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
158500	159500	E=1.5e-15	At4g01980.1	T7B11.25, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
160000	161000	E=2.3e-28	At3g15310.1	K7L4.11, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
160500	161500	E=1.6e-89	At3g15310.1	K7L4.11, expressed protein, GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown] GO:0005554 [molecular_function unknown]	Inserted fragment within model
161000	162000	E=1.6e-72	At5g32621.1	F15I15.2, expressed protein, GO:0005554 [molecular_function unknown] GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown]	Inserted fragment within model
161500	162500	E=9.0e-09	At5g32621.1	F15I15.2, expressed protein, GO:0005554 [molecular_function unknown] GO:0000004 [biological_process unknown] GO:0008372 [cellular_component unknown]	Inserted fragment within model
169000	170000	E=4.6e-26	At5g28250.1	T8M17.20, Ulp1 protease family protein, GO:0008234 [cysteine-type peptidase activity] GO:0006508 [proteolysis and peptidolysis]	Inserted fragment within model
170500	171500	E=1.2e-	At4g17810.1	FCAALL.130, zinc finger (C2H2 type) family protein, GO:0003676	Conserved

		59		[nucleic acid binding] GO:0008270 [zinc ion binding] GO:0003700 [transcription factor activity]	collinear gene
171000	172000	E=5.4e-82	At4g17810.1	FCAALL.130, zinc finger (C2H2 type) family protein, GO:0003676 [nucleic acid binding] GO:0008270 [zinc ion binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
171500	172500	E=6.2e-18	At4g17810.1	FCAALL.130, zinc finger (C2H2 type) family protein, GO:0003676 [nucleic acid binding] GO:0008270 [zinc ion binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
177500	178500	E=3.1e-53	At4g17830.1	FCAALL.133, peptidase M20/M25/M40 family protein, GO:0008237 [metallopeptidase activity] GO:0006508 [proteolysis and peptidolysis]	Conserved collinear gene
178000	179000	E=5.8e-103	At4g17830.1	FCAALL.133, peptidase M20/M25/M40 family protein, GO:0008237 [metallopeptidase activity] GO:0006508 [proteolysis and peptidolysis]	Conserved collinear gene
178500	179500	E=8.7e-79	At4g17830.1	FCAALL.133, peptidase M20/M25/M40 family protein, GO:0008237 [metallopeptidase activity] GO:0006508 [proteolysis and peptidolysis]	Conserved collinear gene
179000	180000	E=4.7e-61	At4g17830.1	FCAALL.133, peptidase M20/M25/M40 family protein, GO:0008237 [metallopeptidase activity] GO:0006508 [proteolysis and peptidolysis]	Conserved collinear gene
179500	180500	E=4.4e-41	At4g17830.1	FCAALL.133, peptidase M20/M25/M40 family protein, GO:0008237 [metallopeptidase activity] GO:0006508 [proteolysis and peptidolysis]	Conserved collinear gene
180000	181000	E=7.0e-83	At4g17840.1	T6K21.20, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
180500	181500	E=1.5e-45	At2g35260.1	T4C15.7, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
181000	182000	E=6.1e-31	At4g17840.1	T6K21.20, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
181500	182500	E=6.1e-18	At4g17840.1	T6K21.20, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
184000	185000	E=3.9e-12	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
184500	185500	E=3.9e-12	At2g05950.1	T6P5.15, hypothetical protein, GO:0005554 [molecular_function unknown]	Predicted transposon
189000	190000	E=3.3e-07	At4g17850.1	T6K21.30, hypothetical protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
189500	190500	E=2.1e-10	At4g17850.1	T6K21.30, hypothetical protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
199000	200000	E=6.3e-10	At4g17850.1	T6K21.30, hypothetical protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
199500	200500	E=1.7e-15	At4g17850.1	T6K21.30, hypothetical protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
204000	205000	E=8.8e-11	At3g43220.1	F7K15.70, phosphoinositide phosphatase family protein, GO:0004439 [phosphoinositide 5-phosphatase activity]	Inserted fragment outside gene

					models
204500	205500	E=8.8e-11	At3g43220.1	F7K15.70, phosphoinositide phosphatase family protein, GO:0004439 [phosphoinositide 5-phosphatase activity]	Inserted fragment outside gene models
212500	213500	E=6.0e-16	At2g31700.1	T9H9.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
213000	214000	E=7.2e-07	At2g31700.1	T9H9.22, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment outside gene models
214000	215000	E=2.1e-06	At3g24255.1	K13K6.3, expressed protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
214500	215500	E=8.3e-16	At1g21330.1	F24J8.25, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment within model
215000	216000	E=3.3e-10	At4g36970.1	AP22.30, remorin family protein, GO:0003677 [DNA binding]	Inserted fragment outside gene models
215500	216500	E=3.3e-10	At4g36970.1	AP22.30, remorin family protein, GO:0003677 [DNA binding]	Inserted fragment outside gene models
218000	219000	E=7.2e-16	At4g20880.1	T13K14.40, ethylene-responsive nuclear protein / ethylene-regulated nuclear protein (ERT2), GO:0005554 [molecular_function unknown]	Inserted fragment within model
218500	219500	E=7.2e-16	At4g20880.1	T13K14.40, ethylene-responsive nuclear protein / ethylene-regulated nuclear protein (ERT2), GO:0005554 [molecular_function unknown]	Inserted fragment within model
223000	224000	E=5.3e-32	At4g17870.1	T6K21.50, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
223500	224500	E=5.7e-86	At4g17870.1	T6K21.50, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
224000	225000	E=2.7e-49	At4g17870.1	T6K21.50, expressed protein, GO:0005554 [molecular_function unknown]	Conserved collinear gene
226000	227000	E=1.6e-07	At3g32904.1	T7B9.24, hypothetical protein, GO:0005554 [molecular_function unknown]	Inserted fragment

					outside gene models
231500	232500	E=7.7e-77	At4g17880.1	T6K21.60, basic helix-loop-helix (bHLH) family protein, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
232000	233000	E=1.5e-115	At4g17880.1	T6K21.60, basic helix-loop-helix (bHLH) family protein, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
232500	233500	E=2.3e-103	At4g17880.1	T6K21.60, basic helix-loop-helix (bHLH) family protein, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
233000	234000	E=5.7e-94	At4g17880.1	T6K21.60, basic helix-loop-helix (bHLH) family protein, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene
233500	234500	E=1.1e-33	At4g17880.1	T6K21.60, basic helix-loop-helix (bHLH) family protein, GO:0003677 [DNA binding] GO:0003700 [transcription factor activity]	Conserved collinear gene