Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
BM073967	1.65E-12	Mo17<F1<B73	9.66	10	ns		
CD484534	1.19E-10	Mo17<F1<B73	2.39	10	>ref|XP 450808.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD25837.1| unknown protein [Oryza sativa (japonica cultivar-group)]	172	7E-56
					>ref|NP 563872.1| unknown protein [Arabidopsis thaliana]gb|AAM63692.1| unknown [Arabidopsis thaliana] gb|AAD39574.1| T10O24.14 [Arabidopsis thaliana]	179	3E-29
DV489965	2.07E-10	B73<F1<Mo17	3.47	3	>ref|XP_474978.1| OSJNBb0015G09.12 [Oryza sativa (japonica cultivar-group)]emb|CAE03918.2| OSJNBb0015G09.12 [Oryza sativa (japonica cultivar-group)] emb|CAE01956.2| OSJNBb0071D01.2 [Oryza sativa (japonica cultivar-group)]	226	2E-67
					>gb|ABB55396.1| unknown [Solanum tuberosum]	224	2E-42
					>dbj|BAD46596.1| unknown protein [Oryza sativa (japonica cultivar-group)]	237	6E-36
					>ref|NP_683315.1| unknown protein [Arabidopsis thaliana]gb|AAL32926.1| Unknown protein [Arabidopsis thaliana] gb|AAN65076.1| Unknown protein [Arabidopsis thaliana]	233	3E-30
					>gb|AAF79893.1| Contains similarity to pigpen protein from Mus musculus gb|AF224264and contains protein of unknown function DUF78 PF|01918 domain. ESTs gb|N38077, gb|BE037702, gb|AV442191, gb|AV441368, gb|Z17998, gb|AV527266, gb|AV520794, gb|AI997847, gb|AV543000 come from this gene. [Arabidopsis thaliana]	538	8E-30
BM074100	5.26E-10	Mo17<F1<B73	2.19	10	>ref|XP 473945.1| OSJNBa0053K19.11 [Oryza sativa (japonica cultivar-group)]emb|CAE03503.2| OSJNBa0053K19.11 [Oryza sativa (japonica cultivar-group)]	408	1E-32
					>emb|CAA81081.1| T-protein [Solanum tuberosum]sp|P54260|GCST_SOLTU Aminomethyltransferase, mitochondrial precursor (Glycine cleavage system T protein) (GCVT)	406	1E-28
					>emb|CAA81077.1| T protein [Flaveria pringlei]sp|P49363|GCST_FLAPR Aminomethyltransferase, mitochondrial precursor (Glycine cleavage system T protein) (GCVT)	407	4E-28
					>emb|CAB16917.1| T-Protein precursor [Flaveria trinervia]sp|O23936|GCST_FLATR Aminomethyltransferase, mitochondrial precursor (Glycine cleavage system T protein) (GCVT)	407	4E-28
					>emb|CAA94902.1| T-protein [Flaveria anomala]sp|O49849|GCST_FLAAN Aminomethyltransferase, mitochondrial precursor (Glycine cleavage system T protein) (GCVT)	407	4E-28
BM073112	1.12E-09	Mo17<F1<B73	5.42	10	>ref|XP_479601.1| unknown protein [Oryza sativa (japonica cultivar-group)]ref|XP_506581.1| PREDICTED OJ1200_C08.123 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD30292.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAC10351.1| unknown protein [Oryza sativa (japonica cultivar-group)]	247	3E-63
					>ref|XP 472660.1| OSJNBa0086B14.2 [Oryza sativa (japonica cultivar-group)]emb|CAD40830.1| OSJNBa0086B14.2 [Oryza sativa (japonica cultivar-group)]	245	2E-27
					>dbj|BAB11562.1| unnamed protein product [Arabidopsis thaliana]	234	5E-24
					>ref|NP 201343.2| unknown protein [Arabidopsis thaliana]	252	5E-24
					>emb|CAB79348.1| putative protein [Arabidopsis thaliana]emb|CAB45073.1| putative protein [Arabidopsis thaliana]	208	7E-23
BM350737	1.83E-09	Mo17<F1<B73	3.88	10	ns		
BM073177	1.94E-09	Mo17<B73=F1	7.5	10	>gb|AAT40079.1| MPI [Zea perennis]gb|AAT40071.1| MPI [Zea perennis] gb|AAT40067.1| MPI [Zea diploperennis]	71	2E-22
					>gb|ABA34107.1| maize protease inhibitor [Zea mays subsp. parviglumis]	70	2E-22
					>gb|ABA34116.1| maize protease inhibitor [Zea mays subsp. parviglumis]	70	2E-22
					>gb|AAT40086.1| MPI [Zea perennis]gb|AAT40083.1| MPI [Zea perennis] gb|AAT40082.1| MPI [Zea perennis] gb|AAT40081.1| MPI [Zea perennis] gb|AAT40080.1| MPI [Zea perennis] gb|AAT40078.1| MPI [Zea perennis] gb|AAT40075.1| MPI [Zea perennis] gb|AAT40074.1| MPI [Zea perennis] gb|AAT40073.1| MPI [Zea perennis] gb|AAT40072.1| MPI [Zea perennis] gb|AAT40070.1| MPI [Zea diploperennis] gb|AAT40069.1| MPI [Zea diploperennis] gb|AAT40068.1| MPI [Zea diploperennis] gb|AAT40066.1| MPI [Zea diploperennis] gb|AAT40065.1| MPI [Zea diploperennis] gb|AAT40064.1| MPI [Zea diploperennis] gb|AAT40062.1| MPI [Zea diploperennis] gb|AAT40061.1| MPI [Zea diploperennis] gb|AAT40060.1| MPI [Zea diploperennis] gb|AAT40059.1| MPI [Zea diploperennis] gb|AAT40058.1| MPI [Zea diploperennis]	72	3E-22
					>gb|ABA34112.1| maize protease inhibitor [Zea mays subsp. parviglumis]	71	3E-22
DV490536	2.04E-09	Mo17<F1<B73	2.12	10	>gb|AAX11351.1| cathepsin B-like cysteine protease [Oryza sativa (japonicacultivar-group)]	358	3E-75
					>emb|CAC83720.1| cathepsin B [Hordeum vulgare subsp. vulgare]	344	3E-74
					>emb|CAA46810.1| cathepsin B [Triticum aestivum]	305	2E-73
					>emb|CAA46811.1| cathepsin B [Triticum aestivum]	353	5E-68
					>dbj|BAD94873.1| cathepsin B-like cysteine proteinase like protein [Arabidopsisthaliana]	183	5E-63
CD058791	3.65E-09	Mo17<F1<B73	1.9	10	>ref|XP_475712.1| putative GTP-binding protein Rab7a [Oryza sativa (japonicacultivar-group)] gb|AAT01314.1| putative GTP-binding protein Rab7a [Oryza sativa (japonica cultivar-group)]	206	1E-95
					>sp|Q40787|RAB7 PENCL Ras-related protein Rab7 (Possible apospory-associated protein)gb|AAA85273.1| possible apospory-associated protein	206	1E-95
					>gb|AAO67728.1| small GTP binding protein [Oryza sativa (indica cultivar-group)]	206	1E-94
					>gb|ABB29958.1| unknown [Solanum tuberosum]gb|ABB02623.1| unknown [Solanum tuberosum]	206	4E-93
					>gb|AAQ72787.1| putative GTP-binding protein [Cucumis sativus]	206	6E-93
BM348874	3.90E-09	Mo17<F1<B73	2.93	10	ns		
CD650745	6.08E-09	Mo17<F1<B73	2.5	10	>gb|AAL76334.1| putative G-box binding protein [Oryza sativa]dbj|BAD45657.1| G-box binding protein-like [Oryza sativa (japonica cultivar-group)] gb|AAB65433.1| HvB12D homolog [Oryza sativa]	89	9E-40

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>emb|CAA70936.1| B12Dg1 [Hordeum vulgare subsp. vulgare]emb|CAA54065.1| HvB12D [Hordeum vulgare subsp. vulgare]	87	8E-36
					>gb|AAD22104.1| B12D protein [Ipomoea batatas]	90	3E-33
					>ref|NP_190397.1| unknown protein [Arabidopsis thaliana]emb|CAB51061.1| B12D-like protein [Arabidopsis thaliana] gb|AAL91215.1| B12D-like protein [Arabidopsis thaliana] gb|AAN65070.1| B12D-like protein [Arabidopsis thaliana] pir||T13003 hypothetical protein T24C20.20 - Arabidopsis thaliana	88	7E-29
					>ref|XP_477421.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]dbj|BAC84633.1| putative B12D protein [Oryza sativa (japonica cultivar-group)] dbj|BAD31625.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]	98	8E-28
BG842925	6.85E-09	Mo17<F1<B73	2.77	10	>ref|XP_462851.1| B1146F03.16 [Oryza sativa (japonica cultivar-group)]dbj|BAB93161.1| putative CP12 [Oryza sativa (japonica cultivar-group)] dbj|BAB19776.1| contains EST AU078264(S21150)~unknown protein [Oryza sativa (japonica cultivar-group)]	124	3E-31
					>emb|CAA96570.1| CP12 [Pisum sativum]	127	9E-23
					>gb|AAV63570.1| auxin-induced putative CP12 domain-containing protein [Arachishypogaea]	73	7E-22
					>ref|NP_566100.2| CP12-1 [Arabidopsis thaliana]gb|AAM47914.1| putative chloroplast protein CP12 [Arabidopsis thaliana] gb|AAL32917.1| putative chloroplast protein CP12 [Arabidopsis thaliana]	124	1E-21
					>emb|CAA96568.1| CP12 [Spinacia oleracea]	124	1E-20
CD484655	8.17E-09	Mo17<F1<B73	1.84	10	>ref|XP_475712.1| putative GTP-binding protein Rab7a [Oryza sativa (japonicacultivar-group)] gb|AAT01314.1| putative GTP-binding protein Rab7a [Oryza sativa (japonica cultivar-group)]	206	2E-78
					>sp|Q40787|RAB7 PENCL Ras-related protein Rab7 (Possible apospory-associated protein)gb|AAA85273.1| possible apospory-associated protein	206	2E-78
					>gb|AAO67728.1| small GTP binding protein [Oryza sativa (indica cultivar-group)]	206	5E-77
					>sp|O24461|RAB7 PRUAR Ras-related protein Rab7gb|AAB71504.1| Rab7 GTP binding protein [Prunus armeniaca]	207	3E-70
					>emb|CAA98171.1| RAB7D [Lotus corniculatus var. japonicus]	207	1E-69
DV942590	1.67E-08	B73<F1=Mo17	2.81	2	ns		
BG841472	1.74E-08	B73<F1=Mo17	4.66	3	>emb|CAJ20024.1| putative cystatin [Zea mays]dbj|BAA09666.1| cysteine proteinase inhibitor [Zea mays] gb|AAY57865.1| cysteine proteinase inhibitor [Zea mays subsp. parviglumis]	134	3E-61
					>emb|CAA60610.1| cysteine proteinase inhibitor [Zea mays]	134	7E-61
					>gb|AAY57868.1| cysteine proteinase inhibitor [Zea mays subsp. parviglumis]gb|AAY57864.1| cysteine proteinase inhibitor [Zea mays subsp. parviglumis]	134	9E-60
					>dbj|BAA07327.1| cystatin II [Zea mays]	134	4E-58
					>gb|AAY57859.1| cysteine proteinase inhibitor [Zea mays subsp. parviglumis]	134	4E-58
BG840972	1.81E-08	Mo17<F1<B73	7.03	10	ns		
BM073611	2.10E-08	Mo17<B73=F1	22.77	10	ns		
CD661828	2.20E-08	B73<F1<Mo17	3.64	3	>gb|AAP94583.1| putative protein [Zea mays]	786	6E-6
CB815723	2.43E-08	B73<F1=Mo17	2.99	2	>emb|CAJ20023.1| putative cystatin [Zea mays]	135	5E-46
					>sp|P31726|CYT1 MAIZE Cystatin-1 precursor (Cystatin I) (Corn kernel cysteine proteinaseinhibitor) dbj|BAA01472.1| corn cystatin I [Zea mays]	135	2E-45
					>emb|CAA60634.1| cysteine proteinase inhibitor [Sorghum bicolor]	130	6E-43
					>emb|CAJ20024.1| putative cystatin [Zea mays]dbj|BAA09666.1| cysteine proteinase inhibitor [Zea mays] gb|AAY57865.1| cysteine proteinase inhibitor [Zea mays subsp. parviglumis]	134	6E-43
					>emb|CAA60610.1| cysteine proteinase inhibitor [Zea mays]	134	1E-42
CB886241	3.18E-08	Mo17<F1<B73	2.33	10	>dbj|BAD53494.1| putative Synoviolin 1 [Oryza sativa (japonica cultivar-group)]dbj|BAD53976.1| putative Synoviolin 1 [Oryza sativa (japonica cultivar-group)]	500	3E-10
					>ref|NP_188230.1| protein binding / ubiquitin-protein ligase/ zinc ion binding[Arabidopsis thaliana] gb|AAY57599.1| RING finger family protein [Arabidopsis thaliana] dbj|BAB02675.1| unnamed protein product [Arabidopsis thaliana] dbj|BAC41836.1| putative zinc finger protein [Arabidopsis thaliana]	492	3E-9
					>ref|NP_849843.3| protein binding / ubiquitin-protein ligase/ zinc ion binding[Arabidopsis thaliana] gb|AAR23700.1| At1g65040 [Arabidopsis thaliana] dbj|BAD42325.1| Hrd1p like protein [Arabidopsis thaliana]	460	9E-9
					>gb|AAF06038.1| Contains a PF|00097 Zinc finger, C3HC4 type (RING finger) domain.ESTs gb|N96912 and gb|AI994359 come from this gene. [Arabidopsis thaliana]	496	9E-9
					>ref|NP_176684.3| protein binding / ubiquitin-protein ligase/ zinc ion binding[Arabidopsis thaliana]	389	9E-9
BG874023	3.44E-08	Mo17<F1<B73	2.5	10	>ref|NP_917838.1| putative chloroplast 50S ribosomal protein L31 [Oryza sativa(japonica cultivar-group)] dbj|BAB90423.1| chloroplast 50S ribosomal protein L31-like [Oryza sativa (japonica cultivar-group)] dbj|BAB90722.1| chloroplast 50S ribosomal protein L31-like [Oryza sativa (japonica cultivar-group)]	135	1E-19
CB605161	3.69E-08	B73<F1<Mo17	2.82	3	>gb|AAC04265.1| (S)-adenosyl-L-methionine:delta 24-sterol methyltransferase [Zeamays]	344	3E-64
					>gb|AAB70886.1| endosperm C-24 sterol methyltransferase [Zea mays]	344	3E-64
					>ref|XP_477078.1| cycloartenol-C24-methyltransferase [Oryza sativa (japonicacultivar-group)] dbj|BAC83238.1| cycloartenol-C24-methyltransferase [Oryza sativa (japonica cultivar-group)] sp|Q6ZIX2|SMT1 ORYSA Cycloartenol-C-24-methyltransferase 1 (24-sterol C-methyltransferase 1) (Sterol C-methyltransferase 1)	344	5E-63
					>gb|AAC34988.1| cycloartenol-C24-methyltransferase [Oryza sativa subsp. japonica]	349	5E-63
					>gb|AAC34951.1| S-adenosyl-methionine-sterol-C- methyltransferase [Nicotianatabacum]	346	1E-60
BM079312	4.07E-08	B73<F1=Mo17	2.94	3	>ref|XP_450323.1| putative indole-3-glycerol phosphate synthase [Oryza sativa(japonica cultivar-group)] dbj|BAD23563.1| putative indole-3-glycerol phosphate synthase [Oryza sativa (japonica cultivar-group)]	381	2E-35

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|XP_481579.1| putative indole-3-glycerol phosphate synthase [Oryza sativa(japonica cultivar-group)] dbj|BAD01725.1| putative indole-3-glycerol phosphate synthase [Oryza sativa (japonica cultivar-group)] dbj|BAD10429.1| putative indole-3-glycerol phosphate synthase [Oryza sativa (japonica cultivar-group)]	399	3E-33
					>ref|XP_472804.1| OSJNBa0016O02.9 [Oryza sativa (japonica cultivar-group)]emb|CAE05999.3| OSJNBa0016O02.9 [Oryza sativa (japonica cultivar-group)]	393	2E-29
					>ref|NP_199633.1| indole-3-glycerol-phosphate synthase [Arabidopsis thaliana]gb|AAL31111.1| AT5g48220/MIF21_11 [Arabidopsis thaliana] gb|AAK97693.1| AT5g48220/MIF21_11 [Arabidopsis thaliana] gb|AAK91344.1| AT5g48220/MIF21_11 [Arabidopsis thaliana] dbj|BAA97002.1| indole-3-glycerol phosphate synthase [Arabidopsis thaliana]	379	1E-27
					>dbj|BAC42166.1| putative indole-3-glycerol phosphate synthase [Arabidopsisthaliana]	259	5E-26
AF153448	5.59E-08	F1=Mo17<B73	2.14	9	>gb|AAD38068.1| nitrate reductase [Zea mays]	910	0E+0
					>sp|P17571|NIA1 MAIZE Nitrate reductase [NADH] (NR)	621	0E+0
					>gb|AAA03202.1| NADH:nitrate reductase	618	0E+0
					>gb|AAA33483.1| nitrate reductase	501	0E+0
					>pir||S19254 nitrate reductase (NADH) (EC 1.7.1.1) flavin chain (clone Zmnr1) -maize (fragment)	617	0E+0
BG840917	5.60E-08	Mo17<F1<B73	3.86	10	>gb|AAC24570.1| trypsin inhibitor [Zea mays]	174	5E-71
					>ref|XP_549976.1| putative Bowman Birk trypsin inhibitor [Oryza sativa (japonicacultivar-group)] dbj|BAD52865.1| putative Bowman Birk trypsin inhibitor [Oryza sativa (japonica cultivar-group)] dbj|BAD52690.1| putative Bowman Birk trypsin inhibitor [Oryza sativa (japonica cultivar-group)]	186	6E-32
					>emb|CAB88393.1| putative Bowman Birk tryspin inhibitor [Oryza sativa (indicacultivar-group)]	190	2E-29
					>ref|NP_909066.1| putative Bowman Birk tryspin inhibitor [Oryza sativa (japonicacultivar-group)] dbj|BAB21176.1| putative Bowman Birk tryspin inhibitor [Oryza sativa (japonica cultivar-group)]	218	3E-29
					>emb|CAB88391.1| putative Bowman Birk trypsin inhibitor [Oryza sativa (indicacultivar-group)]	185	4E-29
DV490909	7.59E-08	Mo17<F1<B73	2.42	10	ns		
DV490507	8.39E-08	Mo17<F1<B73	3.79	10	>dbj|BAD53494.1| putative Synoviolin 1 [Oryza sativa (japonica cultivar-group)]dbj|BAD53976.1| putative Synoviolin 1 [Oryza sativa (japonica cultivar-group)]	500	2E-20
					>ref|NP_188230.1| protein binding / ubiquitin-protein ligase/ zinc ion binding[Arabidopsis thaliana] gb|AAY57599.1| RING finger family protein [Arabidopsis thaliana] dbj|BAB02675.1| unnamed protein product [Arabidopsis thaliana] dbj|BAC41836.1| putative zinc finger protein [Arabidopsis thaliana]	492	8E-20
					>ref|NP_849843.3| protein binding / ubiquitin-protein ligase/ zinc ion binding[Arabidopsis thaliana] gb|AAR23700.1| At1g65040 [Arabidopsis thaliana] dbj|BAD42325.1| Hrd1p like protein [Arabidopsis thaliana]	460	4E-19
					>gb|AAF06038.1| Contains a PF|00097 Zinc finger, C3HC4 type (RING finger) domain.ESTs gb|N96912 and gb|AI994359 come from this gene. [Arabidopsis thaliana]	496	4E-19
					>ref|NP_176684.3| protein binding / ubiquitin-protein ligase/ zinc ion binding[Arabidopsis thaliana]	389	4E-19
DV490386	9.87E-08	B73<F1<Mo17	2.22	4	>gb|AAO16692.1| putative Xa1-like protein [Sorghum bicolor]	1284	1E-83
					>emb|CAD45028.1| NBS-LRR disease resistance protein homologue [Hordeum vulgare]	1366	2E-50
					>dbj|BAD29495.1| putative bacterial blight-resistance protein Xa1 [Oryza sativa(japonica cultivar-group)] dbj|BAD28895.1| putative bacterial blight-resistance protein Xa1 [Oryza sativa (japonica cultivar-group)]	1394	3E-50
					>emb|CAD45025.1| NBS-LRR disease resistance protein homologue [Hordeum vulgare]	1440	5E-49
					>gb|AAM94158.1| putative RGA protein 567A-4.7 [Aegilops tauschii]	874	8E-49
DV491578	1.05E-07	Mo17<F1<B73	4.02	9	>gb|AAL59230.1| sesquiterpene cyclase [Zea mays]	631	3E-51
					>gb|AAK73113.1| sesquiterpene cyclase [Zea mays]gb|AAG37841.1| sesquiterpene cyclase 1 [Zea mays]	592	6E-51
					>gb|AAV64216.1| stc [Zea mays]	665	6E-51
					>ref|NP_908798.1| putative sesquiterpene cyclase 1 [Oryza sativa (japonicacultivar-group)] dbj|BAB63870.1| putative terpene synthase 4 [Oryza sativa (japonica cultivar-group)]	547	2E-30
					>ref|XP_480262.1| putative sesquiterpene cyclase 1 [Oryza sativa (japonicacultivar-group)] dbj|BAC99543.1| putative sesquiterpene cyclase 1 [Oryza sativa (japonica cultivar-group)]	605	2E-28
BM074072	1.11E-07	Mo17<F1<B73	9.37	10	>dbj|BAD73736.1| putative heme A:farnesyltransferase [Oryza sativa (japonicacultivar-group)] dbj|BAD73506.1| putative heme A:farnesyltransferase [Oryza sativa (japonica cultivar-group)]	435	1E-14
					>ref|NP_918047.1| putative heme A farnesyltransferase homolog [Oryza sativa (japonicacultivar-group)]	449	1E-14
					>ref|NP_566019.1| prenyltransferase/ protoheme IX farnesyltransferase [Arabidopsisthaliana] gb|AAM45064.1| putative heme A [Arabidopsis thaliana] gb|AAK76626.1| putative heme A:farnesyltransferase [Arabidopsis thaliana] gb|AAM14960.1| putative heme A:farnesyltransferase [Arabidopsis thaliana] gb|AAC27454.3| putative heme A:farnesyltransferase [Arabidopsis thaliana]	431	5E-11
BM078960	2.16E-07	Mo17<F1<B73	2.17	10	>ref|XP_462851.1| B1146F03.16 [Oryza sativa (japonica cultivar-group)]dbj|BAB93161.1| putative CP12 [Oryza sativa (japonica cultivar-group)] dbj|BAB19776.1| contains EST AU078264(S21150)~unknown protein [Oryza sativa (japonica cultivar-group)]	124	2E-26
					>emb|CAA96570.1| CP12 [Pisum sativum]	127	4E-22
					>gb|AAV63570.1| auxin-induced putative CP12 domain-containing protein [Arachishypogaea]	73	1E-21
					>ref|NP_566100.2| CP12-1 [Arabidopsis thaliana]gb|AAM47914.1| putative chloroplast protein CP12 [Arabidopsis thaliana] gb|AAL32917.1| putative chloroplast protein CP12 [Arabidopsis thaliana]	124	6E-21

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>ref|NP_191800.1| CP12-2 [Arabidopsis thaliana]gb|AAM45071.1| putative CP12 protein precursor [Arabidopsis thaliana] gb|AAM20142.1| putative CP12 protein precursor [Arabidopsis thaliana] emb|CAB82955.1| CP12 protein precursor-like protein [Arabidopsis thaliana]	131	3E-20
AI861151	2.85E-07	B73<F1<Mo17	2.23	4	>gb|AAO16692.1| putative Xa1-like protein [Sorghum bicolor]	1284	2E-68
					>dbj|BAD29495.1| putative bacterial blight-resistance protein Xa1 [Oryza sativa(japonica cultivar-group)] dbj|BAD28895.1| putative bacterial blight-resistance protein Xa1 [Oryza sativa (japonica cultivar-group)]	1394	8E-40
					>emb|CAD45028.1| NBS-LRR disease resistance protein homologue [Hordeum vulgare]	1366	5E-37
					>ref|XP_464903.1| putative bacterial blight-resistance protein Xa1 [Oryza sativa(japonica cultivar-group)] dbj|BAD20050.1| putative bacterial blight-resistance protein Xa1 [Oryza sativa (japonica cultivar-group)]	1237	2E-36
					>emb|CAD45025.1| NBS-LRR disease resistance protein homologue [Hordeum vulgare]	1440	3E-36
BG842276	3.08E-07	Mo17<B73=F1	2.05	11	>dbj|BAD68857.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD68744.1| unknown protein [Oryza sativa (japonica cultivar-group)]	58	1E-10
					>ref|NP 917167.1| P0039G05.22 [Oryza sativa (japonica cultivar-group)]	54	1E-10
CD001309	3.24E-07	Mo17<B73=F1	1.43	10	>ref|XP_478414.1| putative translational inhibitor protein [Oryza sativa (japonicacultivar-group)] dbj|BAC20708.1| putative translational inhibitor protein [Oryza sativa (japonica cultivar-group)] dbj|BAD31311.1| putative translational inhibitor protein [Oryza sativa (japonica cultivar-group)]	180	4E-58
					>dbj|BAD00048.1| perchloric acid soluble translation inhibitor protein homolog[Gentiana triflora] dbj|BAC66487.1| translation-inhibitor protein [Gentiana triflora]	188	5E-54
					>ref|NP_188674.1| endoribonuclease [Arabidopsis thaliana]gb|AAK53030.1| AT3g20390/MQC12_15 [Arabidopsis thaliana] gb|AAL31178.1| AT3g20390/MQC12 15 [Arabidopsis thaliana] gb|AAM63246.1| translational inhibitor protein, putative [Arabidopsis thaliana]	187	1E-52
					>dbj|BAB02821.1| unnamed protein product [Arabidopsis thaliana]	143	1E-52
					>emb|CAE56534.1| Hypothetical protein CBG24261 [Caenorhabditis briggsae]	172	1E-32
BM348610	3.27E-07	Mo17<F1<B73	1.97	10	>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	6E-18
					>gb|ABA94002.1| NBS-LRR resistance protein, putative [Oryza sativa (japonicacultivar-group)]	1386	3E-17
					>gb|ABA97248.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]gb|ABB51090.1| mannose-specific jacalin-related lectin [Oryza sativa (japonica cultivar-group)]	306	3E-16
					>ref|XP_470893.1| putative salt-induced protein [Oryza sativa (japonicacultivar-group)] gb|AAP12924.1| putative salt-induced protein [Oryza sativa (japonica cultivar-group)] gb|AAK55472.1| putative salt-induced protein [Oryza sativa (japonica cultivar-group)]	191	1E-14
					>gb|ABA93998.1| stripe rust resistance protein Yr10 [Oryza sativa (japonicacultivar-group)]	1384	1E-14
DV549526	3.52E-07	Mo17<F1<B73	2.11	10	ns		
BM073941	3.83E-07	Mo17<B73=F1	87.98	10	>gb|AAX96835.1| Similar to beta-amyrin synthase [Oryza sativa (japonicacultivar-group)] gb|ABA92749.1| beta-amyrin synthase, putative [Oryza sativa (japonica cultivar-group)]	548	2E-48
					>emb|CAC84558.1| beta-amyrin synthase [Avena strigosa]gb|AAT38897.1| beta-amyrin synthase [Avena strigosa]	757	4E-41
					>gb|AAT38896.1| beta-amyrin synthase [Avena prostrata]	757	4E-41
					>gb|AAT38895.1| beta-amyrin synthase [Avena longiglumis]	757	4E-41
					>gb|AAT38894.1| beta-amyrin synthase [Avena longiglumis]	757	4E-41
CD573354	3.89E-07	Mo17<F1<B73	1.73	10	>gb|AAU44034.1| putative tonneau 2 [Oryza sativa (japonica cultivar-group)]	488	2E-62
					>ref|NP_568364.1| FASS (FASS 1) [Arabidopsis thaliana]gb|AAM44936.1| unknown protein [Arabidopsis thaliana] gb|AAK26026.1| unknown protein [Arabidopsis thaliana] gb|AAG35778.1| tonneau 2 [Arabidopsis thaliana] gb|AAG35792.1| tonneau 2 [Arabidopsis thaliana]	480	3E-59
BM080257	4.13E-07	Mo17<F1<B73	2.07	10	>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	2E-23
					>gb|ABA94002.1| NBS-LRR resistance protein, putative [Oryza sativa (japonicacultivar-group)]	1386	8E-23
					>gb|ABA97248.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]gb|ABB51090.1| mannose-specific jacalin-related lectin [Oryza sativa (japonica cultivar-group)]	306	2E-21
					>ref|NP_908901.1| Mannose-Binding Rice Lectin [Oryza sativa (japonicacultivar-group)] gb|AAK82986.1| salt-induced protein [Oryza sativa (japonica cultivar-group)] gb|AAL30827.1| lectin-like protein [Oryza sativa] dbj|BAB93403.1| salT gene product [Oryza sativa (japonica cultivar-group)] dbj|BAB63898.1| salT gene product [Oryza sativa (japonica cultivar-group)] dbj|BAA25369.1| MRL [Oryza sativa (japonica cultivar-group)]	145	6E-21
					>emb|CAA81059.1| salT [Oryza sativa]gb|AAB23484.1| 15 kda organ-specific salt-induced protein [Oryza sativa] sp|P24120|SALT_ORYSA Salt stress-induced protein (Salt protein)	145	8E-21
CB331053	4.26E-07	Mo17<F1<B73	2.06	10	ns		
BM332688	4.35E-07	Mo17<F1<B73	1.95	10	>ref|XP 473776.1| OSJNBa0041A02.14 [Oryza sativa (japonica cultivar-group)]emb|CAD41867.2| OSJNBa0041A02.14 [Oryza sativa (japonica cultivar-group)]	396	8E-59
					>emb|CAA67728.1| pectinacetylesterase precursor [Vigna radiata var. radiata]	399	3E-43
					>ref|NP_193677.2| carboxylic ester hydrolase [Arabidopsis thaliana]gb|AAU45212.1| At4g19420 [Arabidopsis thaliana] gb|AAT70429.1| At4g19420 [Arabidopsis thaliana]	397	1E-39
					>dbj|BAD94548.1| pectinacetylesterase like protein [Arabidopsis thaliana]	195	1E-39
					>ref|XP_467338.1| putative pectin acetylesterase [Oryza sativa (japonicacultivar-group)] dbj|BAD08059.1| putative pectin acetylesterase [Oryza sativa (japonica cultivar-group)] dbj|BAD07550.1| putative pectin acetylesterase [Oryza sativa (japonica cultivar-group)]	397	9E-37
BM338343	4.48E-07	B73<F1<Mo17	3.74	3	ns		

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
BM073284	5.60E-07	B73<F1=Mo17	16.57	3	>sp|P56879|CIRB CHAPA Circulin-B (CIRB)	31	7E-7
CB331466	5.96E-07	Mo17<F1<B73	2.38	10	>dbj|BAD53494.1| putative Synoviolin 1 [Oryza sativa (japonica cultivar-group)]dbj|BAD53976.1| putative Synoviolin 1 [Oryza sativa (japonica cultivar-group)]	500	1E-31
					>ref|NP_188230.1| protein binding / ubiquitin-protein ligase/ zinc ion binding[Arabidopsis thaliana] gb|AAY57599.1| RING finger family protein [Arabidopsis thaliana] dbj|BAB02675.1| unnamed protein product [Arabidopsis thaliana] dbj|BAC41836.1| putative zinc finger protein [Arabidopsis thaliana]	492	4E-26
					>ref|NP_849843.3| protein binding / ubiquitin-protein ligase/ zinc ion binding[Arabidopsis thaliana] gb|AAR23700.1| At1g65040 [Arabidopsis thaliana] dbj|BAD42325.1| Hrd1p like protein [Arabidopsis thaliana]	460	3E-24
					>ref|NP 176684.3| protein binding / ubiquitin-protein ligase/ zinc ion binding[Arabidopsis thaliana]	389	3E-24
					>gb|AAF06038.1| Contains a PF|00097 Zinc finger, C3HC4 type (RING finger) domain.ESTs gb|N96912 and gb|AI994359 come from this gene. [Arabidopsis thaliana]	496	2E-20
CD661786	6.09E-07	Mo17<F1<B73	2.62	10	>ref|XP 470140.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAO65872.1| unknown protein [Oryza sativa (japonica cultivar-group)]	474	3E-9
					>ref|NP_190229.1| transporter [Arabidopsis thaliana]emb|CAB62036.1| putative protein [Arabidopsis thaliana] gb|AAM78037.1| AT3g46450/F18L15_170 [Arabidopsis thaliana] gb|AAM19794.1| AT3g46450/F18L15 170 [Arabidopsis thaliana]	486	1E-6
					>ref|NP 974390.1| transporter [Arabidopsis thaliana]	494	1E-6
BM350119	6.58E-07	Mo17<F1<B73	2.54	10	>gb|AAT77407.1| unknown protein [Oryza sativa (japonica cultivar-group)]	297	6E-52
					>dbj|BAB74712.1| all3013 [Nostoc sp. PCC 7120]ref|NP 487053.1| hypothetical protein all3013 [Nostoc sp. PCC 7120]	247	1E-33
					>gb|ABA20522.1| Protein of unknown function DUF561 [Anabaena variabilis ATCC 29413]ref|YP_321417.1| Protein of unknown function DUF561 [Anabaena variabilis ATCC 29413]	247	5E-33
					>ref|ZP_00514859.1| Protein of unknown function DUF561 [Crocosphaera watsonii WH 8501]gb|EAM52697.1| Protein of unknown function DUF561 [Crocosphaera watsonii WH 8501]	246	3E-32
					>ref|ZP 00107581.1| COG0294: Dihydropteroate synthase and related enzymes [Nostocpunctiforme PCC 73102]	248	4E-32
DV550757	6.72E-07	Mo17<F1<B73	3.86	9	>dbj|BAD72327.1| unknown protein [Oryza sativa (japonica cultivar-group)]	650	2E-59
					>ref|NP_200157.2| ORG1; ATP binding / kinase/ protein kinase/ proteinserine/threonine kinase [Arabidopsis thaliana] gb|AAL38683.1| unknown protein [Arabidopsis thaliana]	590	5E-27
					>ref|NP_851182.1| ORG1; ATP binding / kinase/ protein kinase/ proteinserine/threonine kinase [Arabidopsis thaliana] ref|NP_001032069.1| ORG1; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] gb|AAP37769.1| At5g53450 [Arabidopsis thaliana] dbj|BAA97322.1| unnamed protein product [Arabidopsis thaliana] gb|AAN72012.1| putative protein [Arabidopsis thaliana]	670	5E-27
BG841837	7.62E-07	Mo17<F1<B73	2.38	9	ns		
BM336348	7.72E-07	Mo17<F1<B73	1.7	10	>dbj|BAD28236.1| putative ASR2 [Oryza sativa (japonica cultivar-group)]	105	6E-10
					>gb|AAY98008.1| ASR3 [Solanum habrochaites]gb|AAY98005.1| ASR3 [Lycopersicon peruvianum var. humifusum] gb|AAY98004.1| ASR3 [Lycopersicon cheesmaniae]	108	1E-9
					>gb|AAY98007.1| ASR3 [Lycopersicon chilense]	108	1E-9
					>gb|AAY98003.1| ASR3 [Lycopersicon esculentum var. cerasiforme]	108	1E-9
					>gb|AAP46155.1| ASR-like protein 1 [Hevea brasiliensis]	108	3E-9
CB280860	8.51E-07	Mo17<F1<B73	3.79	9	ns		
BM074011	9.71E-07	Mo17<F1<B73	2.08	10	>emb|CAA48641.1| type II light-harvesting chlorophyll a /b-binding protein [Zeamays]	229	9E-9
					>gb|AAC28490.1| photosystem II type II chlorophyll a/b binding protein [Sorghumbicolor]	191	9E-9
					>gb|AAA18555.1| putative. light-harvesting chlorophyll A/B binding protein	35	3E-8
					>ref|NP_178585.1| LHCB2.1; chlorophyll binding [Arabidopsis thaliana]gb|AAD31358.1| putative chlorophyll a/b binding protein [Arabidopsis thaliana] gb|AAK96540.1| At2g05100/F15L11.2 [Arabidopsis thaliana] gb|AAK96468.1| At2g05100/F15L11.2 [Arabidopsis thaliana] gb|AAN71932.1| putative chlorophyll a/b binding protein [Arabidopsis thaliana]	265	4E-8
					>gb|AAT81763.1| chlorophyll a/b binding protein [Oryza sativa (japonicacultivar-group)]	263	4E-8
DV550511	9.76E-07	Mo17<F1<B73	2.93	10	>gb|AAY26526.1| 12-oxo-phytodienoic acid reductase [Zea mays]	372	4E-33
					>emb|CAD89605.1| oxo-phytodienoic acid reductase [Oryza sativa (japonicacultivar-group)]	237	3E-23
					>dbj|BAD35835.1| putative 12-oxophytodienoic acid reductase [Oryza sativa (japonicacultivar-group)] dbj|BAD35327.1| putative 12-oxophytodienoic acid reductase [Oryza sativa (japonica cultivar-group)]	264	3E-23
					>dbj|BAD35833.1| putative 12-oxophytodienoic acid reductase [Oryza sativa (japonicacultivar-group)] dbj|BAD35325.1| putative 12-oxophytodienoic acid reductase [Oryza sativa (japonica cultivar-group)]	376	3E-23
					>emb|CAD89604.1| oxo-phytodienoic acid reductase [Oryza sativa (japonicacultivar-group)] dbj|BAD35834.1| 12-oxophytodienoic acid reductase [Oryza sativa (japonica cultivar-group)] dbj|BAD35326.1| 12-oxophytodienoic acid reductase [Oryza sativa (japonica cultivar-group)] dbj|BAD26703.1| 12-oxo-phytodienoic acid reductase [Oryza sativa (japonica cultivar-group)] dbj|BAC20139.1| 12-oxophytodienoic acid reductase [Oryza sativa] pir||JC8028 cis-12-oxo-phytodienoic acid-reductase 1 - rice	380	3E-23
BM334482	1.03E-06	Mo17<F1<B73	2.37	9	ns		
DV493868	1.15E-06	Mo17<B73=F1	2.19	10	ns		

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
BM080645	1.27E-06	Mo17<B73<F1	2.08	11	>dbj|BAD68857.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD68744.1| unknown protein [Oryza sativa (japonica cultivar-group)]	58	1E-10
					>ref|NP 917167.1| P0039G05.22 [Oryza sativa (japonica cultivar-group)]	54	1E-10
BM333995	1.38E-06	Mo17<F1<B73	1.86	10	>gb|AAV88601.1| low temperature and salt responsive protein [Pennisetum glaucum]	56	4E-17
					>ref|XP_479247.1| putative low temperature and salt responsive protein [Oryza sativa(japonica cultivar-group)] gb|AAS72305.1| drought-induced hydrophobic protein [Oryza sativa (japonica cultivar-group)] dbj|BAC16385.1| putative low temperature and salt responsive protein [Oryza sativa (japonica cultivar-group)] sp|Q8H5T6|LTI6A_ORYSA Hydrophobic protein LTI6A (Low temperature-induced protein 6A) gb|AAT37941.1| low temperature-induced low molecular weight integral membrane protein LTI6a [Oryza sativa (japonica cultivar-group)]	56	6E-16
					>ref|NP 908456.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]	537	4E-14
					>dbj|BAD34659.1| plasma membrane protein 3 [Leymus chinensis]	54	6E-13
					>dbj|BAD34658.1| plasma membrane protein 3 [Leymus chinensis]	54	8E-13
DV550844	1.53E-06	B73<F1=Mo17	2.05	3	ns		
BM379118	1.56E-06	Mo17<F1<B73	1.89	10	>ref|XP_475416.1| putative 40S ribosomal protein S26 [Oryza sativa (japonicacultivar-group)] gb|AAT01360.1| putative 40S ribosomal protein S26 [Oryza sativa (japonica cultivar-group)]	194	5E-32
					>dbj|BAD87076.1| putative ribosomal protein S26 [Oryza sativa (japonicacultivar-group)] dbj|BAD73505.1| putative ribosomal protein S26 [Oryza sativa (japonica cultivar-group)]	133	5E-32
					>sp|P49216|RS26 ORYSA 40S ribosomal protein S26 (S31)dbj|BAA07208.1| ribosomal protein S31 [Oryza sativa (japonica cultivar-group)]	133	5E-31
					>gb|AAD47346.1| ribosomal protein S26 [Pisum sativum]	130	2E-26
					>ref|NP_191193.1| structural constituent of ribosome [Arabidopsis thaliana]emb|CAB87433.1| 40S ribosomal protein S26 homolog [Arabidopsis thaliana] gb|AAM91494.1| AT3g56340/F18O21 300 [Arabidopsis thaliana] gb|AAK63990.1| AT3g56340/F18O21 300 [Arabidopsis thaliana]	130	1E-25
CB885848	1.56E-06	Mo17<F1<B73	1.5	9	ns		
BM080387	1.59E-06	Mo17<B73=F1	1.84	10	>ref|NP_915433.1| putative triosephosphate isomerase [Oryza sativa (japonicacultivar-group)] dbj|BAB93230.1| putative triosephosphate isomerase [Oryza sativa (japonica cultivar-group)]	255	1E-55
					>ref|XP_462797.1| putative triosephosphate isomerase [Oryza sativa (japonicacultivar-group)] dbj|BAB21144.1| putative triosephosphate isomerase [Oryza sativa (japonica cultivar-group)] dbj|BAB43989.1| putative triosephosphate isomerase [Oryza sativa (japonica cultivar-group)] sp|P48494|TPIS_ORYSA Triosephosphate isomerase, cytosolic (TIM) (Triose-phosphate isomerase) gb|AAA18541.1| triosephosphate isomerase	253	3E-51
					>gb|AAB81110.1| triosephosphate isomerase 1 [Zea mays]sp|P12863|TPIS_MAIZE Triosephosphate isomerase, cytosolic (TIM) (Triose-phosphate isomerase) dbj|BAA00009.1| triosephosphate isomerase [Zea mays]	253	8E-50
					>gb|ABA46792.1| triosphosphate isomerase-like protein [Solanum tuberosum]	257	3E-49
					>emb|CAA81487.1| triosephosphate isomerase [Secale cereale]sp|P46226|TPIS_SECCE Triosephosphate isomerase, cytosolic (TIM) (Triose-phosphate isomerase) prf||2109226A triosephosphate isomerase	253	5E-49
BM073783	1.66E-06	Mo17<B73=F1	26.95	10	ns		
CD662028	1.67E-06	Mo17<F1<B73	1.61	10	ns		
DV490342	1.69E-06	B73<F1=Mo17	1.99	3	>gb|AAO72582.1| unknown [Oryza sativa (japonica cultivar-group)]	168	1E-69
					>ref|NP_567639.1| unknown protein [Arabidopsis thaliana]gb|AAK93755.1| unknown protein [Arabidopsis thaliana] gb|AAK28638.1| unknown protein [Arabidopsis thaliana]	202	4E-62
					>gb|AAM62876.1| unknown [Arabidopsis thaliana]	202	4E-62
					>gb|AAT85217.1| unknown protein [Oryza sativa (japonica cultivar-group)]	229	3E-61
					>ref|NP_192392.1| unknown protein [Arabidopsis thaliana]emb|CAB80848.1| putative protein [Arabidopsis thaliana] gb|AAM10171.1| unknown protein [Arabidopsis thaliana] gb|AAL24428.1| Unknown protein [Arabidopsis thaliana] gb|AAM67017.1| unknown [Arabidopsis thaliana] gb|AAD03444.1| contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana]	139	2E-59
BM073887	1.97E-06	Mo17<F1<B73	1.64	10	>gb|AAV66923.1| peroxiredoxin Q [Triticum aestivum]	217	1E-46
					>dbj|BAD35223.1| putative peroxiredoxin Q [Oryza sativa (japonica cultivar-group)]	217	3E-45
					>gb|AAS46230.1| peroxiredoxin Q [Populus balsamifera subsp. trichocarpa x Populusdeltoides]	213	8E-44
					>dbj|BAA90524.1| peroxiredoxin Q [Sedum lineare]	186	7E-43
					>dbj|BAD04985.1| peroxiredoxin Q [Gentiana triflora]	217	6E-42
CB380836	2.03E-06	Mo17<F1<B73	1.59	10	ns		
CB351538	2.05E-06	Mo17<F1<B73	1.75	10	>ref|XP 472647.1| OSJNBa0027P08.12 [Oryza sativa (japonica cultivar-group)]emb|CAD40966.2| OSJNBa0027P08.12 [Oryza sativa (japonica cultivar-group)]	198	3E-43
					>dbj|BAD44498.1| hypothetical protein [Arabidopsis thaliana]dbj|BAD43285.1| hypothetical protein [Arabidopsis thaliana]	201	6E-20
DV622216	2.12E-06	B73=F1<Mo17	1.74	4	>ref|XP_550490.1| putative beta 1,3 glucan synthase [Oryza sativa (japonicacultivar-group)] dbj|BAD67750.1| putative beta 1,3 glucan synthase [Oryza sativa (japonica cultivar-group)]	1771	3E-34
					>gb|AAY90061.1| putative 1,3-beta-glucan synthase 12 [Triticum aestivum]	108	1E-33
					>ref|NP_912451.1| Putative callose synthase [Oryza sativa (japonica cultivar-group)]gb|AAO15292.1| Putative callose synthase [Oryza sativa (japonica cultivar-group)]	2055	1E-27

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP 850271.1| ATGSL08 (GLUCAN SYNTHASE-LIKE 8); 1,3-beta-glucan synthase/transferase, transferring glycosyl groups [Arabidopsis thaliana]	1680	2E-27
					>gb|AAD31571.1| putative glucan synthase [Arabidopsis thaliana]	784	2E-27
BM348583	2.16E-06	Mo17<B73=F1	26	10	>ref|XP_482909.1| putative cytochrome P450 [Oryza sativa (japonica cultivar-group)]dbj|BAD09367.1| putative cytochrome P450 [Oryza sativa (japonica cultivar-group)]	510	2E-6
BG841156	2.46E-06	B73<F1=Mo17	2.02	2	>ref|XP_550207.1| putative carboxypeptidase D [Oryza sativa (japonicacultivar-group)] dbj|BAD61439.1| putative carboxypeptidase D [Oryza sativa (japonica cultivar-group)]	471	7E-74
					>emb|CAB58992.1| serine carboxypeptidase II-1 [Hordeum vulgare subsp. vulgare]gb|AAB31591.1| CP-MII.1=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 324 aa] sp|P55747|CBP21_HORVU Serine carboxypeptidase II-1 precursor (CP-MII.1) [Contains: Serine carboxypeptidase II-1 chain A; Serine carboxypeptidase II-1 chain B]	324	2E-71
					>ref|NP_909340.1| putative carboxypeptidase D [Oryza sativa (japonicacultivar-group)] dbj|BAB08188.1| Similar to Hordeum vulgare carboxypeptidase D precursor (T05701) [Oryza sativa (japonica cultivar-group)]	490	5E-71
					>gb|AAV43957.1| putative serine carboxypeptidase II [Oryza sativa (japonicacultivar-group)]	483	7E-61
					>sp||P08819_2 [Segment 2 of 2] Serine carboxypeptidase II (Carboxypeptidase D)(CPDW-II) (CP-WII) [Contains: Serine carboxypeptidase II chain A; Serine carboxypeptidase II chain B] pdb|1BCS|B Chain B, Complex Of The Wheat Serine Carboxypeptidase, Cpdw-Ii, With The Microbial Peptide Aldehyde Inhibitor, Chymostatin, And Arginine At 100 Degrees Kelvin pdb|1BCR|B Chain B, Complex Of The Wheat Serine Carboxypeptidase, Cpdw-Ii, With The Microbial Peptide Aldehyde Inhibitor, Antipain, And Arginine At Room Temperature prf||1408164B CPase II B	160	6E-58
BG842726	2.48E-06	Mo17<F1<B73	1.95	10	>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	2E-23
					>gb|ABA94002.1| NBS-LRR resistance protein, putative [Oryza sativa (japonicacultivar-group)]	1386	3E-22
					>gb|ABA97248.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]gb|ABB51090.1| mannose-specific jacalin-related lectin [Oryza sativa (japonica cultivar-group)]	306	2E-21
					>ref|NP_908901.1| Mannose-Binding Rice Lectin [Oryza sativa (japonicacultivar-group)] gb|AAK82986.1| salt-induced protein [Oryza sativa (japonica cultivar-group)] gb|AAL30827.1| lectin-like protein [Oryza sativa] dbj|BAB93403.1| salT gene product [Oryza sativa (japonica cultivar-group)] dbj|BAB63898.1| salT gene product [Oryza sativa (japonica cultivar-group)] dbj|BAA25369.1| MRL [Oryza sativa (japonica cultivar-group)]	145	5E-21
					>emb|CAA81059.1| salT [Oryza sativa]gb|AAB23484.1| 15 kda organ-specific salt-induced protein [Oryza sativa] sp|P24120|SALT_ORYSA Salt stress-induced protein (Salt protein)	145	6E-21
CD527338	2.49E-06	B73<F1<Mo17	1.56	3	>emb|CAA55022.1| beta tubulin [Oryza sativa (japonica cultivar-group)]	447	3E-66
					>emb|CAE52516.1| beta tubulin [Setaria viridis]	448	3E-66
					>ref|NP_915874.1| tubulin beta chain [Oryza sativa (japonica cultivar-group)]dbj|BAB92274.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] dbj|BAA06381.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|P45960|TBB4 ORYSA Tubulin beta-4 chain (Beta-4 tubulin)	447	3E-66
					>gb|AAA66495.1| beta-tubulin	447	3E-66
					>sp|Q41783|TBB6 MAIZE Tubulin beta-6 chain (Beta-6 tubulin)gb|AAA20186.1| beta-6 tubulin	446	3E-66
CB605250	2.56E-06	Mo17<F1<B73	1.82	10	ns		
CD001318	2.61E-06	Mo17<F1<B73	1.68	10	>gb|AAO72574.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]	409	8E-69
					>ref|XP_464689.1| putative elongation factor 1-gamma [Oryza sativa (japonicacultivar-group)] dbj|BAD17614.1| putative elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]	414	8E-69
					>ref|XP_464690.1| Elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]dbj|BAD17615.1| Elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)] sp|Q9ZRI7|EF1G ORYSA Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) dbj|BAA34206.1| elongation factor 1B gamma [Oryza	418	1E-68
					>gb|AAO72563.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]	413	2E-66
					>dbj|BAD61932.1| putative elongation factor 1 gamma [Oryza sativa (japonicacultivar-group)] dbj|BAD61828.1| putative elongation factor 1 gamma [Oryza sativa (japonica cultivar-group)]	416	2E-66
CB833609	2.68E-06	Mo17<B73=F1	2.27	10	ns		
DV621316	2.70E-06	Mo17<F1<B73	2.42	10	ns		
BM079864	2.91E-06	B73<F1<Mo17	4.31	3	>sp|P56879|CIRB CHAPA Circulin-B (CIRB)	31	8E-7
DV622490	3.02E-06	Mo17<B73=F1	1.89	10	>gb|AAV50043.1| metallothionein-like protein [Saccharum hybrid cultivar]	81	1E-6
DV491214	3.29E-06	Mo17<B73=F1	1.84	10	>ref|XP_475718.1| putative gamma-glutamyl hydrolase [Oryza sativa (japonicacultivar-group)] gb|AAT01320.1| putative gamma-glutamyl hydrolase [Oryza sativa (japonica cultivar-group)]	337	3E-98
					>ref|NP_565186.2| catalytic/ gamma-glutamyl hydrolase [Arabidopsis thaliana]gb|AAM20068.1| putative gamma glutamyl hydrolase [Arabidopsis thaliana] gb|AAL49804.1| putative gamma glutamyl hydrolase [Arabidopsis thaliana] sp|O65355|GGH_ARATH Gamma-glutamyl hydrolase precursor (Gamma-Glu-X carboxypeptidase) (Conjugase) (GH)	347	4E-69
					>gb|AAC83041.1| Strong similarity to gb|AF067141 gamma-glutamyl hydrolase fromArabidopsis thaliana. ESTs gb|R83955, gb|T45062, gb|T22220, gb|AA586207, gb|AI099851 and gb|AI00672 come from this gene pir||F96815 hypothetical protein F9K20.28 [imported] - Arabidopsis thaliana	327	4E-69
					>gb|AAC33745.1| gamma-glutamyl hydrolase [Arabidopsis thaliana]pir||T52030 gamma-glutamyl hydrolase [imported] - Arabidopsis thaliana	326	2E-68
					>ref|NP_177987.1| catalytic/ gamma-glutamyl hydrolase [Arabidopsis thaliana]ref|NP_974172.1| catalytic/ gamma-glutamyl hydrolase [Arabidopsis thaliana] gb|AAD30570.1| putative gamma-glutamyl hydrolase [Arabidopsis thaliana]	348	2E-67

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
CB334713	3.32E-06	Mo17<F1<B73	2.27	10	>dbj|BAD53494.1| putative Synoviolin 1 [Oryza sativa (japonica cultivar-group)]dbj|BAD53976.1| putative Synoviolin 1 [Oryza sativa (japonica cultivar-group)]	500	1E-31
					>ref|NP_188230.1| protein binding / ubiquitin-protein ligase/ zinc ion binding[Arabidopsis thaliana] gb|AAY57599.1| RING finger family protein [Arabidopsis thaliana] dbj|BAB02675.1| unnamed protein product [Arabidopsis thaliana] dbj|BAC41836.1| putative zinc finger protein [Arabidopsis thaliana]	492	5E-26
					>ref|NP_849843.3| protein binding / ubiquitin-protein ligase/ zinc ion binding[Arabidopsis thaliana] gb|AAR23700.1| At1g65040 [Arabidopsis thaliana] dbj|BAD42325.1| Hrd1p like protein [Arabidopsis thaliana]	460	5E-24
					>ref|NP_176684.3| protein binding / ubiquitin-protein ligase/ zinc ion binding[Arabidopsis thaliana]	389	5E-24
					>gb|AAF06038.1| Contains a PF|00097 Zinc finger, C3HC4 type (RING finger) domain.ESTs gb|N96912 and gb|AI994359 come from this gene. [Arabidopsis thaliana]	496	3E-20
CB605258	3.38E-06	Mo17<F1<B73	1.54	10	ns		
CD661852	3.42E-06	Mo17<F1<B73	1.56	10	>ref|NP_912417.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]gb|AAP06860.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	117	1E-15
					>ref|NP_192563.2| unknown protein [Arabidopsis thaliana]gb|AAN15541.1| unknown protein [Arabidopsis thaliana] gb|AAL62398.1| unknown protein [Arabidopsis thaliana]	113	5E-9
AI615090	3.65E-06	Mo17<F1<B73	2.14	10	>ref|XP_550034.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD52799.1| unknown protein [Oryza sativa (japonica cultivar-group)]	489	2E-13
					>ref|XP_550033.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD52798.1| unknown protein [Oryza sativa (japonica cultivar-group)]	526	9E-9
CD661780	3.65E-06	Mo17<F1<B73	1.56	10	ns		
CB334529	3.75E-06	B73<F1=Mo17	1.49	3	>emb|CAA55022.1| beta tubulin [Oryza sativa (japonica cultivar-group)]	447	2E-80
					>emb|CAE52516.1| beta tubulin [Setaria viridis]	448	2E-80
					>ref|NP_915874.1| tubulin beta chain [Oryza sativa (japonica cultivar-group)]dbj|BAB92274.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] dbj|BAA06381.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|P45960|TBB4_ORYSA Tubulin beta-4 chain (Beta-4 tubulin)	447	2E-80
					>gb|AAA66495.1| beta-tubulin	447	2E-80
					>sp|Q41783|TBB6_MAIZE Tubulin beta-6 chain (Beta-6 tubulin)gb|AAA20186.1| beta-6 tubulin	446	2E-80
CD670393	3.76E-06	Mo17<B73=F1	3.47	10	>ref|XP_480212.1| WD-40 repeat protein-like [Oryza sativa (japonica cultivar-group)]dbj|BAC99788.1| WD-40 repeat protein-like [Oryza sativa (japonica cultivar-group)]	1150	8E-7
BG840776	3.77E-06	Mo17<F1<B73	2.01	10	>gb|AAM22751.1| one helix protein [Deschampsia antarctica]	110	2E-24
					>gb|AAP23938.1| one helix protein [Ipomoea nil]	116	2E-24
					>gb|ABA98252.1| one helix protein [Oryza sativa (japonica cultivar-group)]	113	4E-24
					>gb|AAM62880.1| one helix protein OHP [Arabidopsis thaliana]	110	5E-23
					>ref|NP_195832.1| OHP (ONE HELIX PROTEIN) [Arabidopsis thaliana]emb|CAB82985.1| one helix protein (OHP) [Arabidopsis thaliana] gb|AAM10146.1| one helix protein (OHP) [Arabidopsis thaliana] gb|AAL32924.1| one helix protein (OHP) [Arabidopsis thaliana] gb|AAC25108.1| one helix protein [Arabidopsis thaliana]	110	5E-23
CD568360	3.89E-06	B73<F1<Mo17	2.28	3	>gb|AAV67827.1| unknown protein [Oryza sativa (japonica cultivar-group)]	400	1E-35
					>ref|XP_475819.1| unknown protein [Oryza sativa (japonica cultivar-group)]	358	6E-27
					>ref|XP_465099.1| hydrolase, alpha/beta fold family protein-like [Oryza sativa(japonica cultivar-group)] dbj|BAD23358.1| hydrolase, alpha/beta fold family protein-like [Oryza sativa (japonica cultivar-group)]	289	9E-10
					>dbj|BAA97145.1| unnamed protein product [Arabidopsis thaliana]	438	3E-9
					>ref|NP_974930.1| catalytic/ hydrolase [Arabidopsis thaliana]ref|NP_001032065.1| catalytic/ hydrolase [Arabidopsis thaliana]	396	3E-9
CD527368	4.00E-06	B73<F1=Mo17	1.61	3	ns		
BG842228	4.03E-06	Mo17<F1<B73	2.1	10	>ref|XP_479171.1| putative alanine aminotransferase [Oryza sativa (japonicacultivar-group)] dbj|BAC79995.1| putative alanine aminotransferase [Oryza sativa (japonica cultivar-group)] dbj|BAC79866.1| putative alanine aminotransferase [Oryza sativa (japonica cultivar-group)]	486	2E-21
					>gb|AAV64237.1| putative alanine aminotransferase [Zea mays]	516	4E-21
					>gb|AAV64199.1| putative alanine aminotransferase [Zea mays]	516	4E-21
					>emb|CAE54279.1| putative alanine aminotransferase [Triticum aestivum]	113	7E-20
					>emb|CAA49199.1| alanine aminotransferase [Panicum miliaceum]sp|P34106|ALA2_PANMI Alanine aminotransferase 2 (GPT) (Glutamic--pyruvic transaminase 2) (Glutamic--alanine transaminase 2) (ALAAT-2)	482	1E-18
BM075132	4.40E-06	Mo17<F1<B73	2.18	9	>gb|AAW48295.1| pore-forming toxin-like protein Hfr-2 [Triticum aestivum]	492	3E-9
CD651747	4.71E-06	Mo17<F1<B73	1.61	10	ns		
BM340381	4.80E-06	Mo17<B73=F1	10.73	10	ns		
CD484960	5.53E-06	Mo17<B73<F1	1.66	12	>gb|AAF71261.2| beta-glucosidase aggregating factor precursor [Zea mays]	306	2E-37
					>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	6E-35
					>gb|AAR20919.1| jasmonate-induced protein [Triticum aestivum]	304	2E-34
					>gb|ABA97248.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]gb|ABB51090.1| mannose-specific jacalin-related lectin [Oryza sativa (japonica cultivar-group)]	306	3E-34
					>gb|AAB72098.1| 32 kDa protein [Hordeum vulgare]	306	5E-34

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
CB603943	5.73E-06	Mo17<B73=F1	1.65	10	>ref|XP_493844.1| putative glutathione S-transferase [Oryza sativa (japonicacultivar-group)] gb|AAN64482.1| putative glutathione S-transferase [Oryza sativa (japonica cultivar-group)]	244	2E-50
					>emb|CAA76758.1| putative In2.1 protein [Triticum aestivum]	243	1E-41
					>ref|XP_493845.1| putative glutathione S-transferase [Oryza sativa (japonicacultivar-group)] gb|AAN64486.1| putative glutathione S-transferase [Oryza sativa (japonica cultivar-group)]	255	1E-40
					>gb|AAF70831.1| XIG [Oryza sativa]	243	1E-40
					>emb|CAA41447.1| In2-1 [Zea mays]sp|P49248|IN21 MAIZE IN2-1 protein	243	1E-39
BM073594	6.07E-06	B73<F1=Mo17	2.04	3	>ref|NP_915626.1| putative uricase [Oryza sativa (japonica cultivar-group)]dbj|BAC01199.1| putative uricase [Oryza sativa (japonica cultivar-group)] dbj|BAB63819.1| putative uricase [Oryza sativa (japonica cultivar-group)]	307	3E-68
					>gb|AAA33994.1| nodulin 35	309	1E-52
					>prf||1109273A nodulin 35	309	4E-52
					>sp|O04104|URID SOYBN Uricase II isozyme 2 (Urate oxidase) (Nodulin 35) (N-35)(Non-symbiotic uricase) dbj|BAA19672.1| nodulin 35 [Glycine max]	309	7E-52
					>sp|P53763|URIC PHAVU Uricase II (Urate oxidase) (Nodule-specific uricase)gb|AAB97726.1| uricase II [Phaseolus vulgaris]	308	2E-51
CD484869	6.13E-06	Mo17<B73=F1	1.78	10	>gb|AAV50043.1| metallothionein-like protein [Saccharum hybrid cultivar]	81	3E-10
					>gb|AAS88721.1| metallothionein-like protein [Cynodon dactylon]	81	5E-9
					>emb|CAC40757.1| putative metallothionein-like protein type 2B [Atropa belladonna]	81	1E-8
					>ref|NP_909265.1| putative metallothionein-like protein [Oryza sativa (japonicacultivar-group)] dbj|BAD52374.1| metallothionein [Oryza rufipogon] dbj|BAD52373.1| metallothionein [Oryza rufipogon] dbj|BAD52372.1| metallothionein [Oryza rufipogon] dbj|BAD52371.1| metallothionein [Oryza rufipogon] dbj|BAD52370.1| metallothionein [Oryza rufipogon] dbj|BAD52369.1| metallothionein [Oryza rufipogon] dbj|BAD52368.1| metallothionein [Oryza rufipogon] dbj|BAD52367.1| metallothionein [Oryza rufipogon] dbj|BAD52366.1| metallothionein [Oryza rufipogon] dbj|BAD52365.1| metallothionein [Oryza rufipogon] dbj|BAD52364.1| metallothionein [Oryza rufipogon] dbj|BAD52363.1| metallothionein [Oryza rufipogon] dbj|BAD52362.1| metallothionein [Oryza rufipogon] dbj|BAB44010.1| putative metallothionein-like protein [Oryza sativa (japonica cultivar-group)] dbj|BAA14038.1| metallothionein-like protein [Oryza sativa] sp|P94029|MT21 ORYSA Metallothionein-like protein type 2 gb|AAC49627.1| metallothionein-like type 2	82	3E-8
					>gb|AAP80616.1| metallothionein [Triticum aestivum]	114	7E-8
BM072868	6.18E-06	Mo17<B73=F1	2.01	11	>dbj|BAD68857.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD68744.1| unknown protein [Oryza sativa (japonica cultivar-group)]	58	2E-12
					>ref|NP 917167.1| P0039G05.22 [Oryza sativa (japonica cultivar-group)]	54	1E-11
DV622257	6.54E-06	B73<F1<Mo17	1.5	3	>ref|XP 479905.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD08860.1| unknown protein [Oryza sativa (japonica cultivar-group)]	184	5E-31
					>ref|NP 176927.1| unknown protein [Arabidopsis thaliana]gb|AAM63870.1| unknown [Arabidopsis thaliana] gb|AAG28897.1| F12A21.27 [Arabidopsis thaliana]	163	2E-22
					>gb|AAM63820.1| unknown [Arabidopsis thaliana]	168	6E-22
					>ref|NP 564215.1| unknown protein [Arabidopsis thaliana]	168	6E-22
					>dbj|BAD82112.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD82771.1| unknown protein [Oryza sativa (japonica cultivar-group)]	171	4E-20
BM347617	6.84E-06	Mo17<F1<B73	3.37	10	ns		
CB281986	7.07E-06	Mo17<F1<B73	1.78	10	>gb|AAV59386.1| putative nucleoside diphosphate kinase [Oryza sativa (japonicacultivar-group)] ref|XP_476035.1| putative nucleoside diphosphate kinase [Oryza sativa (japonica cultivar-group)] gb|AAW57792.1| putative nucleoside diphosphate kinase [Oryza sativa (japonica cultivar-group)]	239	7E-31
					>gb|AAF08537.1| nucleoside diphosphate kinase [Pisum sativum]	233	6E-20
					>gb|AAM65336.1| nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana]	237	6E-19
					>ref|NP_567690.1| ATP binding / nucleoside diphosphate kinase [Arabidopsis thaliana]emb|CAB81308.1| hypothetical protein [Arabidopsis thaliana] emb|CAB43890.1| hypothetical protein [Arabidopsis thaliana] dbj|BAC42534.1| unknown protein [Arabidopsis thaliana] dbj|BAB19789.1| nucleoside diphosphate kinase 4 [Arabidopsis thaliana] sp|Q8LAH8|NDK4_ARATH Nucleoside diphosphate kinase IV, chloroplast/mitochondrial precursor (NDK IV) (NDP kinase IV) (NDPK IV) (Nucleoside diphosphate kinase 4)	237	2E-18
					>ref|NP_192839.1| NDPK3 (NUCLEOSIDE DIPHOSPHATE KINASE 3); ATP binding / nucleosidediphosphate kinase [Arabidopsis thaliana] emb|CAB81202.1| nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana] emb|CAB40069.1| nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana] gb|AAL33810.1| putative nucleoside diphosphate kinase 3 [Arabidopsis thaliana] gb|AAK59688.1| putative nucleoside diphosphate kinase ndpk3 [Arabidopsis thaliana] sp|O49203|NDK3_ARATH Nucleoside diphosphate kinase III, chloroplast/mitochondrial precursor (NDK III) (NDP kinase III) (NDPK III) gb|AAC33956.1| contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] gb|AAC00512.1| nucleoside diphosphate kinase 3 [Arabidopsis thaliana]	238	3E-16
BM339765	7.37E-06	Mo17<B73=F1	8.01	10	ns		
DV550939	7.70E-06	Mo17<F1<B73	2.17	9	>ref|XP 470990.1| OSJNBb0085F13.14 [Oryza sativa (japonica cultivar-group)]emb|CAE02767.2| OSJNBb0085F13.14 [Oryza sativa (japonica cultivar-group)]	623	8E-74
					>emb|CAA40137.1| arginine decarboxylase [Avena sativa]sp|P22220|SPE1 AVESA Arginine decarboxylase (ARGDC) (ADC)	607	3E-67
					>emb|CAB64599.1| arginine decarboxylase 1 [Datura stramonium]	724	4E-35
					>emb|CAA85773.1| arginine decarboxylase [Pisum sativum]sp|Q43075|SPE1 PEA Arginine decarboxylase (ARGDC) (ADC)	728	7E-35
					>dbj|BAE71301.1| putative arginine decarboxylase [Trifolium pratense]	729	7E-35
CB604486	7.96E-06	Mo17<F1<B73	2.45	10	>ref|NP 912448.1| Unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAO15289.1| Unknown protein [Oryza sativa (japonica cultivar-group)]	240	5E-81

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_568767.1| oxidoreductase, acting on paired donors, with incorporation orreduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors [Arabidopsis thaliana] gb|AAM63324.1| unknown [Arabidopsis thaliana]	227	6E-58
					>dbj|BAA97223.1| unnamed protein product [Arabidopsis thaliana]	250	6E-58
					>gb|AAO42850.1| At5g51880 [Arabidopsis thaliana]	227	1E-57
					>ref|XP 452140.1| unnamed protein product [Kluyveromyces lactis]emb|CAH02533.1| unnamed protein product [Kluyveromyces lactis NRRL Y-1140]	227	2E-23
DV621428	8.08E-06	B73<F1=Mo17	2.14	3	>dbj|BAD38037.1| F-box protein-like [Oryza sativa (japonica cultivar-group)]dbj|BAD38264.1| F-box protein-like [Oryza sativa (japonica cultivar-group)]	428	2E-11
					>ref|XP_482875.1| F-box protein family-like [Oryza sativa (japonica cultivar-group)]dbj|BAD09570.1| F-box protein family-like [Oryza sativa (japonica cultivar-group)]	394	3E-9
					>ref|NP_172548.2| unknown protein [Arabidopsis thaliana]gb|AAU95433.1| At1g10780 [Arabidopsis thaliana] gb|AAT71950.1| At1g10780 [Arabidopsis thaliana] gb|AAD31335.1| T16B5.8 [Arabidopsis thaliana]	418	3E-6
DV621711	8.54E-06	B73<F1=Mo17	1.57	3	>ref|XP 474220.1| OSJNBa0084K01.4 [Oryza sativa (japonica cultivar-group)]emb|CAE04832.1| OSJNBa0084K01.4 [Oryza sativa (japonica cultivar-group)]	176	5E-61
					>gb|AAM67107.1| transcription co-activator-like protein [Arabidopsis thaliana]	168	2E-47
					>gb|AAV84520.1| At5g03220 [Arabidopsis thaliana]ref|NP_195942.1| unknown protein [Arabidopsis thaliana] emb|CAB86089.1| putative protein [Arabidopsis thaliana] gb|AAG40347.1| AT5g03220 [Arabidopsis thaliana] dbj|BAC42181.1| unknown protein [Arabidopsis thaliana] dbj|BAB08382.1| transcriptional co-activator-like protein [Arabidopsis thaliana]	168	6E-47
					>emb|CAB83310.1| transcriptional co-activator-like protein [Arabidopsis thaliana]gb|AAM19916.1| At5g03505/C320EPL23M [Arabidopsis thaliana] gb|AAL91616.1| At5g03505/C320EPL23M [Arabidopsis thaliana]	168	8E-47
					>ref|NP 195970.1| unknown protein [Arabidopsis thaliana]	443	4E-46
CD651118	8.78E-06	Mo17<B73=F1	1.89	11	>ref|XP_550093.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD61477.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAD61068.1| unknown protein [Oryza sativa (japonica cultivar-group)]	436	5E-91
					>ref|NP_912342.1| putative sulfolipid synthase [Oryza sativa (japonicacultivar-group)] gb|AAP06834.1| putative sulfolipid synthase [Oryza sativa (japonica cultivar-group)]	415	4E-79
					>ref|XP_476339.1| putative sulfolipid synthase [Oryza sativa (japonicacultivar-group)] dbj|BAD31817.1| putative sulfolipid synthase [Oryza sativa (japonica cultivar-group)]	479	1E-76
					>gb|AAK76635.1| unknown protein [Arabidopsis thaliana]	434	5E-75
					>ref|NP_568085.2| SQD2 (SULFOQUINOVOSYLDIACYLGLYCEROL 2); UDP-sulfoquinovose:DAGsulfoquinovosyltransferase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] gb|AAM18913.1| sulfolipid synthase [Arabidopsis thaliana] gb|AAO64198.1| unknown protein [Arabidopsis thaliana]	510	5E-75
BG842033	9.59E-06	Mo17<F1<B73	2	10	>gb|AAC37357.1| catalasesp|P18123|CATA3 MAIZE Catalase isozyme 3	496	5E-50
					>emb|CAA31057.1| unnamed protein product [Zea mays]	495	1E-39
					>gb|AAA33441.1| catalase isozyme 3 (EC 1.11.1.6)	495	1E-39
					>emb|CAH61266.1| catalase [Secale cereale]	494	6E-37
					>gb|AAC17730.1| catalase 2 [Hordeum vulgare]	394	1E-36
AW066844	9.82E-06	Mo17<F1<B73	2.09	10	ns		
BM074414	9.91E-06	Mo17<F1<B73	1.77	10	ns		
BG841239	1.01E-05	Mo17<F1<B73	17.07	10	>gb|AAV44016.1| unknown protein [Oryza sativa (japonica cultivar-group)]	468	4E-76
					>ref|NP_181336.1| unknown protein [Arabidopsis thaliana]gb|AAM45095.1| unknown protein [Arabidopsis thaliana] gb|AAL87350.1| unknown protein [Arabidopsis thaliana] gb|AAD32771.1| unknown protein [Arabidopsis thaliana]	419	9E-56
					>ref|XP 684280.1| PREDICTED: hypothetical protein XP 679188 [Danio rerio]	406	1E-9
					>ref|XP 688439.1| PREDICTED: hypothetical protein XP 683347 [Danio rerio]	273	1E-9
					>ref|XP 684100.1| PREDICTED: hypothetical protein XP 679008 [Danio rerio]	382	4E-9
CD001440	1.04E-05	Mo17<F1<B73	1.99	10	>gb|AAL76334.1| putative G-box binding protein [Oryza sativa]dbj|BAD45657.1| G-box binding protein-like [Oryza sativa (japonica cultivar-group)] gb|AAB65433.1| HvB12D homolog [Oryza sativa]	89	1E-39
					>emb|CAA70936.1| B12Dg1 [Hordeum vulgare subsp. vulgare]emb|CAA54065.1| HvB12D [Hordeum vulgare subsp. vulgare]	87	1E-35
					>gb|AAD22104.1| B12D protein [Ipomoea batatas]	90	3E-33
					>ref|NP_190397.1| unknown protein [Arabidopsis thaliana]emb|CAB51061.1| B12D-like protein [Arabidopsis thaliana] gb|AAL91215.1| B12D-like protein [Arabidopsis thaliana] gb|AAN65070.1| B12D-like protein [Arabidopsis thaliana] pir||T13003 hypothetical protein T24C20.20 - Arabidopsis thaliana	88	9E-29
					>ref|XP_477421.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]dbj|BAC84633.1| putative B12D protein [Oryza sativa (japonica cultivar-group)] dbj|BAD31625.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]	98	1E-27
DV490389	1.05E-05	Mo17<F1<B73	1.8	10	>gb|AAX11351.1| cathepsin B-like cysteine protease [Oryza sativa (japonicacultivar-group)]	358	3E-90
					>emb|CAC83720.1| cathepsin B [Hordeum vulgare subsp. vulgare]	344	2E-88
					>emb|CAA46810.1| cathepsin B [Triticum aestivum]	305	4E-88
					>emb|CAA46811.1| cathepsin B [Triticum aestivum]	353	1E-81
					>emb|CAA57522.1| cathepsin B-like cysteine proteinase [Nicotiana rustica]	356	8E-76

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15 % FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
CD001771	1.26E-05	B73<F1<Mo17	1.45	4	>emb|CAA33620.1| GAPDH [Zea mays]sp|P08735|G3PC MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 1	337	1E-68
					>emb|CAA30151.1| unnamed protein product [Zea mays]	337	1E-68
					>emb|CAA51676.1| glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zeamays] sp|Q09054|G3PD_MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 2 gb|AAA87880.1| glyceraldehyde-3-phosphate dehydrogenase gb|AAA87578.1| cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2	337	9E-67
					>gb|AAQ55397.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp.spontaneum] gb|AAQ55396.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55394.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55393.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55391.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55389.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55387.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55386.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55385.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55384.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55381.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55380.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55379.1| glyceraldehyde-3-phosphate dehydrogenase	245	8E-66
					>emb|CAA42901.1| glyceraldehyde 3-phosphate dehydrogenase [Hordeum vulgare]sp|P26517|G3PX_HORVU Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	337	8E-66
CB334677	1.27E-05	Mo17<F1<B73	2.05	10	>gb|ABA97485.1| transposon protein, putative, mutator sub-class [Oryza sativa(japonica cultivar-group)]	563	1E-13
					>ref|NP 918060.1| B1129H01.16 [Oryza sativa (japonica cultivar-group)]	732	1E-12
					>ref|NP 909653.1| putative transposon protein [Oryza sativa]gb|AAK50592.1| putative transposon protein [Oryza sativa]	475	3E-11
DV492345	1.30E-05	B73<F1<Mo17	1.88	3	>dbj|BAD28535.1| unknown protein [Oryza sativa (japonica cultivar-group)]	159	9E-62
					>ref|NP_190345.1| unknown protein [Arabidopsis thaliana]emb|CAB61987.1| putative protein [Arabidopsis thaliana] gb|AAL85048.1| unknown protein [Arabidopsis thaliana] gb|AAK76632.1| unknown protein [Arabidopsis thaliana]	408	2E-22
CD001891	1.30E-05	Mo17<F1<B73	1.69	10	ns		
CB886466	1.36E-05	Mo17<F1<B73	1.74	10	>ref|XP_475416.1| putative 40S ribosomal protein S26 [Oryza sativa (japonicacultivar-group)] gb|AAT01360.1| putative 40S ribosomal protein S26 [Oryza sativa (japonica cultivar-group)]	194	8E-32
					>dbj|BAD87076.1| putative ribosomal protein S26 [Oryza sativa (japonicacultivar-group)] dbj|BAD73505.1| putative ribosomal protein S26 [Oryza sativa (japonica cultivar-group)]	133	8E-32
					>sp|P49216|RS26 ORYSA 40S ribosomal protein S26 (S31)dbj|BAA07208.1| ribosomal protein S31 [Oryza sativa (japonica cultivar-group)]	133	6E-31
					>gb|AAD47346.1| ribosomal protein S26 [Pisum sativum]	130	2E-27
					>ref|NP_191193.1| structural constituent of ribosome [Arabidopsis thaliana]emb|CAB87433.1| 40S ribosomal protein S26 homolog [Arabidopsis thaliana] gb|AAM91494.1| AT3g56340/F18O21 300 [Arabidopsis thaliana] gb|AAK63990.1| AT3g56340/F18O21 300 [Arabidopsis thaliana]	130	2E-26
CD058853	1.38E-05	Mo17<F1<B73	1.59	10	ns		
CB250081	1.41E-05	Mo17<B73=F1	2.36	10	>dbj|BAD37611.1| putative ethylene-inducible CTR1-like protein kinase [Oryza sativa(japonica cultivar-group)]	1112	1E-90
					>dbj|BAD72566.1| putative salt-inducible protein kinase [Oryza sativa (japonicacultivar-group)] dbj|BAD72309.1| putative salt-inducible protein kinase [Oryza sativa (japonica cultivar-group)]	1273	2E-83
					>emb|CAD42651.1| putative protein kinase [Hordeum vulgare subsp. vulgare]	226	2E-80
					>ref|NP_190276.1| ATP binding / protein kinase/ protein serine/threonine kinase/protein-tyrosine kinase [Arabidopsis thaliana] emb|CAB51173.1| putative protein [Arabidopsis thaliana]	1171	3E-80
					>ref|XP 476333.1| contains EST D23238(C2469)~kinase-like protein [Oryza sativa(japonica cultivar-group)]	1270	1E-79
BM334318	1.54E-05	Mo17<F1<B73	2.28	10	ns		
BM073998	1.67E-05	Mo17<F1<B73	2.06	10	>ref|NP 914795.1| putative thioredoxin [Oryza sativa (japonica cultivar-group)]dbj|BAB90300.1| putative thioredoxin F [Oryza sativa (japonica cultivar-group)]	187	1E-51
					>sp|O81332|TRXF MESCR Thioredoxin F-type, chloroplast precursor (TRX-F)gb|AAC19392.1| thioredoxin F precursor [Mesembryanthemum crystallinum]	191	5E-46
					>emb|CAA45098.1| thioredoxin F [Pisum sativum]gb|AAC49357.1| thioredoxin f sp|P29450|TRXF PEA Thioredoxin F-type, chloroplast precursor (TRX-F)	182	3E-45
					>ref|NP_197144.1| electron transporter/ thiol-disulfide exchange intermediate[Arabidopsis thaliana] gb|AAL15192.1| putative thioredoxin f2 protein [Arabidopsis thaliana] gb|AAK44171.1| putative thioredoxin f2 protein [Arabidopsis thaliana] dbj|BAB09607.1| thioredoxin f2 [Arabidopsis thaliana] sp|Q9XFH9|TRXF2 ARATH Thioredoxin F-type 2, chloroplast precursor (TRX-F2) gb|AAD35004.1| thioredoxin f2 [Arabidopsis thaliana]	185	2E-44
					>ref|NP_186922.1| electron transporter/ thiol-disulfide exchange intermediate[Arabidopsis thaliana] gb|AAF26987.1| thioredoxin f1 [Arabidopsis thaliana] gb|AAM20355.1| putative thioredoxin f1 protein [Arabidopsis thaliana] gb|AAL38832.1| putative thioredoxin f1 protein [Arabidopsis thaliana] gb|AAM61345.1| thioredoxin f1 [Arabidopsis thaliana] sp|Q9XFH8|TRXF1 ARATH Thioredoxin F-type 1, chloroplast precursor (TRX-F1)	178	3E-43
CB381452	1.76E-05	Mo17<B73=F1	1.93	10	ns		
DV490644	1.78E-05	B73<F1<Mo17	1.7	3	ns		
CD527629	1.83E-05	Mo17<B73=F1	1.66	10	ns		
CB250100	1.93E-05	B73<F1<Mo17	1.9	4	ns		

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
CD484493	2.03E-05	F1=Mo17<B73	1.69	9	>ref|XP_466081.1| copper chaperone homolog CCH [Oryza sativa (japonicacultivar-group)] dbj|BAD25440.1| copper chaperone homolog CCH [Oryza sativa (japonica cultivar-group)] gb|AAF15285.1| copper chaperone homolog CCH [Oryza sativa]	132	2E-25
					>dbj|BAD73816.1| putative copper chaperone [Oryza sativa (japonica cultivar-group)]	252	1E-24
					>ref|NP_191183.1| CCH [Arabidopsis thaliana]emb|CAB87423.1| copper homeostasis factor [Arabidopsis thaliana] gb|AAK32872.1| AT3g56240/F18O21_200 [Arabidopsis thaliana] gb|AAL47423.1| AT3g56240/F18O21_200 [Arabidopsis thaliana] gb|AAM62878.1| copper homeostasis factor [Arabidopsis thaliana] gb|AAC33510.1| copper homeostasis factor [Arabidopsis thaliana]	121	5E-24
					>emb|CAE51321.1| chopper chaperone [Hordeum vulgare subsp. vulgare]	112	9E-24
					>gb|AAP06757.1| copper chaperone [Lycopersicon esculentum]	81	1E-23
BM073598	2.08E-05	Mo17<F1<B73	2.08	10	ns		
DV550769	2.08E-05	B73<F1=Mo17	2.48	3	>ref|XP 473863.1| OSJNBa0070C17.11 [Oryza sativa (japonica cultivar-group)]emb|CAE05204.3| OSJNBa0070C17.11 [Oryza sativa (japonica cultivar-group)]	154	3E-8
					>ref|XP 473862.1| OSJNBa0070C17.10 [Oryza sativa (japonica cultivar-group)]emb|CAE05203.3| OSJNBa0070C17.10 [Oryza sativa (japonica cultivar-group)]	202	2E-6
CB834083	2.09E-05	B73<F1=Mo17	1.6	3	>dbj|BAD28519.1| unknown protein [Oryza sativa (japonica cultivar-group)]	416	9E-47
					>dbj|BAD28520.1| unknown protein [Oryza sativa (japonica cultivar-group)]	308	8E-32
					>ref|XP 482498.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD01195.1| unknown protein [Oryza sativa (japonica cultivar-group)]	427	3E-22
					>dbj|BAD04851.1| hypothetical protein [Solanum tuberosum]	390	1E-10
					>dbj|BAD04852.2| hypothetical protein [Nicotiana benthamiana]	380	6E-9
BM349300	2.36E-05	Mo17<B73=F1	1.95	10	>gb|AAP46155.1| ASR-like protein 1 [Hevea brasiliensis]	108	1E-15
					>gb|AAP37981.1| ASR2 [Lycopersicon peruvianum var. humifusum]	112	2E-15
					>gb|AAP37983.1| ASR2 [Lycopersicon cheesmanii]gb|AAP37982.1| ASR2 [Lycopersicon esculentum var. cerasiforme] gb|AAA99440.2| ABA- and ripening-induced protein; ABA-induced protein; ripening-induced protein [Lycopersicon esculentum]	114	2E-15
					>emb|CAA52873.1| Asr2 [Lycopersicon esculentum]sp|P37219|ASR2 LYCES Abscisic stress ripening protein 2	114	2E-15
					>gb|AAL27561.1| abscisic acid response protein [Cucumis melo]gb|AAL27560.1| abscisic acid response protein [Cucumis melo]	112	3E-15
BG874176	2.40E-05	Mo17<F1<B73	2.12	10	ns		
DV549670	2.68E-05	Mo17<B73=F1	3.39	10	>gb|AAC24570.1| trypsin inhibitor [Zea mays]	174	2E-45
					>ref|NP_909091.1| putative Bowman Birk trypsin inhibitor [Oryza sativa (japonicacultivar-group)] dbj|BAB18291.1| putative Bowman Birk trypsin inhibitor [Oryza sativa (japonica cultivar-group)]	179	2E-23
					>ref|XP_549976.1| putative Bowman Birk trypsin inhibitor [Oryza sativa (japonicacultivar-group)] dbj|BAD52865.1| putative Bowman Birk trypsin inhibitor [Oryza sativa (japonica cultivar-group)] dbj|BAD52690.1| putative Bowman Birk trypsin inhibitor [Oryza sativa (japonica cultivar-group)]	186	4E-21
					>emb|CAB88391.1| putative Bowman Birk trypsin inhibitor [Oryza sativa (indicacultivar-group)]	185	6E-20
					>ref|NP_909067.1| putative Bowman Birk trypsin inhibitor [Oryza sativa (japonicacultivar-group)] dbj|BAB55531.1| putative Bowman Birk trypsin inhibitor [Oryza sativa (japonica cultivar-group)] dbj|BAB21177.1| putative Bowman Birk tryspin inhibitor [Oryza sativa (japonica cultivar-group)]	181	6E-20
DV550358	2.76E-05	B73<F1=Mo17	1.42	3	>ref|XP 549829.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD44834.1| unknown protein [Oryza sativa (japonica cultivar-group)]	363	2E-57
					>ref|NP 908351.1| P0436E04.10 [Oryza sativa (japonica cultivar-group)]	359	2E-57
					>ref|XP_468251.1| unknown protein [Oryza sativa (japonica cultivar-group)]ref|XP_507026.1| PREDICTED OJ1695_H09.11 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD19269.1| unknown protein [Oryza sativa (japonica cultivar-group)]	365	4E-56
					>ref|NP_191004.1| ubiquitin-protein ligase/ zinc ion binding [Arabidopsis thaliana]emb|CAB81801.1| RING finger-like protein [Arabidopsis thaliana] gb|AAN18187.1| At3g54360/T12E18_50 [Arabidopsis thaliana] gb|AAK95259.1| AT3g54360/T12E18_50 [Arabidopsis thaliana] gb|AAM63273.1| RING finger-like protein [Arabidopsis thaliana]	405	2E-43
					>emb|CAH89580.1| hypothetical protein [Pongo pygmaeus]	571	1E-8
CD527360	2.87E-05	B73<F1=Mo17	1.48	3	>dbj|BAD34415.1| unknown protein [Oryza sativa (japonica cultivar-group)]	206	2E-53
					>ref|NP_196729.1| unknown protein [Arabidopsis thaliana]emb|CAB87686.1| putative protein [Arabidopsis thaliana] gb|AAM51276.1| unknown protein [Arabidopsis thaliana] gb|AAL36156.1| unknown protein [Arabidopsis thaliana] gb|AAM10172.1| putative protein [Arabidopsis thaliana] gb|AAL32939.1| putative protein [Arabidopsis thaliana] gb|AAM65551.1| unknown [Arabidopsis thaliana]	207	4E-41
					>emb|CAD52808.1| hypothetical protein [Plasmodium falciparum 3D7]ref|NP 705571.1| hypothetical protein [Plasmodium falciparum 3D7]	450	3E-7
CD484245	3.00E-05	Mo17<F1<B73	1.64	10	>dbj|BAD44921.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD44911.1| unknown protein [Oryza sativa (japonica cultivar-group)]	90	3E-14
					>gb|AAM64550.1| unknown [Arabidopsis thaliana]	102	2E-11
					>gb|AAO42921.1| At4g16146 [Arabidopsis thaliana]dbj|BAC43640.1| unknown protein [Arabidopsis thaliana]	102	2E-10
					>ref|NP 567486.1| unknown protein [Arabidopsis thaliana]	102	2E-10
					>gb|ABA97694.1| expressed protein [Oryza sativa (japonica cultivar-group)]	95	2E-7
CD527382	3.04E-05	Mo17<F1<B73	1.76	10	>ref|XP_463020.1| putative Acyl-CoA-binding protein [Oryza sativa (japonicacultivar-group)] gb|AAR10857.1| putative Acyl-CoA-binding protein [Oryza sativa (japonica cultivar-group)]	155	2E-39
					>ref|NP_913999.1| putative Acyl-CoA binding protein (ACBP) [Oryza sativa (japonicacultivar-group)] dbj|BAC99898.1| putative Acyl-CoA binding protein (ACBP) [Oryza sativa (japonica cultivar-group)] dbj|BAC57826.1| putative Acyl-CoA binding protein (ACBP) [Oryza sativa (japonica cultivar-group)]	91	3E-39

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>dbj|BAB85987.1| Acyl-CoA-binding protein [Panax ginseng]	87	2E-38
					>gb|AAP82942.1| acyl-CoA-binding protein [Tropaeolum majus]	90	7E-38
					>emb|CAB56693.1| Acyl-CoA binding protein (ACBP) [Digitalis lanata]	92	3E-37
DV551208	3.08E-05	Mo17<F1<B73	1.7	10	>dbj|BAD52915.1| esterase/lipase/thioesterase-like protein [Oryza sativa (japonicacultivar-group)]	698	1E-73
					>dbj|BAD52912.1| esterase/lipase/thioesterase-like protein [Oryza sativa (japonicacultivar-group)]	682	6E-61
					>ref|NP_564662.1| catalytic [Arabidopsis thaliana]gb|AAC64874.1| Contains similarity to gi|2924495 hypothetical protein Rv1920 from Mycobacterium tuberculosis genome gb|AL022020. [Arabidopsis thaliana] gb|AAM63493.1| unknown [Arabidopsis thaliana] gb|AAO64893.1| At1g54570 [Arabidopsis thaliana] dbj|BAC43090.1| unknown protein [Arabidopsis thaliana]	704	2E-45
					>ref|NP_566801.1| catalytic [Arabidopsis thaliana]gb|AAL07256.1| unknown protein [Arabidopsis thaliana] gb|AAK25855.1| unknown protein [Arabidopsis thaliana] dbj|BAB01231.1| unnamed protein product [Arabidopsis thaliana]	701	4E-43
					>ref|NP 198929.1| catalytic [Arabidopsis thaliana]dbj|BAB09715.1| unnamed protein product [Arabidopsis thaliana]	702	2E-41
CB381619	3.08E-05	Mo17<B73=F1	1.73	10	>emb|CAE00870.1| TA8 protein [Oryza sativa (japonica cultivar-group)]	197	3E-64
					>ref|XP_482379.1| putative RNA binding protein [Oryza sativa (japonicacultivar-group)] ref|XP_507581.1| PREDICTED OSJNBa0007M04.13 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_507230.1| PREDICTED OSJNBa0007M04.13 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC99692.1| putative RNA binding protein [Oryza sativa (japonica cultivar-group)]	214	3E-64
					>gb|AAL76994.1| RNA binding protein [Elaeis oleifera]	218	2E-55
					>gb|ABB87134.1| RNA binding protein-like protein [Solanum tuberosum]	217	9E-54
					>ref|NP_196080.1| RNA binding / nucleic acid binding [Arabidopsis thaliana]emb|CAB85566.1| rna binding protein-like [Arabidopsis thaliana] gb|AAM67546.1| putative RNA binding protein [Arabidopsis thaliana] gb|AAL36178.1| putative rna binding protein [Arabidopsis thaliana] gb|AAL06954.1| AT5g04600/T32M21 200 [Arabidopsis thaliana] gb|AAK55702.1| AT5g04600/T32M21 200 [Arabidopsis thaliana]	222	3E-45
DV490870	3.09E-05	B73<F1<Mo17	1.64	4	>gb|ABA94201.1| glutamyl-tRNA(Gln) amidotransferase, B subunit [Oryza sativa(japonica cultivar-group)]	544	1E-63
					>ref|NP_564530.1| GATB (GLU-ADT SUBUNIT B); carbon-nitrogen ligase, with glutamine asamido-N-donor / glutamyl-tRNA(Gln) amidotransferase/ ligase [Arabidopsis thaliana] gb|AAL67097.1| At1g48520/T1N15_12 [Arabidopsis thaliana] gb|AAL06883.1| At1g48520/T1N15_12 [Arabidopsis thaliana] gb|AAG29096.1| Glu-tRNA(Gln) amidotransferase subunit B [Arabidopsis thaliana]	550	2E-53
					>dbj|BAC09946.1| Glu-tRNA(Gln) amidotransferase subunit B [Thermosynechococcuselongatus BP-1] sp|Q8DGC4|GATB_SYNEL Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (Asp/Glu-ADT subunit B) ref|NP_683184.1| aspartyl/glutamyl-tRNA amidotransferase subunit B [Thermosynechococcus elongatus BP-1]	500	3E-41
					>gb|AAF79700.1| T1N15.14 [Arabidopsis thaliana]	618	4E-40
					>dbj|BAD79576.1| glutamyl-tRNA(Gln) amidotransferase subunit B [Synechococcuselongatus PCC 6301] ref|YP_172096.1| aspartyl/glutamyl-tRNA amidotransferase subunit B [Synechococcus elongatus PCC 6301]	494	5E-38
CB815946	3.32E-05	Mo17<F1<B73	1.68	9	>ref|NP_179430.1| TTN5 (TITAN 5); GTP binding [Arabidopsis thaliana]gb|AAL34222.1| putative ADP-ribosylation factor [Arabidopsis thaliana] gb|AAK59514.1| putative ADP-ribosylation factor [Arabidopsis thaliana] gb|AAM22961.1| ARL2 G-protein [Arabidopsis thaliana] gb|AAD15498.1| putative ADP-ribosylation factor [Arabidopsis thaliana] gb|AAM65870.1| putative ADP-ribosylation factor [Arabidopsis thaliana] sp|Q9ZPX1|ARF5_ARATH Probable ADP-ribosylation factor At2g18390	185	3E-28
					>gb|EAL35698.1| ADP-ribosylation factor-like protein 2 (ARL2) [Cryptosporidiumhominis] ref|XP_665925.1| ADP-ribosylation factor-like protein 2 (ARL2) [Cryptosporidium hominis]	151	6E-25
					>gb|EAN77845.1| ADP-ribosylation factor 6, putative [Trypanosoma brucei]ref|XP 822673.1| ADP-ribosylation factor 6 [Trypanosoma brucei]	186	2E-24
					>gb|EAN90243.1| ADP-ribosylation factor, putative [Trypanosoma cruzi]ref|XP 812094.1| ADP-ribosylation factor [Trypanosoma cruzi strain CL Brener]	186	2E-24
					>ref|XP 394559.1| PREDICTED: similar to ADP-ribosylation factor-like 2 [Apismellifera]	184	4E-24
DV496085	3.38E-05	Mo17<B73=F1	1.83	11	>ref|NP_919594.1| putative purple acid phosphatase [Oryza sativa (japonicacultivar-group)] gb|AAL34937.1| Putative purple acid phosphatase [Oryza sativa] gb|AAP51881.1| Ser/Thr protein phosphatase, putative [Oryza sativa (japonica cultivar-group)]	335	4E-38
					>gb|AAT37529.1| purple acid phosphatase 1 [Solanum tuberosum]	328	2E-29
					>ref|NP_566587.1| ATACP5; protein serine/threonine phosphatase [Arabidopsis thaliana]gb|AAV69751.1| putative purple acid phosphatase [Arabidopsis thaliana] gb|AAO24567.1| At3g17790 [Arabidopsis thaliana] dbj|BAB02702.1| purple acid phosphatase-like protein [Arabidopsis thaliana] emb|CAB63938.1| acid phosphatase type 5 [Arabidopsis thaliana] emb|CAC09923.1| acid phosphatase type 5 [Arabidopsis thaliana]	338	2E-28
					>gb|AAM61192.1| acid phosphatase type 5 [Arabidopsis thaliana]	338	8E-28
					>gb|ABA94168.1| Ser/Thr protein phosphatase family protein, putative [Oryza sativa(japonica cultivar-group)]	264	3E-27
BM334587	3.53E-05	Mo17<B73=F1	2.6	10	>gb|AAG34827.1| glutathione S-transferase GST 19 [Zea mays]	225	3E-8
DV494678	3.79E-05	Mo17<B73=F1	1.63	10	>gb|AAO72563.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]	413	3E-85
					>dbj|BAD61932.1| putative elongation factor 1 gamma [Oryza sativa (japonicacultivar-group)] dbj|BAD61828.1| putative elongation factor 1 gamma [Oryza sativa (japonica cultivar-group)]	416	3E-85
					>ref|XP_464690.1| Elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]dbj|BAD17615.1| Elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)] sp|Q9ZRI7|EF1G ORYSA Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) dbj|BAA34206.1| elongation factor 1B gamma [Oryza	418	2E-84

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|AAO72574.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]	409	4E-84
					>ref|XP_464689.1| putative elongation factor 1-gamma [Oryza sativa (japonicacultivar-group)] dbj|BAD17614.1| putative elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]	414	4E-84
CD001334	3.95E-05	Mo17<F1<B73	1.66	10	>dbj|BAD54696.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]dbj|BAD34409.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	75	6E-28
					>dbj|BAC43353.1| unknown protein [Arabidopsis thaliana]	71	3E-26
					>gb|EAA00792.2| ENSANGP00000020123 [Anopheles gambiae str. PEST]ref|XP 320694.2| ENSANGP00000020123 [Anopheles gambiae str. PEST]	81	2E-10
					>dbj|BAE63661.1| unnamed protein product [Aspergillus oryzae]	117	5E-9
					>ref|NP_652380.2| CG13018-PA [Drosophila melanogaster]gb|AAY55593.1| IP03340p [Drosophila melanogaster] gb|AAF58293.2| CG13018-PA [Drosophila melanogaster]	79	1E-8
CB351635	3.97E-05	B73<F1=Mo17	1.56	2	>gb|AAM16247.1| AT5g62700/MRG21 12 [Arabidopsis thaliana]gb|AAK32919.1| AT5g62700/MRG21 12 [Arabidopsis thaliana]	353	4E-44
					>gb|AAQ92664.1| beta-tubulin 3 [Gossypium hirsutum]sp|Q6VAF8|TBB3 GOSHI Tubulin beta-3 chain (Beta-3 tubulin)	430	4E-44
					>emb|CAA55022.1| beta tubulin [Oryza sativa (japonica cultivar-group)]	447	9E-44
					>emb|CAE52516.1| beta tubulin [Setaria viridis]	448	9E-44
					>ref|NP_915874.1| tubulin beta chain [Oryza sativa (japonica cultivar-group)]dbj|BAB92274.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] dbj|BAA06381.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|P45960|TBB4 ORYSA Tubulin beta-4 chain (Beta-4 tubulin)	447	9E-44
AI586887	4.00E-05	Mo17<B73=F1	2.63	10	>dbj|BAD73259.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD73143.1| unknown protein [Oryza sativa (japonica cultivar-group)]	266	3E-16
					>ref|NP 918653.1| P0520B06.19 [Oryza sativa (japonica cultivar-group)]	258	3E-16
					>ref|NP_192449.1| unknown protein [Arabidopsis thaliana]ref|NP_001031586.1| unknown protein [Arabidopsis thaliana] emb|CAB81082.1| putative protein [Arabidopsis thaliana] gb|AAQ62419.1| At4g05400 [Arabidopsis thaliana] dbj|BAD43333.1| putative protein [Arabidopsis thaliana]	250	6E-12
DV494611	4.09E-05	Mo17<B73=F1	2.03	10	>dbj|BAD27782.1| unknown protein [Oryza sativa (japonica cultivar-group)]	174	4E-55
					>gb|AAM61727.1| unknown [Arabidopsis thaliana]	173	4E-46
					>gb|AAV63879.1| hypothetical protein [Arabidopsis thaliana]ref|NP_565558.1| unknown protein [Arabidopsis thaliana] gb|AAM76748.1| hypothetical protein [Arabidopsis thaliana] gb|AAC63664.1| expressed protein [Arabidopsis thaliana]	173	9E-46
					>dbj|BAC42221.1| unknown protein [Arabidopsis thaliana]	173	9E-46
					>emb|CAB79768.1| putative protein [Arabidopsis thaliana]	217	5E-40
CD484310	4.13E-05	Mo17<B73=F1	1.5	10	>ref|XP_478414.1| putative translational inhibitor protein [Oryza sativa (japonicacultivar-group)] dbj|BAC20708.1| putative translational inhibitor protein [Oryza sativa (japonica cultivar-group)] dbj|BAD31311.1| putative translational inhibitor protein [Oryza sativa (japonica cultivar-group)]	180	3E-58
					>dbj|BAD00048.1| perchloric acid soluble translation inhibitor protein homolog[Gentiana triflora] dbj|BAC66487.1| translation-inhibitor protein [Gentiana triflora]	188	5E-54
					>ref|NP_188674.1| endoribonuclease [Arabidopsis thaliana]gb|AAK53030.1| AT3g20390/MQC12_15 [Arabidopsis thaliana] gb|AAL31178.1| AT3g20390/MQC12 15 [Arabidopsis thaliana] gb|AAM63246.1| translational inhibitor protein, putative [Arabidopsis thaliana]	187	8E-53
					>dbj|BAB02821.1| unnamed protein product [Arabidopsis thaliana]	143	8E-53
					>emb|CAE56534.1| Hypothetical protein CBG24261 [Caenorhabditis briggsae]	172	1E-32
DV491049	4.16E-05	Mo17<B73=F1	1.88	10	>emb|CAA92107.1| cytochrome c oxidase, Vc subunit [Hordeum vulgare subsp. vulgare]sp|Q42841|COX5C_HORVU Cytochrome c oxidase polypeptide Vc (Cytochrome c oxidase subunit 5c)	63	2E-13
					>gb|ABA98934.1| Cytochrome c oxidase subunit Vc [Oryza sativa (japonicacultivar-group)] sp|Q9SXX7|COX5C_ORYSA Cytochrome c oxidase polypeptide Vc (Cytochrome c oxidase subunit 5c) dbj|BAA77682.1| cytochrome c oxidase subunit 5c [Oryza sativa (japonica cultivar-group)]	63	4E-13
					>gb|AAL67939.1| cytochrome c oxidase subunit 5c [Helianthus annuus]sp|Q8VY39|CX5C2_HELAN Cytochrome c oxidase polypeptide Vc-2 (Cytochrome c oxidase subunit 5c-2)	64	2E-11
					>gb|AAL67938.1| cytochrome c oxidase subunit 5c [Helianthus annuus]sp|Q8VY40|CX5C1_HELAN Cytochrome c oxidase polypeptide Vc-1 (Cytochrome c oxidase subunit 5c-1)	63	2E-11
					>gb|AAB31231.1| cytochrome c oxidase subunit Vc [Ipomoea batatas]emb|CAA37470.1| unnamed protein product [Ipomoea batatas] sp|P19173|COX5C_IPOBA Cytochrome c oxidase polypeptide Vc (Cytochrome c oxidase subunit 5c)	64	3E-10
CD058607	4.17E-05	B73<F1=Mo17	1.51	3	>dbj|BAC78569.1| katanin [Oryza sativa (japonica cultivar-group)]dbj|BAD87507.1| katanin [Oryza sativa (japonica cultivar-group)]	386	3E-25
					>ref|NP 916186.1| katanin p60 subunit A 1-like [Oryza sativa (japonicacultivar-group)]	428	3E-25
					>dbj|BAD73366.1| katanin p60 subunit A 1-like [Oryza sativa (japonicacultivar-group)] dbj|BAD73313.1| katanin p60 subunit A 1-like [Oryza sativa (japonica cultivar-group)]	152	2E-22
					>dbj|BAD73365.1| vacuolar protein sorting factor 4B-like [Oryza sativa (japonicacultivar-group)] dbj|BAD73312.1| vacuolar protein sorting factor 4B-like [Oryza sativa (japonica cultivar-group)]	410	2E-22
					>ref|NP 916872.1| putative katanin [Oryza sativa (japonica cultivar-group)]	411	2E-22
CB334483	4.22E-05	Mo17<F1<B73	1.54	10	ns		
CA998709	4.28E-05	Mo17<B73=F1	1.45	10	>emb|CAI64400.1| thioredoxin h1 protein [Zea mays]	128	1E-59
					>ref|XP_475666.1| putative thioredoxin H-type (TRX-H) (TrxTa) [Oryza sativa (japonicacultivar-group)] gb|AAT44260.1| putative thioredoxin H-type (TRX-H) (TrxTa) [Oryza sativa (japonica cultivar-group)]	121	3E-47

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

<table>
<tr><th>GenBank accession no.</th><th>Overall P value</th><th>Significant pattern</th><th>Fold change†</th><th>Sector‡</th><th>BLAST annotation*</th><th>Score</th><th>E value</th></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAB20886.1| thioredoxin h [Oryza sativa (japonica cultivar-group)]</td><td>121</td><td>3E-47</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAF88067.1| thioredoxin H [Triticum aestivum]emb|CAB96931.1| thioredoxin h [Triticum aestivum]</td><td>125</td><td>1E-43</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAP72291.1| thioredoxin h isoform 2; HvTrxh2 [Hordeum vulgare subsp. vulgare]</td><td>122</td><td>1E-43</td></tr>
<tr><td>BM073357</td><td>4.32E-05</td><td>Mo17<B73=F1</td><td>2.15</td><td>10</td><td>>gb|ABA98519.1| hAT family dimerisation domain, putative [Oryza sativa (japonicacultivar-group)]</td><td>337</td><td>8E-8</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>prf||2021344A activator-like transposable element</td><td>804</td><td>3E-7</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_920480.1| putative activator-like transposable element [Oryza sativa(japonica cultivar-group)] gb|AAM18172.1| Putative activator-like transposable element [Oryza sativa (japonica cultivar-group)] gb|AAP52767.1| hAT family dimerisation domain, putative [Oryza sativa (japonica cultivar-group)]</td><td>737</td><td>5E-7</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_471074.1| OSJNBa0020P07.19 [Oryza sativa (japonica cultivar-group)]emb|CAE01302.2| OSJNBa0020P07.19 [Oryza sativa (japonica cultivar-group)]</td><td>741</td><td>7E-7</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA25635.1| unnamed protein product [Zea mays]</td><td>221</td><td>9E-7</td></tr>
<tr><td>DV494490</td><td>4.35E-05</td><td>B73<F1=Mo17</td><td>1.57</td><td>3</td><td>>ref|XP_474220.1| OSJNBa0084K01.4 [Oryza sativa (japonica cultivar-group)]emb|CAE04832.1| OSJNBa0084K01.4 [Oryza sativa (japonica cultivar-group)]</td><td>176</td><td>3E-41</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAM67107.1| transcription co-activator-like protein [Arabidopsis thaliana]</td><td>168</td><td>2E-32</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAV84520.1| At5g03220 [Arabidopsis thaliana]ref|NP_195942.1| unknown protein [Arabidopsis thaliana] emb|CAB86089.1| putative protein [Arabidopsis thaliana] gb|AAG40347.1| AT5g03220 [Arabidopsis thaliana] dbj|BAC42181.1| unknown protein [Arabidopsis thaliana] dbj|BAB08382.1| transcriptional co-activator-like protein [Arabidopsis thaliana]</td><td>168</td><td>2E-32</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAB83310.1| transcriptional co-activator-like protein [Arabidopsis thaliana]gb|AAM19916.1| At5g03505/C320EPL23M [Arabidopsis thaliana] gb|AAL91616.1| At5g03505/C320EPL23M [Arabidopsis thaliana]</td><td>168</td><td>9E-32</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_913999.1| putative Acyl-CoA binding protein (ACBP) [Oryza sativa (japonicacultivar-group)] dbj|BAC99898.1| putative Acyl-CoA binding protein (ACBP) [Oryza sativa (japonica cultivar-group)] dbj|BAC57826.1| putative Acyl-CoA binding protein (ACBP) [Oryza sativa (japonica cultivar-group)]</td><td>91</td><td>6E-39</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAB85987.1| Acyl-CoA-binding protein [Panax ginseng]</td><td>87</td><td>4E-38</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAP82942.1| acyl-CoA-binding protein [Tropaeolum majus]</td><td>90</td><td>2E-37</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAB56693.1| Acyl-CoA binding protein (ACBP) [Digitalis lanata]</td><td>92</td><td>6E-37</td></tr>
<tr><td>BM078903</td><td>4.40E-05</td><td>Mo17<B73=F1</td><td>2.3</td><td>10</td><td>>gb|AAY26525.1| 12-oxo-phytodienoic acid reductase [Zea mays]</td><td>371</td><td>4E-61</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAB62248.1| old-yellow-enzyme homolog [Catharanthus roseus]</td><td>379</td><td>9E-44</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|ABA26969.1| TO18-1 [Taraxacum officinale]</td><td>125</td><td>9E-42</td></tr>
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<tr><td>CB334576</td><td>4.52E-05</td><td>Mo17<B73=F1</td><td>1.46</td><td>10</td><td>>ref|XP_483643.1| putative cytochrome p450 (CYP78A9) [Oryza sativa (japonicacultivar-group)] dbj|BAD09934.1| putative cytochrome p450 (CYP78A9) [Oryza sativa (japonica cultivar-group)]</td><td>551</td><td>2E-47</td></tr>
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<tr><td>CB350976</td><td>4.67E-05</td><td>Mo17<F1<B73</td><td>1.52</td><td>9</td><td>>ref|NP_917838.1| putative chloroplast 50S ribosomal protein L31 [Oryza sativa(japonica cultivar-group)] dbj|BAB90423.1| chloroplast 50S ribosomal protein L31-like [Oryza sativa (japonica cultivar-group)] dbj|BAB90722.1| chloroplast 50S ribosomal protein L31-like [Oryza sativa (japonica cultivar-group)]</td><td>135</td><td>5E-25</td></tr>
<tr><td>CB604817</td><td>4.72E-05</td><td>Mo17<F1<B73</td><td>1.7</td><td>10</td><td>>gb|AAV50048.1| S27 ribosomal protein [Saccharum hybrid cultivar]gb|AAC97381.1| 40S ribosomal protein S27 homolog [Zea mays]</td><td>86</td><td>4E-38</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAC42163.1| putative ribosomal protein S27 [Hordeum vulgare subsp. vulgare]emb|CAC42162.1| putative ribosomal protein S27 [Hordeum vulgare subsp. vulgare] emb|CAC42134.1| putative ribosomal protein S27 [Hordeum vulgare subsp. vulgare] emb|CAA59732.2| putative zinc finger protein [Hordeum vulgare subsp. vulgare] sp|Q96564|RS27_HORVU 40S ribosomal protein S27 (Manganese efficiency-related protein 1)</td><td>86</td><td>9E-38</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_465641.1| 40S ribosomal protein S27 [Oryza sativa (japonica cultivar-group)]dbj|BAD22060.1| 40S ribosomal protein S27 [Oryza sativa (japonica cultivar-group)]</td><td>86</td><td>3E-37</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAV50037.1| ribosomal protein S27 [Saccharum hybrid cultivar]</td><td>84</td><td>4E-37</td></tr>
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<tr><td>DV490268</td><td>4.86E-05</td><td>Mo17<F1<B73</td><td>1.8</td><td>10</td><td>>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]</td><td>307</td><td>4E-26</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|ABA94002.1| NBS-LRR resistance protein, putative [Oryza sativa (japonicacultivar-group)]</td><td>1386</td><td>1E-24</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_908901.1| Mannose-Binding Rice Lectin [Oryza sativa (japonicacultivar-group)] gb|AAK82986.1| salt-induced protein [Oryza sativa (japonica cultivar-group)] gb|AAL30827.1| lectin-like protein [Oryza sativa] dbj|BAB93403.1| salT gene product [Oryza sativa (japonica cultivar-group)] dbj|BAB63898.1| salT gene product [Oryza sativa (japonica cultivar-group)] dbj|BAA25369.1| MRL [Oryza sativa (japonica cultivar-group)]</td><td>145</td><td>1E-22</td></tr>
</table>

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>gb|ABA97248.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]gb|ABB51090.1| mannose-specific jacalin-related lectin [Oryza sativa (japonica cultivar-group)]	306	1E-22
					>emb|CAA81059.1| salT [Oryza sativa]gb|AAB23484.1| 15 kda organ-specific salt-induced protein [Oryza sativa] sp|P24120|SALT_ORYSA Salt stress-induced protein (Salt protein)	145	1E-22
CB616939	4.97E-05	Mo17<B73=F1	1.64	10	ns		
CD001132	5.00E-05	Mo17<B73=F1	1.65	10	ns		
BM073127	5.01E-05	Mo17<F1<B73	1.85	10	>ref|NP_920316.1| putative transposon protein [Oryza sativa (japonica cultivar-group)]gb|AAN05390.1| putative transposon protein [Oryza sativa (japonica cultivar-group)] gb|AAP52603.1| transposon protein, putative, CACTA, En/Spm sub-class [Oryza sativa (japonica cultivar-group)]	1620	5E-6
					>gb|ABA97584.1| transposon protein, putative, CACTA, En/Spm sub-class [Oryza sativa(japonica cultivar-group)]	1599	5E-6
CB240057	5.09E-05	Mo17<F1<B73	1.52	10	>ref|NP_564010.1| unknown protein [Arabidopsis thaliana]gb|AAK62433.1| Unknown protein [Arabidopsis thaliana] gb|AAP13425.1| At1g16880 [Arabidopsis thaliana] gb|AAF99845.1| Unknown protein [Arabidopsis thaliana]	290	2E-15
					>ref|NP 973847.1| unknown protein [Arabidopsis thaliana]	213	2E-15
					>gb|AAM64912.1| unknown [Arabidopsis thaliana]	301	2E-8
					>ref|NP_196094.1| amino acid binding [Arabidopsis thaliana]emb|CAB86016.1| putative protein [Arabidopsis thaliana] gb|AAM48021.1| putative protein [Arabidopsis thaliana] gb|AAL62393.1| putative protein [Arabidopsis thaliana] dbj|BAB08978.1| unnamed protein product [Arabidopsis thaliana]	301	2E-8
					>gb|ABA95833.1| ACT domain, putative [Oryza sativa (japonica cultivar-group)]	279	3E-6
CD573503	5.09E-05	Mo17<B73=F1	1.37	10	>emb|CAE04894.3| OSJNBa0042I15.16 [Oryza sativa (japonica cultivar-group)]sp|Q7XLX6|S1FA2 ORYSA DNA-binding protein S1FA2	80	2E-7
					>emb|CAE04896.3| OSJNBa0042I15.18 [Oryza sativa (japonica cultivar-group)]sp|P42553|S1FA1 ORYSA DNA-binding protein S1FA1	76	4E-6
BM334805	5.44E-05	Mo17<F1<B73	1.78	10	>gb|AAV88601.1| low temperature and salt responsive protein [Pennisetum glaucum]	56	3E-17
					>ref|XP_479247.1| putative low temperature and salt responsive protein [Oryza sativa(japonica cultivar-group)] gb|AAS72305.1| drought-induced hydrophobic protein [Oryza sativa (japonica cultivar-group)] dbj|BAC16385.1| putative low temperature and salt responsive protein [Oryza sativa (japonica cultivar-group)] sp|Q8H5T6|LTI6A_ORYSA Hydrophobic protein LTI6A (Low temperature-induced protein 6A) gb|AAT37941.1| low temperature-induced low molecular weight integral membrane protein LTI6a [Oryza sativa (japonica cultivar-group)]	56	2E-16
					>ref|NP 908456.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]	537	3E-14
					>dbj|BAD34659.1| plasma membrane protein 3 [Leymus chinensis]	54	3E-13
					>dbj|BAD34658.1| plasma membrane protein 3 [Leymus chinensis]	54	4E-13
CD527395	5.45E-05	Mo17<F1<B73	1.59	10	>dbj|BAD34362.1| ankyrin-like protein [Oryza sativa (japonica cultivar-group)]dbj|BAD34405.1| ankyrin-like protein [Oryza sativa (japonica cultivar-group)]	562	1E-42
					>ref|XP 483595.1| ankyrin-like protein [Oryza sativa (japonica cultivar-group)]dbj|BAD08980.1| ankyrin-like protein [Oryza sativa (japonica cultivar-group)]	528	1E-36
					>ref|NP 180741.1| protein binding [Arabidopsis thaliana]gb|AAD32290.1| ankyrin-like protein [Arabidopsis thaliana]	662	3E-28
					>ref|NP 172055.1| protein binding [Arabidopsis thaliana]gb|AAD30616.1| Hypothetical protein [Arabidopsis thaliana]	627	3E-27
					>ref|NP_172250.1| protein binding [Arabidopsis thaliana]gb|AAF75083.1| It contains Ank repeat PF|00023. EST gb|AI996003 comes from this gene. [Arabidopsis thaliana]	543	7E-23
BG840742	5.48E-05	Mo17<F1<B73	2.65	10	ns		
BM072919	5.57E-05	Mo17<F1<B73	2.24	10	ns		
CD001508	6.00E-05	Mo17<F1<B73	1.5	10	>gb|AAV28627.1| putative 60S ribosomal protein L31 [Zea mays]	124	5E-39
					>dbj|BAD61612.1| putative 60S ribosomal protein L31 [Oryza sativa (japonicacultivar-group)]	124	3E-38
					>ref|XP_467485.1| putative 60S ribosomal protein L31 [Oryza sativa (japonicacultivar-group)] dbj|BAD12898.1| putative 60S ribosomal protein L31 [Oryza sativa (japonica cultivar-group)]	123	1E-37
					>ref|XP_483237.1| putative 60S ribosomal protein L31 [Oryza sativa (japonicacultivar-group)] dbj|BAD10170.1| putative 60S ribosomal protein L31 [Oryza sativa (japonica cultivar-group)] dbj|BAD08833.1| putative 60S ribosomal protein L31 [Oryza sativa (japonica cultivar-group)]	122	1E-37
					>gb|AAF42953.1| 80S ribosomal protein L31 [Perilla frutescens]sp|Q9M573|RL31 PERFR 60S ribosomal protein L31	121	2E-36
BM335672	6.09E-05	Mo17<B73=F1	1.58	10	ns		
CD661842	6.20E-05	Mo17<B73=F1	1.42	10	>sp|O48557|RL17 MAIZE 60S ribosomal protein L17gb|AAB88619.1| ribosomal protein L17 [Zea mays]	171	6E-85
					>ref|XP_450351.1| putative ribosomal protein L17 [Oryza sativa (japonicacultivar-group)] ref|XP_507427.1| PREDICTED P0523B07.46 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_506642.1| PREDICTED P0523B07.46 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD23752.1| putative ribosomal protein L17 [Oryza sativa (japonica cultivar-group)] dbj|BAD23438.1| putative ribosomal protein L17 [Oryza sativa (japonica cultivar-group)]	171	8E-79
					>ref|XP_483472.1| putative ribosomal protein L17 [Oryza sativa (japonicacultivar-group)] dbj|BAD09119.1| putative ribosomal protein L17 [Oryza sativa (japonica cultivar-group)] dbj|BAD09020.1| putative ribosomal protein L17 [Oryza sativa (japonica cultivar-group)]	171	1E-77
					>emb|CAA44599.1| ribosomal protein L17-2 [Hordeum vulgare subsp. vulgare]sp|P35267|RL172 HORVU 60S ribosomal protein L17-2	172	9E-76
					>gb|AAG49551.1| ribosomal protein L17-1 [Poa secunda]	171	4E-75
DV495669	6.26E-05	Mo17<B73=F1	1.8	10	>emb|CAE00870.1| TA8 protein [Oryza sativa (japonica cultivar-group)]	197	1E-22

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>ref|XP_482379.1| putative RNA binding protein [Oryza sativa (japonicacultivar-group)] ref|XP_507581.1| PREDICTED OSJNBa0007M04.13 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_507230.1| PREDICTED OSJNBa0007M04.13 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC99692.1| putative RNA binding protein [Oryza sativa (japonica cultivar-group)]	214	1E-22
					>gb|ABB87134.1| RNA binding protein-like protein [Solanum tuberosum]	217	6E-16
					>gb|AAL76994.1| RNA binding protein [Elaeis oleifera]	218	1E-14
					>ref|NP_196080.1| RNA binding / nucleic acid binding [Arabidopsis thaliana]emb|CAB85566.1| rna binding protein-like [Arabidopsis thaliana] gb|AAM67546.1| putative RNA binding protein [Arabidopsis thaliana] gb|AAL36178.1| putative rna binding protein [Arabidopsis thaliana] gb|AAL06954.1| AT5g04600/T32M21 200 [Arabidopsis thaliana] gb|AAK55702.1| AT5g04600/T32M21 200 [Arabidopsis thaliana]	222	3E-13
BM073364	6.47E-05	Mo17<F1<B73	1.69	9	>gb|ABA94031.1| Rubredoxin, putative [Oryza sativa (japonica cultivar-group)]	151	3E-18
					>ref|NP_568749.1| electron transporter/ metal ion binding [Arabidopsis thaliana]gb|AAL85079.1| unknown protein [Arabidopsis thaliana] gb|AAK92703.1| unknown protein [Arabidopsis thaliana] gb|AAM63852.1| unknown [Arabidopsis thaliana] dbj|BAB08747.1| unnamed protein product [Arabidopsis thaliana]	154	4E-15
CD001176	6.48E-05	Mo17<B73=F1	1.33	10	>emb|CAE04894.3| OSJNBa0042I15.16 [Oryza sativa (japonica cultivar-group)]sp|Q7XLX6|S1FA2 ORYSA DNA-binding protein S1FA2	80	1E-7
					>emb|CAE04896.3| OSJNBa0042I15.18 [Oryza sativa (japonica cultivar-group)]sp|P42553|S1FA1 ORYSA DNA-binding protein S1FA1	76	2E-6
CB815948	6.75E-05	B73<F1=Mo17	1.46	3	>emb|CAA37061.1| unnamed protein product [Zea mays]sp|P18026|TBB2 MAIZE Tubulin beta-2 chain (Beta-2 tubulin)	444	2E-59
					>gb|AAT94032.1| beta-tubulin [Oryza sativa (japonica cultivar-group)]dbj|BAC82429.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|Q76FS3|TBB6 ORYSA Tubulin beta-6 chain (Beta-6 tubulin)	444	5E-59
					>emb|CAA55022.1| beta tubulin [Oryza sativa (japonica cultivar-group)]	447	6E-59
					>emb|CAE52516.1| beta tubulin [Setaria viridis]	448	6E-59
					>ref|NP_915874.1| tubulin beta chain [Oryza sativa (japonica cultivar-group)]dbj|BAB92274.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] dbj|BAA06381.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|P45960|TBB4 ORYSA Tubulin beta-4 chain (Beta-4 tubulin)	447	6E-59
BM333794	6.82E-05	F1=Mo17<B73	1.82	9	ns		
CB815646	6.90E-05	Mo17<F1<B73	2.41	9	>dbj|BAD27782.1| unknown protein [Oryza sativa (japonica cultivar-group)]	174	3E-57
					>gb|AAM61727.1| unknown [Arabidopsis thaliana]	173	1E-47
					>gb|AAV63879.1| hypothetical protein [Arabidopsis thaliana]ref|NP_565558.1| unknown protein [Arabidopsis thaliana] gb|AAM76748.1| hypothetical protein [Arabidopsis thaliana] gb|AAC63664.1| expressed protein [Arabidopsis thaliana]	173	2E-47
					>dbj|BAC42221.1| unknown protein [Arabidopsis thaliana]	173	2E-47
					>ref|NP 567848.1| unknown protein [Arabidopsis thaliana]gb|AAM62730.1| unknown [Arabidopsis thaliana]	173	1E-42
BG874044	7.33E-05	F1=Mo17<B73	1.87	9	ns		
BM349987	7.38E-05	Mo17<B73=F1	1.83	10	>gb|AAX95073.1| Fructose-bisphosphate aldolase class-I [Oryza sativa (japonicacultivar-group)] gb|ABA91633.1| Fructose-bisphosphate aldolase class-I [Oryza sativa (japonica cultivar-group)]	363	2E-85
					>gb|AAX95072.1| Fructose-bisphosphate aldolase class-I [Oryza sativa (japonicacultivar-group)] gb|ABA91632.1| Fructose-bisphosphate aldolase class-I [Oryza sativa (japonica cultivar-group)] sp|Q40677|ALFC ORYSA Fructose-bisphosphate aldolase, chloroplast precursor (ALDP)	388	2E-85
					>dbj|BAA02730.1| chloroplastic aldolase [Oryza sativa]	388	3E-84
					>gb|AAF74220.1| fructose 1,6-bisphosphate aldolase precursor [Avena sativa]	388	9E-82
					>gb|AAB70542.1| aldolase [Oryza sativa]	362	1E-80
DV621225	7.60E-05	B73<F1=Mo17	1.66	3	>gb|AAT94032.1| beta-tubulin [Oryza sativa (japonica cultivar-group)]dbj|BAC82429.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|Q76FS3|TBB6 ORYSA Tubulin beta-6 chain (Beta-6 tubulin)	444	7E-72
					>emb|CAA55022.1| beta tubulin [Oryza sativa (japonica cultivar-group)]	447	1E-71
					>emb|CAE52516.1| beta tubulin [Setaria viridis]	448	1E-71
					>ref|NP_915874.1| tubulin beta chain [Oryza sativa (japonica cultivar-group)]dbj|BAB92274.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] dbj|BAA06381.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|P45960|TBB4 ORYSA Tubulin beta-4 chain (Beta-4 tubulin)	447	1E-71
					>gb|AAA66495.1| beta-tubulin	447	1E-71
CB331824	7.80E-05	Mo17<F1<B73	1.42	10	>ref|XP_464199.1| putative ribosomal protein S14 [Oryza sativa (japonicacultivar-group)] ref|XP_506724.1| PREDICTED OJ9003_G05.34 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD25218.1| putative ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]	150	9E-63
					>ref|XP_472410.1| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)]emb|CAE02065.2| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)] dbj|BAD29299.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)] dbj|BAD27798.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]	151	1E-61
					>sp|P19950|RS141 MAIZE 40S ribosomal protein S14 (Clone MCH1)	149	5E-61
					>gb|AAO41731.1| cytoplasmic ribosomal protein S14 [Brassica napus]	150	4E-60
					>gb|ABC01912.1| ribosomal protein S14-like protein [Solanum tuberosum]gb|ABB87124.1| hypothetical protein [Solanum tuberosum]	150	2E-59
CD650795	8.14E-05	Mo17<B73=F1	1.7	10	>dbj|BAD87076.1| putative ribosomal protein S26 [Oryza sativa (japonicacultivar-group)] dbj|BAD73505.1| putative ribosomal protein S26 [Oryza sativa (japonica cultivar-group)]	133	4E-33

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|XP_475416.1| putative 40S ribosomal protein S26 [Oryza sativa (japonicacultivar-group)] gb|AAT01360.1| putative 40S ribosomal protein S26 [Oryza sativa (japonica cultivar-group)]	194	7E-33
					>sp|P49216|RS26 ORYSA 40S ribosomal protein S26 (S31)dbj|BAA07208.1| ribosomal protein S31 [Oryza sativa (japonica cultivar-group)]	133	6E-32
					>gb|AAD47346.1| ribosomal protein S26 [Pisum sativum]	130	2E-27
					>ref|NP_191193.1| structural constituent of ribosome [Arabidopsis thaliana]emb|CAB87433.1| 40S ribosomal protein S26 homolog [Arabidopsis thaliana] gb|AAM91494.1| AT3g56340/F18O21 300 [Arabidopsis thaliana] gb|AAK63990.1| AT3g56340/F18O21 300 [Arabidopsis thaliana]	130	2E-26
CD485155	8.24E-05	Mo17<B73=F1	1.5	10	>emb|CAB90214.1| putative elongation factor 1 beta [Hordeum vulgare subsp. vulgare]	226	3E-40
					>gb|AAR15081.1| translational elongation factor 1 subunit Bbeta [Pisum sativum]	231	2E-39
					>ref|XP_479153.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)]ref|XP_506463.1| PREDICTED P0616D06.117 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC16499.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)] dbj|BAA04903.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)] sp|Q40680|EF1D ORYSA Elongation factor 1-delta (EF-1-delta) (Elongation factor 1B-beta) (eEF-1B beta)	229	8E-39
					>gb|AAU89237.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)]dbj|BAA34599.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)] dbj|BAA34598.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)]	226	8E-39
					>gb|ABA81875.1| putative elongation factor 1B alpha-subunit0like [Solanumtuberosum] gb|ABA40427.1| unknown [Solanum tuberosum]	227	2E-38
CD573184	8.26E-05	B73<F1<Mo17	1.39	4	>emb|CAA55021.1| beta tubulin [Oryza sativa (japonica cultivar-group)]	383	3E-98
					>emb|CAE52517.1| beta tubulin [Setaria viridis]	448	3E-98
					>emb|CAE52516.1| beta tubulin [Setaria viridis]	448	3E-98
					>gb|AAL92118.1| beta-tubulin [Gossypium hirsutum]gb|AAL92026.1| tubulin beta-1 [Gossypium hirsutum]	445	3E-98
					>gb|AAM10035.1| beta tubulin [Arabidopsis thaliana]gb|AAK96884.1| beta tubulin [Arabidopsis thaliana]	449	3E-98
BM333861	8.49E-05	Mo17<B73=F1	1.7	10	>ref|XP 473776.1| OSJNBa0041A02.14 [Oryza sativa (japonica cultivar-group)]emb|CAD41867.2| OSJNBa0041A02.14 [Oryza sativa (japonica cultivar-group)]	396	3E-29
					>emb|CAA67728.1| pectinacetylesterase precursor [Vigna radiata var. radiata]	399	2E-20
					>ref|NP_193677.2| carboxylic ester hydrolase [Arabidopsis thaliana]gb|AAU45212.1| At4g19420 [Arabidopsis thaliana] gb|AAT70429.1| At4g19420 [Arabidopsis thaliana]	397	1E-18
					>dbj|BAD94548.1| pectinacetylesterase like protein [Arabidopsis thaliana]	195	1E-18
					>ref|XP_467338.1| putative pectin acetylesterase [Oryza sativa (japonicacultivar-group)] dbj|BAD08059.1| putative pectin acetylesterase [Oryza sativa (japonica cultivar-group)] dbj|BAD07550.1| putative pectin acetylesterase [Oryza sativa (japonica cultivar-group)]	397	9E-17
BM340087	8.54E-05	Mo17<B73=F1	4.19	10	>ref|NP 912448.1| Unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAO15289.1| Unknown protein [Oryza sativa (japonica cultivar-group)]	240	1E-53
					>ref|NP_568767.1| oxidoreductase, acting on paired donors, with incorporation orreduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors [Arabidopsis thaliana] gb|AAM63324.1| unknown [Arabidopsis thaliana]	227	1E-41
					>gb|AAO42850.1| At5g51880 [Arabidopsis thaliana]	227	1E-41
					>dbj|BAA97223.1| unnamed protein product [Arabidopsis thaliana]	250	1E-41
					>ref|XP 452140.1| unnamed protein product [Kluyveromyces lactis]emb|CAH02533.1| unnamed protein product [Kluyveromyces lactis NRRL Y-1140]	227	3E-24
DV942309	8.58E-05	Mo17<B73=F1	2.25	10	ns		
CB331490	8.76E-05	Mo17<B73=F1	1.59	10	>ref|XP_464689.1| putative elongation factor 1-gamma [Oryza sativa (japonicacultivar-group)] dbj|BAD17614.1| putative elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]	414	2E-63
					>dbj|BAD61932.1| putative elongation factor 1 gamma [Oryza sativa (japonicacultivar-group)] dbj|BAD61828.1| putative elongation factor 1 gamma [Oryza sativa (japonica cultivar-group)]	416	7E-62
					>ref|XP_464690.1| Elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]dbj|BAD17615.1| Elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)] sp|Q9ZRI7|EF1G ORYSA Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) dbj|BAA34206.1| elongation factor 1B gamma [Oryza	418	7E-62
					>gb|AAO72563.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]	413	2E-60
					>gb|AAO72574.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]	409	4E-59
CD527738	8.87E-05	Mo17<B73=F1	10.2	10	>gb|AAQ01160.1| transmembrane protein kinase [Oryza sativa (japonica cultivar-group)]	999	5E-6
					>ref|XP_550586.1| putative transmembrane protein kinase [Oryza sativa (japonicacultivar-group)] dbj|BAD67663.1| putative transmembrane protein kinase [Oryza sativa (japonica cultivar-group)] dbj|BAD44800.1| putative transmembrane protein kinase [Oryza sativa (japonica cultivar-group)]	980	5E-6
CD568357	9.01E-05	Mo17<B73=F1	1.52	10	>dbj|BAD68931.1| polygalacturonase PG1-like [Oryza sativa (japonica cultivar-group)]	538	4E-22
					>ref|XP_475942.1| putative polygalacturonase [Oryza sativa (japonica cultivar-group)]gb|AAU10689.1| putative polygalacturonase [Oryza sativa (japonica cultivar-group)] gb|AAT39158.1| putative polygalacturonase [Oryza sativa (japonica cultivar-group)]	571	1E-14
					>gb|AAD39587.1| 10A19I.1 [Oryza sativa (japonica cultivar-group)]	184	1E-14
BM333756	9.07E-05	Mo17<B73=F1	1.52	10	>gb|ABA93830.1| beta-hydroxysteroid dehydrogenase, putative [Oryza sativa (japonicacultivar-group)]	340	8E-32
					>gb|ABA93829.1| beta-hydroxysteroid dehydrogenase, putative [Oryza sativa (japonicacultivar-group)]	354	8E-32
					>ref|XP 465933.1| putative steroleosin [Oryza sativa (japonica cultivar-group)]dbj|BAD23082.1| putative steroleosin [Oryza sativa (japonica cultivar-group)]	357	9E-10
					>ref|XP 465935.1| putative steroleosin [Oryza sativa (japonica cultivar-group)]dbj|BAD23084.1| putative steroleosin [Oryza sativa (japonica cultivar-group)]	395	7E-7
DV622182	9.17E-05	Mo17<F1<B73	1.79	10	>gb|AAT75242.1| putative N2,N2-dimethylguanosine tRNA methyltransferase [Oryzasativa (japonica cultivar-group)]	608	3E-24

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>gb|AAL86317.1| putative N2,N2-dimethylguanine tRNA methyltransferase [Arabidopsisthaliana]	670	3E-19
					>ref|NP 197085.2| RNA binding / S-adenosylmethionine-dependent methyltransferase/tRNA (guanine-N2-)-methyltransferase [Arabidopsis thaliana]	691	3E-19
					>emb|CAC01780.1| N2, N2-dimethylguanine tRNA methyltransferase-like protein[Arabidopsis thaliana]	684	3E-19
					>sp|Q9LFU5|TRM1_ARATH Probable N(2),N(2)-dimethylguanosine tRNA methyltransferase(tRNA(guanine-26,N(2)-N(2)) methyltransferase) (tRNA 2,2-dimethylguanosine-26 methyltransferase) (tRNA(m(2,2)G26)dimethyltransferase)	586	3E-19
BM074489	9.25E-05	Mo17<F1<B73	1.79	9	>ref|XP_465863.1| putative cytochrome P450 [Oryza sativa (japonica cultivar-group)]dbj|BAD23217.1| putative cytochrome P450 [Oryza sativa (japonica cultivar-group)]	525	9E-48
					>ref|XP_465865.1| putative cytochrome P450 [Oryza sativa (japonica cultivar-group)]dbj|BAD23219.1| putative cytochrome P450 [Oryza sativa (japonica cultivar-group)]	524	3E-47
					>ref|XP_465864.1| putative cytochrome P450 [Oryza sativa (japonica cultivar-group)]dbj|BAD23218.1| putative cytochrome P450 [Oryza sativa (japonica cultivar-group)]	509	7E-46
					>ref|XP_469849.1| putative cytochrome P450 [Oryza sativa (japonica cultivar-group)]gb|AAK63940.1| putative cytochrome P450 [Oryza sativa (japonica cultivar-group)]	512	4E-37
					>ref|XP_469850.1| putative cytochrome P450 [Oryza sativa (japonica cultivar-group)]gb|AAK63920.1| putative cytochrome P450 [Oryza sativa (japonica cultivar-group)]	732	6E-37
CD568378	9.25E-05	B73<F1<Mo17	1.41	4	>emb|CAA86728.1| calcium-binding protein [Zea mays]emb|CAA61939.1| Calreticulin precursor [Zea mays] prf||2205314A calreticulin	421	1E-72
					>gb|AAW02798.1| calreticulin-like protein [Triticum aestivum]	415	9E-70
					>ref|XP_477252.1| putative Calreticulin precursor [Oryza sativa (japonicacultivar-group)] dbj|BAD31962.1| putative Calreticulin precursor [Oryza sativa (japonica cultivar-group)] dbj|BAC82933.1| putative Calreticulin precursor [Oryza sativa (japonica cultivar-group)]	429	2E-68
					>ref|XP_477251.1| putative Calreticulin precursor [Oryza sativa (japonicacultivar-group)] ref|XP_507358.1| PREDICTED OJ1058_C08.28-2 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_506239.1| PREDICTED OJ1058_C08.28-2 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD31961.1| putative Calreticulin precursor [Oryza sativa (japonica cultivar-group)] dbj|BAC82932.1| putative Calreticulin precursor [Oryza sativa (japonica cultivar-group)] sp|Q9SLY8|CRTC ORYSA Calreticulin precursor	424	2E-68
					>dbj|BAA88900.1| calcium-binding protein [Oryza sativa]	424	2E-68
CD484346	9.32E-05	Mo17<F1<B73	1.48	10	>ref|XP_475416.1| putative 40S ribosomal protein S26 [Oryza sativa (japonicacultivar-group)] gb|AAT01360.1| putative 40S ribosomal protein S26 [Oryza sativa (japonica cultivar-group)]	194	5E-27
					>dbj|BAD87076.1| putative ribosomal protein S26 [Oryza sativa (japonicacultivar-group)] dbj|BAD73505.1| putative ribosomal protein S26 [Oryza sativa (japonica cultivar-group)]	133	5E-27
					>sp|P49216|RS26 ORYSA 40S ribosomal protein S26 (S31)dbj|BAA07208.1| ribosomal protein S31 [Oryza sativa (japonica cultivar-group)]	133	5E-26
					>gb|AAD47346.1| ribosomal protein S26 [Pisum sativum]	130	7E-22
					>ref|NP_191193.1| structural constituent of ribosome [Arabidopsis thaliana]emb|CAB87433.1| 40S ribosomal protein S26 homolog [Arabidopsis thaliana] gb|AAM91494.1| AT3g56340/F18O21 300 [Arabidopsis thaliana] gb|AAK63990.1| AT3g56340/F18O21 300 [Arabidopsis thaliana]	130	2E-21
CB816603	1.04E-04	Mo17<B73=F1	1.71	10	ns		
CB240017	1.08E-04	Mo17<F1<B73	1.72	10	>ref|XP_482379.1| putative RNA binding protein [Oryza sativa (japonicacultivar-group)] ref|XP_507581.1| PREDICTED OSJNBa0007M04.13 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_507230.1| PREDICTED OSJNBa0007M04.13 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC99692.1| putative RNA binding protein [Oryza sativa (japonica cultivar-group)]	214	5E-22
					>gb|ABB87134.1| RNA binding protein-like protein [Solanum tuberosum]	217	1E-17
					>gb|AAL76994.1| RNA binding protein [Elaeis oleifera]	218	5E-17
					>ref|NP_196080.1| RNA binding / nucleic acid binding [Arabidopsis thaliana]emb|CAB85566.1| rna binding protein-like [Arabidopsis thaliana] gb|AAM67546.1| putative RNA binding protein [Arabidopsis thaliana] gb|AAL36178.1| putative rna binding protein [Arabidopsis thaliana] gb|AAL06954.1| AT5g04600/T32M21 200 [Arabidopsis thaliana] gb|AAK55702.1| AT5g04600/T32M21 200 [Arabidopsis thaliana]	222	2E-15
					>emb|CAE00870.1| TA8 protein [Oryza sativa (japonica cultivar-group)]	197	5E-14
BM078579	1.08E-04	Mo17<B73=F1	1.73	10	>dbj|BAD53225.1| myosin heavy chain-like [Oryza sativa (japonica cultivar-group)]	755	8E-50
					>ref|NP 917406.1| putative myosin-like protein my5 [Oryza sativa (japonicacultivar-group)]	574	3E-45
					>gb|AAD17931.2| unconventional myosin heavy chain [Zea mays]	1529	3E-30
					>dbj|BAD72949.1| myosin XI [Nicotiana tabacum]	1529	1E-29
					>gb|AAB71529.1| unconventional myosin [Helianthus annuus]	1528	6E-29
BM074160	1.09E-04	Mo17<F1<B73	1.74	10	>gb|AAV32180.1| unknown protein [Oryza sativa (japonica cultivar-group)]	536	7E-40
					>ref|NP_568306.1| metal ion binding [Arabidopsis thaliana]gb|AAL06982.1| AT5g14910/F2G14_30 [Arabidopsis thaliana] gb|AAK62653.1| AT5g14910/F2G14_30 [Arabidopsis thaliana] gb|AAM63286.1| unknown [Arabidopsis thaliana]	178	5E-23
					>emb|CAC01810.1| putative protein [Arabidopsis thaliana]	175	7E-21
DV550600	1.10E-04	B73<F1<Mo17	1.56	3	>ref|XP_475374.1| putative histone H2A [Oryza sativa (japonica cultivar-group)]gb|AAT39181.1| putative histone H2A [Oryza sativa (japonica cultivar-group)] gb|AAT39174.1| putative histone H2A [Oryza sativa (japonica cultivar-group)]	163	2E-39
					>ref|NP 918596.1| putative histone H2A [Oryza sativa (japonica cultivar-group)]dbj|BAB44136.1| putative histone H2A [Oryza sativa (japonica cultivar-group)]	159	2E-38

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>gb|AAT08680.1| histone H2A [Hyacinthus orientalis]	152	3E-38
					>gb|AAT08677.1| histone H2A [Hyacinthus orientalis]	152	3E-38
					>gb|AAF65769.1| histone H2A [Euphorbia esula]sp|Q9M531|H2A EUPES Histone H2A	153	1E-37
CD651672	1.11E-04	Mo17<F1<B73	1.52	9	>gb|AAC19375.1| acireductone dioxygenase 2 [Oryza sativa]	198	1E-92
					>gb|AAX55895.1| aci-reductone dioxygenase-like protein [Oryza sativa (japonicacultivar-group)]	198	3E-92
					>gb|AAN06863.1| Putative probable submergence induced, nickel-binding protein 2A[Oryza sativa (japonica cultivar-group)]	254	2E-90
					>dbj|BAB61039.1| iron-deficiency induced gene [Hordeum vulgare]	198	9E-89
					>gb|AAC05511.1| acireductone dioxygenase 1 [Oryza sativa]	199	2E-81
DV549653	1.13E-04	Mo17<B73=F1	1.61	11	>gb|AAT35818.1| abscisic stress ripening protein-like protein [Musa acuminata]	143	3E-13
					>gb|AAX96480.1| abscisic acid- and stress-induced protein - rice [Oryza sativa(japonica cultivar-group)] gb|AAX92999.1| abscisic acid- and stress-induced protein - rice [Oryza sativa (japonica cultivar-group)] gb|AAB96681.1| abscisic acid- and stress-inducible protein [Oryza sativa] gb|ABA91705.1| abscisic acid- and stress-induced protein [Oryza sativa (japonica cultivar-group)]	138	8E-13
					>gb|AAR23420.1| ASR protein [Ginkgo biloba]	181	1E-12
					>gb|AAT57940.1| 22 kDa drought-inducible protein [Saccharum hybrid cultivar]dbj|BAB68268.1| drought inducible 22 kD protein [Saccharum officinarum]	142	4E-12
					>gb|AAB02692.1| LP3-1	126	1E-10
BM073756	1.14E-04	F1=Mo17<B73	2.49	9	>gb|AAL24473.1| beta-expansin OsEXPB11 [Oryza sativa]	292	1E-28
					>ref|XP_467145.1| putative beta-expansin [Oryza sativa (japonica cultivar-group)]dbj|BAD25736.1| putative beta-expansin [Oryza sativa (japonica cultivar-group)] dbj|BAD25773.1| putative beta-expansin [Oryza sativa (japonica cultivar-group)]	292	1E-28
					>dbj|BAD06319.1| putative beta-expansin [Triticum aestivum]	289	1E-20
					>gb|AAK56127.1| beta-expansin 4 [Zea mays]	308	3E-20
					>gb|AAS48886.1| expansin EXPB9 [Triticum aestivum]	289	4E-20
BM334196	1.17E-04	Mo17<F1<B73	1.56	10	>ref|NP_917838.1| putative chloroplast 50S ribosomal protein L31 [Oryza sativa(japonica cultivar-group)] dbj|BAB90423.1| chloroplast 50S ribosomal protein L31-like [Oryza sativa (japonica cultivar-group)] dbj|BAB90722.1| chloroplast 50S ribosomal protein L31-like [Oryza sativa (japonica cultivar-group)]	135	6E-56
					>gb|AAC77927.1| similar to chloroplast 50S ribosomal protein L31 [Medicago sativa]	133	2E-23
					>ref|NP_565109.1| EMB2184; structural constituent of ribosome [Arabidopsis thaliana]gb|AAL15224.1| putative chloroplast 50S ribosomal protein L31 [Arabidopsis thaliana] gb|AAK44041.1| putative chloroplast 50S ribosomal protein L31 [Arabidopsis thaliana] gb|AAM65248.1| chloroplast 50S ribosomal protein L31, putative [Arabidopsis thaliana] gb|AAG13073.1| Unknown protein [Arabidopsis thaliana]	144	6E-23
					>ref|YP 477812.1| ribosomal protein L31 [Cyanobacteria bacterium Yellowstone B-Prime]	74	1E-15
					>ref|YP_474877.1| ribosomal protein L31 [Cyanobacteria bacterium Yellowstone A-Prime]gb|ABC99614.1| ribosomal protein L31 [Cyanobacteria bacterium Yellowstone A-Prime]	73	5E-15
CB381450	1.19E-04	Mo17<F1<B73	1.5	10	>dbj|BAD22765.1| glycoprotein [Bromus inermis]	134	7E-66
					>ref|XP_466813.1| putative hydroxyproline-rich glycoprotein 1 [Oryza sativa (japonicacultivar-group)] dbj|BAD21553.1| putative hydroxyproline-rich glycoprotein 1 [Oryza sativa (japonica cultivar-group)] dbj|BAD22517.1| putative hydroxyproline-rich glycoprotein 1 [Oryza sativa (japonica cultivar-group)]	134	1E-65
					>ref|XP_473172.1| OSJNBb0070J16.13 [Oryza sativa (japonica cultivar-group)]emb|CAE01917.2| OSJNBb0070J16.13 [Oryza sativa (japonica cultivar-group)] emb|CAE02348.2| OSJNBb0072M01.9 [Oryza sativa (japonica cultivar-group)]	134	2E-65
					>gb|ABA40467.1| glycoprotein-like protein [Solanum tuberosum]	134	7E-60
					>dbj|BAA83469.1| Csf-1 [Cucumis sativus]	138	3E-56
DV491489	1.19E-04	Mo17<B73=F1	2.2	10	ns		
CD484569	1.22E-04	B73<F1<Mo17	1.47	3	>emb|CAA05772.1| Ubiquitin carrier protein [Zea mays]	169	1E-28
					>ref|XP_475366.1| putative ubiquitin-conjugating enzyme E2 [Oryza sativa (japonicacultivar-group)] gb|AAT39166.1| putative ubiquitin-conjugating enzyme E2 [Oryza sativa (japonica cultivar-group)]	169	2E-28
					>gb|AAC12662.1| ubiquitin-conjugating enzyme protein E2 [Zea mays]	169	2E-28
					>ref|NP_915413.1| putative Ubiquitin carrier protein UBC7 [Oryza sativa (japonicacultivar-group)] dbj|BAB93210.1| putative ubiquitin carrier protein UBC7 [Oryza sativa (japonica cultivar-group)] dbj|BAB67890.1| putative ubiquitin carrier protein UBC7 [Oryza sativa (japonica cultivar-group)]	169	5E-28
					>sp|P25868|UBC7 WHEAT Ubiquitin-conjugating enzyme E2 7 (Ubiquitin-protein ligase 7)(Ubiquitin carrier protein 7)	168	4E-26
CB815767	1.26E-04	Mo17<B73=F1	1.5	11	>gb|ABA97248.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]gb|ABB51090.1| mannose-specific jacalin-related lectin [Oryza sativa (japonica cultivar-group)]	306	6E-29
					>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	4E-27
					>gb|AAR20919.1| jasmonate-induced protein [Triticum aestivum]	304	5E-27
					>gb|AAA87041.1| putative 32.6 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72096.1| 32 kDa protein [Hordeum vulgare]	304	7E-27
					>gb|AAF71261.2| beta-glucosidase aggregating factor precursor [Zea mays]	306	9E-27
DV489556	1.27E-04	B73=F1<Mo17	1.7	4	>emb|CAE17316.1| villin 1 [Nicotiana tabacum]	559	4E-20
					>gb|AAD54660.1| actin bundling protein ABP135 [Lilium longiflorum]	965	2E-18

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>emb|CAE17317.1| villin 2 [Nicotiana tabacum]	520	4E-18
					>ref|NP 567048.1| VLN3 (VILLIN 3); actin binding [Arabidopsis thaliana]	965	1E-16
					>emb|CAB68147.1| villin 3 fragment [Arabidopsis thaliana]pir||T45819 villin 3 homolog F28O9.260 - Arabidopsis thaliana (fragment)	383	1E-16
CD568560	1.27E-04	Mo17<B73=F1	1.55	10	>ref|XP_464690.1| Elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]dbj|BAD17615.1| Elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)] sp|Q9ZRI7|EF1G ORYSA Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) dbj|BAA34206.1| elongation factor 1B gamma [Oryza	418	4E-33
					>gb|AAO72574.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]	409	9E-33
					>ref|XP_464689.1| putative elongation factor 1-gamma [Oryza sativa (japonicacultivar-group)] dbj|BAD17614.1| putative elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]	414	9E-33
					>gb|AAO72563.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]	413	3E-32
					>dbj|BAD61932.1| putative elongation factor 1 gamma [Oryza sativa (japonicacultivar-group)] dbj|BAD61828.1| putative elongation factor 1 gamma [Oryza sativa (japonica cultivar-group)]	416	3E-32
BG874123	1.28E-04	Mo17<F1<B73	1.74	9	ns		
CB351652	1.28E-04	Mo17<F1<B73	1.58	9	>gb|AAT08007.1| putative zinc finger protein [Zea mays]	303	2E-6
CD484490	1.34E-04	Mo17<B73=F1	1.47	10	>dbj|BAD54480.1| putative tRNA intron endonuclease [Oryza sativa (japonicacultivar-group)] dbj|BAD54220.1| putative tRNA intron endonuclease [Oryza sativa (japonica cultivar-group)] sp|Q5Z6B1|SEN2 ORYSA Probable tRNA-splicing endonuclease subunit Sen2 (tRNA-intron endonuclease Sen2)	293	5E-33
					>gb|ABA94597.1| tRNA intron endonuclease, catalytic C-terminal domain, putative[Oryza sativa (japonica cultivar-group)]	292	6E-32
					>ref|NP_190145.1| ATSEN1 (SPLICING ENDONUCLEASE 1); tRNA-intron endonuclease[Arabidopsis thaliana] emb|CAB75488.1| putative protein [Arabidopsis thaliana] dbj|BAD94688.1| putative protein [Arabidopsis thaliana] sp|Q9M1E8|SEN21_ARATH tRNA-splicing endonuclease subunit Sen2-1 (AtSen1) (tRNA-intron endonuclease Sen2-1)	237	4E-12
					>dbj|BAA88628.1| tRNA intron endonuclease [Arabidopsis thaliana]dbj|BAA88627.1| tRNA intron endonuclease [Arabidopsis thaliana]	237	5E-12
					>ref|NP 974966.1| SEN2 (SPLICING ENDONUCLEASE 2); tRNA-intron endonuclease[Arabidopsis thaliana]	255	3E-11
BM073434	1.36E-04	F1<B73=Mo17	2.05	6	>gb|AAC25630.1| pathogenesis related protein-5 [Zea mays]gb|ABA34043.1| pathogenesis-related protein 5 [Zea mays subsp. parviglumis]	172	5E-66
					>gb|ABA34036.1| pathogenesis-related protein 5 [Zea mays subsp. parviglumis]gb|ABA34035.1| pathogenesis-related protein 5 [Zea mays subsp. parviglumis] gb|ABA34034.1| pathogenesis-related protein 5 [Zea mays subsp. parviglumis] gb|ABA34033.1| pathogenesis-related protein 5 [Zea mays subsp. parviglumis] prf||1906392A thaumatin-like protein	174	5E-66
					>gb|ABA34044.1| pathogenesis-related protein 5 [Zea mays subsp. parviglumis]gb|ABA34041.1| pathogenesis-related protein 5 [Zea mays subsp. parviglumis]	174	1E-65
					>gb|ABA34042.1| pathogenesis-related protein 5 [Zea mays subsp. parviglumis]gb|ABA34040.1| pathogenesis-related protein 5 [Zea mays subsp. parviglumis] gb|ABA34038.1| pathogenesis-related protein 5 [Zea mays subsp. parviglumis] gb|ABA34037.1| pathogenesis-related protein 5 [Zea mays subsp. parviglumis]	174	5E-63
					>gb|ABA34032.1| pathogenesis-related protein 5 [Zea mays subsp. parviglumis]	176	5E-63
DV491669	1.37E-04	Mo17<F1<B73	2.13	9	>ref|XP_466191.1| putative suppressor of actin 1 [Oryza sativa (japonicacultivar-group)] dbj|BAD33306.1| inositol 5-phosphatase 3-like protein [Oryza sativa (japonica cultivar-group)]	597	4E-47
					>gb|AAX96819.1| Similar to SAC domain protein 7 [Oryza sativa (japonicacultivar-group)] gb|ABA92882.1| SAC domain protein 7, putative [Oryza sativa (japonica cultivar-group)]	311	7E-37
					>ref|NP_190714.2| phosphoinositide 5-phosphatase [Arabidopsis thaliana]gb|AAP49840.1| SAC domain protein 7 [Arabidopsis thaliana] gb|AAK64136.1| unknown protein [Arabidopsis thaliana] gb|AAK25977.1| unknown protein [Arabidopsis thaliana] gb|AAP41368.1| SAC1-like protein AtSAC1c [Arabidopsis thaliana]	597	3E-24
					>gb|AAP49839.1| SAC domain protein 6 [Arabidopsis thaliana]gb|AAP41367.1| SAC1-like protein AtSAC1b [Arabidopsis thaliana]	593	2E-22
					>dbj|BAB10407.1| unnamed protein product [Arabidopsis thaliana]	626	2E-22
DV942182	1.37E-04	Mo17<B73=F1	2.58	10	ns		
CB886283	1.38E-04	Mo17<B73=F1	1.85	10	>ref|XP_482379.1| putative RNA binding protein [Oryza sativa (japonicacultivar-group)] ref|XP_507581.1| PREDICTED OSJNBa0007M04.13 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_507230.1| PREDICTED OSJNBa0007M04.13 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC99692.1| putative RNA binding protein [Oryza sativa (japonica cultivar-group)]	214	2E-72
					>emb|CAE00870.1| TA8 protein [Oryza sativa (japonica cultivar-group)]	197	2E-64
					>gb|AAL76994.1| RNA binding protein [Elaeis oleifera]	218	1E-60
					>gb|ABB87134.1| RNA binding protein-like protein [Solanum tuberosum]	217	6E-59
					>ref|NP_196080.1| RNA binding / nucleic acid binding [Arabidopsis thaliana]emb|CAB85566.1| rna binding protein-like [Arabidopsis thaliana] gb|AAM67546.1| putative RNA binding protein [Arabidopsis thaliana] gb|AAL36178.1| putative rna binding protein [Arabidopsis thaliana] gb|AAL06954.1| AT5g04600/T32M21 200 [Arabidopsis thaliana] gb|AAK55702.1| AT5g04600/T32M21 200 [Arabidopsis thaliana]	222	1E-49
CD568722	1.41E-04	Mo17<F1<B73	1.53	10	>gb|AAP80664.1| S28 ribosomal protein [Triticum aestivum]	86	5E-25
					>emb|CAA04565.1| rpS28 [Hordeum vulgare subsp. vulgare]	65	3E-24
					>emb|CAA57636.1| small subunit ribosomal protein S28 [Zea mays]sp|P46302|RS28 MAIZE 40S ribosomal protein S28	65	4E-24
					>emb|CAA10103.1| ribosomal protein S28 [Prunus persica]emb|CAA10102.1| ribosomal protein S28 [Prunus persica] emb|CAA10101.1| ribosomal protein S28 [Prunus persica]	65	1E-22

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|AAM78552.1| ribosomal protein small subunit 28 [Helianthus annuus]	65	4E-22
CB886238	1.41E-04	Mo17<F1<B73	1.88	10	>ref|XP_482526.1| putative dihydrolipoamide acetyltransferase [Oryza sativa (japonicacultivar-group)] dbj|BAC99341.1| putative dihydrolipoamide acetyltransferase [Oryza sativa (japonica cultivar-group)] dbj|BAD01179.1| putative dihydrolipoamide acetyltransferase [Oryza sativa (japonica cultivar-group)]	475	5E-89
					>gb|AAK76609.2| putative dihydrolipoamide S-acetyltransferase [Arabidopsisthaliana]	369	6E-84
					>dbj|BAB01047.1| dihydrolipoamide S-acetyltransferase [Arabidopsis thaliana]	432	6E-84
					>ref|NP_189215.1| LTA2 (PLASTID E2 SUBUNIT OF PYRUVATE DECARBOXYLASE);acyltransferase/ dihydrolipoyllysine-residue acetyltransferase/ protein binding [Arabidopsis thaliana] gb|AAK59863.1| AT3g25860/MPE11_1 [Arabidopsis thaliana] gb|AAN86176.1| putative dihydrolipoamide S-acetyltransferase [Arabidopsis thaliana] gb|AAD55139.1| dihydrolipoamide S-acetyltransferase [Arabidopsis thaliana]	480	6E-84
					>dbj|BAD36253.1| putative mono-lipoyl E2 [Oryza sativa (japonica cultivar-group)]	501	2E-79
CA998647	1.43E-04	Mo17<B73=F1	1.33	11	>gb|AAF71261.2| beta-glucosidase aggregating factor precursor [Zea mays]	306	3E-40
					>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	9E-38
					>gb|AAR20919.1| jasmonate-induced protein [Triticum aestivum]	304	1E-36
					>gb|AAA87042.1| putative 32.7 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72097.1| 32 kDa protein [Hordeum vulgare]	304	2E-36
					>gb|AAB72098.1| 32 kDa protein [Hordeum vulgare]	306	2E-35
CB251903	1.50E-04	Mo17<B73=F1	1.82	10	>emb|CAA46876.1| DNA-binding protein [Zea mays]pir||T03640 high mobility group protein MNB1b - maize (fragment)	168	1E-22
					>gb|AAM95942.1| nucleosome/chromatin assembly factor group D protein [Zea mays]emb|CAA41220.1| high mobility group protein [Zea mays] emb|CAB46752.1| HMGa protein [Zea mays] sp|P27347|MNB1B MAIZE DNA-binding protein MNB1B (HMG1-like protein)	157	4E-22
					>gb|AAP21609.1| HMGB1 [Oryza sativa (indica cultivar-group)]gb|AAN28722.1| HMG1 protein [Oryza sativa (indica cultivar-group)] dbj|BAD61823.1| HMGB1 [Oryza sativa (japonica cultivar-group)] gb|AAC78104.1| high mobility group protein [Oryza sativa]	157	7E-21
					>emb|CAA77641.1| high mobility group protein [Triticum aestivum]sp|P40621|HMGL WHEAT HMG1/2-like protein	161	3E-20
					>emb|CAA90679.1| HMG1/2-like protein [Hordeum vulgare subsp. vulgare]	160	2E-19
CD661736	1.51E-04	Mo17<F1<B73	1.43	10	>emb|CAE05511.1| OSJNBa0038P21.4 [Oryza sativa (japonica cultivar-group)]	221	4E-70
					>sp|Q08069|RS8 MAIZE 40S ribosomal protein S8gb|AAB06330.1| ribosomal protein S8	221	3E-67
					>ref|XP_465742.1| putative 40S ribosomal protein S8 [Oryza sativa (japonicacultivar-group)] ref|XP_506804.1| PREDICTED P0483C08.42 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD21871.1| putative 40S ribosomal protein S8 [Oryza sativa (japonica cultivar-group)] dbj|BAD21876.1| putative 40S ribosomal protein S8 [Oryza sativa (japonica cultivar-group)]	220	4E-67
					>sp|P49199|RS8 ORYSA 40S ribosomal protein S8dbj|BAA07207.1| ribosomal protein S8 [Oryza sativa (japonica cultivar-group)]	220	5E-63
					>gb|ABA46755.1| unknown [Solanum tuberosum]	224	2E-62
CB605494	1.53E-04	B73<F1=Mo17	1.64	3	>gb|AAW88509.1| beta-tubulin [Lolium perenne]	321	6E-85
					>emb|CAA55021.1| beta tubulin [Oryza sativa (japonica cultivar-group)]	383	6E-85
					>emb|CAE52517.1| beta tubulin [Setaria viridis]	448	6E-85
					>emb|CAE52516.1| beta tubulin [Setaria viridis]	448	6E-85
					>gb|AAL92118.1| beta-tubulin [Gossypium hirsutum]gb|AAL92026.1| tubulin beta-1 [Gossypium hirsutum]	445	6E-85
CD573372	1.56E-04	Mo17<B73=F1	1.68	10	>ref|XP_475712.1| putative GTP-binding protein Rab7a [Oryza sativa (japonicacultivar-group)] gb|AAT01314.1| putative GTP-binding protein Rab7a [Oryza sativa (japonica cultivar-group)]	206	e-110
					>sp|Q40787|RAB7 PENCL Ras-related protein Rab7 (Possible apospory-associated protein)gb|AAA85273.1| possible apospory-associated protein	206	e-110
					>gb|AAO67728.1| small GTP binding protein [Oryza sativa (indica cultivar-group)]	206	e-109
					>sp|O24461|RAB7 PRUAR Ras-related protein Rab7gb|AAB71504.1| Rab7 GTP binding protein [Prunus armeniaca]	207	e-103
					>emb|CAA98171.1| RAB7D [Lotus corniculatus var. japonicus]	207	e-102
BM073340	1.64E-04	B73<F1=Mo17	2.92	3	>gb|AAB47967.1| nonspecific lipid transfer protein [Hordeum vulgare]	96	5E-23
					>ref|XP_475853.1| putative lipid transfer protein [Oryza sativa (japonicacultivar-group)] gb|AAT39264.1| putative lipid transfer protein [Oryza sativa (japonica cultivar-group)]	94	6E-22
					>ref|NP_564532.1| lipid binding [Arabidopsis thaliana]gb|AAM14109.1| putative lipid transfer protein [Arabidopsis thaliana] gb|AAK76553.1| putative lipid transfer protein [Arabidopsis thaliana]	94	3E-16
					>gb|AAG60123.1| lipid transfer protein, putative [Arabidopsis thaliana]	87	3E-16
					>ref|XP_475855.1| putative lipid transfer protein [Oryza sativa (japonicacultivar-group)] gb|AAT85180.1| putative lipid transfer protein [Oryza sativa (japonica cultivar-group)] gb|AAT39266.1| putative lipid transfer protein [Oryza sativa (japonica cultivar-group)]	96	5E-16
CD568718	1.66E-04	Mo17<F1<B73	1.6	10	>ref|XP_473550.1| OSJNBa0088I22.17 [Oryza sativa (japonica cultivar-group)]emb|CAE75904.1| OSJNBa0088I22.17 [Oryza sativa (japonica cultivar-group)]	464	1E-75
CA829976	1.67E-04	Mo17<B73=F1	1.7	11	>gb|AAF71261.2| beta-glucosidase aggregating factor precursor [Zea mays]	306	7E-36
					>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	9E-36
					>gb|AAR20919.1| jasmonate-induced protein [Triticum aestivum]	304	1E-34
					>gb|ABA97248.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]gb|ABB51090.1| mannose-specific jacalin-related lectin [Oryza sativa (japonica cultivar-group)]	306	2E-34

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>gb|AAA87041.1| putative 32.6 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72096.1| 32 kDa protein [Hordeum vulgare]	304	2E-34
CB380870	1.68E-04	Mo17<B73<F1	1.44	11	>gb|AAA87042.1| putative 32.7 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72097.1| 32 kDa protein [Hordeum vulgare]	304	6E-19
					>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	1E-18
					>gb|AAB72098.1| 32 kDa protein [Hordeum vulgare]	306	2E-18
					>gb|AAA87041.1| putative 32.6 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72096.1| 32 kDa protein [Hordeum vulgare]	304	2E-18
					>gb|ABA96669.1| jakalin homolog [Oryza sativa (japonica cultivar-group)]	258	6E-17
BG841183	1.69E-04	Mo17<B73=F1	1.59	10	>gb|AAU10802.1| 'putative endo-1,3;1,4-beta-D-glucanase' [Oryza sativa (japonicacultivar-group)]	240	4E-32
					>gb|AAU10803.1| 'putative endo-1,3;1,4-beta-D-glucanase' [Oryza sativa (japonicacultivar-group)]	239	3E-29
					>ref|NP_566732.1| hydrolase [Arabidopsis thaliana]gb|AAM19921.1| AT3g23600/MDB19_9 [Arabidopsis thaliana] gb|AAL36041.1| AT3g23600/MDB19_9 [Arabidopsis thaliana] gb|AAM61180.1| contains similarity to endo-1,3-1,4-beta-D-glucanase [Arabidopsis thaliana] dbj|BAB02778.1| unnamed protein product [Arabidopsis thaliana]	239	3E-21
					>ref|XP_480878.1| putative Endo-1,3;1,4-beta-D-glucanase precursor [Oryza sativa(japonica cultivar-group)] dbj|BAD05237.1| putative Endo-1,3;1,4-beta-D-glucanase precursor [Oryza sativa (japonica cultivar-group)] dbj|BAD05479.1| putative Endo-1,3;1,4-beta-D-glucanase precursor [Oryza sativa (japonica cultivar-group)]	265	2E-20
					>gb|AAX92844.1| Dienelactone hydrolase family, putative [Oryza sativa (japonicacultivar-group)] gb|ABA92619.1| Dienelactone hydrolase family, putative [Oryza sativa (japonica cultivar-group)]	276	2E-20
CD661929	1.70E-04	Mo17<F1<B73	1.62	9	>gb|AAP80664.1| S28 ribosomal protein [Triticum aestivum]	86	1E-25
					>emb|CAA04565.1| rpS28 [Hordeum vulgare subsp. vulgare]	65	9E-25
					>emb|CAA57636.1| small subunit ribosomal protein S28 [Zea mays]sp|P46302|RS28 MAIZE 40S ribosomal protein S28	65	1E-24
					>emb|CAA10103.1| ribosomal protein S28 [Prunus persica]emb|CAA10102.1| ribosomal protein S28 [Prunus persica] emb|CAA10101.1| ribosomal protein S28 [Prunus persica]	65	4E-23
					>gb|AAM78552.1| ribosomal protein small subunit 28 [Helianthus annuus]	65	1E-22
CB331416	1.78E-04	Mo17<F1<B73	1.53	10	>gb|AAM47587.1| unknown protein [Sorghum bicolor]	153	5E-39
					>ref|NP_196413.1| unknown protein [Arabidopsis thaliana]emb|CAB62608.1| putative protein [Arabidopsis thaliana] gb|AAM64297.1| unknown [Arabidopsis thaliana] gb|AAO42799.1| At5g07960 [Arabidopsis thaliana] dbj|BAB09960.1| unnamed protein product [Arabidopsis thaliana] sp|Q9SD88|U139_ARATH UPF0139 protein At5g07960	107	8E-37
					>ref|XP 469825.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAK16184.1| unknown protein [Oryza sativa (japonica cultivar-group)]	93	1E-34
					>ref|XP_643471.1| hypothetical protein DDB0217686 [Dictyostelium discoideum]gb|AAO53170.1| hypothetical protein [Dictyostelium discoideum] gb|EAL69675.1| hypothetical protein DDB0217686 [Dictyostelium discoideum]	98	3E-9
					>gb|AAF16694.1| unknown [Manduca sexta]sp|Q9U516|U139 MANSE Hypothetical UPF0139 protein pMsmaA27	108	4E-8
BM080659	1.81E-04	Mo17<B73=F1	1.74	10	>gb|AAV43816.1| unknown protein [Oryza sativa (japonica cultivar-group)]	200	9E-37
					>gb|ABA81879.1| unknown [Solanum tuberosum]	197	1E-21
					>ref|NP_175926.1| transcription factor [Arabidopsis thaliana]gb|AAT71971.1| At1g55300 [Arabidopsis thaliana] gb|AAR28024.1| TAF7 [Arabidopsis thaliana] gb|AAR25638.1| At1g55300 [Arabidopsis thaliana] gb|AAG51559.1| Serine/arginine-rich protein, putative; 48931-50251 [Arabidopsis thaliana]	203	9E-18
					>ref|NP 001031194.1| transcription factor [Arabidopsis thaliana]	239	2E-16
					>dbj|BAD68329.1| TATA-binding protein-associated factor TAFII55-like [Oryza sativa(japonica cultivar-group)]	193	1E-14
BM073845	1.83E-04	Mo17<B73=F1	2.73	10	>emb|CAH68542.2| OSJNBa0009P12.20 [Oryza sativa (japonica cultivar-group)]	279	7E-29
					>ref|XP_467255.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD07702.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAD07902.1| unknown protein [Oryza sativa (japonica cultivar-group)]	255	2E-22
					>gb|AAM65735.1| unknown [Arabidopsis thaliana]	264	9E-17
					>dbj|BAD44266.1| unknown protein [Arabidopsis thaliana]	264	9E-17
					>dbj|BAD43504.1| unknown protein [Arabidopsis thaliana]	264	9E-17
DV494229	1.83E-04	B73<F1<Mo17	1.35	3	>gb|AAU44177.1| putative actin [Oryza sativa (japonica cultivar-group)]	377	7E-72
					>ref|XP 470336.1| actin [Oryza sativa (japonica cultivar-group)]gb|AAR88568.1| actin [Oryza sativa (japonica cultivar-group)] sp|P17299|ACT3 ORYSA Actin-3	377	7E-72
					>ref|NP_196543.1| ACT7 [Arabidopsis thaliana]gb|AAM20037.1| putative actin 2/7 protein [Arabidopsis thaliana] gb|AAL36336.1| putative ACTIN 2/7 protein [Arabidopsis thaliana] gb|AAM53337.1| actin 2/7 [Arabidopsis thaliana] gb|AAM47998.1| ACTIN 2/7 [Arabidopsis thaliana] gb|AAL32780.1| ACTIN 2/7 [Arabidopsis thaliana] dbj|BAB09402.1| ACTIN 2/7 [Arabidopsis thaliana] sp|P53492|ACT7_ARATH Actin-7 (Actin-2) gb|AAB52506.1| actin7 gb|AAA80356.1| actin-2	377	2E-71
					>gb|AAW78915.1| actin [Triticum aestivum]gb|AAW78911.1| actin [Triticum turgidum] gb|AAN59956.1| actin [Hordeum vulgare]	377	2E-71
					>gb|AAV83799.1| putative actin 1 [Chorispora bungeana]	363	2E-71
DV621976	1.84E-04	B73<F1=Mo17	1.59	2	ns		
DV490246	1.95E-04	F1=Mo17<B73	1.6	9	>gb|AAC37357.1| catalasesp|P18123|CATA3 MAIZE Catalase isozyme 3	496	6E-18
					>emb|CAH61266.1| catalase [Secale cereale]	494	8E-13

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15 % FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|AAC17730.1| catalase 2 [Hordeum vulgare]	394	2E-12
					>sp|P55308|CATA2 HORVU Catalase isozyme 2gb|AAA96948.1| catalase	494	2E-12
					>ref|XP_463870.1| catalase (EC 1.11.1.6) catA-like protein [Oryza sativa (japonicacultivar-group)] dbj|BAD07712.1| catalase catA-like protein [Oryza sativa (japonica cultivar-group)] dbj|BAD07937.1| catalase catA-like protein [Oryza sativa (japonica cultivar-group)]	153	6E-11
CB816143	2.02E-04	Mo17<B73=F1	1.64	10	ns		
CD484515	2.04E-04	Mo17<B73=F1	1.46	10	>ref|XP_479153.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)]ref|XP_506463.1| PREDICTED P0616D06.117 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC16499.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)] dbj|BAA04903.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)] sp|Q40680|EF1D ORYSA Elongation factor 1-delta (EF-1-delta) (Elongation factor 1B-beta) (eEF-1B beta)	229	7E-45
					>gb|AAU89237.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)]dbj|BAA34599.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)] dbj|BAA34598.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)]	226	7E-40
					>emb|CAB90214.1| putative elongation factor 1 beta [Hordeum vulgare subsp. vulgare]	226	5E-39
					>gb|AAR15081.1| translational elongation factor 1 subunit Bbeta [Pisum sativum]	231	5E-38
					>sp|P93447|EF1D_PIMBR Elongation factor 1-delta (EF-1-delta) (Elongation factor 1B-beta)(eEF-1B beta) gb|AAB68395.1| elongation factor 1-beta [Pimpinella brachycarpa]	226	6E-37
DV621200	2.06E-04	B73<F1=Mo17	1.4	3	>ref|XP 479905.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD08860.1| unknown protein [Oryza sativa (japonica cultivar-group)]	184	2E-31
					>ref|NP 176927.1| unknown protein [Arabidopsis thaliana]gb|AAM63870.1| unknown [Arabidopsis thaliana] gb|AAG28897.1| F12A21.27 [Arabidopsis thaliana]	163	6E-23
					>gb|AAM63820.1| unknown [Arabidopsis thaliana]	168	2E-22
					>ref|NP 564215.1| unknown protein [Arabidopsis thaliana]	168	2E-22
					>dbj|BAD82112.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD82771.1| unknown protein [Oryza sativa (japonica cultivar-group)]	171	1E-20
DV942638	2.07E-04	Mo17<F1<B73	1.64	9	>gb|AAX95073.1| Fructose-bisphosphate aldolase class-I [Oryza sativa (japonicacultivar-group)] gb|ABA91633.1| Fructose-bisphosphate aldolase class-I [Oryza sativa (japonica cultivar-group)]	363	2E-16
					>gb|AAX95074.1| Fructose-bisphosphate aldolase class-I [Oryza sativa (japonicacultivar-group)] gb|ABA91631.1| Fructose-bisphosphate aldolase class-I [Oryza sativa (japonica cultivar-group)]	131	2E-16
					>gb|AAX95075.1| Fructose-bisphosphate aldolase class-I [Oryza sativa (japonicacultivar-group)] gb|ABA91630.1| Fructose-bisphosphate aldolase class-I [Oryza sativa (japonica cultivar-group)]	145	2E-16
					>gb|AAB70542.1| aldolase [Oryza sativa]	362	2E-16
					>gb|AAX95072.1| Fructose-bisphosphate aldolase class-I [Oryza sativa (japonicacultivar-group)] gb|ABA91632.1| Fructose-bisphosphate aldolase class-I [Oryza sativa (japonica cultivar-group)] sp|Q40677|ALFC ORYSA Fructose-bisphosphate aldolase, chloroplast precursor (ALDP)	388	2E-16
CD527416	2.08E-04	Mo17<B73=F1	1.76	10	>ref|XP 470431.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAO20079.1| unknown protein [Oryza sativa (japonica cultivar-group)]	158	2E-13
CD058801	2.09E-04	B73<F1=Mo17	1.38	3	>gb|ABA98247.1| Auxin response factor, putative [Oryza sativa (japonicacultivar-group)]	840	7E-27
					>gb|ABA98246.1| Auxin response factor, putative [Oryza sativa (japonicacultivar-group)]	841	7E-27
					>gb|AAG43286.2| putative auxin response factor 1 [Oryza sativa (indicacultivar-group)]	857	3E-26
					>emb|CAC83756.1| auxin response factor 1 [Oryza sativa (japonica cultivar-group)]	836	3E-26
					>gb|ABA93992.1| Auxin response factor, putative [Oryza sativa (japonicacultivar-group)]	811	3E-26
DV490653	2.11E-04	Mo17<F1<B73	3.44	10	>ref|XP_477553.1| putative cytochrome P450 71E1 [Oryza sativa (japonicacultivar-group)] dbj|BAD31248.1| putative cytochrome P450 71E1 [Oryza sativa (japonica cultivar-group)] dbj|BAC55732.1| putative cytochrome P450 71E1 [Oryza sativa (japonica cultivar-group)]	538	1E-50
					>gb|AAC39318.1| cytochrome P450 CYP71E1 [Sorghum bicolor]sp|O48958|C71E1_SORBI Cytochrome P450 71E1 (4-hydroxyphenylacetaldehyde oxime monooxygenase)	531	2E-41
					>ref|NP_910063.1| putative cytochrome P450 [Oryza sativa (japonica cultivar-group)]gb|AAO37955.1| putative cytochrome P450 [Oryza sativa (japonica cultivar-group)] gb|AAO20056.1| putative cytochrome P450 protein [Oryza sativa (japonica cultivar-group)]	527	1E-39
					>dbj|BAB02437.1| cytochrome P450 [Arabidopsis thaliana]	434	2E-39
					>ref|NP_189247.1| CYP71B17; heme binding / iron ion binding / monooxygenase/ oxygenbinding [Arabidopsis thaliana] dbj|BAB02436.1| cytochrome P450 [Arabidopsis thaliana] sp|Q9LTM6|C71BH ARATH Cytochrome P450 71B17	502	4E-38
CB329795	2.11E-04	B73<F1=Mo17	1.39	3	>emb|CAA55022.1| beta tubulin [Oryza sativa (japonica cultivar-group)]	447	2E-72
					>emb|CAE52516.1| beta tubulin [Setaria viridis]	448	2E-72
					>ref|NP_915874.1| tubulin beta chain [Oryza sativa (japonica cultivar-group)]dbj|BAB92274.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] dbj|BAA06381.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|P45960|TBB4 ORYSA Tubulin beta-4 chain (Beta-4 tubulin)	447	2E-72
					>gb|AAA66495.1| beta-tubulin	447	2E-72
					>sp|Q41783|TBB6 MAIZE Tubulin beta-6 chain (Beta-6 tubulin)gb|AAA20186.1| beta-6 tubulin	446	2E-72
CB815751	2.14E-04	Mo17<F1<B73	1.57	10	ns		
DV490309	2.14E-04	Mo17<B73=F1	1.52	10	>ref|XP_467076.1| chaperone protein dnaJ-like [Oryza sativa (japonicacultivar-group)] dbj|BAD26566.1| chaperone protein dnaJ-like [Oryza sativa (japonica cultivar-group)]	332	3E-8

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_974975.1| unknown protein [Arabidopsis thaliana]ref|NP_200975.1| unknown protein [Arabidopsis thaliana] gb|AAN31107.1| At5g61670/k11j9_190 [Arabidopsis thaliana] gb|AAM51301.1| unknown protein [Arabidopsis thaliana] gb|AAL38842.1| unknown protein [Arabidopsis thaliana] gb|AAM19804.1| AT5g61670/k11j9 190 [Arabidopsis thaliana] gb|AAM61134.1| unknown [Arabidopsis thaliana] dbj|BAB09011.1| unnamed protein product [Arabidopsis thaliana]	307	3E-8
					>dbj|BAD29300.1| chaperone protein dnaJ-related-like [Oryza sativa (japonicacultivar-group)] dbj|BAD27799.1| chaperone protein dnaJ-related-like [Oryza sativa (japonica cultivar-group)]	314	1E-7
					>ref|NP_196231.2| unknown protein [Arabidopsis thaliana]gb|AAM91684.1| unknown protein [Arabidopsis thaliana] gb|AAL59969.1| unknown protein [Arabidopsis thaliana]	315	1E-6
					>dbj|BAA98202.1| unnamed protein product [Arabidopsis thaliana]	319	1E-6
CD527794	2.16E-04	Mo17<B73=F1	1.48	10	>gb|AAP92747.1| ribosomal L9-like protein [Oryza sativa (japonica cultivar-group)]	190	2E-77
					>sp|P49210|RL9 ORYSA 60S ribosomal protein L9dbj|BAA19798.1| YK426 [Oryza sativa]	190	2E-77
					>ref|XP_463799.1| putative 60S ribosomal protein L9 [Oryza sativa (japonicacultivar-group)] dbj|BAD07825.1| putative 60S ribosomal protein L9 [Oryza sativa (japonica cultivar-group)]	183	4E-75
					>ref|XP 506675.1| PREDICTED OJ1435 F07.31 gene product [Oryza sativa (japonicacultivar-group)]	192	4E-75
					>gb|ABA81856.1| unknown [Solanum tuberosum]	194	6E-69
CB834053	2.20E-04	Mo17<B73=F1	1.68	10	ns		
CB604224	2.20E-04	Mo17<B73=F1	1.59	10	>emb|CAI64400.1| thioredoxin h1 protein [Zea mays]	128	6E-60
					>ref|XP_475666.1| putative thioredoxin H-type (TRX-H) (TrxTa) [Oryza sativa (japonicacultivar-group)] gb|AAT44260.1| putative thioredoxin H-type (TRX-H) (TrxTa) [Oryza sativa (japonica cultivar-group)]	121	2E-47
					>dbj|BAB20886.1| thioredoxin h [Oryza sativa (japonica cultivar-group)]	121	2E-47
					>gb|AAF88067.1| thioredoxin H [Triticum aestivum]emb|CAB96931.1| thioredoxin h [Triticum aestivum]	125	6E-44
					>gb|AAP72291.1| thioredoxin h isoform 2; HvTrxh2 [Hordeum vulgare subsp. vulgare]	122	6E-44
CD058888	2.23E-04	B73<F1=Mo17	1.54	3	>dbj|BAC78569.1| katanin [Oryza sativa (japonica cultivar-group)]dbj|BAD87507.1| katanin [Oryza sativa (japonica cultivar-group)]	386	5E-33
					>ref|NP 916186.1| katanin p60 subunit A 1-like [Oryza sativa (japonicacultivar-group)]	428	3E-29
					>dbj|BAD73365.1| vacuolar protein sorting factor 4B-like [Oryza sativa (japonicacultivar-group)] dbj|BAD73312.1| vacuolar protein sorting factor 4B-like [Oryza sativa (japonica cultivar-group)]	410	6E-20
					>ref|NP 916872.1| putative katanin [Oryza sativa (japonica cultivar-group)]	411	6E-20
					>ref|NP_565791.1| ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding[Arabidopsis thaliana] gb|AAC26698.2| putative katanin [Arabidopsis thaliana] gb|AAM61422.1| putative katanin [Arabidopsis thaliana]	384	1E-11
DV943338	2.39E-04	Mo17<B73=F1	3.2	10	ns		
CB815724	2.41E-04	B73<F1<Mo17	1.55	3	>gb|AAP85378.1| RNA binding protein Rp120 [Oryza sativa (japonica cultivar-group)]gb|AAP85377.1| RNA binding protein Rp120 [Oryza sativa (japonica cultivar-group)]	986	2E-61
					>ref|XP_466019.1| RNA binding protein Rp120 [Oryza sativa (japonica cultivar-group)]dbj|BAD26152.1| RNA binding protein Rp120 [Oryza sativa (japonica cultivar-group)] dbj|BAD25376.1| RNA binding protein Rp120 [Oryza sativa (japonica cultivar-group)]	986	2E-61
					>dbj|BAC06184.1| 110 kDa 4SNc-Tudor domain protein [Pisum sativum]	989	6E-42
					>dbj|BAB32793.1| 110 kDa 4SNc-Tudor domain protein [Pisum sativum]	699	6E-42
					>ref|NP 196352.2| nuclease/ nucleic acid binding [Arabidopsis thaliana]gb|AAL57629.1| AT5g07350/T2I1 60 [Arabidopsis thaliana]	991	6E-39
DV550868	2.51E-04	B73<F1<Mo17	3.64	3	>dbj|BAD37901.1| CREG2-protein-like [Oryza sativa (japonica cultivar-group)]dbj|BAD37864.1| CREG2-protein-like [Oryza sativa (japonica cultivar-group)]	215	7E-14
CB381221	2.51E-04	Mo17<B73=F1	1.45	10	ns		
DV622653	2.51E-04	Mo17<F1<B73	1.39	9	>ref|NP_568778.1| oxidoreductase, acting on NADH or NADPH [Arabidopsis thaliana]gb|AAL79599.1| AT5g52840/MXC20_6 [Arabidopsis thaliana] gb|AAL06910.1| AT5g52840/MXC20_6 [Arabidopsis thaliana] dbj|BAB10432.1| unnamed protein product [Arabidopsis thaliana] sp|Q9FLX7|NUFM_ARATH Probable NADH-ubiquinone oxidoreductase 18 kDa subunit, mitochondrial precursor (Complex I-18Kd) (CI-18Kd)	169	2E-40
					>gb|AAL32032.1| NADH-ubiquinone oxidoreductase [Retama raetam]	153	3E-38
					>ref|NP 680745.1| unknown protein [Arabidopsis thaliana]	115	6E-8
					>gb|AAU44524.1| hypothetical protein AT4G28005 [Arabidopsis thaliana]	112	8E-8
					>ref|XP 504293.1| hypothetical protein [Yarrowia lipolytica]emb|CAG79892.1| unnamed protein product [Yarrowia lipolytica CLIB122]	146	6E-6
DV622495	2.52E-04	B73<F1<Mo17	1.56	4	>gb|ABA91469.1| long-chain acyl-CoA synthetase [Oryza sativa (japonicacultivar-group)]	709	4E-73
					>gb|ABA96460.1| long-chain acyl-CoA synthetase [Oryza sativa (japonicacultivar-group)]	683	7E-70
					>gb|ABA96459.1| long-chain acyl-CoA synthetase [Oryza sativa (japonicacultivar-group)]	707	7E-70
					>gb|AAM28873.1| long chain acyl-CoA synthetase 6 [Arabidopsis thaliana]	701	2E-61
					>dbj|BAB40450.1| long-chain acyl-CoA synthetase [Arabidopsis thaliana]	701	2E-61
CD650760	2.56E-04	Mo17<B73=F1	1.46	10	>ref|XP_475712.1| putative GTP-binding protein Rab7a [Oryza sativa (japonicacultivar-group)] gb|AAT01314.1| putative GTP-binding protein Rab7a [Oryza sativa (japonica cultivar-group)]	206	1E-69

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>sp|Q40787|RAB7 PENCL Ras-related protein Rab7 (Possible apospory-associated protein)gb|AAA85273.1| possible apospory-associated protein	206	1E-69
					>gb|AAO67728.1| small GTP binding protein [Oryza sativa (indica cultivar-group)]	206	3E-68
					>sp|O24461|RAB7 PRUAR Ras-related protein Rab7gb|AAB71504.1| Rab7 GTP binding protein [Prunus armeniaca]	207	2E-61
					>emb|CAA98171.1| RAB7D [Lotus corniculatus var. japonicus]	207	7E-61
DV621279	2.57E-04	Mo17<F1<B73	1.31	9	>gb|AAU44173.1| unknown protein [Oryza sativa (japonica cultivar-group)]	401	8E-60
					>dbj|BAA75685.1| WREBP-2 [Nicotiana tabacum]	371	1E-23
					>ref|XP_466167.1| putative WREBP-2 [Oryza sativa (japonica cultivar-group)]dbj|BAD15483.1| putative WREBP-2 [Oryza sativa (japonica cultivar-group)]	342	9E-22
					>dbj|BAB83613.1| unknown protein [Arabidopsis thaliana]	339	9E-22
					>ref|NP_849323.1| nucleic acid binding / zinc ion binding [Arabidopsis thaliana]	387	9E-22
CD573009	2.61E-04	Mo17<F1<B73	1.57	10	ns		
BG841731	2.66E-04	Mo17<B73=F1	2.44	10	>emb|CAA46641.1| heat shock protein 17.2 [Zea mays]	152	6E-62
					>emb|CAA63901.1| heat shock protein 17.0 [Pennisetum glaucum]	152	4E-55
					>ref|XP_462737.1| putative heat shock protein [Oryza sativa (japonicacultivar-group)] emb|CAA43210.1| 16.9 KD low molecular weight heat shock protein [Oryza sativa] dbj|BAB64126.1| putative heat shock protein [Oryza sativa (japonica cultivar-group)] sp|P27777|HSP11_ORYSA 16.9 kDa class I heat shock protein gb|AAA33909.1| 16.9 kDa heat shock protein prf||1908439A heat shock protein 16.9A	150	2E-54
					>emb|CAA63902.1| heat shock protein 16.9 [Pennisetum glaucum]	150	3E-54
					>ref|XP_462738.1| putative heat shock protein [Oryza sativa (japonicacultivar-group)] dbj|BAB64127.1| putative heat shock protein [Oryza sativa (japonica cultivar-group)] gb|AAA33910.1| 16.9 kDa heat shock protein prf||1908439B heat shock protein 16.9B	150	3E-54
BG842066	2.71E-04	Mo17<B73=F1	1.59	11	>gb|AAB06331.1| novel protein	143	1E-71
					>gb|AAD45283.1| unknown [Zea mays]	128	1E-61
					>ref|XP_474394.1| OSJNBa0032F06.15 [Oryza sativa (japonica cultivar-group)]emb|CAE03432.2| OSJNBa0032F06.15 [Oryza sativa (japonica cultivar-group)]	145	9E-55
					>ref|XP_466973.1| putative elicitor-responsive gene-3 [Oryza sativa (japonicacultivar-group)] dbj|BAD25356.1| putative elicitor-responsive gene-3 [Oryza sativa (japonica cultivar-group)]	143	1E-38
					>gb|AAM63058.1| putative elicitor-responsive gene [Arabidopsis thaliana]	147	4E-38
DV492715	2.79E-04	B73<F1=Mo17	1.7	3	>gb|ABA99609.1| hypothetical protein LOC_Os12g44170 [Oryza sativa (japonicacultivar-group)]	859	4E-61
					>ref|NP_973860.1| ATP binding / damaged DNA binding [Arabidopsis thaliana]ref|NP_173324.1| ATP binding / damaged DNA binding [Arabidopsis thaliana] gb|AAO50545.1| unknown protein [Arabidopsis thaliana] dbj|BAC42129.1| unknown protein [Arabidopsis thaliana]	860	8E-51
					>gb|AAF79278.1| F14D16.2 [Arabidopsis thaliana]	977	8E-51
					>ref|NP_177613.1| ATP binding / damaged DNA binding [Arabidopsis thaliana]gb|AAD55301.1| Contains 2 PF|01535 DUF domains. [Arabidopsis thaliana]	855	3E-48
					>ref|NP_180698.1| ATP binding / damaged DNA binding [Arabidopsis thaliana]gb|AAD26479.1| unknown protein [Arabidopsis thaliana]	918	4E-7
CD527329	2.84E-04	Mo17<B73=F1	1.62	10	>gb|AAT74541.1| tyrosine-specific protein phosphatase protein [Oryza sativa]	225	5E-70
					>ref|NP_171993.1| phosphoprotein phosphatase [Arabidopsis thaliana]gb|AAC97999.1| ESTs gb|H36249, gb|AA59732 and gb|AA651219 come from this gene. [Arabidopsis thaliana] gb|AAO63274.1| At1g05000 [Arabidopsis thaliana] sp|Q9ZVN4|Y1500 ARATH Probable tyrosine-protein phosphatase At1g05000	215	8E-62
					>ref|XP_450177.1| putative tyrosine specific protein phosphatase protein [Oryzasativa (japonica cultivar-group)] dbj|BAD22288.1| putative tyrosine specific protein phosphatase protein [Oryza sativa (japonica cultivar-group)]	222	1E-60
					>pdb|1XRI|B Chain B, X-Ray Structure Of A Putative Phosphoprotein PhosphataseFrom Arabidopsis Thaliana Gene At1g05000 pdb|1XRI|A Chain A, X-Ray Structure Of A Putative Phosphoprotein Phosphatase From Arabidopsis Thaliana Gene At1g05000	151	2E-59
					>gb|AAX20039.1| tyrosine specific protein phosphatase family protein [Capsicumannuum]	225	4E-59
DV489704	2.88E-04	Mo17<B73=F1	1.88	10	>ref|XP_472942.1| OSJNBa0081L15.18 [Oryza sativa (japonica cultivar-group)]emb|CAE02006.2| OJ000223_09.8 [Oryza sativa (japonica cultivar-group)] emb|CAE03156.2| OSJNBa0081L15.18 [Oryza sativa (japonica cultivar-group)]	505	2E-83
					>gb|AAL79959.1| glucose-6-phosphate dehydrogenase [Oryza sativa (japonicacultivar-group)]	505	2E-82
					>dbj|BAA97664.1| glucose-6-phosphate dehydrogenase [Triticum aestivum]	509	8E-82
					>dbj|BAA97662.1| glucose-6-phosphate dehydrogenase [Triticum aestivum]	509	5E-81
					>ref|XP_466575.1| putative glucose-6-phosphate dehydrogenase [Oryza sativa (japonicacultivar-group)] dbj|BAD22150.1| putative glucose-6-phosphate dehydrogenase [Oryza sativa (japonica cultivar-group)]	517	7E-81
DV495282	2.91E-04	B73<F1=Mo17	1.51	3	ns		
CD001799	2.95E-04	Mo17<B73=F1	1.6	10	ns		
CB815390	3.06E-04	Mo17<F1<B73	2.11	10	>ref|XP_473146.1| OSJNBa0004N05.10 [Oryza sativa (japonica cultivar-group)]emb|CAE03386.2| OSJNBa0004N05.10 [Oryza sativa (japonica cultivar-group)]	465	3E-10
					>ref|NP_171899.1| unknown protein [Arabidopsis thaliana]gb|AAD10667.1| Unknown protein [Arabidopsis thaliana]	418	7E-7
					>ref|NP_199217.1| unknown protein [Arabidopsis thaliana]gb|AAP37859.1| At5g44040 [Arabidopsis thaliana] gb|AAM20395.1| putative protein [Arabidopsis thaliana] dbj|BAB09064.1| unnamed protein product [Arabidopsis thaliana]	416	2E-6
CD568379	3.13E-04	Mo17<F1<B73	1.49	10	>ref|NP_922765.1| putative chloroplast-targeted beta-amylase [Oryza sativa (japonicacultivar-group)] gb|AAG60205.1| putative chloroplast-targeted beta-amylase [Oryza sativa] gb|AAP55052.1| chloroplast-targeted beta-amylase, putative [Oryza sativa (japonica cultivar-group)]	544	2E-28

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>emb|CAI39244.1| beta-amylase [Glycine max]	540	2E-19
					>gb|AAK84008.1| beta-amylase PCT-BMYI [Solanum tuberosum]	545	7E-18
					>emb|CAB46051.1| putative beta-amylase [Arabidopsis thaliana]emb|CAB80980.1| putative beta-amylase [Arabidopsis thaliana]	498	6E-17
					>ref|NP_567523.1| CT-BMY; beta-amylase [Arabidopsis thaliana]emb|CAB58423.1| beta-amylase enzyme [Arabidopsis thaliana] gb|AAM65134.1| putative beta-amylase [Arabidopsis thaliana]	548	6E-17
CD568411	3.16E-04	F1=Mo17<B73	1.78	9	>dbj|BAB10218.1| unnamed protein product [Arabidopsis thaliana]	454	2E-35
					>ref|NP_198810.2| oxidoreductase [Arabidopsis thaliana]gb|AAP81799.1| At5g39940 [Arabidopsis thaliana] gb|AAO00853.1| putative protein [Arabidopsis thaliana]	480	2E-35
					>gb|ABA99608.1| hypothetical protein LOC_Os12g44160 [Oryza sativa (japonicacultivar-group)]	418	5E-31
					>gb|ABA22117.1| Fumarate reductase/succinate dehydrogenase flavoprotein-like[Anabaena variabilis ATCC 29413] ref|YP_323012.1| Fumarate reductase/succinate dehydrogenase flavoprotein-like [Anabaena variabilis ATCC 29413]	413	9E-24
					>dbj|BAB76255.1| all4556 [Nostoc sp. PCC 7120]ref|NP_488596.1| hypothetical protein all4556 [Nostoc sp. PCC 7120]	370	6E-23
CB885354	3.18E-04	Mo17<B73=F1	1.75	10	>gb|AAV50043.1| metallothionein-like protein [Saccharum hybrid cultivar]	81	7E-17
					>ref|NP_909265.1| putative metallothionein-like protein [Oryza sativa (japonicacultivar-group)] dbj|BAD52374.1| metallothionein [Oryza rufipogon] dbj|BAD52373.1| metallothionein [Oryza rufipogon] dbj|BAD52372.1| metallothionein [Oryza rufipogon] dbj|BAD52371.1| metallothionein [Oryza rufipogon] dbj|BAD52370.1| metallothionein [Oryza rufipogon] dbj|BAD52369.1| metallothionein [Oryza rufipogon] dbj|BAD52368.1| metallothionein [Oryza rufipogon] dbj|BAD52367.1| metallothionein [Oryza rufipogon] dbj|BAD52366.1| metallothionein [Oryza rufipogon] dbj|BAD52365.1| metallothionein [Oryza rufipogon] dbj|BAD52364.1| metallothionein [Oryza rufipogon] dbj|BAD52363.1| metallothionein [Oryza rufipogon] dbj|BAD52362.1| metallothionein [Oryza rufipogon] dbj|BAB44010.1| putative metallothionein-like protein [Oryza sativa (japonica cultivar-group)] dbj|BAA14038.1| metallothionein-like protein [Oryza sativa] sp|P94029|MT21_ORYSA Metallothionein-like protein type 2 gb|AAC49627.1| metallothionein-like type 2	82	6E-15
					>gb|AAS88721.1| metallothionein-like protein [Cynodon dactylon]	81	1E-14
					>emb|CAB53392.1| metallothionein [Eichhornia crassipes]emb|CAB53390.1| metallothionein [Eichhornia crassipes] emb|CAA09025.1| unnamed protein product [Eichhornia crassipes] emb|CAA09024.1| unnamed protein product [Eichhornia crassipes] emb|CAA09023.1| unnamed protein product [Eichhornia crassipes]	77	4E-14
					>gb|AAT08692.1| type 2 metallothionein-like protein [Hyacinthus orientalis]	85	2E-13
DV491284	3.20E-04	F1=Mo17<B73	1.54	9	>ref|NP_908456.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]	537	3E-15
					>gb|AAQ84111.1| Clt1 [Poncirus trifoliata]	54	5E-13
					>dbj|BAD34658.1| plasma membrane protein 3 [Leymus chinensis]	54	6E-13
					>gb|AAS72306.1| drought-induced hydrophobic protein [Oryza sativa (japonicacultivar-group)] gb|AAM46894.1| early drought induced protein [Oryza sativa (indica cultivar-group)] sp|Q6AT93|LTI6B_ORYSA Hydrophobic protein LTI6B (Low temperature-induced protein 6B) gb|AAT37942.1| low temperature-induced low molecular weight integral membrane protein LTI6b [Oryza sativa (japonica cultivar-group)]	55	6E-13
					>gb|AAV88601.1| low temperature and salt responsive protein [Pennisetum glaucum]	56	8E-13
DV549392	3.23E-04	B73<F1=Mo17	1.58	3	>gb|AAV28626.1| Bet v I allergen [Zea mays]	154	5E-61
					>ref|XP_472791.1| OSJNBb0048E02.12 [Oryza sativa (japonica cultivar-group)]emb|CAD40936.1| OSJNBb0048E02.12 [Oryza sativa (japonica cultivar-group)]	157	5E-49
					>gb|AAF87152.1| T23E23.17 [Arabidopsis thaliana]	418	1E-23
					>ref|NP_173813.1| unknown protein [Arabidopsis thaliana]emb|CAC83600.1| major latex-like protein [Arabidopsis thaliana] gb|AAL31239.1| At1g24020/T23E23_22 [Arabidopsis thaliana] gb|AAK96470.1| At1g24020/T23E23_22 [Arabidopsis thaliana] sp|Q93VR4|ML423_ARATH MLP-like protein 423	155	4E-23
					>gb|AAM65899.1| pollen allergen-like protein [Arabidopsis thaliana]	155	6E-23
BM381047	3.24E-04	Mo17<B73=F1	1.33	10	ns		
CB605079	3.25E-04	Mo17<F1<B73	1.45	10	>ref|XP_467724.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD15772.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAD15729.1| unknown protein [Oryza sativa (japonica cultivar-group)]	181	4E-20
CB239984	3.30E-04	Mo17<B73=F1	1.84	10	ns		
CB833959	3.34E-04	Mo17<B73=F1	1.37	10	ns		
BM074056	3.35E-04	Mo17<B73=F1	4.72	10	>ref|XP_470719.1| putative polyprotein [Oryza sativa]gb|AAL82521.1| putative polyprotein [Oryza sativa]	408	3E-13
					>ref|XP_472450.1| OSJNBb0108J11.11 [Oryza sativa (japonica cultivar-group)]emb|CAE02919.3| OSJNBb0108J11.11 [Oryza sativa (japonica cultivar-group)]	815	1E-12
					>gb|AAL68644.1| polyprotein [Oryza sativa (japonica cultivar-group)]	933	5E-12
					>gb|AAL76001.1| putative gag-pol polyprotein [Zea mays]	2396	1E-11
					>ref|XP_471847.1| OSJNBb0062H02.17 [Oryza sativa (japonica cultivar-group)]emb|CAE05600.2| OSJNBa0054D14.1 [Oryza sativa (japonica cultivar-group)] emb|CAD40278.2| OSJNBb0062H02.17 [Oryza sativa (japonica cultivar-group)]	1629	1E-11
CB380802	3.40E-04	Mo17<B73=F1	1.36	10	>gb|AAT08750.1| ribosomal protein L7 [Hyacinthus orientalis]	129	3E-39
					>gb|AAM64816.1| Ribosomal protein L7Ae-like [Arabidopsis thaliana]	128	2E-38
					>ref|NP_197516.1| RNA binding / structural constituent of ribosome [Arabidopsisthaliana] gb|AAM16174.1| AT5g20160/F5O24_50 [Arabidopsis thaliana] gb|AAK82476.1| AT5g20160/F5O24_50 [Arabidopsis thaliana] gb|AAM64557.1| ribosomal protein L7Ae-like [Arabidopsis thaliana]	128	7E-38

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>emb|CAB79193.1| Ribosomal protein L7Ae-like (fragment) [Arabidopsis thaliana]emb|CAB52812.1| Ribosomal protein L7Ae-like (fragment) [Arabidopsis thaliana]	108	1E-37
					>ref|NP 193969.1| RNA binding / structural constituent of ribosome [Arabidopsisthaliana] gb|AAM63731.1| Ribosomal protein L7Ae-like [Arabidopsis thaliana]	128	1E-37
BG842466	3.44E-04	Mo17<F1<B73	2.23	10	>dbj|BAD81539.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]dbj|BAD81466.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	70	1E-10
					>gb|AAM61511.1| unknown [Arabidopsis thaliana]	70	2E-7
					>gb|AAO64205.1| unknown protein [Arabidopsis thaliana]	92	2E-7
CB604802	3.67E-04	F1=Mo17<B73	1.33	9	>gb|AAL73485.1| repressor protein [Oryza sativa]	296	3E-68
					>gb|AAL73486.1| repressor protein [Triticum aestivum]	312	5E-68
					>emb|CAB93720.1| DR1-like protein [Arabidopsis thaliana]	162	8E-58
					>ref|NP 001031927.1| unknown protein [Arabidopsis thaliana]	158	1E-57
					>gb|AAL73489.1| repressor protein [Glycine max]	156	5E-57
BM336433	3.67E-04	F1=Mo17<B73	1.36	9	>emb|CAA77595.1| Plastid ribosomal protein CL15 [Pisum sativum]sp|P31165|RK15 PEA 50S ribosomal protein L15, chloroplast precursor (CL15)	258	1E-39
					>emb|CAA77593.1| Plastid ribosomal protein CL15 [Arabidopsis thaliana]pir||R5MUL5 ribosomal protein L15 precursor, chloroplast - Arabidopsis thaliana	277	7E-39
					>ref|NP_189221.1| RPL15 [Arabidopsis thaliana]gb|AAL15231.1| putative 50S ribosomal protein L15, chloroplast precursor [Arabidopsis thaliana] gb|AAK44050.1| putative 50S ribosomal protein L15, chloroplast precursor [Arabidopsis thaliana] gb|AAL11595.1| AT3g25920/MPE11_7 [Arabidopsis thaliana] gb|AAM61054.1| 50S ribosomal protein L15, chloroplast precursor [Arabidopsis thaliana] dbj|BAB01055.1| chloroplast 50S ribosomal protein L15 [Arabidopsis thaliana] sp|P25873|RK15 ARATH 50S ribosomal protein L15, chloroplast precursor (CL15)	277	7E-39
					>emb|CAA77592.1| plastid ribosomal protein CL15 [Arabidopsis thaliana]	273	7E-39
					>dbj|BAD80072.1| 50S ribosomal protein L15 [Synechococcus elongatus PCC 6301]ref|YP_172592.1| 50S ribosomal protein L15 [Synechococcus elongatus PCC 6301] ref|YP_401232.1| ribosomal protein L15 [Synechococcus elongatus PCC 7942] sp|Q5N0U8|RL15_SYNP6 50S ribosomal protein L15 dbj|BAA22466.1| 50S ribosomal protein L15 [Synechococcus sp.] gb|ABB58245.1| ribosomal protein L15 [Synechococcus elongatus PCC 7942]	147	7E-18
CD528067	3.70E-04	Mo17<B73=F1	1.31	10	>dbj|BAD28633.1| unknown protein [Oryza sativa (japonica cultivar-group)]	291	1E-55
					>gb|AAU43966.1| unknown protein [Oryza sativa (japonica cultivar-group)]	273	7E-42
					>ref|NP_565465.1| LCV1 [Arabidopsis thaliana]gb|AAM91311.1| unknown protein [Arabidopsis thaliana] gb|AAD24400.2| expressed protein [Arabidopsis thaliana] gb|AAL62439.1| unknown protein [Arabidopsis thaliana] gb|AAM61503.1| unknown [Arabidopsis thaliana]	256	2E-37
					>gb|AAM10356.1| At2g20120/T2G17.8 [Arabidopsis thaliana]gb|AAK95310.1| At2g20120/T2G17.8 [Arabidopsis thaliana]	268	1E-36
					>ref|NP_565464.1| COV1 (CONTINUOUS VASCULAR RING) [Arabidopsis thaliana]gb|AAD24385.1| expressed protein [Arabidopsis thaliana] gb|AAO41858.1| putative membrane protein COV [Arabidopsis thaliana] gb|AAM61543.1| unknown [Arabidopsis thaliana]	268	1E-36
CB603818	3.78E-04	Mo17<F1<B73	1.48	9	ns		
BM073205	3.83E-04	B73<F1<Mo17	1.75	4	>gb|AAU03113.1| putative o-methyltransferase ZRP4 [Oryza sativa (japonicacultivar-group)] gb|AAT01304.1| putative o-methyltransferase ZRP4 [Oryza sativa (japonica cultivar-group)]	367	1E-36
					>gb|AAU03114.1| putative o-methyltransferase ZRP4 [Oryza sativa (japonicacultivar-group)] gb|AAT01305.1| putative o-methyltransferase ZRP4 [Oryza sativa (japonica cultivar-group)]	370	5E-36
					>gb|ABA98340.1| o-methyltransferase zrp4 [Oryza sativa (japonica cultivar-group)]	359	1E-34
					>sp|P47917|ZRP4 MAIZE O-methyltransferase ZRP4 (OMT)gb|AAA18532.1| O-methyltransferase	364	8E-34
					>gb|ABA98018.1| caffeic acid methyl transferase, putative [Oryza sativa (japonicacultivar-group)]	127	8E-33
CB351677	3.89E-04	Mo17<F1<B73	1.59	10	>sp|P05621|H2B2 WHEAT Histone H2B.2	149	1E-36
					>ref|NP_909288.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]dbj|BAB44045.1| putative histone H2B [Oryza sativa (japonica cultivar-group)] dbj|BAB03624.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	153	2E-36
					>ref|XP_475912.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]gb|AAU44113.1| putative histone H2B [Oryza sativa (japonica cultivar-group)] gb|AAT69583.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	152	3E-36
					>ref|XP 475367.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]gb|AAT39167.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	124	3E-36
					>ref|NP 909263.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]dbj|BAB44008.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	153	4E-36
CB280863	3.90E-04	Mo17<B73=F1	1.51	10	>pir||JS0731 wound-inducible basic protein - kidney beandbj|BAA02299.1| 5.8 kb basic protein [Phaseolus vulgaris] sp|Q09020|PR4_PHAVU WOUND-INDUCED BASIC PROTEIN gb|AAA33774.1| basic protein	47	2E-11
					>ref|NP_187379.1| unknown protein [Arabidopsis thaliana]gb|AAF20223.1| putative wound-induced basic protein [Arabidopsis thaliana] gb|AAP21314.1| At3g07230 [Arabidopsis thaliana] gb|AAN72039.1| putative wound-induced basic protein [Arabidopsis thaliana]	46	5E-9
BM073252	3.92E-04	Mo17<B73=F1	1.46	10	>dbj|BAD27890.1| putative vacuolar protein sorting; Vps29p [Oryza sativa (japonicacultivar-group)]	188	2E-59
					>ref|NP_190365.3| hydrolase/ protein serine/threonine phosphatase [Arabidopsisthaliana] ref|NP_974400.1| hydrolase/ protein serine/threonine phosphatase [Arabidopsis thaliana] emb|CAB41864.1| putative protein [Arabidopsis thaliana] gb|AAO42341.1| unknown protein [Arabidopsis thaliana] gb|AAO22602.1| unknown protein [Arabidopsis thaliana]	190	3E-53
					>ref|NP 974399.1| protein serine/threonine phosphatase [Arabidopsis thaliana]	180	3E-53
					>ref|XP 796390.1| PREDICTED: similar to Vacuolar protein sorting 29 (Vesicle proteinsorting 29) [Strongylocentrotus purpuratus]	182	2E-38

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>emb|CAE50610.1| novel protein similar to human and mouse vacuolar protein sorting29 (yeast) (VPS29) [Danio rerio] ref|XP_707443.1| PREDICTED: similar to Vacuolar protein sorting 29 isoform 2 [Danio rerio] ref|NP_956331.1| vacuolar protein sorting 29 [Danio rerio] gb|AAH71331.1| Vacuolar protein sorting 29 [Danio rerio] gb|AAH45981.1| Vacuolar protein sorting 29 [Danio rerio]	182	1E-36
BM073588	3.96E-04	Mo17<B73=F1	1.51	10	>ref|XP 469523.1| putative DNA-binding protein [Oryza sativa]gb|AAK18838.1| putative DNA-binding protein [Oryza sativa]	161	2E-64
					>gb|AAZ20287.1| ubiquitin-conjugating enzyme 2 [Arachis hypogaea]	159	3E-54
					>gb|ABA26987.1| TO38-23 [Taraxacum officinale]	138	3E-49
					>gb|AAT01417.1| ubiquitin-conjugating enzyme family protein [Tamarix androssowii]	146	6E-49
					>gb|ABB29951.1| ubiquitin-conjugating enzyme family protein-like [Solanumtuberosum] gb|ABA40444.1| ubiquitin-conjugating enzyme family protein-like protein [Solanum tuberosum]	146	8E-49
DV550635	3.99E-04	B73<F1=Mo17	1.87	3	ns		
CB334575	4.03E-04	Mo17<B73=F1	1.55	11	>gb|ABA94167.1| purple acid phosphatase precursor, putative [Oryza sativa (japonicacultivar-group)]	294	4E-74
					>ref|NP_919594.1| putative purple acid phosphatase [Oryza sativa (japonicacultivar-group)] gb|AAL34937.1| Putative purple acid phosphatase [Oryza sativa] gb|AAP51881.1| Ser/Thr protein phosphatase, putative [Oryza sativa (japonica cultivar-group)]	335	8E-73
					>gb|AAT37529.1| purple acid phosphatase 1 [Solanum tuberosum]	328	5E-67
					>ref|NP_172923.3| hydrolase/ protein serine/threonine phosphatase [Arabidopsisthaliana] gb|AAT95435.1| putative purple acid phosphatase [Arabidopsis thaliana] gb|AAN41277.1| putative purple acid phosphatase [Arabidopsis thaliana]	366	1E-66
					>gb|AAL49808.2| putative purple acid phosphatase [Arabidopsis thaliana]	352	1E-66
DV491369	4.05E-04	B73<F1<Mo17	2.06	3	>emb|CAB80425.1| hypothetical protein [Arabidopsis thaliana]emb|CAB38299.1| hypothetical protein [Arabidopsis thaliana]	87	1E-10
CB815830	4.11E-04	Mo17<F1<B73	1.41	9	>ref|XP 450543.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD23593.1| unknown protein [Oryza sativa (japonica cultivar-group)]	177	4E-22
					>ref|NP_565877.1| unknown protein [Arabidopsis thaliana]dbj|BAD94470.1| hypothetical protein [Arabidopsis thaliana] gb|AAM61046.1| unknown [Arabidopsis thaliana]	78	3E-11
					>gb|AAO42916.1| At3g54082 [Arabidopsis thaliana]dbj|BAC43618.1| unknown protein [Arabidopsis thaliana] dbj|BAC42414.1| unknown protein [Arabidopsis thaliana]	78	7E-11
					>dbj|BAD94948.1| hypothetical protein [Arabidopsis thaliana]	78	9E-11
DV942210	4.20E-04	Mo17<B73=F1	1.55	10	>gb|AAT08725.1| histone H4 [Hyacinthus orientalis]	103	1E-37
					>dbj|BAB71814.1| histone H4 [Citrus jambhiri]	102	1E-37
					>ref|NP_563793.1| DNA binding [Arabidopsis thaliana]ref|NP_850660.1| DNA binding [Arabidopsis thaliana] ref|NP_180441.1| HIS4 [Arabidopsis thaliana] ref|NP_568911.1| DNA binding [Arabidopsis thaliana] ref|NP_568918.1| DNA binding [Arabidopsis thaliana] ref|NP_190941.1| DNA binding [Arabidopsis thaliana] ref|NP_563797.1| DNA binding [Arabidopsis thaliana] ref|NP_850939.1| DNA binding [Arabidopsis thaliana] ref|NP_190179.1| DNA binding [Arabidopsis thaliana] ref|XP_475394.1| histone H4 [Oryza sativa (japonica cultivar-group)] ref|XP_475383.1| putative histone H4 [Oryza sativa (japonica cultivar-group)] ref|NP_912452.1| Unknown protein [Oryza sativa (japonica cultivar-group)] ref|XP_467181.1| histone H4 [Oryza sativa (japonica cultivar-group)] ref|NP_922551.1| histone H4 [Oryza sativa (japonica cultivar-group)] ref|NP_915374.1| putative histone H4 [Oryza sativa (japonica cultivar-group)] ref|NP_910647.1| histone H4 [Oryza sativa (japonica cultivar-group)] ref|XP 473659.1| OSJNBa0088A01.17 [Oryza sativa (japonica cultivar-group)] gb|AAU90170.1| histone H4 [Oryza sativa	103	1E-37
					>sp|P62786|H42 WHEAT Histone H4 variant TH091gb|AAA34292.1| histone H4	103	1E-37
					>prf||1101277A histone H4	102	1E-37
CB885823	4.21E-04	F1=Mo17<B73	1.4	9	>gb|AAK06838.1| glyoxalase I [Avicennia marina]	184	7E-65
					>emb|CAA12028.1| Glyoxalase I [Cicer arietinum]sp|O49818|LGUL_CICAR Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)	186	1E-62
					>ref|NP_849609.1| calmodulin binding / lactoylglutathione lyase [Arabidopsisthaliana] ref|NP_172291.1| calmodulin binding / lactoylglutathione lyase [Arabidopsis thaliana] ref|NP_001030995.1| calmodulin binding / lactoylglutathione lyase [Arabidopsis thaliana] gb|AAT41850.1| At1g08110 [Arabidopsis thaliana] gb|AAN72031.1| glyoxalase I, putative [Arabidopsis thaliana] sp|Q8H0V3|LGUL_ARATH Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)	185	9E-62
					>ref|NP 001030996.1| calmodulin binding / lactoylglutathione lyase [Arabidopsisthaliana]	235	9E-62
					>emb|CAA73691.1| Glyoxalase I [Brassica juncea]sp|O04885|LGUL_BRAJU Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)	185	3E-61
DV491351	4.26E-04	B73<F1<Mo17	1.6	3	>gb|AAF79839.1| T6D22.14 [Arabidopsis thaliana]	2254	2E-18
					>ref|NP_849608.1| MOM (MAINTENANCE OF METHYLATION) [Arabidopsis thaliana]ref|NP_563806.1| MOM (MAINTENANCE OF METHYLATION) [Arabidopsis thaliana] gb|AAF73381.1| MOM [Arabidopsis thaliana]	2001	2E-18
					>gb|AAF73380.1| MOM [Arabidopsis thaliana]	2001	2E-18
CB816440	4.26E-04	Mo17<B73=F1	1.61	10	ns		
DV491703	4.27E-04	Mo17<F1<B73	2.48	9	ns		
CB381627	4.29E-04	Mo17<B73=F1	1.41	10	>dbj|BAD54696.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]dbj|BAD34409.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	75	9E-28
					>dbj|BAC43353.1| unknown protein [Arabidopsis thaliana]	71	1E-26

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|EAA00792.2| ENSANGP00000020123 [Anopheles gambiae str. PEST]ref|XP 320694.2| ENSANGP00000020123 [Anopheles gambiae str. PEST]	81	2E-10
					>dbj|BAE63661.1| unnamed protein product [Aspergillus oryzae]	117	1E-9
					>ref|NP_652380.2| CG13018-PA [Drosophila melanogaster]gb|AAY55593.1| IP03340p [Drosophila melanogaster] gb|AAF58293.2| CG13018-PA [Drosophila melanogaster]	79	2E-8
CB334308	4.31E-04	Mo17<B73=F1	1.28	10	>gb|AAM08320.1| small Ran-related GTP-binding protein [Triticum aestivum]gb|AAL30396.1| small Ras-related GTP-binding protein [Triticum aestivum]	221	3E-14
					>ref|XP_475914.1| GTP-binding nuclear protein RAN-B1 [Oryza sativa (japonicacultivar-group)] gb|AAT69585.1| GTP-binding nuclear protein RAN-B1 [Oryza sativa (japonica cultivar-group)] dbj|BAA81911.1| Ran [Oryza sativa (japonica cultivar-group)] dbj|BAB82438.1| small GTP-binding protein (Ran2) [Oryza sativa (japonica cultivar-group)]	221	3E-14
					>gb|AAD18006.1| Ran-related GTP binding protein [Zea mays]	170	3E-13
					>emb|CAC10213.1| GTP-binding protein [Cicer arietinum]	221	2E-12
					>gb|AAM12880.1| GTP-binding protein [Helianthus annuus]	221	2E-12
BM080173	4.37E-04	Mo17<B73=F1	3.91	10	>emb|CAF31501.1| putative acid phosphatase [Hordeum vulgare subsp. vulgare]emb|CAB71336.2| putative acid phosphatase [Hordeum vulgare subsp. vulgare]	272	5E-49
					>emb|CAA11075.1| acid phosphatase [Glycine max]	264	1E-46
					>gb|AAU90121.1| putative acid phosphatase [Oryza sativa (japonica cultivar-group)]gb|AAW56902.1| putative acid phosphatase [Oryza sativa (japonica cultivar-group)]	265	3E-44
					>gb|AAW56914.1| putative acid phosphatase [Oryza sativa (japonica cultivar-group)]gb|AAW56899.1| putative acid phosphatase [Oryza sativa (japonica cultivar-group)]	243	2E-43
					>gb|AAV31208.1| unknow protein [Oryza sativa (japonica cultivar-group)]gb|AAW56911.1| putative acid phosphatase [Oryza sativa (japonica cultivar-group)]	250	2E-42
DV490613	4.39E-04	Mo17<B73=F1	4.01	10	>ref|XP 463025.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAR10853.1| unknown protein [Oryza sativa (japonica cultivar-group)]	490	8E-20
					>ref|XP_480216.1| unknown protein [Oryza sativa (japonica cultivar-group)]ref|XP_507142.1| PREDICTED OJ9990_A01.113 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC99902.1| unknown protein [Oryza sativa (japonica cultivar-group)]	470	6E-19
CB617072	4.39E-04	B73<F1=Mo17	1.46	3	>gb|AAL73043.1| histone H1-like protein [Zea mays]	244	4E-26
					>emb|CAA40362.1| H1 histone [Zea mays]sp|P23444|H1 MAIZE Histone H1	246	3E-16
					>ref|NP 909937.1| histone-like protein [Oryza sativa (japonica cultivar-group)]gb|AAO37519.1| histone-like protein [Oryza sativa (japonica cultivar-group)]	293	3E-16
					>dbj|BAA87331.1| variant of histone H1 [Lilium longiflorum]	231	3E-16
					>dbj|BAA25203.1| histone H1 [Triticum aestivum]	284	8E-16
DV489877	4.40E-04	Mo17<F1<B73	1.89	10	>dbj|BAD28383.1| putative tripeptidyl peptidase II [Oryza sativa (japonicacultivar-group)]	1359	2E-35
					>emb|CAB79085.1| putative protein [Arabidopsis thaliana]emb|CAB45880.1| putative protein [Arabidopsis thaliana]	1396	2E-30
					>gb|AAM20148.1| unknown protein [Arabidopsis thaliana]	1346	2E-30
					>ref|NP 193817.2| TPP2 (TRIPEPTIDYL PEPTIDASE II); subtilase [Arabidopsis thaliana]	1380	2E-30
					>gb|AAL27553.1| hypothetical protein [Musa acuminata]	234	2E-25
AI665898	4.44E-04	B73<F1=Mo17	1.84	3	>dbj|BAD45275.1| putative 24 kDa seed maturation protein [Oryza sativa (japonicacultivar-group)]	265	6E-45
					>gb|ABB51093.1| reticulon [Hordeum vulgare]	204	8E-45
					>dbj|BAD27895.1| putative 24 kDa seed maturation protein [Oryza sativa (japonicacultivar-group)]	230	3E-41
					>ref|NP_913448.1| P0492F05.25 [Oryza sativa (japonica cultivar-group)]dbj|BAB32723.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAB92114.1| unknown protein [Oryza sativa (japonica cultivar-group)]	279	1E-28
					>gb|ABC01908.1| putative 24 kDa seed maturation protein-like protein [Solanumtuberosum]	255	7E-28
CB251978	4.46E-04	B73<F1=Mo17	1.37	3	ns		
DV489688	4.70E-04	B73<F1=Mo17	1.9	3	ns		
BG841274	4.74E-04	Mo17<F1<B73	1.67	10	>gb|AAC28490.1| photosystem II type II chlorophyll a/b binding protein [Sorghumbicolor]	191	2E-37
					>emb|CAA48641.1| type II light-harvesting chlorophyll a /b-binding protein [Zeamays]	229	5E-37
					>gb|AAT81763.1| chlorophyll a/b binding protein [Oryza sativa (japonicacultivar-group)]	263	4E-36
					>gb|AAC15992.1| chlorophyll a/b binding protein [Oryza sativa]	263	2E-35
					>dbj|BAA00537.1| type II light-harvesting chlorophyll a/b-binding protein [Oryzasativa (japonica cultivar-group)]	263	3E-35
CD001060	4.81E-04	Mo17<F1<B73	1.54	10	>gb|AAG46061.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]ref|XP 469258.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	322	2E-23
					>gb|ABA99954.1| hypothetical protein LOC Os12g43780 [Oryza sativa (japonicacultivar-group)]	150	3E-14
BM266692	4.91E-04	Mo17<F1<B73	9	10	>ref|XP_479102.1| unknown protein [Oryza sativa (japonica cultivar-group)]ref|XP_506454.1| PREDICTED OSJNBa0072I06.5 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC84850.1| unknown protein [Oryza sativa (japonica cultivar-group)]	245	1E-9
CD059030	4.93E-04	Mo17<B73=F1	1.41	11	>sp|P23346|SODC5 MAIZE Superoxide dismutase [Cu-Zn] 4AP	152	2E-77
					>emb|CAB57992.1| superoxide dismutase-4AP [Zea mays]sp|P23345|SODC4 MAIZE Superoxide dismutase [Cu-Zn] 4A	152	1E-76
					>emb|CAB57993.1| superoxide dismutase-4A [Zea mays]gb|AAB49913.1| superoxide dismutase 4A	152	2E-75

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>sp|P28757|SODC2_ORYSA Superoxide dismutase [Cu-Zn] 2gb|AAC14465.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00800.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)]	152	3E-71
					>gb|AAY56345.1| cytoplasmic copper/zinc-superoxide dismutase [Oryza sativa (indicacultivar-group)] sp|P28756|SODC1_ORYSA Superoxide dismutase [Cu-Zn] 1 gb|AAC14464.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00799.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)] prf||2111424A Cu/Zn superoxide dismutase	152	3E-70
CB410998	5.09E-04	Mo17<B73=F1	1.52	10	>ref|XP_482710.1| unknown protein [Oryza sativa (japonica cultivar-group)]ref|XP_507588.1| PREDICTED OJ1117_F10.6 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_507250.1| PREDICTED OJ1117_F10.6 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD08781.1| unknown protein [Oryza sativa (japonica cultivar-group)]	464	2E-79
					>ref|XP 482707.1| fiber protein-like [Oryza sativa (japonica cultivar-group)]dbj|BAD08741.1| fiber protein-like [Oryza sativa (japonica cultivar-group)]	683	3E-70
					>ref|NP 189910.2| DNA binding / protein binding / zinc ion binding [Arabidopsisthaliana] gb|AAQ82841.1| At3g43240 [Arabidopsis thaliana]	747	1E-54
					>emb|CAB89045.1| putative protein [Arabidopsis thaliana]	717	1E-53
					>ref|XP 482708.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]dbj|BAD08779.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	301	2E-30
CB815754	5.09E-04	B73<F1<Mo17	1.43	4	>ref|XP_476775.1| putative DNA-directed RNA polymerase II 13.6K chain [Oryza sativa(japonica cultivar-group)] dbj|BAC83620.1| putative DNA-directed RNA polymerase II 13.6K chain [Oryza sativa (japonica cultivar-group)]	120	6E-58
					>ref|NP_190777.1| ATRPB13.6; DNA binding / DNA-directed RNA polymerase [Arabidopsisthaliana] emb|CAB41329.1| DNA-directed RNA polymerase II 13.6K chain [Arabidopsis thaliana] gb|AAO64919.1| At3g52090 [Arabidopsis thaliana] gb|AAB02849.1| RNA polymerase II 13.6 kDa subunit sp|Q38859|RPB11_ARATH DNA-directed RNA polymerase II 13.6 kDa polypeptide pir||S71204 DNA-directed RNA polymerase (EC 2.7.7.6) II 13.6K chain - Arabidopsis thaliana	116	1E-49
					>emb|CAF90169.1| unnamed protein product [Tetraodon nigroviridis]	117	1E-28
					>gb|EAL33630.1| GA19897-PA [Drosophila pseudoobscura]	117	1E-28
					>ref|NP_609836.1| CG6840-PA [Drosophila melanogaster]gb|AAF53606.1| CG6840-PA [Drosophila melanogaster] sp|Q9VJE4|RPB11_DROME DNA-directed RNA polymerase II 13.3 kDa polypeptide (RPB11)	117	2E-28
BG874095	5.11E-04	Mo17<B73=F1	1.85	10	>tpg|DAA00299.1| TPA: putative phytosulfokine peptide precursor [Zea mays]	102	6E-38
					>ref|XP_470620.1| Putative Phytosulfokines precursor [Oryza sativa (japonicacultivar-group)] gb|AAM19137.1| Putative Phytosulfokines precursor [Oryza sativa (japonica cultivar-group)] gb|AAO00693.1| Putative Phytosulfokines precursor [Oryza sativa (japonica cultivar-group)]	101	5E-14
CD651787	5.14E-04	Mo17<B73=F1	1.47	10	>ref|XP_479153.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)]ref|XP_506463.1| PREDICTED P0616D06.117 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC16499.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)] dbj|BAA04903.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)] sp|Q40680|EF1D ORYSA Elongation factor 1-delta (EF-1-delta) (Elongation factor 1B-beta) (eEF-1B beta)	229	2E-40
					>gb|AAU89237.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)]dbj|BAA34599.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)] dbj|BAA34598.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)]	226	8E-34
					>gb|AAR15081.1| translational elongation factor 1 subunit Bbeta [Pisum sativum]	231	7E-33
					>emb|CAB90214.1| putative elongation factor 1 beta [Hordeum vulgare subsp. vulgare]	226	4E-32
					>sp|P93447|EF1D_PIMBR Elongation factor 1-delta (EF-1-delta) (Elongation factor 1B-beta)(eEF-1B beta) gb|AAB68395.1| elongation factor 1-beta [Pimpinella brachycarpa]	226	5E-32
DV491446	5.16E-04	B73<F1<Mo17	6.34	3	ns		
BG841152	5.18E-04	F1=Mo17<B73	1.8	9	>gb|AAG34839.1| glutathione S-transferase GST 31 [Zea mays]	232	7E-45
					>gb|AAG34842.1| glutathione S-transferase GST 34 [Zea mays]	225	4E-39
					>ref|NP_922426.1| putative glutathione S-transferase [Oryza sativa (japonicacultivar-group)] gb|AAM12496.1| putative glutathione S-transferase [Oryza sativa (japonica cultivar-group)] gb|AAP54713.1| glutathione S-transferase, putative [Oryza sativa (japonica cultivar-group)]	255	3E-30
					>ref|NP_922425.1| putative glutathione S-transferase [Oryza sativa (japonicacultivar-group)] gb|AAK98543.1| putative glutathione S-transferase OsGSTU15 [Oryza sativa (japonica cultivar-group)] gb|AAM12500.1| putative glutathione S-transferase [Oryza sativa (japonica cultivar-group)] gb|AAP54712.1| glutathione S-transferase, putative [Oryza sativa (japonica cultivar-group)]	244	2E-28
					>gb|ABB47914.1| glutathione S-transferase, putative [Oryza sativa (japonicacultivar-group)]	130	2E-28
CB331056	5.26E-04	Mo17<B73=F1	1.4	10	>gb|AAK06838.1| glyoxalase I [Avicennia marina]	184	2E-19
					>emb|CAA12028.1| Glyoxalase I [Cicer arietinum]sp|O49818|LGUL_CICAR Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)	186	6E-19
					>ref|NP_849609.1| calmodulin binding / lactoylglutathione lyase [Arabidopsisthaliana] ref|NP_172291.1| calmodulin binding / lactoylglutathione lyase [Arabidopsis thaliana] ref|NP_001030995.1| calmodulin binding / lactoylglutathione lyase [Arabidopsis thaliana] gb|AAT41850.1| At1g08110 [Arabidopsis thaliana] gb|AAN72031.1| glyoxalase I, putative [Arabidopsis thaliana] sp|Q8H0V3|LGUL_ARATH Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)	185	2E-18
					>ref|NP 001030996.1| calmodulin binding / lactoylglutathione lyase [Arabidopsisthaliana]	235	2E-18
					>gb|AAF79827.1| T6D22.20 [Arabidopsis thaliana]	196	2E-18
CD484616	5.33E-04	F1=Mo17<B73	1.39	9	ns		
BM332662	5.34E-04	Mo17<B73=F1	1.61	10	ns		

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
BM335631	5.43E-04	Mo17<B73=F1	7.89	10	>emb|CAA44165.1| unnamed protein product [Zea mays]	611	1E-44
					>gb|AAA21566.1| MudrA [Zea mays]gb|AAA81535.1| mudrA gene product	823	1E-44
					>gb|AAB48408.1| MURAZC [Zea mays]	823	3E-44
					>gb|AAN40034.1| putative MURAZC [Zea mays]	566	7E-41
					>ref|XP_507157.1| PREDICTED P0035F08.13 gene product [Oryza sativa (japonicacultivar-group)]	373	6E-37
CD001481	5.43E-04	Mo17<B73=F1	1.23	10	>ref|XP_475453.1| putative 60S ribosomal protein L24 [Oryza sativa (japonicacultivar-group)] gb|AAT01333.1| putative 60S ribosomal protein L24 [Oryza sativa (japonica cultivar-group)]	161	1E-43
					>dbj|BAD82702.1| putative 60S ribosomal protein L24 [Oryza sativa (japonicacultivar-group)]	162	6E-43
					>ref|NP_911528.1| putative 60S ribosomal protein L24 [Oryza sativa (japonicacultivar-group)] dbj|BAD30738.1| putative 60S ribosomal protein L24 [Oryza sativa (japonica cultivar-group)] dbj|BAC06922.1| putative 60S ribosomal protein L24 [Oryza sativa (japonica cultivar-group)]	160	1E-42
					>emb|CAA63960.1| L24 ribosomal protein [Hordeum vulgare subsp. vulgare]sp|P50888|RL24_HORVU 60S ribosomal protein L24	162	9E-42
					>gb|AAG13986.1| 60S ribosomal protein L24 [Prunus avium]sp|Q9FUL4|RL24_PRUAV 60S ribosomal protein L24	186	5E-40
DV622327	5.44E-04	Mo17<F1<B73	1.36	10	ns		
BM073390	5.56E-04	B73<F1<Mo17	6.27	3	ns		
DV490312	5.57E-04	Mo17<B73=F1	1.68	10	>gb|AAO72563.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]	413	1E-53
					>dbj|BAD61932.1| putative elongation factor 1 gamma [Oryza sativa (japonicacultivar-group)] dbj|BAD61828.1| putative elongation factor 1 gamma [Oryza sativa (japonica cultivar-group)]	416	1E-53
					>ref|XP_464690.1| Elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]dbj|BAD17615.1| Elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)] sp|Q9ZRI7|EF1G_ORYSA Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) dbj|BAA34206.1| elongation factor 1B gamma [Oryza	418	8E-53
					>gb|AAO72574.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]	409	2E-52
					>ref|XP_464689.1| putative elongation factor 1-gamma [Oryza sativa (japonicacultivar-group)] dbj|BAD17614.1| putative elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]	414	2E-52
CB605387	5.61E-04	B73<F1<Mo17	1.3	3	>ref|XP_507607.1| PREDICTED P0562A06.14 gene product [Oryza sativa (japonicacultivar-group)] ref|XP_507335.1| PREDICTED P0562A06.14 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_483765.1| putative 40S ribosomal protein S25 (RPS25B) [Oryza sativa (japonica cultivar-group)] dbj|BAD13135.1| putative 40S ribosomal protein S25 (RPS25B) [Oryza sativa (japonica cultivar-group)]	108	2E-11
					>dbj|BAD46219.1| putative 40S ribosomal protein 25S [Oryza sativa (japonicacultivar-group)]	108	6E-11
					>ref|NP_179752.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAD23647.1| 40S ribosomal protein S25 [Arabidopsis thaliana] gb|AAM10294.1| At2g21580/F2G1.15 [Arabidopsis thaliana] gb|AAK82474.1| At2g21580/F2G1.15 [Arabidopsis thaliana] pir||H84602 40S ribosomal protein S25 [imported] - Arabidopsis thaliana sp|Q9SIK2|RS25A_ARATH 40S ribosomal protein S25-1	108	6E-11
					>ref|NP_001031390.1| structural constituent of ribosome [Arabidopsis thaliana]	107	6E-11
					>ref|NP_195631.1| structural constituent of ribosome [Arabidopsis thaliana]emb|CAB80583.1| ribosomal protein S25 [Arabidopsis thaliana] emb|CAB43635.1| ribosomal protein S25 [Arabidopsis thaliana] gb|AAL15350.1| AT4g39200/T22F8_100 [Arabidopsis thaliana] gb|AAK59777.1| AT4g39200/T22F8_100 [Arabidopsis thaliana] gb|AAM62797.1| ribosomal protein S25 [Arabidopsis thaliana] sp|Q9T029|RS25B_ARATH 40S ribosomal protein S25-2 pir||T08568 ribosomal protein S25, cytosolic - Arabidopsis thaliana	108	3E-10
DV621333	5.62E-04	Mo17<B73=F1	1.39	10	>gb|AAC19375.1| acireductone dioxygenase 2 [Oryza sativa]	198	2E-92
					>gb|AAX55895.1| aci-reductone dioxygenase-like protein [Oryza sativa (japonicacultivar-group)]	198	5E-92
					>gb|AAN06863.1| Putative probable submergence induced, nickel-binding protein 2A[Oryza sativa (japonica cultivar-group)]	254	3E-90
					>dbj|BAB61039.1| iron-deficiency induced gene [Hordeum vulgare]	198	1E-88
					>gb|AAC05511.1| acireductone dioxygenase 1 [Oryza sativa]	199	3E-81
BM341094	5.79E-04	Mo17<B73=F1	1.56	10	>ref|XP_474686.1| OSJNBb0006L01.5 [Oryza sativa (japonica cultivar-group)]emb|CAE04393.2| OSJNBb0006L01.5 [Oryza sativa (japonica cultivar-group)]	253	2E-61
					>gb|AAM61464.1| electron transfer flavoprotein beta-subunit-like [Arabidopsisthaliana]	251	3E-53
					>ref|NP_199156.1| electron transporter [Arabidopsis thaliana]gb|AAL38600.1| AT5g43430/MWF20_14 [Arabidopsis thaliana] gb|AAK74015.1| AT5g43430/MWF20_14 [Arabidopsis thaliana] dbj|BAA97422.1| electron transfer flavoprotein beta-subunit-like [Arabidopsis thaliana]	251	3E-53
					>ref|ZP_00509545.1| Electron transfer flavoprotein beta-subunit [Polaromonas sp. JS666]gb|EAM36351.1| Electron transfer flavoprotein beta-subunit [Polaromonas sp. JS666]	249	5E-43
					>gb|AAH59787.1| MGC68596 protein [Xenopus laevis]	254	1E-41
CB603863	5.82E-04	Mo17<F1<B73	1.54	10	>ref|NP_908597.1| putative endo-1,3(4)-beta-glucanase [Oryza sativa (japonicacultivar-group)] dbj|BAB92772.1| putative endo-1,3(4)-beta-glucanase [Oryza sativa (japonica cultivar-group)]	499	2E-41
					>ref|NP_192138.1| hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana]emb|CAB80722.1| putative endo-1, 4-beta glucanase [Arabidopsis thaliana] gb|AAM26639.1| AT4g02290/T2H3_5 [Arabidopsis thaliana] gb|AAL85001.1| AT4g02290/T2H3_5 [Arabidopsis thaliana] gb|AAC28173.1| T2H3.5 [Arabidopsis thaliana]	516	1E-31
					>gb|AAA80495.1| endo-1,4-beta-glucanase precursor	510	2E-31
					>gb|ABC70313.1| endo-1,4-beta-glucanase precursor [Glycine max]	414	3E-31

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>gb|AAC12684.1| endo-beta-1,4-glucanase [Pinus radiata]	510	5E-31
DV493407	5.83E-04	B73=F1<Mo17	1.97	5	>gb|AAR91199.1| cytochrome c oxidase subunit 2 [Zea mays]sp|P00412|COX2 MAIZE Cytochrome c oxidase subunit 2 (Cytochrome c oxidase polypeptide II)	260	3E-26
					>sp|P00413|COX2 WHEAT Cytochrome c oxidase subunit 2 (Cytochrome c oxidase polypeptideII)	260	3E-26
					>emb|CAA37048.1| cytochrome-c oxidase [Triticum aestivum]	260	1E-25
					>emb|CAA24094.1| cytochrome oxidase subunit II [Zea mays]	260	3E-24
					>emb|CAA24093.1| cytochrome oxidase subunit II [Zea mays]	274	3E-24
CB833618	5.88E-04	B73<F1=Mo17	1.51	3	>emb|CAA55022.1| beta tubulin [Oryza sativa (japonica cultivar-group)]	447	6E-67
					>emb|CAE52516.1| beta tubulin [Setaria viridis]	448	6E-67
					>ref|NP_915874.1| tubulin beta chain [Oryza sativa (japonica cultivar-group)]dbj|BAB92274.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] dbj|BAA06381.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|P45960|TBB4 ORYSA Tubulin beta-4 chain (Beta-4 tubulin)	447	6E-67
					>gb|AAA66495.1| beta-tubulin	447	6E-67
					>sp|Q41783|TBB6 MAIZE Tubulin beta-6 chain (Beta-6 tubulin)gb|AAA20186.1| beta-6 tubulin	446	6E-67
DV621288	5.90E-04	B73<F1=Mo17	1.38	3	>gb|AAV88604.1| voltage dependent anion channel protein [Pennisetum glaucum]gb|AAV88603.1| voltage dependent anion channel protein [Pennisetum glaucum] gb|AAP46186.1| PgPOR29 [Pennisetum glaucum]	277	9E-83
					>gb|AAO72587.1| porin-like protein [Oryza sativa (japonica cultivar-group)]	277	5E-79
					>emb|CAA63968.1| pom30 [Solanum tuberosum]	276	4E-57
					>gb|ABB16970.1| POM30-like protein [Solanum tuberosum]	275	4E-57
					>gb|AAQ87022.1| VDAC2.1 [Lotus corniculatus var. japonicus]	276	4E-54
DV490747	6.11E-04	F1=Mo17<B73	1.35	8	>dbj|BAD27593.1| putative aspartate transaminase [Oryza sativa (japonicacultivar-group)]	432	6E-57
					>dbj|BAA23814.1| aspartate aminotransferase [Oryza sativa (japonica cultivar-group)]	132	7E-56
					>dbj|BAD54126.1| aspartate transaminase precursor, mitochondrial [Oryza sativa(japonica cultivar-group)]	430	1E-55
					>emb|CAA45024.1| aspartate aminotransferase [Panicum miliaceum]dbj|BAA04993.1| aspartate aminotransferase [Panicum miliaceum]	428	1E-55
					>dbj|BAA23815.1| aspartate aminotransferase [Oryza sativa (japonica cultivar-group)]	430	1E-55
CD527160	6.14E-04	Mo17<B73=F1	1.44	11	>gb|AAF71261.2| beta-glucosidase aggregating factor precursor [Zea mays]	306	1E-33
					>gb|AAR20919.1| jasmonate-induced protein [Triticum aestivum]	304	9E-33
					>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	2E-32
					>gb|AAA87041.1| putative 32.6 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72096.1| 32 kDa protein [Hordeum vulgare]	304	3E-32
					>gb|ABA97248.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]gb|ABB51090.1| mannose-specific jacalin-related lectin [Oryza sativa (japonica cultivar-group)]	306	3E-32
CB885343	6.15E-04	Mo17<B73=F1	1.45	10	>emb|CAI64401.1| thioredoxin h2 protein [Zea mays]	122	7E-57
					>pdb|1WMJ|A Chain A, Solution Structure Of Thioredoxin Type H From Oryza Sativa	130	8E-39
					>ref|XP_476912.1| Thioredoxin H-type (TRX-H) [Oryza sativa (japonica cultivar-group)]dbj|BAD30186.1| Thioredoxin H-type (TRX-H) [Oryza sativa (japonica cultivar-group)] dbj|BAC79928.1| Thioredoxin H-type (TRX-H) [Oryza sativa (japonica cultivar-group)] dbj|BAA04864.1| thioredoxin h [Oryza sativa (japonica cultivar-group)] sp|Q42443|TRXH_ORYSA Thioredoxin H-type (TRX-H) (Phloem sap 13 kDa protein 1) gb|AAB51522.1| thioredoxin h [Oryza sativa] dbj|BAA05546.1| thioredoxin h [Oryza sativa]	122	1E-38
					>gb|AAL67139.1| thioredoxin H [Triticum aestivum]	118	6E-37
					>gb|AAP72290.1| thioredoxin h isoform 1; HvTrxh1 [Hordeum vulgare subsp. vulgare]	118	2E-36
BM266437	6.18E-04	F1=Mo17<B73	2.11	9	>ref|XP_479799.1| putative glycine-rich protein [Oryza sativa (japonicacultivar-group)] dbj|BAD33105.1| putative glycine-rich protein [Oryza sativa (japonica cultivar-group)] dbj|BAD09035.1| putative glycine-rich protein [Oryza sativa (japonica cultivar-group)]	328	6E-19
DV493328	6.23E-04	Mo17<B73=F1	2.11	10	>ref|NP_916873.1| ubiquitin-conjugating enzyme E2 [Oryza sativa (japonicacultivar-group)] dbj|BAC01179.1| putative ubiquitin-conjugating enzyme E2 [Oryza sativa (japonica cultivar-group)] dbj|BAB84382.1| putative ubiquitin-conjugating enzyme E2 [Oryza sativa (japonica cultivar-group)]	153	2E-65
					>ref|NP_564011.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme[Arabidopsis thaliana] gb|AAL31253.1| At1g16890/F17F16.16 [Arabidopsis thaliana] gb|AAK96500.1| At1g16890/F17F16.16 [Arabidopsis thaliana] gb|AAM63831.1| E2, ubiquitin-conjugating enzyme, putative [Arabidopsis thaliana] gb|AAF99844.1| Putative ubiquitin-conjugating enzyme E2 [Arabidopsis thaliana] gb|AAY44875.1| ubiquitinating enzyme [Arabidopsis thaliana]	153	6E-65
					>gb|AAZ20286.1| ubiquitin-conjugating enzyme 1 [Arachis hypogaea]	153	1E-64
					>ref|NP_565192.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme[Arabidopsis thaliana] gb|AAN18113.1| At1g78870/F9K20_8 [Arabidopsis thaliana] gb|AAK83603.1| At1g78870/F9K20_8 [Arabidopsis thaliana] gb|AAM63067.1| E2, ubiquitin-conjugating enzyme, putative [Arabidopsis thaliana] gb|AAY44874.1| ubiquitinating enzyme [Arabidopsis thaliana]	153	3E-64
					>ref|NP_849678.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme[Arabidopsis thaliana]	120	4E-63
BG840735	6.31E-04	Mo17<F1<B73	1.51	9	>gb|AAK63010.1| heme oxygenase 1 [Sorghum bicolor]	184	1E-30
					>dbj|BAD35463.1| putative heme oxygenase 1 [Oryza sativa (japonica cultivar-group)]	289	3E-28
					>gb|AAK63012.1| heme oxygenase 1 [Lycopersicon esculentum]	278	1E-23

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>emb|CAD80091.1| putative heme oxygenase 1 [Momordica charantia]	129	6E-23
					>gb|AAG42008.2| putative heme oxygenase HO1 [Arabidopsis thaliana]	268	4E-22
DV550895	6.40E-04	Mo17<B73=F1	1.76	10	>ref|XP_473296.1| OSJNBb0039L24.13 [Oryza sativa (japonica cultivar-group)]emb|CAE04574.1| OSJNBb0039L24.13 [Oryza sativa (japonica cultivar-group)]	206	2E-20
					>gb|AAM63910.1| remorin [Arabidopsis thaliana]	202	3E-15
					>ref|NP_197764.1| DNA binding [Arabidopsis thaliana]gb|AAN15335.1| Unknown protein [Arabidopsis thaliana] gb|AAK62451.1| Unknown protein [Arabidopsis thaliana] dbj|BAB10048.1| unnamed protein product [Arabidopsis thaliana]	202	3E-15
					>ref|NP_974824.1| DNA binding [Arabidopsis thaliana]	201	3E-15
					>gb|AAD28506.1| remorin 1 [Lycopersicon esculentum]	197	8E-15
DV943052	6.45E-04	Mo17<B73=F1	2.97	10	ns		
BM269155	6.48E-04	Mo17<B73=F1	1.76	10	ns		
DV550769	6.65E-04	B73=F1<Mo17	1.97	4	>ref|XP_473863.1| OSJNBa0070C17.11 [Oryza sativa (japonica cultivar-group)]emb|CAE05204.3| OSJNBa0070C17.11 [Oryza sativa (japonica cultivar-group)]	154	3E-8
					>ref|XP_473862.1| OSJNBa0070C17.10 [Oryza sativa (japonica cultivar-group)]emb|CAE05203.3| OSJNBa0070C17.10 [Oryza sativa (japonica cultivar-group)]	202	2E-6
BG842405	6.71E-04	Mo17<B73=F1	1.48	10	>dbj|BAA32348.1| ferredoxin [Zea mays]	140	4E-22
					>sp|P27789|FER5_MAIZE Ferredoxin-5, chloroplast precursor (Ferredoxin V) (Fd V)gb|AAA33462.1| ferredoxin prf||1907324A ferredoxin:ISOTYPE=V	135	1E-19
					>sp|P27787|FER1_MAIZE Ferredoxin-1, chloroplast precursor (Ferredoxin I) (Fd I)gb|AAA33460.1| ferredoxin gb|AAA33459.1| ferredoxin prf||1907324B ferredoxin:ISOTYPE=I	150	4E-17
					>pdb|1GAQ|B Chain B, Crystal Structure Of The Complex Between Ferredoxin AndFerredoxin-Nadp+ Reductase	98	4E-17
					>ref|XP_479678.1| Ferredoxin I, chloroplast precursor [Oryza sativa (japonicacultivar-group)] ref|XP_507559.1| PREDICTED OJ1300_E01.1 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_507558.1| PREDICTED OJ1300_E01.1 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_507082.1| PREDICTED OJ1300_E01.1 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD08924.1| Ferredoxin I, chloroplast precursor [Oryza sativa (japonica cultivar-group)] sp|P11051|FER1_ORYSA Ferredoxin-1, chloroplast precursor (Ferredoxin I) (Anti-disease protein 1) pir||FERZ ferredoxin [2Fe-2S] I precursor - rice dbj|BAA06436.1| ferredoxin [Oryza sativa (japonica cultivar-group)]	139	5E-17
DV494441	6.74E-04	B73<F1=Mo17	1.44	3	>emb|CAA33620.1| GAPDH [Zea mays]sp|P08735|G3PC_MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 1	337	3E-89
					>emb|CAA30151.1| unnamed protein product [Zea mays]	337	8E-89
					>emb|CAA51676.1| glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zeamays] sp|Q09054|G3PD_MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 2 gb|AAA87880.1| glyceraldehyde-3-phosphate dehydrogenase gb|AAA87578.1| cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2	337	2E-87
					>gb|AAA33466.1| glyceraldehyde-3-phosphate dehydrogenase [Zea mays]	247	2E-87
					>emb|CAA42901.1| glyceraldehyde 3-phosphate dehydrogenase [Hordeum vulgare]sp|P26517|G3PX_HORVU Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	337	2E-84
BM335843	6.86E-04	Mo17<B73=F1	1.61	10	>gb|AAT77918.1| putative NUDIX hydrolase [Oryza sativa (japonica cultivar-group)]	183	3E-47
					>ref|NP_911373.2| MutT-like protein [Oryza sativa (japonica cultivar-group)]dbj|BAD31700.1| MutT-like protein [Oryza sativa (japonica cultivar-group)] dbj|BAC16411.2| MutT-like protein [Oryza sativa (japonica cultivar-group)]	182	3E-37
					>ref|NP_566428.1| hydrolase [Arabidopsis thaliana]gb|AAG40353.1| AT3g12600 [Arabidopsis thaliana] gb|AAK49630.1| AT3g12600/T2E22_108 [Arabidopsis thaliana] gb|AAG51020.1| unknown protein; 22985-21799 [Arabidopsis thaliana] dbj|BAB02251.1| unnamed protein product [Arabidopsis thaliana] gb|AAO11575.1| At3g12600/T2E22_108 [Arabidopsis thaliana] sp|Q9LHK1|NUD16_ARATH Nudix hydrolase 16, mitochondrial precursor (AtNUDT16)	180	9E-29
					>ref|XP_465994.1| MutT-like protein [Oryza sativa (japonica cultivar-group)]dbj|BAD26313.1| MutT-like protein [Oryza sativa (japonica cultivar-group)]	204	2E-16
					>gb|ABA94049.1| hydrolase, NUDIX family, putative [Oryza sativa (japonicacultivar-group)]	217	1E-15
DV622613	6.87E-04	Mo17<B73=F1	1.35	11	>emb|CAA29928.1| unnamed protein product [Zea mays]sp|P12653|GSTF1_MAIZE Glutathione S-transferase I (GST-I) (GST-29) (GST class-phi)	214	2E-72
					>gb|AAA72758.1| glutathione S-transferase	214	2E-72
					>pdb|1BYE|D Chain D, Glutathione S-Transferase I From Mais In Complex WithAtrazine Glutathione Conjugate pdb|1BYE|C Chain C, Glutathione S-Transferase I From Mais In Complex With Atrazine Glutathione Conjugate pdb|1BYE|B Chain B, Glutathione S-Transferase I From Mais In Complex With Atrazine Glutathione Conjugate pdb|1BYE|A Chain A, Glutathione S-Transferase I From Mais In Complex With Atrazine Glutathione Conjugate	213	2E-72
					>gb|AAA33470.1| glutathione S-transferase Igb|AAA33469.1| glutathione S-transferase I prf||1303351A transferase,glutathione S	214	1E-71
					>pdb|1AXD|B Chain B, Structure Of Glutathione S-Transferase-I Bound With TheLigand Lactoylglutathione pdb|1AXD|A Chain A, Structure Of Glutathione S-Transferase-I Bound With The Ligand Lactoylglutathione	209	5E-70
CD484423	6.87E-04	Mo17<B73=F1	1.28	10	>gb|AAF71261.2| beta-glucosidase aggregating factor precursor [Zea mays]	306	3E-36
					>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	3E-34
					>gb|AAR20919.1| jasmonate-induced protein [Triticum aestivum]	304	1E-33
					>gb|ABA97248.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]gb|ABB51090.1| mannose-specific jacalin-related lectin [Oryza sativa (japonica cultivar-group)]	306	2E-33
					>gb|AAB72098.1| 32 kDa protein [Hordeum vulgare]	306	7E-33
DV550469	6.87E-04	B73=F1<Mo17	1.73	4	>gb|ABA94013.1| hypothetical protein LOC_Os11g32320 [Oryza sativa (japonicacultivar-group)]	265	1E-33

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

<table>
<tr><th>GenBank accession no.</th><th>Overall P value</th><th>Significant pattern</th><th>Fold change[†]</th><th>Sector[‡]</th><th>BLAST annotation*</th><th>Score</th><th>E value</th></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_566797.1| unknown protein [Arabidopsis thaliana]gb|AAM98166.1| expressed protein [Arabidopsis thaliana] gb|AAM64687.1| unknown [Arabidopsis thaliana] gb|AAP13402.1| At3g26710 [Arabidopsis thaliana] dbj|BAB01734.1| unnamed protein product [Arabidopsis thaliana]</td><td>267</td><td>9E-24</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA66820.1| hypothetical protein [Arabidopsis thaliana]</td><td>216</td><td>7E-19</td></tr>
<tr><td>CB331508</td><td>6.96E-04</td><td>Mo17<B73=F1</td><td>1.34</td><td>10</td><td>>sp|P19950|RS141 MAIZE 40S ribosomal protein S14 (Clone MCH1)</td><td>149</td><td>1E-46</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_472410.1| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)]emb|CAE02065.2| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)] dbj|BAD29299.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)] dbj|BAD27798.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]</td><td>151</td><td>2E-46</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_464199.1| putative ribosomal protein S14 [Oryza sativa (japonicacultivar-group)] ref|XP_506724.1| PREDICTED OJ9003_G05.34 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD25218.1| putative ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]</td><td>150</td><td>2E-46</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>sp|P19951|RS142 MAIZE 40S ribosomal protein S14 (Clone MCH2)</td><td>150</td><td>2E-46</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAO41731.1| cytoplasmic ribosomal protein S14 [Brassica napus]</td><td>150</td><td>7E-46</td></tr>
<tr><td>DV621991</td><td>7.03E-04</td><td>B73=F1<Mo17</td><td>1.33</td><td>4</td><td>>ref|NP_915675.1| putative protein kinase SPK-3 [Oryza sativa (japonicacultivar-group)] dbj|BAB89813.1| serine/threonine protein kinase SAPK4 [Oryza sativa (japonica cultivar-group)] dbj|BAB64101.1| serine/threonine protein kinase SAPK4 [Oryza sativa (japonica cultivar-group)] dbj|BAD18000.1| serine/threonine protein kinase SAPK4 [Oryza sativa (japonica cultivar-group)] sp|Q5N942|SAPK4_ORYSA Serine/threonine-protein kinase SAPK4 (Osmotic stress/abscisic acid-activated protein kinase 4)</td><td>360</td><td>3E-70</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_472550.1| OSJNBa0084A10.11 [Oryza sativa (japonica cultivar-group)]dbj|BAD18003.1| serine/threonine protein kinase SAPK7 [Oryza sativa (japonica cultivar-group)] sp|Q7XQP4|SAPK7 ORYSA Serine/threonine-protein kinase SAPK7 (Osmotic stress/abscisic acid-activated protein kinase 7)</td><td>359</td><td>2E-59</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAB68961.1| protein kinase 3 [Glycine max]</td><td>351</td><td>4E-59</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAE03037.3| OSJNBa0084A10.12 [Oryza sativa (japonica cultivar-group)]</td><td>407</td><td>4E-59</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAU43772.1| putative salt-inducible protein kinase [Zea mays]</td><td>364</td><td>6E-59</td></tr>
<tr><td>DV492325</td><td>7.09E-04</td><td>Mo17<F1<B73</td><td>1.84</td><td>9</td><td>>ref|XP 473945.1| OSJNBa0053K19.11 [Oryza sativa (japonica cultivar-group)]emb|CAE03503.2| OSJNBa0053K19.11 [Oryza sativa (japonica cultivar-group)]</td><td>408</td><td>5E-60</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA81081.1| T-protein [Solanum tuberosum]sp|P54260|GCST_SOLTU Aminomethyltransferase, mitochondrial precursor (Glycine cleavage system T protein) (GCVT)</td><td>406</td><td>1E-53</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA81077.1| T protein [Flaveria pringlei]sp|P49363|GCST_FLAPR Aminomethyltransferase, mitochondrial precursor (Glycine cleavage system T protein) (GCVT)</td><td>407</td><td>2E-52</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA94902.1| T-protein [Flaveria anomala]sp|O49849|GCST_FLAAN Aminomethyltransferase, mitochondrial precursor (Glycine cleavage system T protein) (GCVT)</td><td>407</td><td>2E-52</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAB16917.1| T-Protein precursor [Flaveria trinervia]sp|O23936|GCST_FLATR Aminomethyltransferase, mitochondrial precursor (Glycine cleavage system T protein) (GCVT)</td><td>407</td><td>6E-52</td></tr>
<tr><td>DV621817</td><td>7.26E-04</td><td>B73=F1<Mo17</td><td>1.42</td><td>4</td><td>>gb|AAT93850.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAS98480.1| unknown protein [Oryza sativa (japonica cultivar-group)]</td><td>989</td><td>3E-53</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAB87716.1| putative protein [Arabidopsis thaliana]</td><td>955</td><td>5E-47</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP 196717.2| catalytic [Arabidopsis thaliana]</td><td>978</td><td>5E-47</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP 795069.1| PREDICTED: similar to CG2943-PA [Strongylocentrotus purpuratus]</td><td>204</td><td>4E-16</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAI22235.1| novel protein [Homo sapiens]</td><td>971</td><td>6E-16</td></tr>
<tr><td>CD485034</td><td>7.32E-04</td><td>F1=Mo17<B73</td><td>1.51</td><td>9</td><td>>dbj|BAD73816.1| putative copper chaperone [Oryza sativa (japonica cultivar-group)]</td><td>252</td><td>8E-8</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_466081.1| copper chaperone homolog CCH [Oryza sativa (japonicacultivar-group)] dbj|BAD25440.1| copper chaperone homolog CCH [Oryza sativa (japonica cultivar-group)] gb|AAF15285.1| copper chaperone homolog CCH [Oryza sativa]</td><td>132</td><td>8E-8</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_191183.1| CCH [Arabidopsis thaliana]emb|CAB87423.1| copper homeostasis factor [Arabidopsis thaliana] gb|AAK32872.1| AT3g56240/F18O21_200 [Arabidopsis thaliana] gb|AAL47423.1| AT3g56240/F18O21_200 [Arabidopsis thaliana] gb|AAM62878.1| copper homeostasis factor [Arabidopsis thaliana] gb|AAC33510.1| copper homeostasis factor [Arabidopsis thaliana]</td><td>121</td><td>1E-7</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAE51321.1| chopper chaperone [Hordeum vulgare subsp. vulgare]</td><td>112</td><td>2E-7</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAF15286.1| copper chaperone homolog CCH [Glycine max]</td><td>130</td><td>4E-6</td></tr>
<tr><td>CB886106</td><td>7.33E-04</td><td>Mo17<B73=F1</td><td>1.38</td><td>10</td><td>ns</td><td></td><td></td></tr>
<tr><td>DV621876</td><td>7.34E-04</td><td>Mo17<B73=F1</td><td>1.46</td><td>10</td><td>>dbj|BAD22146.1| putative 26S proteasome non-ATPase regulatory subunit 6 (26Sproteasome regulatory particle non-ATPase subunit 7) (OsRPN7) [Oryza sativa (japonica cultivar-group)]</td><td>388</td><td>2E-61</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_472939.1| OSJNBa0081L15.15 [Oryza sativa (japonica cultivar-group)]emb|CAD41392.2| OJ000223_09.5 [Oryza sativa (japonica cultivar-group)] emb|CAE03153.2| OSJNBa0081L15.15 [Oryza sativa (japonica cultivar-group)] sp|Q8W425|PSD6_ORYSA 26S proteasome non-ATPase regulatory subunit 6 (26S proteasome regulatory particle non-ATPase subunit 7) (OsRPN7) dbj|BAB78486.1| 26S proteasome regulatory particle non-ATPase subunit7 [Oryza sativa (japonica cultivar-group)]</td><td>389</td><td>7E-59</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAC32134.1| KIAA0107-like protein [Picea mariana]</td><td>232</td><td>5E-57</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_567709.1| unknown protein [Arabidopsis thaliana]ref|NP_974611.1| unknown protein [Arabidopsis thaliana] gb|AAP86665.1| 26S proteasome subunit RPN7 [Arabidopsis thaliana] gb|AAN31800.1| putative proteasome regulatory subunit [Arabidopsis thaliana] gb|AAM13268.1| putative proteasome regulatory subunit [Arabidopsis thaliana] gb|AAK96691.1| putative proteasome regulatory subunit [Arabidopsis thaliana] gb|AAM65400.1| putative proteasome regulatory subunit [Arabidopsis thaliana] sp|Q93Y35|PSD6 ARATH Probable 26S proteasome non-ATPase regulatory subunit 6</td><td>387</td><td>2E-54</td></tr>
</table>

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>emb|CAB79392.1| putative proteasome regulatory subunit [Arabidopsis thaliana]emb|CAB41122.1| putative proteasome regulatory subunit [Arabidopsis thaliana] pir||T06666 26S proteasome regulatory particle chain RPN7 homolog F6I7.30 - Arabidopsis thaliana	406	1E-52
CB617292	7.41E-04	Mo17<F1<B73	1.41	10	>ref|XP_468402.1| putative NADH dehydrogenase [Oryza sativa (japonicacultivar-group)] dbj|BAD22016.1| putative NADH dehydrogenase [Oryza sativa (japonica cultivar-group)] dbj|BAD21515.1| putative NADH dehydrogenase [Oryza sativa (japonica cultivar-group)]	408	8E-87
					>ref|NP_565469.1| unknown protein [Arabidopsis thaliana]gb|AAT68351.1| hypothetical protein At2g20360 [Arabidopsis thaliana] gb|AAK93749.1| putative NADH-ubiquinone oxireductase [Arabidopsis thaliana] gb|AAK59545.1| putative NADH-ubiquinone oxireductase [Arabidopsis thaliana] gb|AAD21752.2| putative NADH-ubiquinone oxireductase [Arabidopsis thaliana] gb|AAX23820.1| hypothetical protein At2g20360 [Arabidopsis thaliana]	402	6E-61
					>ref|XP 508942.1| PREDICTED: NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9,39kDa [Pan troglodytes]	347	2E-32
					>emb|CAH92896.1| hypothetical protein [Pongo pygmaeus]	377	3E-32
					>gb|AAH91192.1| Ndufa9 protein [Rattus norvegicus]	370	3E-32
CD484530	7.44E-04	B73<F1<Mo17	1.58	4	>ref|XP_483802.1| putative ripening regulated protein DDTFR18 [Oryza sativa (japonicacultivar-group)] dbj|BAD09618.1| putative ripening regulated protein DDTFR18 [Oryza sativa (japonica cultivar-group)]	434	2E-71
					>ref|NP 194294.2| antiporter/ drug transporter [Arabidopsis thaliana]	488	7E-62
					>ref|XP_483803.1| putative ripening regulated protein DDTFR18 [Oryza sativa (japonicacultivar-group)] dbj|BAD09619.1| putative ripening regulated protein DDTFR18 [Oryza sativa (japonica cultivar-group)]	451	9E-62
					>ref|NP 567173.3| antiporter/ drug transporter/ transporter [Arabidopsis thaliana]	542	3E-60
					>gb|AAO42212.1| unknown protein [Arabidopsis thaliana]	514	8E-60
CB604570	7.45E-04	B73=F1<Mo17	1.39	4	>emb|CAA37828.1| unnamed protein product [Petroselinum crispum]sp|P19177|H2A PETCR Histone H2A	149	2E-39
					>gb|AAT08677.1| histone H2A [Hyacinthus orientalis]	152	7E-39
					>sp|P02276|H2A2 WHEAT Histone H2A.2.1	151	7E-39
					>sp|P40280|H2A MAIZE Histone H2Agb|AAB04687.1| histone H2A	159	7E-39
					>ref|NP 918596.1| putative histone H2A [Oryza sativa (japonica cultivar-group)]dbj|BAB44136.1| putative histone H2A [Oryza sativa (japonica cultivar-group)]	159	9E-39
DV942339	7.61E-04	B73<F1=Mo17	1.62	3	>ref|NP_922361.1| putative Ste20-related protein kinase [Oryza sativa (japonicacultivar-group)] gb|AAG13441.1| putative Ste20-related protein kinase [Oryza sativa (japonica cultivar-group)]	643	3E-46
					>ref|NP_912431.1| Putative Ste20-related protein kinase [Oryza sativa (japonicacultivar-group)] gb|AAO17022.1| Putative Ste20-related protein kinase [Oryza sativa (japonica cultivar-group)]	645	1E-25
					>ref|NP 192811.3| ATP binding / kinase/ protein kinase/ protein serine/threoninekinase/ protein-tyrosine kinase [Arabidopsis thaliana]	708	3E-14
					>ref|NP_194141.2| ATP binding / kinase/ protein kinase/ protein serine/threoninekinase/ protein-tyrosine kinase [Arabidopsis thaliana] gb|AAM91677.1| unknown protein [Arabidopsis thaliana] gb|AAM14047.1| unknown protein [Arabidopsis thaliana]	709	2E-11
					>emb|CAB81174.1| putative protein kinase [Arabidopsis thaliana]	693	5E-11
CB334571	7.67E-04	Mo17<B73=F1	1.41	11	>emb|CAI64400.1| thioredoxin h1 protein [Zea mays]	128	1E-40
					>ref|XP_475666.1| putative thioredoxin H-type (TRX-H) (TrxTa) [Oryza sativa (japonicacultivar-group)] gb|AAT44260.1| putative thioredoxin H-type (TRX-H) (TrxTa) [Oryza sativa (japonica cultivar-group)]	121	3E-32
					>dbj|BAB20886.1| thioredoxin h [Oryza sativa (japonica cultivar-group)]	121	3E-32
					>gb|AAP72291.1| thioredoxin h isoform 2; HvTrxh2 [Hordeum vulgare subsp. vulgare]	122	1E-31
					>gb|AAF88067.1| thioredoxin H [Triticum aestivum]emb|CAB96931.1| thioredoxin h [Triticum aestivum]	125	5E-31
DV550678	7.90E-04	Mo17<B73=F1	1.44	10	>gb|AAV50043.1| metallothionein-like protein [Saccharum hybrid cultivar]	81	9E-7
					>gb|AAS88721.1| metallothionein-like protein [Cynodon dactylon]	81	2E-6
CB834045	7.90E-04	Mo17<B73=F1	1.39	10	>ref|XP 463045.1| expressed protein [Oryza sativa (japonica cultivar-group)]gb|AAS07181.1| expressed protein [Oryza sativa (japonica cultivar-group)]	91	5E-18
					>emb|CAJ13713.1| hypothetical protein [Capsicum chinense]	96	1E-16
					>ref|NP_850005.1| unknown protein [Arabidopsis thaliana]gb|AAK00397.1| unknown protein [Arabidopsis thaliana] gb|AAG41478.1| unknown protein [Arabidopsis thaliana] gb|AAL06786.1| At2g20820/F5H14.21 [Arabidopsis thaliana] gb|AAG40023.1| At2g20820 [Arabidopsis thaliana] gb|AAK55709.1| At2g20820/F5H14.21 [Arabidopsis thaliana]	93	2E-15
					>ref|NP_850006.1| unknown protein [Arabidopsis thaliana]gb|AAD20913.2| expressed protein [Arabidopsis thaliana] gb|AAM67005.1| unknown [Arabidopsis thaliana]	102	9E-6
DV493051	7.95E-04	B73<F1=Mo17	1.47	3	>emb|CAA33620.1| GAPDH [Zea mays]sp|P08735|G3PC MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 1	337	1E-66
					>emb|CAA30151.1| unnamed protein product [Zea mays]	337	3E-66
					>emb|CAA51676.1| glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zeamays] sp|Q09054|G3PD_MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 2 gb|AAA87880.1| glyceraldehyde-3-phosphate dehydrogenase gb|AAA87578.1| cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2	337	5E-65
					>gb|AAA33466.1| glyceraldehyde-3-phosphate dehydrogenase [Zea mays]	247	5E-65
					>emb|CAA42901.1| glyceraldehyde 3-phosphate dehydrogenase [Hordeum vulgare]sp|P26517|G3PX_HORVU Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	337	2E-62

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
CD484434	7.98E-04	Mo17<B73=F1	1.43	11	>ref|NP 910221.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAA90629.1| unknown protein [Oryza sativa (japonica cultivar-group)]	230	7E-42
					>gb|AAM64310.1| unknown [Arabidopsis thaliana]	230	6E-33
					>gb|AAL66902.1| unknown protein [Arabidopsis thaliana]gb|AAK96864.1| Unknown protein [Arabidopsis thaliana]	230	2E-32
					>ref|NP 566447.1| unknown protein [Arabidopsis thaliana]dbj|BAB01412.1| unnamed protein product [Arabidopsis thaliana]	230	4E-32
					>gb|AAF00144.1| predicted protein [Oryza sativa]	98	1E-19
BM334092	8.06E-04	Mo17<F1<B73	1.56	10	>dbj|BAD69005.1| putative DsPTP1 protein [Oryza sativa (japonica cultivar-group)]	199	1E-45
					>ref|NP 914134.1| OJ1460 H08.3 [Oryza sativa (japonica cultivar-group)]	196	1E-45
					>gb|ABA02563.1| dual-specificity protein-like phosphatase 2 [Zea mays]	170	2E-39
					>dbj|BAE44441.1| dual specificity protein tyrosine phosphatase 1 [Solanum tuberosum]	179	3E-25
					>ref|NP_189003.1| phosphoprotein phosphatase/ protein tyrosine/serine/threoninephosphatase [Arabidopsis thaliana] emb|CAA77232.1| DsPTP1 protein [Arabidopsis thaliana]	198	7E-25
CD058547	8.07E-04	Mo17<F1<B73	1.28	9	>gb|ABA95929.1| CBS domain, putative [Oryza sativa (japonica cultivar-group)]	542	2E-66
					>gb|AAX93000.1| CBS domain, putative [Oryza sativa (japonica cultivar-group)]gb|ABA91621.1| CBS domain, putative [Oryza sativa (japonica cultivar-group)]	575	1E-61
					>ref|NP 190863.3| unknown protein [Arabidopsis thaliana]emb|CAB86899.1| putative protein [Arabidopsis thaliana]	556	2E-57
					>gb|AAN15439.1| putative protein [Arabidopsis thaliana]gb|AAM91587.1| putative protein [Arabidopsis thaliana]	469	2E-57
					>ref|XP 463645.1| P0592G05.9 [Oryza sativa (japonica cultivar-group)]	553	5E-52
DV621151	8.16E-04	B73<F1=Mo17	1.35	3	>gb|AAX96124.1| adenylate kinase b (ec 2.7.4.3) (atp-amp transphosphorylase) [Oryzasativa (japonica cultivar-group)] gb|ABA92960.1| adenylate kinase b [Oryza sativa (japonica cultivar-group)] sp|Q08480|KAD2_ORYSA Adenylate kinase B (ATP-AMP transphosphorylase) dbj|BAA01181.1| adenylate kinase-b [Oryza sativa]	243	6E-84
					>gb|ABA96905.1| adenylate kinase a [Oryza sativa (japonica cultivar-group)]sp|Q08479|KAD1_ORYSA Adenylate kinase A (ATP-AMP transphosphorylase) dbj|BAA01180.1| adenylate kinase-a [Oryza sativa]	241	3E-82
					>ref|NP_201145.1| ADK1 (ADENYLATE KINASE 1); ATP binding / adenylate kinase/nucleotide kinase/ phosphotransferase, phosphate group as acceptor [Arabidopsis thaliana] gb|AAL85071.1| putative adenylate kinase [Arabidopsis thaliana] gb|AAK64049.1| putative adenylate kinase [Arabidopsis thaliana] gb|AAM61739.1| adenylate kinase [Arabidopsis thaliana] dbj|BAB08805.1| adenylate kinase [Arabidopsis thaliana] sp|O82514|KAD1_ARATH Adenylate kinase 1 (ATP-AMP transphosphorylase 1)	246	2E-77
					>gb|AAM63345.1| adenylate kinase [Arabidopsis thaliana]	248	3E-77
					>ref|NP_199848.1| ATP binding / adenylate kinase/ nucleotide kinase/phosphotransferase, phosphate group as acceptor [Arabidopsis thaliana] gb|AAO44077.1| At5g50370 [Arabidopsis thaliana] dbj|BAB09456.1| adenylate kinase [Arabidopsis thaliana] sp|Q9FK35|KAD2_ARATH Adenylate kinase 2 (ATP-AMP transphosphorylase 2)	248	3E-76
CD510512	8.22E-04	Mo17<B73=F1	1.34	10	>ref|XP_469784.1| putative potassium channel protein [Oryza sativa (japonicacultivar-group)] gb|AAO32309.1| putative outward rectifying potassium channel [Oryza sativa (japonica cultivar-group)] gb|AAR87255.1| putative potassium channel protein [Oryza sativa (japonica cultivar-group)] gb|AAP68365.1| putative potassium channel protein [Oryza sativa (japonica cultivar-group)]	347	8E-45
					>gb|AAX08090.1| outward-rectifying potassium channel [Hordeum vulgare subsp.vulgare]	349	1E-42
					>gb|AAD16279.1| pulvinus outward-rectifying channel for potassium SPOCK1 [Samaneasaman]	352	1E-25
					>ref|XP_476391.1| putative outward-rectifying potassium channel KCO1 [Oryza sativa(japonica cultivar-group)] dbj|BAD30634.1| putative outward-rectifying potassium channel KCO1 [Oryza sativa (japonica cultivar-group)] dbj|BAC06932.1| putative outward-rectifying potassium channel KCO1 [Oryza sativa (japonica cultivar-group)]	349	4E-25
					>gb|AAF97863.1| outward-rectifying potassium channel KCO1 [Eucalyptuscamaldulensis] gb|AAF97727.1| Eucalyptus camaldulensis outward-rectifying potassium channel mRNA, complete cds	348	2E-23
BM350368	8.24E-04	F1=Mo17<B73	1.44	9	>gb|AAU90205.1| unknown protein [Oryza sativa (japonica cultivar-group)]	144	1E-34
					>dbj|BAD82673.1| unknown protein [Oryza sativa (japonica cultivar-group)]	156	3E-10
					>ref|NP 915497.1| P0005H10.22 [Oryza sativa (japonica cultivar-group)]	272	3E-10
					>ref|NP 001030865.1| unknown protein [Arabidopsis thaliana]	146	4E-8
BM072886	8.41E-04	Mo17<B73=F1	1.42	10	>ref|NP_921803.1| putative PGPD14 protein (pollen germination related protein) [Oryzasativa (japonica cultivar-group)] gb|AAP54090.1| CHY zinc finger, putative [Oryza sativa (japonica cultivar-group)]	266	3E-44
					>gb|ABB47748.1| CHY zinc finger, putative [Oryza sativa (japonica cultivar-group)]	222	3E-44
					>gb|AAD02556.1| PGPD14 [Petunia x hybrida]	285	4E-36
					>gb|AAM65683.1| PGPD14 protein [Arabidopsis thaliana]	274	2E-34
					>ref|NP_197683.1| ubiquitin-protein ligase/ zinc ion binding [Arabidopsis thaliana]gb|AAK96553.1| AT5g22920/MRN17_15 [Arabidopsis thaliana] gb|AAY57617.1| RING finger family protein [Arabidopsis thaliana] dbj|BAB10613.1| PGPD14 protein [Arabidopsis thaliana] gb|AAO11551.1| At5g22920/MRN17 15 [Arabidopsis thaliana]	291	3E-34
BM350562	8.51E-04	Mo17<B73=F1	2.23	10	>ref|NP_922208.1| putative folylpolyglutamate synthetase [Oryza sativa (japonicacultivar-group)] gb|AAG13624.1| putative folylpolyglutamate synthetase [Oryza sativa (japonica cultivar-group)]	546	2E-29

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP 196217.2| ATDFB (A. THALIANA DHFS-FPGS HOMOLOG B);tetrahydrofolylpolyglutamate synthase [Arabidopsis thaliana]	571	1E-27
					>ref|NP 001031840.1| ATDFB (A. THALIANA DHFS-FPGS HOMOLOG B);tetrahydrofolylpolyglutamate synthase [Arabidopsis thaliana]	513	1E-27
					>emb|CAC80839.2| dihydrofolate synthetase /folylpolyglutamate synthetase[Arabidopsis thaliana]	571	2E-27
					>ref|NP_567026.3| ATDFD (A. THALIANA DHFS-FPGS HOMOLOG D);tetrahydrofolylpolyglutamate synthase [Arabidopsis thaliana] emb|CAC82079.1| folylpolyglutamate-dihydrofolate synthetase [Arabidopsis thaliana]	492	3E-25
CB381724	8.52E-04	Mo17<B73=F1	1.72	10	>ref|XP 473874.1| OSJNBa0070C17.22 [Oryza sativa (japonica cultivar-group)]emb|CAE05215.3| OSJNBa0070C17.22 [Oryza sativa (japonica cultivar-group)]	438	5E-10
DV549332	8.56E-04	B73<F1=Mo17	1.45	3	ns		
BM073332	8.59E-04	Mo17<B73=F1	4.38	10	ns		
CD650951	8.61E-04	F1=Mo17<B73	1.32	9	>ref|NP_921998.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]gb|AAG13576.1| hypothetical protein [Oryza sativa] gb|AAP54285.1| hypothetical protein LOC Os10g33820 [Oryza sativa (japonica cultivar-group)]	460	1E-46
					>ref|NP 850276.1| unknown protein [Arabidopsis thaliana]	433	2E-7
CD527239	8.83E-04	Mo17<B73=F1	1.32	10	>ref|NP_910779.1| putative NADH dehydrogenase [Oryza sativa (japonicacultivar-group)] ref|XP_506513.1| PREDICTED P0503D09.102 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC16718.1| putative NADH dehydrogenase [Oryza sativa (japonica cultivar-group)]	504	4E-9
DV490806	8.84E-04	B73<F1<Mo17	1.48	4	>ref|NP_915675.1| putative protein kinase SPK-3 [Oryza sativa (japonicacultivar-group)] dbj|BAB89813.1| serine/threonine protein kinase SAPK4 [Oryza sativa (japonica cultivar-group)] dbj|BAB64101.1| serine/threonine protein kinase SAPK4 [Oryza sativa (japonica cultivar-group)] dbj|BAD18000.1| serine/threonine protein kinase SAPK4 [Oryza sativa (japonica cultivar-group)] sp|Q5N942|SAPK4_ORYSA Serine/threonine-protein kinase SAPK4 (Osmotic stress/abscisic acid-activated protein kinase 4)	360	1E-48
					>dbj|BAD82014.1| serine/threonine protein kinase SAPK4-like protein [Oryza sativa(japonica cultivar-group)] dbj|BAD81709.1| serine/threonine protein kinase SAPK4-like protein [Oryza sativa (japonica cultivar-group)]	168	1E-48
					>ref|XP_472550.1| OSJNBa0084A10.11 [Oryza sativa (japonica cultivar-group)]dbj|BAD18003.1| serine/threonine protein kinase SAPK7 [Oryza sativa (japonica cultivar-group)] sp|Q7XQP4|SAPK7 ORYSA Serine/threonine-protein kinase SAPK7 (Osmotic stress/abscisic acid-activated protein kinase 7)	359	7E-37
					>emb|CAE03037.3| OSJNBa0084A10.12 [Oryza sativa (japonica cultivar-group)]	407	7E-37
					>gb|AAU43772.1| putative salt-inducible protein kinase [Zea mays]	364	3E-36
CD058870	9.04E-04	B73=F1<Mo17	1.39	4	>ref|XP_479103.1| putative transcription factor [Oryza sativa (japonicacultivar-group)] dbj|BAC84851.1| putative transcription factor [Oryza sativa (japonica cultivar-group)]	297	1E-8
DV493904	9.11E-04	B73<F1=Mo17	1.55	3	>ref|XP_468386.1| diphthamide synthesis DPH2-like [Oryza sativa (japonicacultivar-group)] ref|XP_507043.1| PREDICTED OJ1293_E04.32 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD22000.1| diphthamide synthesis DPH2-like [Oryza sativa (japonica cultivar-group)] dbj|BAD21677.1| diphthamide synthesis DPH2-like [Oryza sativa (japonica cultivar-group)]	474	5E-46
					>ref|NP_201009.1| unknown protein [Arabidopsis thaliana]gb|AAM51395.1| unknown protein [Arabidopsis thaliana] gb|AAM13884.1| unknown protein [Arabidopsis thaliana]	453	4E-22
					>dbj|BAB10164.1| unnamed protein product [Arabidopsis thaliana]	468	4E-22
					>ref|NP 001025887.1| DPH1 homolog [Gallus gallus]emb|CAG32664.1| hypothetical protein [Gallus gallus]	409	4E-13
					>ref|XP_759185.1| hypothetical protein UM03038.1 [Ustilago maydis 521]gb|EAK84039.1| hypothetical protein UM03038.1 [Ustilago maydis 521] sp|Q4PA25|DPH1 USTMA Diphthamide biosynthesis protein 1	609	1E-10
CB351542	9.27E-04	B73<F1=Mo17	1.58	3	>dbj|BAB11155.1| unnamed protein product [Arabidopsis thaliana]	1105	2E-28
					>ref|NP_196314.2| unknown protein [Arabidopsis thaliana]gb|AAL91294.1| AT5g06970/MOJ9_14 [Arabidopsis thaliana] gb|AAO11640.1| At5g06970/MOJ9_14 [Arabidopsis thaliana]	1101	2E-28
					>ref|XP 469322.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAP68377.1| unknown protein [Oryza sativa (japonica cultivar-group)]	1078	8E-28
					>gb|AAK14418.1| unknown protein [Oryza sativa]	1049	8E-28
					>ref|NP 192904.2| unknown protein [Arabidopsis thaliana]	985	2E-8
DV621059	9.30E-04	B73<F1=Mo17	1.56	3	>gb|ABA95760.1| expressed protein [Oryza sativa (japonica cultivar-group)]	292	2E-59
					>gb|ABA91405.1| expressed protein [Oryza sativa (japonica cultivar-group)]	308	6E-59
					>ref|NP_196037.2| calcium ion binding [Arabidopsis thaliana]emb|CAC05499.1| EF-hand Calcium binding protein-like [Arabidopsis thaliana] gb|AAP68277.1| At5g04170 [Arabidopsis thaliana] gb|AAL91231.1| EF-hand calcium binding protein-like [Arabidopsis thaliana]	354	1E-54
					>ref|NP_187641.2| calcium ion binding [Arabidopsis thaliana]gb|AAT85768.1| At3g10300 [Arabidopsis thaliana] gb|AAL32576.1| Unknown protein [Arabidopsis thaliana]	335	2E-53
					>emb|CAB63845.1| putative cysteine protease [Pisum sativum]	286	5E-43
CB885897	9.38E-04	Mo17<B73=F1	1.29	10	>emb|CAA29928.1| unnamed protein product [Zea mays]sp|P12653|GSTF1 MAIZE Glutathione S-transferase I (GST-I) (GST-29) (GST class-phi)	214	4E-84
					>gb|AAA72758.1| glutathione S-transferase	214	4E-84
					>pdb|1BYE|D Chain D, Glutathione S-Transferase I From Mais In Complex WithAtrazine Glutathione Conjugate pdb|1BYE|C Chain C, Glutathione S-Transferase I From Mais In Complex With Atrazine Glutathione Conjugate pdb|1BYE|B Chain B, Glutathione S-Transferase I From Mais In Complex With Atrazine Glutathione Conjugate pdb|1BYE|A Chain A, Glutathione S-Transferase I From Mais In Complex With Atrazine Glutathione Conjugate	213	4E-84
					>gb|AAA33470.1| glutathione S-transferase Igb|AAA33469.1| glutathione S-transferase I prf||1303351A transferase,glutathione S	214	2E-83

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>pdb|1AXD|B Chain B, Structure Of Glutathione S-Transferase-I Bound With TheLigand Lactoylglutathione pdb|1AXD|A Chain A, Structure Of Glutathione S-Transferase-I Bound With The Ligand Lactoylglutathione	209	9E-82
BM079296	9.38E-04	Mo17<B73=F1	1.78	10	>gb|AAU94637.1| SNARE 13 [Oryza sativa (japonica cultivar-group)]	266	2E-37
					>ref|XP_479265.1| vesicle soluble NSF attachment protein receptor-like protein [Oryzasativa (japonica cultivar-group)] dbj|BAC16405.1| vesicle soluble NSF attachment protein receptor-like protein [Oryza sativa (japonica cultivar-group)]	266	2E-37
					>gb|AAU94636.1| SNARE 12 [Oryza sativa (japonica cultivar-group)]	275	8E-34
					>ref|NP_909819.1| putative vesicle soluble NSF attachment protein receptor [Oryzasativa] gb|AAG46143.1| putative vesicle soluble NSF attachment protein receptor [Oryza sativa]	275	8E-34
					>ref|NP_175258.2| ATNPSN12; protein transporter [Arabidopsis thaliana]gb|AAL92119.1| NPSN12 [Arabidopsis thaliana] gb|AAO63335.1| At1g48240 [Arabidopsis thaliana] dbj|BAC41993.1| unknown protein [Arabidopsis thaliana] gb|AAF79516.1| F21D18.4 [Arabidopsis thaliana] sp|Q9LNH6|NPS12_ARATH Novel plant SNARE 12 (AtNPSN12)	265	3E-30
DV622391	9.46E-04	B73<F1<Mo17	1.28	3	>dbj|BAD72326.1| unknown protein [Oryza sativa (japonica cultivar-group)]	568	4E-25
					>dbj|BAD72325.1| eukaryotic translation initiation factor 3 subunit 10-like [Oryzasativa (japonica cultivar-group)]	1350	2E-22
DV549774	9.47E-04	B73=F1<Mo17	1.97	4	>ref|XP 472585.1| OSJNBa0006B20.8 [Oryza sativa (japonica cultivar-group)]emb|CAD40816.2| OSJNBa0006B20.8 [Oryza sativa (japonica cultivar-group)]	717	4E-9
					>ref|NP 189286.1| unknown protein [Arabidopsis thaliana]dbj|BAB01836.1| selenium-binding protein-like [Arabidopsis thaliana]	700	9E-7
CD058617	9.60E-04	B73<F1=Mo17	1.39	2	>emb|CAA55022.1| beta tubulin [Oryza sativa (japonica cultivar-group)]	447	3E-70
					>emb|CAE52516.1| beta tubulin [Setaria viridis]	448	3E-70
					>ref|NP_915874.1| tubulin beta chain [Oryza sativa (japonica cultivar-group)]dbj|BAB92274.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] dbj|BAA06381.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|P45960|TBB4 ORYSA Tubulin beta-4 chain (Beta-4 tubulin)	447	3E-70
					>gb|AAA66495.1| beta-tubulin	447	3E-70
					>sp|Q41783|TBB6 MAIZE Tubulin beta-6 chain (Beta-6 tubulin)gb|AAA20186.1| beta-6 tubulin	446	3E-70
DV489510	9.61E-04	F1=Mo17<B73	1.65	8	ns		
DV491117	9.73E-04	B73<F1=Mo17	1.54	3	>ref|NP_915015.1| putative SnRK1-interacting protein 1 [Oryza sativa (japonicacultivar-group)] dbj|BAB92460.1| putative SnRK1-interacting protein 1 [Oryza sativa (japonica cultivar-group)] dbj|BAC07318.1| putative SnRK1-interacting protein 1 [Oryza sativa (japonica cultivar-group)]	188	9E-35
					>emb|CAB97356.1| SnRK1-interacting protein 1 [Hordeum vulgare subsp. vulgare]	188	2E-33
					>ref|NP_849876.1| unknown protein [Arabidopsis thaliana]ref|NP_177287.1| unknown protein [Arabidopsis thaliana] gb|AAN15699.1| unknown protein [Arabidopsis thaliana] gb|AAM91575.1| unknown protein [Arabidopsis thaliana] gb|AAG51886.1| hypothetical protein; 63020-64147 [Arabidopsis thaliana]	176	3E-29
					>dbj|BAD34413.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	227	5E-17
					>ref|NP_199598.1| unknown protein [Arabidopsis thaliana]dbj|BAD43427.1| unknown protein [Arabidopsis thaliana] dbj|BAB11334.1| unnamed protein product [Arabidopsis thaliana]	199	1E-16
DV490357	9.73E-04	B73<F1=Mo17	10.26	3	>ref|XP 478231.1| ribosomal protein-like [Oryza sativa (japonica cultivar-group)]dbj|BAD31045.1| ribosomal protein-like [Oryza sativa (japonica cultivar-group)]	258	6E-39
					>gb|ABA96831.1| transposon protein, putative, ping/pong/SNOOPY sub-class [Oryzasativa (japonica cultivar-group)]	511	1E-38
					>gb|ABA95927.1| transposon protein, putative, ping/pong/SNOOPY sub-class [Oryzasativa (japonica cultivar-group)]	450	1E-38
					>gb|AAQ56372.1| hypothetical protein OSJNBa0017M13.23 [Oryza sativa (japonicacultivar-group)]	291	2E-37
					>ref|XP 481524.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	270	2E-37
DV490980	9.82E-04	B73<F1<Mo17	4.56	4	ns		
DV494865	9.83E-04	Mo17<B73=F1	1.9	10	>gb|AAL76334.1| putative G-box binding protein [Oryza sativa]dbj|BAD45657.1| G-box binding protein-like [Oryza sativa (japonica cultivar-group)] gb|AAB65433.1| HvB12D homolog [Oryza sativa]	89	3E-40
					>emb|CAA70936.1| B12Dg1 [Hordeum vulgare subsp. vulgare]emb|CAA54065.1| HvB12D [Hordeum vulgare subsp. vulgare]	87	4E-37
					>gb|AAD22104.1| B12D protein [Ipomoea batatas]	90	1E-33
					>ref|NP_190397.1| unknown protein [Arabidopsis thaliana]emb|CAB51061.1| B12D-like protein [Arabidopsis thaliana] gb|AAL91215.1| B12D-like protein [Arabidopsis thaliana] gb|AAN65070.1| B12D-like protein [Arabidopsis thaliana] pir||T13003 hypothetical protein T24C20.20 - Arabidopsis thaliana	88	4E-30
					>ref|XP_477421.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]dbj|BAC84633.1| putative B12D protein [Oryza sativa (japonica cultivar-group)] dbj|BAD31625.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]	98	1E-27
CA829967	9.92E-04	Mo17<F1<B73	2.29	10	>ref|NP 921503.1| putative polyprotein [Oryza sativa (japonica cultivar-group)]	434	5E-74
					>gb|ABB47623.1| oxidoreductase, aldo/keto reductase family [Oryza sativa (japonicacultivar-group)]	343	5E-74
					>gb|AAT08681.1| aldo/keto reductase [Hyacinthus orientalis]	209	4E-64
					>dbj|BAD61512.1| putative auxin-induced protein [Oryza sativa (japonicacultivar-group)]	344	4E-60
					>gb|AAX11684.1| perakine reductase [Rauvolfia serpentina]	337	7E-58
CB331024	9.95E-04	B73<F1<Mo17	1.56	4	>gb|AAR91093.1| hypothetical protein [Zea mays]	140	4E-62
					>gb|AAR91173.1| hypothetical protein [Zea mays]	101	8E-26
					>gb|AAR91168.1| hypothetical protein [Zea mays]	105	4E-13
CD484865	9.96E-04	B73<F1=Mo17	1.41	3	>gb|AAO43185.1| S-adenosylmethionine decarboxylase leader [Narcissuspseudonarcissus]	51	2E-11

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>emb|CAD41510.3| OSJNBa0029H02.4 [Oryza sativa (japonica cultivar-group)]	450	2E-11
					>gb|AAR84407.1| S-adenosylmethionine decarboxylase uORF [Daucus carota]	53	6E-11
					>gb|AAC48988.1| putative	51	6E-11
					>gb|AAB03864.1| putative ORF; conserved in 5' leaders of plant SAMdC [Pisumsativum]	54	7E-11
BM073917	9.97E-04	Mo17<B73=F1	1.5	10	ns		
DV491701	1.00E-03	Mo17<B73=F1	1.43	10	>gb|ABA98275.1| ribosomal protein L4/L1 family, putative [Oryza sativa (japonicacultivar-group)]	288	1E-19
					>gb|ABA94446.1| ribosomal protein L4/L1 family, putative [Oryza sativa (japonicacultivar-group)]	286	4E-19
					>gb|AAM62769.1| 50S ribosomal protein L4 [Arabidopsis thaliana]	300	1E-17
					>ref|NP_565463.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAD24390.2| 50S ribosomal protein L4 [Arabidopsis thaliana] gb|AAL62411.1| 50S ribosomal protein L4 [Arabidopsis thaliana] gb|AAN72167.1| 50S ribosomal protein L4 [Arabidopsis thaliana]	300	3E-17
					>gb|AAL28955.1| LD33485p [Drosophila melanogaster]ref|NP_524939.1| CG5818-PA [Drosophila melanogaster] gb|AAF53526.1| CG5818-PA [Drosophila melanogaster]	296	8E-7
DV490619	1.00E-03	Mo17<B73=F1	2.16	10	>ref|XP_463160.1| putative protein kinase [Oryza sativa (japonica cultivar-group)]gb|AAR00606.1| putative protein kinase [Oryza sativa (japonica cultivar-group)] dbj|BAD18006.2| serine/threonine protein kinase SAPK10 [Oryza sativa (japonica cultivar-group)] sp|Q75H77|SAPKA_ORYSA Serine/threonine-protein kinase SAPK10 (Osmotic stress/abscisic acid-activated protein kinase 10)	362	3E-26
					>dbj|BAD18005.1| serine/threonine protein kinase SAPK9 [Oryza sativa (japonicacultivar-group)] sp|Q75V57|SAPK9_ORYSA Serine/threonine-protein kinase SAPK9 (Osmotic stress/abscisic acid-activated protein kinase 9) gb|ABA99733.1| protein kinase-like protein [Oryza sativa (japonica cultivar-group)]	361	1E-24
					>ref|XP_469888.1| putative serine-threonine protein kinase [Oryza sativa (japonicacultivar-group)] gb|AAP50965.1| putative serine-threonine protein kinase [Oryza sativa (japonica cultivar-group)] dbj|BAD18004.1| serine/threonine protein kinase SAPK8 [Oryza sativa (japonica cultivar-group)] sp|Q7Y0B9|SAPK8_ORYSA Serine/threonine-protein kinase SAPK8 (Osmotic stress/abscisic acid-activated protein kinase 8)	371	3E-19
					>emb|CAB80112.1| protein kinase-like protein [Arabidopsis thaliana]emb|CAA19877.1| protein kinase-like protein [Arabidopsis thaliana]	357	3E-18
					>ref|NP_567945.1| OST1 (OPEN STOMATA 1); kinase/ protein kinase [Arabidopsisthaliana] emb|CAC87047.1| protein kinase [Arabidopsis thaliana] gb|AAM10100.1| protein kinase-like protein [Arabidopsis thaliana] gb|AAK96815.1| protein kinase - like protein [Arabidopsis thaliana]	362	3E-18
BM336405	1.02E-03	Mo17<B73=F1	1.35	10	>ref|XP_467453.1| putative diphosphate-fructose-6-phosphate 1-phosphotransferasealpha chain [Oryza sativa (japonica cultivar-group)] dbj|BAD07793.1| putative diphosphate-fructose-6-phosphate 1-phosphotransferase alpha chain [Oryza sativa (japonica cultivar-group)]	617	7E-37
					>dbj|BAD33246.1| putative Pyrophosphate--fructose 6-phosphate 1-phosphotransferasealpha subunit [Oryza sativa (japonica cultivar-group)]	617	3E-36
					>emb|CAA83682.1| pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinuscommunis] sp|Q41140|PFPA_RICCO Pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit (PFP) (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPi-PFK)	617	2E-31
					>dbj|BAD95089.1| putative pyrophosphate-dependent phosphofructokinase alpha subunit[Arabidopsis thaliana]	310	1E-30
					>ref|NP_177781.1| 6-phosphofructokinase [Arabidopsis thaliana]gb|AAG51940.1| putative pyrophosphate-dependent phosphofructokinase alpha subunit; 63231-59202 [Arabidopsis thaliana]	617	1E-30
CB334535	1.02E-03	F1=Mo17<B73	1.52	9	>emb|CAD29296.1| plasma membrane H+ ATPase [Oryza sativa (japonica cultivar-group)]gb|ABA99607.1| plasma-membrane proton-efflux P-type ATPase [Oryza sativa (japonica cultivar-group)]	956	3E-61
					>gb|AAT81733.1| H-ATPase [Oryza sativa (japonica cultivar-group)]emb|CAD29294.1| plasma membrane H+ ATPase [Oryza sativa (japonica cultivar-group)]	956	8E-61
					>ref|XP_476966.1| plasma membrane H+ ATPase [Oryza sativa (japonica cultivar-group)]emb|CAD29295.1| plasma membrane H+ ATPase [Oryza sativa (japonica cultivar-group)] dbj|BAC83861.1| plasma membrane H+ ATPase [Oryza sativa (japonica cultivar-group)]	957	4E-60
					>dbj|BAA06629.1| plasma membrane H+-ATPase [Oryza sativa (japonica cultivar-group)]	957	8E-60
					>gb|AAB60276.1| H(+)-transporting ATPase [Zea mays]	949	2E-58
CB833537	1.04E-03	F1=Mo17<B73	1.65	9	>emb|CAC01750.1| putative protein [Arabidopsis thaliana]	494	3E-14
					>ref|NP 197055.2| unknown protein [Arabidopsis thaliana]	497	3E-14
					>gb|AAU44468.1| hypothetical protein AT3G01015 [Arabidopsis thaliana]gb|AAY78731.1| hypothetical protein At3g01015 [Arabidopsis thaliana]	488	4E-13
					>ref|NP 186749.1| unknown protein [Arabidopsis thaliana]gb|AAG51320.1| hypothetical protein; 557-2776 [Arabidopsis thaliana]	488	4E-13
					>gb|ABA99056.1| expressed protein [Oryza sativa (japonica cultivar-group)]	417	1E-11
DV493987	1.04E-03	Mo17<B73=F1	1.49	10	>gb|ABA96078.1| RNA polymerase Rpb3/Rpb11 dimerisation domain, putative [Oryzasativa (japonica cultivar-group)]	108	3E-40
					>ref|NP_180514.1| ATRPC14; DNA binding / DNA-directed RNA polymerase [Arabidopsisthaliana] ref|NP_001031443.1| ATRPC14; DNA binding / DNA-directed RNA polymerase [Arabidopsis thaliana] gb|AAC95185.1| DNA-directed RNA polymerase 14 kDa subunit (AtRPAC14) [Arabidopsis thaliana] gb|AAO50492.1| putative DNA-directed RNA polymerase 14 kDa subunit (AtRPAC14) [Arabidopsis thaliana] dbj|BAC43525.1| putative DNA-directed RNA polymerase 14 kDa subunit AtRPAC14 [Arabidopsis thaliana] gb|AAC49454.1| Arabidopsis thaliana RNA polymerase I(A) and III(C) 14 kDa subunit gb|AAC49453.1| RNA polymerase I(A) and III(C) 14 kDa subunit	122	3E-26
					>ref|XP_710709.1| RNA polymerase I and III shared subunit Rpc19 [Candida albicansSC5314] ref|XP_710695.1| RNA polymerase I and III shared subunit Rpc19 [Candida albicans SC5314] gb|EAK91461.1| potential RNA Polymerase I and III shared subunit Rpc19 [Candida albicans SC5314] gb|EAK91447.1| potential RNA Polymerase I and III shared subunit Rpc19 [Candida albicans SC5314]	131	2E-17

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

<table>
<tr><th>GenBank accession no.</th><th>Overall P value</th><th>Significant pattern</th><th>Fold change[†]</th><th>Sector[‡]</th><th>BLAST annotation*</th><th>Score</th><th>E value</th></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_475912.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]gb|AAU44113.1| putative histone H2B [Oryza sativa (japonica cultivar-group)] gb|AAT69583.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]</td><td>152</td><td>1E-36</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP 640644.1| hypothetical protein DDB0204674 [Dictyostelium discoideum]gb|EAL66655.1| hypothetical protein DDB0204674 [Dictyostelium discoideum]</td><td>315</td><td>2E-13</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP 794415.1| PREDICTED: similar to CG10222-PA [Strongylocentrotus purpuratus]</td><td>308</td><td>1E-12</td></tr>
<tr><td>CB331781</td><td>1.09E-03</td><td>Mo17<B73=F1</td><td>1.38</td><td>10</td><td>>gb|AAP80858.1| ribosomal protein L19 [Triticum aestivum]</td><td>209</td><td>2E-56</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAT08672.1| ribosomal protein L19 [Hyacinthus orientalis]</td><td>203</td><td>8E-55</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_192132.1| structural constituent of ribosome [Arabidopsis thaliana]emb|CAB80716.1| putative ribosomal protein L19 [Arabidopsis thaliana] gb|AAL66909.1| similar to 60S ribosome protein L19 [Arabidopsis thaliana] gb|AAK62438.1| Similar to 60S ribosome protein L19 [Arabidopsis thaliana] sp|P49693|RL19C ARATH 60S ribosomal protein L19-3</td><td>208</td><td>6E-53</td></tr>
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<tr><td>BG842356</td><td>1.10E-03</td><td>F1=Mo17<B73</td><td>1.7</td><td>9</td><td>ns</td><td></td><td></td></tr>
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<tr><td>CD001762</td><td>1.10E-03</td><td>Mo17<F1<B73</td><td>1.31</td><td>10</td><td>>gb|ABA94601.1| ribosomal protein S4 [Oryza sativa (japonica cultivar-group)]gb|ABA94599.1| ribosomal protein S4 [Oryza sativa (japonica cultivar-group)]</td><td>195</td><td>2E-83</td></tr>
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</table>

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

<table>
<thead>
<tr><th>GenBank accession no.</th><th>Overall P value</th><th>Significant pattern</th><th>Fold change†</th><th>Sector‡</th><th>BLAST annotation*</th><th>Score</th><th>E value</th></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA57636.1| small subunit ribosomal protein S28 [Zea mays]sp|P46302|RS28 MAIZE 40S ribosomal protein S28</td><td>65</td><td>2E-25</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>sp|P49216|RS26 ORYSA 40S ribosomal protein S26 (S31)dbj|BAA07208.1| ribosomal protein S31 [Oryza sativa (japonica cultivar-group)]</td><td>133</td><td>4E-36</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>sp|P49199|RS8 ORYSA 40S ribosomal protein S8dbj|BAA07207.1| ribosomal protein S8 [Oryza sativa (japonica cultivar-group)]</td><td>220</td><td>4E-50</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|ABA46755.1| unknown [Solanum tuberosum]</td><td>224</td><td>4E-49</td></tr>
<tr><td>CD485041</td><td>1.19E-03</td><td>Mo17<B73=F1</td><td>1.38</td><td>11</td><td>>emb|CAB57992.1| superoxide dismutase-4AP [Zea mays]sp|P23345|SODC4 MAIZE Superoxide dismutase [Cu-Zn] 4A</td><td>152</td><td>1E-76</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>sp|P23346|SODC5 MAIZE Superoxide dismutase [Cu-Zn] 4AP</td><td>152</td><td>1E-76</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAB57993.1| superoxide dismutase-4A [Zea mays]gb|AAB49913.1| superoxide dismutase 4A</td><td>152</td><td>2E-74</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>sp|P28757|SODC2_ORYSA Superoxide dismutase [Cu-Zn] 2gb|AAC14465.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00800.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)]</td><td>152</td><td>9E-71</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAY56345.1| cytoplasmic copper/zinc-superoxide dismutase [Oryza sativa (indicacultivar-group)] sp|P28756|SODC1_ORYSA Superoxide dismutase [Cu-Zn] 1 gb|AAC14464.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00799.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)] prf||2111424A Cu/Zn superoxide dismutase</td><td>152</td><td>3E-70</td></tr>
<tr><td>CD484562</td><td>1.20E-03</td><td>Mo17<B73=F1</td><td>1.38</td><td>10</td><td>ns</td><td></td><td></td></tr>
<tr><td>BM350700</td><td>1.20E-03</td><td>F1=Mo17<B73</td><td>1.51</td><td>9</td><td>ns</td><td></td><td></td></tr>
<tr><td>DV491285</td><td>1.21E-03</td><td>F1=Mo17<B73</td><td>1.5</td><td>9</td><td>>emb|CAA77808.1| lactate dehydrogenase [Zea mays]sp|P29038|LDH MAIZE L-lactate dehydrogenase (LDH)</td><td>354</td><td>4E-65</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_463815.1| lactate dehydrogenase [Oryza sativa (japonica cultivar-group)]dbj|BAD28080.1| lactate dehydrogenase [Oryza sativa (japonica cultivar-group)] dbj|BAD07543.1| lactate dehydrogenase [Oryza sativa (japonica cultivar-group)] dbj|BAD06283.1| lactate dehydrogenase [Oryza sativa (japonica cultivar-group)] dbj|BAA02971.1| lactate dehydrogenase [Oryza sativa (japonica cultivar-group)]</td><td>353</td><td>3E-57</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP 506679.1| PREDICTED OJ1212 C06.24 gene product [Oryza sativa (japonicacultivar-group)]</td><td>392</td><td>3E-57</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>sp|P22989|LDHB HORVU L-lactate dehydrogenase B (LDH-B)gb|AAA62697.1| L-lactate dehydrogenase</td><td>344</td><td>3E-57</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>sp|P22988|LDHA HORVU L-lactate dehydrogenase A (LDH-A)gb|AAA62696.1| L-lactate dehydrogenase</td><td>356</td><td>1E-55</td></tr>
</tbody>
</table>

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15 % FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
CD528042	1.21E-03	Mo17<B73=F1	1.4	10	>sp|Q08062|MDHC MAIZE Malate dehydrogenase, cytoplasmicgb|AAB64290.1| cytoplasmic malate dehydrogenase [Zea mays]	332	e-111
					>ref|NP_921996.1| cytoplasmic malate dehydrogenase [Oryza sativa (japonicacultivar-group)] gb|AAG13573.1| cytoplasmic malate dehydrogenase [Oryza sativa] gb|AAP54283.1| cytoplasmic malate dehydrogenase [Oryza sativa (japonica cultivar-group)] gb|AAK26431.1| cytoplasmic malate dehydrogenase [Oryza sativa] sp|Q7XDC8|MDHC ORYSA Malate dehydrogenase, cytoplasmic (PP37)	332	e-104
					>emb|CAC12826.1| malate dehydrogenase [Nicotiana tabacum]	332	e-101
					>gb|AAL11502.1| NAD-dependent malate dehydrogenase [Prunus persica]	332	e-101
					>gb|ABC01890.1| malate dehydrogenase-like protein [Solanum tuberosum]	332	e-101
DV551080	1.21E-03	Mo17<B73=F1	1.69	10	>ref|XP 473776.1| OSJNBa0041A02.14 [Oryza sativa (japonica cultivar-group)]emb|CAD41867.2| OSJNBa0041A02.14 [Oryza sativa (japonica cultivar-group)]	396	4E-99
					>gb|AAM65412.1| pectin acetylesterase [Arabidopsis thaliana]	391	8E-81
					>ref|NP_567585.1| carboxylic ester hydrolase [Arabidopsis thaliana]gb|AAL47339.1| putative pectinacetylesterase protein [Arabidopsis thaliana] gb|AAK96722.1| putative pectinacetylesterase protein [Arabidopsis thaliana] gb|AAM64921.1| putative pectinacetylesterase protein [Arabidopsis thaliana]	391	4E-80
					>ref|NP_199341.1| carboxylic ester hydrolase [Arabidopsis thaliana]gb|AAL15296.1| AT5g45280/K9E15_6 [Arabidopsis thaliana] dbj|BAB10249.1| pectin acetylesterase [Arabidopsis thaliana]	391	7E-80
					>emb|CAA67728.1| pectinacetylesterase precursor [Vigna radiata var. radiata]	399	8E-78
BM075714	1.22E-03	B73<F1=Mo17	1.6	3	ns		
DV550599	1.25E-03	B73<F1=Mo17	2.22	3	>ref|NP_922008.1| putative glucose-6-phosphate/phosphate-translocator [Oryza sativa(japonica cultivar-group)] gb|AAG13577.1| putative glucose-6-phosphate/phosphate-translocator [Oryza sativa]	342	9E-16
					>gb|AAK21346.1| putative phosphate translocator [Oryza sativa (japonicacultivar-group)] gb|ABB47794.1| glucose-6-phosphate/phosphate-translocator, putative [Oryza sativa (japonica cultivar-group)]	370	9E-16
					>ref|XP_466859.1| phosphate translocator-like [Oryza sativa (japonicacultivar-group)] dbj|BAD23725.1| phosphate translocator-like [Oryza sativa (japonica cultivar-group)]	341	3E-8
					>ref|NP 180604.1| unknown protein [Arabidopsis thaliana]gb|AAB63090.1| putative integral membrane protein [Arabidopsis thaliana]	200	5E-6
					>dbj|BAD93797.1| integral membrane protein -like [Arabidopsis thaliana]gb|AAP42755.1| At2g30460 [Arabidopsis thaliana] dbj|BAD44037.1| integral membrane protein -like [Arabidopsis thaliana] dbj|BAD43941.1| integral membrane protein -like [Arabidopsis thaliana] dbj|BAD43929.1| integral membrane protein -like [Arabidopsis thaliana] gb|AAO00831.1| putative integral membrane protein [Arabidopsis thaliana]	353	5E-6
CB815768	1.25E-03	Mo17<B73=F1	2.12	10	ns		
BG841963	1.25E-03	F1=Mo17<B73	1.57	8	>gb|AAB37265.1| S-like RNase	269	1E-81
					>gb|AAF45043.1| RNase S-like protein precursor [Hordeum vulgare]	252	1E-47
					>dbj|BAD34375.1| putative RNase S-like protein precursor [Oryza sativa (japonicacultivar-group)] dbj|BAD34238.1| putative RNase S-like protein precursor [Oryza sativa (japonica cultivar-group)]	251	4E-42
					>dbj|BAD34374.1| putative RNase S-like protein precursor [Oryza sativa (japonicacultivar-group)] dbj|BAD34237.1| putative RNase S-like protein precursor [Oryza sativa (japonica cultivar-group)]	259	4E-42
					>gb|AAM18521.1| S-like RNase [Triticum aestivum]	245	1E-26
CD651033	1.26E-03	F1=Mo17<B73	1.51	9	>ref|XP 549818.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD45509.1| unknown protein [Oryza sativa (japonica cultivar-group)]	265	1E-68
					>ref|NP_908341.1| P0672D08.28 [Oryza sativa (japonica cultivar-group)]dbj|BAB92141.1| contains ESTs AU032851(S13343),AU089731(S13343)~unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAB62639.1| contains ESTs AU032851(S13343),AU089731(S13343)~unknown protein [Oryza sativa (japonica cultivar-group)]	291	3E-64
					>ref|NP_189325.2| ATP binding / shikimate kinase [Arabidopsis thaliana]gb|AAS92323.1| At3g26900 [Arabidopsis thaliana] gb|AAS76227.1| At3g26900 [Arabidopsis thaliana] dbj|BAB01237.1| unnamed protein product [Arabidopsis thaliana]	280	5E-31
					>ref|NP 973507.1| ATP binding / shikimate kinase [Arabidopsis thaliana]	304	3E-14
					>ref|NP 179785.2| ATP binding / shikimate kinase [Arabidopsis thaliana]	303	3E-14
DV494968	1.27E-03	Mo17<B73=F1	1.43	10	ns		
CD670262	1.27E-03	B73<F1=Mo17	1.5	3	>ref|XP_475849.1| putative threonine synthase [Oryza sativa (japonicacultivar-group)] gb|AAT39260.1| putative threonine synthase [Oryza sativa (japonica cultivar-group)]	521	5E-75
					>ref|NP_917055.1| putative threonine synthase [Oryza sativa (japonicacultivar-group)] dbj|BAC10696.1| threonine synthase-like [Oryza sativa (japonica cultivar-group)]	525	1E-66
					>gb|AAB04607.1| threonine synthase	525	2E-56
					>ref|NP_194713.1| MTO2 (METHIONINE OVER-ACCUMULATOR); threonine synthase [Arabidopsisthaliana] emb|CAB79742.1| threonine synthase [Arabidopsis thaliana] emb|CAB43659.1| threonine synthase [Arabidopsis thaliana] sp|Q9S7B5|THRC_ARATH Threonine synthase, chloroplast precursor (TS) dbj|BAA77707.1| threonine synthase [Arabidopsis thaliana]	526	2E-56
					>ref|NP 974637.1| MTO2 (METHIONINE OVER-ACCUMULATOR); threonine synthase [Arabidopsisthaliana]	535	2E-56
DV621529	1.27E-03	B73<F1<Mo17	1.39	3	ns		
DV490323	1.28E-03	Mo17<B73=F1	3.97	10	>ref|XP 473049.1| OSJNBa0029H02.5 [Oryza sativa (japonica cultivar-group)]	326	5E-66

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>emb|CAE01627.3| OSJNBa0029H02.7 [Oryza sativa (japonica cultivar-group)]	387	4E-47
					>ref|NP_194868.1| unknown protein [Arabidopsis thaliana]emb|CAB79858.1| hypothetical protein [Arabidopsis thaliana] emb|CAA16543.1| hypothetical protein [Arabidopsis thaliana]	322	4E-22
					>emb|CAG12982.1| unnamed protein product [Tetraodon nigroviridis]	225	4E-16
					>ref|XP 420012.1| PREDICTED: similar to RIKEN cDNA 2410004I17 [Gallus gallus]	752	5E-16
CD484795	1.28E-03	B73<F1=Mo17	1.42	3	>dbj|BAD88200.1| putative auxin response factor [Oryza sativa (japonicacultivar-group)]	808	9E-34
					>dbj|BAB85913.1| auxin response factor 2 [Oryza sativa]	791	9E-34
					>ref|NP 914881.1| auxin response factor 2 [Oryza sativa (japonica cultivar-group)]	826	9E-34
					>gb|ABA98247.1| Auxin response factor, putative [Oryza sativa (japonicacultivar-group)]	840	2E-24
					>gb|ABA98246.1| Auxin response factor, putative [Oryza sativa (japonicacultivar-group)]	841	2E-24
CA989208	1.30E-03	Mo17<B73=F1	1.43	11	>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	1E-21
					>gb|ABA97248.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]gb|ABB51090.1| mannose-specific jacalin-related lectin [Oryza sativa (japonica cultivar-group)]	306	2E-21
					>gb|AAF71261.2| beta-glucosidase aggregating factor precursor [Zea mays]	306	6E-21
					>gb|AAA87042.1| putative 32.7 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72097.1| 32 kDa protein [Hordeum vulgare]	304	7E-20
					>gb|AAR20919.1| jasmonate-induced protein [Triticum aestivum]	304	6E-19
DV494824	1.31E-03	Mo17<B73=F1	1.81	10	>ref|NP_913999.1| putative Acyl-CoA binding protein (ACBP) [Oryza sativa (japonicacultivar-group)] dbj|BAC99898.1| putative Acyl-CoA binding protein (ACBP) [Oryza sativa (japonica cultivar-group)] dbj|BAC57826.1| putative Acyl-CoA binding protein (ACBP) [Oryza sativa (japonica cultivar-group)]	91	2E-33
					>ref|XP_463020.1| putative Acyl-CoA-binding protein [Oryza sativa (japonicacultivar-group)] gb|AAR10857.1| putative Acyl-CoA-binding protein [Oryza sativa (japonica cultivar-group)]	155	3E-33
					>dbj|BAB85987.1| Acyl-CoA-binding protein [Panax ginseng]	87	4E-31
					>emb|CAB56694.1| Acyl-CoA binding protein (ACBP) [Digitalis lanata]	90	8E-31
					>gb|AAP82942.1| acyl-CoA-binding protein [Tropaeolum majus]	90	1E-30
DV489568	1.31E-03	B73=F1<Mo17	1.53	4	>dbj|BAD52953.1| unknown protein [Oryza sativa (japonica cultivar-group)]	783	1E-43
					>dbj|BAD52952.1| unknown protein [Oryza sativa (japonica cultivar-group)]	895	1E-43
					>ref|NP 916345.1| P0490D09.22 [Oryza sativa (japonica cultivar-group)]	1194	1E-43
					>ref|NP_199176.1| nucleic acid binding [Arabidopsis thaliana]gb|AAO64119.1| unknown protein [Arabidopsis thaliana] gb|AAO42027.1| unknown protein [Arabidopsis thaliana] dbj|BAB11626.1| unnamed protein product [Arabidopsis thaliana]	831	1E-20
CB605563	1.35E-03	Mo17<B73=F1	1.52	10	>ref|NP 910160.1| cytoplasmic ribosomal protein L18 [Oryza sativa]gb|AAV32218.1| cytoplasmic ribosomal protein L18 [Oryza sativa (japonica cultivar-group)]	188	6E-63
					>gb|AAW50985.1| ribosomal protein L18 [Triticum aestivum]	188	6E-61
					>ref|XP_479492.1| putative cytoplasmic ribosomal protein L18 [Oryza sativa (japonicacultivar-group)] dbj|BAD31974.1| putative cytoplasmic ribosomal protein L18 [Oryza sativa (japonica cultivar-group)] dbj|BAC83538.1| putative cytoplasmic ribosomal protein L18 [Oryza sativa (japonica cultivar-group)]	195	1E-57
					>gb|AAA69928.1| cytoplasmic ribosomal protein L18	187	5E-55
					>ref|NP_187210.1| RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome[Arabidopsis thaliana] gb|AAF26138.1| putative 60S ribosomal protein L18 [Arabidopsis thaliana] gb|AAL31164.1| AT3g05590/F18C1_14 [Arabidopsis thaliana] gb|AAK59824.1| AT3g05590/F18C1_14 [Arabidopsis thaliana] sp|P42791|RL18 ARATH 60S ribosomal protein L18	187	5E-55
DV490274	1.39E-03	Mo17<B73=F1	1.61	10	>gb|AAF23902.1| MAP kinase homolog [Oryza sativa]dbj|BAD53617.1| MAP kinase [Oryza sativa (japonica cultivar-group)]	506	1E-32
					>dbj|BAD53616.1| putative MAP kinase [Oryza sativa (japonica cultivar-group)]	580	1E-32
					>gb|AAD52659.1| blast and wounding induced mitogen-activated protein kinase [Oryzasativa]	506	1E-32
					>gb|AAX20165.1| putative MAPK protein kinase [Triticum aestivum]	578	1E-28
					>gb|AAX20166.1| putative MAPK protein kinase [Triticum aestivum]	578	5E-28
CB605044	1.42E-03	B73<F1=Mo17	1.42	3	>ref|XP_464969.1| putative 60S ribosomal protein L27 [Oryza sativa (japonicacultivar-group)] dbj|BAD22201.1| putative 60S ribosomal protein L27 [Oryza sativa (japonica cultivar-group)] dbj|BAD21487.1| putative 60S ribosomal protein L27 [Oryza sativa (japonica cultivar-group)]	137	9E-72
					>ref|NP_922757.1| putative ribosomal protein L27 [Oryza sativa (japonicacultivar-group)] gb|AAG60203.1| putative ribosomal protein L27 [Oryza sativa] gb|AAP55044.1| ribosomal protein L27, putative [Oryza sativa (japonica cultivar-group)]	136	5E-68
					>ref|NP_193236.1| structural constituent of ribosome [Arabidopsis thaliana]emb|CAB10279.1| ribosomal protein [Arabidopsis thaliana] gb|AAM20365.1| putative ribosomal protein [Arabidopsis thaliana] gb|AAL36343.1| putative ribosomal protein [Arabidopsis thaliana] gb|AAM62713.1| ribosomal protein [Arabidopsis thaliana] emb|CAB78542.1| ribosomal protein [Arabidopsis thaliana] sp|P51419|RL27 ARATH 60S ribosomal protein L27	135	5E-57
					>dbj|BAA96367.1| ribosomal protein L27 [Panax ginseng]	135	5E-56
					>ref|NP_188862.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAN15737.1| putative ribosomal protein L27 [Arabidopsis thaliana] gb|AAM14157.1| putative ribosomal protein L27 [Arabidopsis thaliana] gb|AAL36216.1| putative ribosomal protein L27 [Arabidopsis thaliana] gb|AAM96987.1| putative ribosomal protein L27 [Arabidopsis thaliana] gb|AAM13388.1| 60S ribosomal protein L27 [Arabidopsis thaliana] gb|AAL32695.1| 60S ribosomal protein L27 [Arabidopsis thaliana] dbj|BAB03070.1| 60S ribosomal protein L27 [Arabidopsis thaliana]	135	7E-56

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
CB885701	1.44E-03	Mo17<F1<B73	1.68	9	>emb|CAA86227.1| ADP-glucose pyrophosphorylase [Zea mays]sp|P55234|GLGL2_MAIZE Glucose-1-phosphate adenylyltransferase large subunit 2, chloroplast precursor (ADP-glucose synthase) (ADP-glucose pyrophosphorylase) (AGPASE S) (Alpha-D-glucose-1-phosphate adenyl transferase)	521	1E-7
CD484523	1.44E-03	F1=Mo17<B73	1.57	9	>emb|CAD29296.1| plasma membrane H+ ATPase [Oryza sativa (japonica cultivar-group)]gb|ABA99607.1| plasma-membrane proton-efflux P-type ATPase [Oryza sativa (japonica cultivar-group)]	956	5E-36
					>emb|CAA54046.1| H(+)-transporting ATPase [Solanum tuberosum]	956	5E-35
					>gb|AAF98344.1| plasma membrane H+-ATPase [Lycopersicon esculentum]gb|AAD55399.1| plasma membrane H+-ATPase isoform LHA2 [Lycopersicon esculentum]	956	7E-35
					>gb|AAA34096.1| plasma membrane H+ ATPase	440	7E-35
					>gb|AAA34052.1| H+-translocating ATPase	956	7E-35
BM348208	1.45E-03	Mo17<B73=F1	2.03	10	>dbj|BAD45307.1| calcineurin B-like protein 3-like [Oryza sativa (japonicacultivar-group)] dbj|BAD44961.1| calcineurin B-like protein 3-like [Oryza sativa (japonica cultivar-group)]	81	1E-12
					>gb|ABA54184.1| calcineurin B-like protein 9 [Oryza sativa (japonicacultivar-group)]	290	1E-12
					>gb|ABA54181.1| calcineurin B-like protein 6 [Oryza sativa (japonicacultivar-group)]	226	2E-9
					>ref|NP_849485.1| CBL10; calcium ion binding [Arabidopsis thaliana]gb|AAO14864.2| calcineurin B-like protein [Arabidopsis thaliana] dbj|BAC42104.1| unknown protein [Arabidopsis thaliana]	246	2E-8
					>ref|NP_195026.1| CBL10; calcium ion binding [Arabidopsis thaliana]gb|AAO72364.1| calcineurin B-like protein 10 [Arabidopsis thaliana] sp|Q7FRS8|CNB10 ARATH Calcineurin B-like protein 10	256	2E-8
CD527251	1.45E-03	B73=F1<Mo17	1.39	4	>emb|CAA33620.1| GAPDH [Zea mays]sp|P08735|G3PC MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 1	337	4E-74
					>emb|CAA30151.1| unnamed protein product [Zea mays]	337	4E-74
					>emb|CAA51676.1| glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zeamays] sp|Q09054|G3PD_MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 2 gb|AAA87880.1| glyceraldehyde-3-phosphate dehydrogenase gb|AAA87578.1| cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2	337	4E-72
					>gb|AAQ55397.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp.spontaneum] gb|AAQ55396.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55394.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55393.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55391.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55389.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55387.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55386.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55385.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55384.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55381.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55380.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55379.1| glyceraldehyde-3-phosphate dehydrogenase	245	2E-70
					>emb|CAA42901.1| glyceraldehyde 3-phosphate dehydrogenase [Hordeum vulgare]sp|P26517|G3PX_HORVU Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	337	2E-70
CD484488	1.45E-03	Mo17<B73=F1	1.43	11	>gb|ABA91291.1| expressed protein [Oryza sativa (japonica cultivar-group)]	638	3E-32
					>gb|ABA96340.1| expressed protein [Oryza sativa (japonica cultivar-group)]	622	3E-31
					>gb|AAV85703.1| At5g05510 [Arabidopsis thaliana]ref|NP_196170.1| unknown protein [Arabidopsis thaliana] gb|AAT71963.1| At5g05510 [Arabidopsis thaliana] dbj|BAB11540.1| unnamed protein product [Arabidopsis thaliana]	471	4E-21
BM075816	1.45E-03	B73<F1=Mo17	1.45	3	>ref|NP_922302.1| kinesin-like protein [Oryza sativa (japonica cultivar-group)]gb|AAG13527.1| kinesin-like protein [Oryza sativa (japonica cultivar-group)] gb|AAP54589.1| kinesin-like protein [Oryza sativa (japonica cultivar-group)]	859	7E-15
					>ref|NP_565510.1| ATP binding / microtubule motor [Arabidopsis thaliana]gb|AAN12893.1| putative kinesin heavy chain [Arabidopsis thaliana] gb|AAK64143.1| putative kinesin heavy chain [Arabidopsis thaliana] gb|AAD23684.2| putative kinesin heavy chain [Arabidopsis thaliana]	1058	3E-6
BM080794	1.46E-03	Mo17<B73=F1	1.37	10	>gb|AAL36459.1| cytochrome b5 reductase isoform II [Zea mays]	279	3E-48
					>gb|AAT77284.1| putative NADH-cytochrome b5 reductase [Oryza sativa (japonicacultivar-group)]	282	3E-43
					>gb|AAV69021.1| NADH:cytochrome b5 reductase [Vernicia fordii]gb|AAV69019.1| NADH:cytochrome b5 reductase [Vernicia fordii]	280	5E-43
					>gb|AAD17694.1| cytochrome b5 reductase [Zea mays]	279	1E-42
					>dbj|BAD82696.1| putative cytochrome b5 reductase [Oryza sativa (japonicacultivar-group)]	279	5E-42
CD001392	1.46E-03	Mo17<B73=F1	1.35	11	>ref|XP_479153.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)]ref|XP_506463.1| PREDICTED P0616D06.117 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC16499.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)] dbj|BAA04903.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)] sp|Q40680|EF1D ORYSA Elongation factor 1-delta (EF-1-delta) (Elongation factor 1B-beta) (eEF-1B beta)	229	1E-42
					>gb|AAR15081.1| translational elongation factor 1 subunit Bbeta [Pisum sativum]	231	5E-36
					>gb|AAU89237.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)]dbj|BAA34599.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)] dbj|BAA34598.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)]	226	5E-36
					>emb|CAB90214.1| putative elongation factor 1 beta [Hordeum vulgare subsp. vulgare]	226	3E-35
					>sp|P93447|EF1D_PIMBR Elongation factor 1-delta (EF-1-delta) (Elongation factor 1B-beta)(eEF-1B beta) gb|AAB68395.1| elongation factor 1-beta [Pimpinella brachycarpa]	226	2E-34

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
CD568516	1.47E-03	F1=Mo17<B73	1.39	9	>gb|AAX55895.1| aci-reductone dioxygenase-like protein [Oryza sativa (japonicacultivar-group)]	198	1E-80
					>gb|AAC19375.1| acireductone dioxygenase 2 [Oryza sativa]	198	1E-80
					>dbj|BAB61039.1| iron-deficiency induced gene [Hordeum vulgare]	198	1E-76
					>gb|AAN06863.1| Putative probable submergence induced, nickel-binding protein 2A[Oryza sativa (japonica cultivar-group)]	254	3E-76
					>gb|AAC05511.1| acireductone dioxygenase 1 [Oryza sativa]	199	5E-75
CB381074	1.47E-03	Mo17<B73=F1	1.37	10	>ref|XP_480842.1| putative 60S ribosomal protein L7 [Oryza sativa (japonicacultivar-group)] dbj|BAD03800.1| putative 60S ribosomal protein L7 [Oryza sativa (japonica cultivar-group)]	245	2E-69
					>gb|AAW50989.1| ribosomal protein L7 [Triticum aestivum]	244	5E-69
					>ref|XP_473801.1| OSJNBb0015N08.13 [Oryza sativa (japonica cultivar-group)]emb|CAE03885.2| OSJNBb0015N08.13 [Oryza sativa (japonica cultivar-group)] emb|CAE02124.2| OSJNBa0035M09.3 [Oryza sativa (japonica cultivar-group)]	250	4E-68
					>ref|NP_850411.1| structural constituent of ribosome / transcription regulator[Arabidopsis thaliana] gb|AAC23430.1| 60S ribosomal protein L7 [Arabidopsis thaliana] pir||T00692 60S ribosomal protein L7 [imported] - Arabidopsis thaliana	247	3E-62
					>ref|NP_850410.1| structural constituent of ribosome / transcription regulator[Arabidopsis thaliana] gb|AAM10036.1| 60S ribosomal protein L7 [Arabidopsis thaliana] gb|AAL38372.1| 60S ribosomal protein L7 [Arabidopsis thaliana] gb|AAL38617.1| At2g44120/F6E13.25 [Arabidopsis thaliana] gb|AAK96628.1| At2g44120/F6E13.25 [Arabidopsis thaliana] gb|AAM65125.1| 60S ribosomal protein L7 [Arabidopsis thaliana] sp|P60039|RL72_ARATH 60S ribosomal protein L7-2	242	3E-62
DV491346	1.48E-03	F1=Mo17<B73	5.3	8	ns		
DV942317	1.48E-03	F1=Mo17<B73	1.72	9	>dbj|BAD87076.1| putative ribosomal protein S26 [Oryza sativa (japonicacultivar-group)] dbj|BAD73505.1| putative ribosomal protein S26 [Oryza sativa (japonica cultivar-group)]	133	5E-33
					>ref|XP_475416.1| putative 40S ribosomal protein S26 [Oryza sativa (japonicacultivar-group)] gb|AAT01360.1| putative 40S ribosomal protein S26 [Oryza sativa (japonica cultivar-group)]	194	9E-33
					>sp|P49216|RS26 ORYSA 40S ribosomal protein S26 (S31)dbj|BAA07208.1| ribosomal protein S31 [Oryza sativa (japonica cultivar-group)]	133	8E-32
					>gb|AAD47346.1| ribosomal protein S26 [Pisum sativum]	130	2E-27
					>ref|NP_191193.1| structural constituent of ribosome [Arabidopsis thaliana]emb|CAB87433.1| 40S ribosomal protein S26 homolog [Arabidopsis thaliana] gb|AAM91494.1| AT3g56340/F18O21 300 [Arabidopsis thaliana] gb|AAK63990.1| AT3g56340/F18O21 300 [Arabidopsis thaliana]	130	2E-26
BG874137	1.48E-03	Mo17<B73=F1	1.86	10	ns		
CB351321	1.49E-03	F1=Mo17<B73	3.12	9	>ref|XP_464091.1| putative molybdopterin synthase large subunit MOCS2B [Oryza sativa(japonica cultivar-group)] dbj|BAD10257.1| putative molybdopterin synthase large subunit MOCS2B [Oryza sativa (japonica cultivar-group)]	193	2E-25
					>ref|NP_181904.1| unknown protein [Arabidopsis thaliana]emb|CAB71291.1| molybdopterin synthase, large subunit [Arabidopsis thaliana] emb|CAB38428.1| molybdopterin synthase large subunit [Arabidopsis thaliana] gb|AAB64030.1| putative molybdopterin synthase large subunit [Arabidopsis thaliana] gb|AAK32854.1| At2g43760/F18O19.13 [Arabidopsis thaliana] gb|AAN64517.1| At2g43760/F18O19.13 [Arabidopsis thaliana]	198	1E-17
					>emb|CAD80090.1| putative molybdopterin synthase large subunit [Momordica charantia]	110	4E-16
					>gb|AAT43644.1| molybdopterin (MPT) converting factor, subunit 2 [Picrophilustorridus DSM 9790] ref|YP_023837.1| molybdopterin (MPT) converting factor, subunit 2 [Picrophilus torridus DSM 9790]	137	4E-12
					>ref|NP_004522.1| molybdopterin synthase large subunit MOCS2B [Homo sapiens]ref|NP_904327.1| molybdopterin synthase large subunit MOCS2B [Homo sapiens] gb|AAH46097.1| Molybdopterin synthase, large subunit MOCS2B [Homo sapiens] emb|CAG33453.1| MOCS2 [Homo sapiens] gb|AAD14599.1| molybdopterin-synthase large subunit [Homo sapiens] gb|AAF67478.1| molybdenum cofactor biosysthesis protein E [Homo sapiens] gb|AAD13297.1| molybdopterin synthase large subunit [Homo sapiens] sp|O96007|MOS2L_HUMAN Molybdenum cofactor synthesis protein 2 large subunit (Molybdopterin synthase large subunit) (MPT synthase large subunit) (MOCS2B) (MOCO1-B)	188	2E-11
CB381184	1.50E-03	Mo17<B73=F1	1.21	10	>ref|XP_478414.1| putative translational inhibitor protein [Oryza sativa (japonicacultivar-group)] dbj|BAC20708.1| putative translational inhibitor protein [Oryza sativa (japonica cultivar-group)] dbj|BAD31311.1| putative translational inhibitor protein [Oryza sativa (japonica cultivar-group)]	180	6E-56
					>dbj|BAD00048.1| perchloric acid soluble translation inhibitor protein homolog[Gentiana triflora] dbj|BAC66487.1| translation-inhibitor protein [Gentiana triflora]	188	9E-52
					>ref|NP_188674.1| endoribonuclease [Arabidopsis thaliana]gb|AAK53030.1| AT3g20390/MQC12_15 [Arabidopsis thaliana] gb|AAL31178.1| AT3g20390/MQC12 15 [Arabidopsis thaliana] gb|AAM63246.1| translational inhibitor protein, putative [Arabidopsis thaliana]	187	2E-50
					>dbj|BAB02821.1| unnamed protein product [Arabidopsis thaliana]	143	2E-50
					>gb|AAY18881.1| translational inhibitor protein p14.5 [synthetic construct]	161	4E-32
DV551123	1.50E-03	Mo17<B73=F1	1.53	10	>sp|Q10716|CYSP1 MAIZE Cysteine proteinase 1 precursordbj|BAA08244.1| cysteine proteinase [Zea mays]	371	2E-89
					>ref|XP_507484.1| PREDICTED OJ1371_D04.6 gene product [Oryza sativa (japonicacultivar-group)] ref|XP_507483.1| PREDICTED OJ1371_D04.6 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_465566.1| putative cysteine proteinase 1 precursor [Oryza sativa (japonica cultivar-group)] ref|XP_507482.1| PREDICTED OJ1371_D04.6 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_506801.1| PREDICTED OJ1371_D04.6 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD19579.1| putative cysteine proteinase 1 precursor [Oryza sativa (japonica cultivar-group)]	373	1E-82
					>emb|CAA57675.1| cysteine proteinase [Zea mays]	145	9E-81
					>tpe|CAD66657.1| TPA: putative cysteine protease [Hordeum vulgare subsp. vulgare]	377	1E-79
					>gb|AAW21813.1| cysteine protease [Triticum aestivum]	377	2E-79

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
BM349941	1.51E-03	F1=Mo17<B73	1.58	9	>gb|AAG34830.1| glutathione S-transferase GST 22 [Zea mays]	229	2E-22
					>gb|AAG34845.1| glutathione S-transferase GST 37 [Zea mays]	236	3E-10
					>gb|AAM83401.1| glutathione-S-transferase 28e45 [Triticum aestivum]	228	6E-7
					>gb|AAM89393.1| glutathione S-transferase 1 [Aegilops tauschii]gb|AAD10129.1| glutathione S-transferase TSI-1 [Aegilops tauschii] pdb|1GWC|C Chain C, The Structure Of A Tau Class Glutathione S-Transferase From Wheat, Active In Herbicide Detoxification pdb|1GWC|B Chain B, The Structure Of A Tau Class Glutathione S-Transferase From Wheat, Active In Herbicide Detoxification pdb|1GWC|A Chain A, The Structure Of A Tau Class Glutathione S-Transferase From Wheat, Active In Herbicide Detoxification	230	6E-7
					>ref|XP_476737.1| putative glutathione S-transferase GST27 [Oryza sativa (japonicacultivar-group)] ref|XP_506181.1| PREDICTED OSJNBa0050F10.6 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD31777.1| putative glutathione S-transferase GST27 [Oryza sativa (japonica cultivar-group)]	235	8E-7
CB604806	1.52E-03	Mo17<B73=F1	1.29	10	ns		
DV551233	1.52E-03	Mo17<B73=F1	1.75	11	>ref|NP_911744.1| unknown protein [Oryza sativa (japonica cultivar-group)]ref|XP_506244.1| PREDICTED P0021G06.122-2 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC20822.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAC20124.1| unknown protein [Oryza sativa (japonica cultivar-group)]	107	1E-21
					>ref|NP_190014.1| unknown protein [Arabidopsis thaliana]emb|CAB88996.1| putative protein [Arabidopsis thaliana] gb|AAN60290.1| unknown [Arabidopsis thaliana] gb|AAO64023.1| unknown protein [Arabidopsis thaliana] dbj|BAC42815.1| unknown protein [Arabidopsis thaliana]	108	1E-13
					>ref|NP_197620.1| unknown protein [Arabidopsis thaliana]gb|AAL32901.1| Unknown protein [Arabidopsis thaliana] gb|AAP21319.1| At5g22280 [Arabidopsis thaliana] gb|AAM66072.1| unknown [Arabidopsis thaliana] dbj|BAB08326.1| unnamed protein product [Arabidopsis thaliana]	108	2E-13
					>gb|AAO41143.1| unknown protein, 3'-partial [Oryza sativa (japonicacultivar-group)]	53	1E-10
					>dbj|BAD27808.1| unknown protein [Oryza sativa (japonica cultivar-group)]	106	7E-7
CB381189	1.52E-03	F1=Mo17<B73	1.33	9	>ref|XP_464689.1| putative elongation factor 1-gamma [Oryza sativa (japonicacultivar-group)] dbj|BAD17614.1| putative elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]	414	6E-76
					>gb|ABA81876.1| unknown [Solanum tuberosum]	413	1E-67
					>gb|ABB87108.1| putative elongation factor 1-gamma-like [Solanum tuberosum]	414	1E-67
					>gb|AAL87298.1| unknown protein [Arabidopsis thaliana]	345	2E-67
					>gb|AAO72574.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]	409	1E-38
DV550388	1.53E-03	Mo17<B73=F1	1.58	10	>ref|XP_478466.1| putative glucose-6-phosphate/phosphate-transloca tor precursor[Oryza sativa (japonica cultivar-group)] ref|XP_478462.1| putative glucose-6-phosphate/phosphate-transloca tor precursor [Oryza sativa (japonica cultivar-group)] ref|XP_478458.1| putative glucose-6-phosphate/phosphate-transloca tor precursor [Oryza sativa (japonica cultivar-group)] dbj|BAC57677.1| putative glucose-6-phosphate/phosphate- translocator precursor [Oryza sativa (japonica cultivar-group)] dbj|BAC57673.1| putative glucose-6-phosphate/phosphate- translocator precursor [Oryza sativa (japonica cultivar-group)] dbj|BAD30854.1| putative glucose-6-phosphate/phosphate- translocator precursor [Oryza sativa (japonica cultivar-group)]	392	2E-13
					>dbj|BAD94591.1| Similar to glucose-6-phosphate/phosphate-translocator [Arabidopsisthaliana]	110	5E-13
					>ref|NP 564785.1| antiporter/ glucose-6-phosphate transporter [Arabidopsis thaliana]	388	5E-13
					>gb|AAM10041.1| similar to glucose-6-phosphate/phosphate-translocator [Arabidopsisthaliana] gb|AAK68814.1| Similar to glucose-6-phosphate/phosphate-translocator [Arabidopsis thaliana] sp|Q94B38|GPT2 ARATH Glucose-6-phosphate/phosphate translocator 2, chloroplast precursor	388	5E-13
					>gb|AAF86908.1| glucose-6P/phosphate translocator precursor [Mesembryanthemumcrystallinum]	395	6E-13
CB886023	1.53E-03	Mo17<B73=F1	1.76	10	ns		
BM336116	1.55E-03	Mo17<B73=F1	2.68	10	>ref|NP_913526.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]dbj|BAA96586.1| putative SDL-1 protein [Oryza sativa (japonica cultivar-group)]	556	3E-11
DV491012	1.59E-03	B73=F1<Mo17	1.44	5	>ref|XP 474136.1| OSJNBb0059K02.13 [Oryza sativa (japonica cultivar-group)]emb|CAE04503.1| OSJNBb0059K02.13 [Oryza sativa (japonica cultivar-group)]	464	1E-39
					>ref|NP_201525.2| exonuclease [Arabidopsis thaliana]gb|AAL87318.1| unknown protein [Arabidopsis thaliana] gb|AAN71976.1| unknown protein [Arabidopsis thaliana]	782	2E-22
					>ref|NP 190579.1| exonuclease [Arabidopsis thaliana]emb|CAB62118.1| hypothetical protein [Arabidopsis thaliana]	406	3E-21
					>dbj|BAB10958.1| unnamed protein product [Arabidopsis thaliana]	782	4E-21
					>ref|NP_196173.1| exonuclease [Arabidopsis thaliana]gb|AAP81803.1| At5g05540 [Arabidopsis thaliana] dbj|BAB11543.1| unnamed protein product [Arabidopsis thaliana] dbj|BAC43046.1| unknown protein [Arabidopsis thaliana]	466	3E-19
CD510425	1.60E-03	B73<F1<Mo17	1.38	3	>emb|CAE52517.1| beta tubulin [Setaria viridis]	448	2E-63
					>ref|NP_912523.1| Putative beta tubulin [Oryza sativa (japonica cultivar-group)]gb|AAN60482.1| Putative beta tubulin [Oryza sativa (japonica cultivar-group)] sp|Q8H7U1|TBB2 ORYSA Tubulin beta-2 chain (Beta-2 tubulin)	447	2E-63
					>emb|CAA37060.1| beta 1 tubulin [Zea mays]sp|P18025|TBB1 MAIZE Tubulin beta-1 chain (Beta-1 tubulin)	446	1E-62
					>gb|AAL92118.1| beta-tubulin [Gossypium hirsutum]gb|AAL92026.1| tubulin beta-1 [Gossypium hirsutum]	445	2E-62
					>gb|AAQ92668.1| beta-tubulin 9 [Gossypium hirsutum]sp|Q6VAF4|TBB9 GOSHI Tubulin beta-9 chain (Beta-9 tubulin)	445	2E-62
CB605418	1.61E-03	Mo17<B73=F1	1.41	11	>ref|NP_564138.1| protein transporter [Arabidopsis thaliana]gb|AAL34154.1| unknown protein [Arabidopsis thaliana] gb|AAK59479.1| unknown protein [Arabidopsis thaliana] gb|AAF87893.1| Unknown protein [Arabidopsis thaliana]	506	2E-50

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_177823.2| protein transporter [Arabidopsis thaliana]gb|AAQ62873.1| At1g76970 [Arabidopsis thaliana] dbj|BAD94203.1| hypothetical protein [Arabidopsis thaliana]	446	5E-49
					>gb|ABB90835.1| VHS and GAT domain protein [Glycine max]	672	4E-45
					>ref|XP_464916.1| putative VHS domain-containing protein [Oryza sativa (japonicacultivar-group)] dbj|BAD28297.1| putative VHS domain-containing protein [Oryza sativa (japonica cultivar-group)] dbj|BAD21829.1| putative VHS domain-containing protein [Oryza sativa (japonica cultivar-group)]	634	1E-43
					>gb|AAX96736.1| VHS domain [Oryza sativa (japonica cultivar-group)]gb|ABA91946.1| VHS domain [Oryza sativa (japonica cultivar-group)]	109	5E-43
CD661814	1.63E-03	Mo17<B73=F1	1.34	10	>emb|CAA48638.1| cyclophilin [Zea mays]sp|P21569|CYPH_MAIZE Peptidyl-prolyl cis-trans isomerase (PPIase) (Rotamase) (Cyclophilin) (Cyclosporin A-binding protein) gb|AAA63403.1| cyclophilin	172	6E-49
					>gb|AAK60569.1| cyclophilin [Triticum aestivum]	131	7E-41
					>gb|AAK49428.1| cyclophilin A-3 [Triticum aestivum]gb|AAK49426.1| cyclophilin A-1 [Triticum aestivum]	171	2E-40
					>gb|AAK49427.1| cyclophilin A-2 [Triticum aestivum]gb|AAS17067.1| cyclophilin A [Triticum aestivum]	171	2E-40
					>ref|XP_463914.1| peptidylprolyl isomerase Cyp2 [Oryza sativa (japonicacultivar-group)] ref|XP_506694.1| PREDICTED OSJNBb0088N06.23 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD07601.1| peptidylprolyl isomerase Cyp2 [Oryza sativa (japonica cultivar-group)] dbj|BAD08141.1| peptidylprolyl isomerase Cyp2 [Oryza sativa (japonica cultivar-group)] gb|AAA57045.1| cyclophilin 2	172	3E-40
DV491731	1.63E-03	Mo17<B73=F1	1.84	10	ns		
BM341661	1.63E-03	Mo17<B73=F1	1.35	10	>emb|CAJ01693.1| 2-Cys peroxiredoxin [Oryza sativa (japonica cultivar-group)]dbj|BAD27915.1| putative thioredoxin peroxidase [Oryza sativa (japonica cultivar-group)] dbj|BAD28826.1| putative thioredoxin peroxidase [Oryza sativa (japonica cultivar-group)]	261	5E-77
					>gb|AAC78473.1| thioredoxin peroxidase [Secale cereale]	258	2E-75
					>ref|NP_568166.1| antioxidant [Arabidopsis thaliana]gb|AAK00375.1| putative 2-cys peroxiredoxin protein [Arabidopsis thaliana] gb|AAG41453.1| putative 2-cys peroxiredoxin protein [Arabidopsis thaliana] gb|AAM10065.1| 2-cys peroxiredoxin-like protein [Arabidopsis thaliana] gb|AAK96812.1| 2-cys peroxiredoxin-like protein [Arabidopsis thaliana]	273	3E-75
					>gb|AAM62760.1| 2-cys peroxiredoxin-like protein [Arabidopsis thaliana]	271	3E-75
					>dbj|BAB08951.1| 2-cys peroxiredoxin-like protein [Arabidopsis thaliana]	271	3E-75
BM073059	1.65E-03	F1=Mo17<B73	1.37	9	>gb|AAQ84317.1| fiber NTGP1-related protein [Gossypium barbadense]	199	1E-28
					>dbj|BAD81915.1| putative geranylgeranylated protein NTGP1 [Oryza sativa (japonicacultivar-group)]	216	1E-28
					>dbj|BAD87240.1| putative NTGP1 [Oryza sativa (japonica cultivar-group)]	214	5E-28
					>gb|AAT37501.1| putative SNARE protein [Hevea brasiliensis]	199	1E-27
					>gb|AAD00116.1| NTGP1 [Nicotiana tabacum]	199	1E-27
DV491495	1.66E-03	Mo17<B73=F1	1.45	10	>gb|AAW34236.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	166	4E-19
					>ref|XP_468756.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)] ref|XP_468752.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] gb|AAP20855.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] gb|AAP20842.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] sp|P40978|RS19 ORYSA 40S ribosomal protein S19	146	4E-19
					>gb|AAW34237.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	144	3E-16
					>ref|NP_186857.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAF14828.1| putative 40S ribosomal protein S19 [Arabidopsis thaliana] gb|AAL34186.1| putative 40S ribosomal protein S19 [Arabidopsis thaliana] gb|AAK44092.1| putative 40S ribosomal protein S19 [Arabidopsis thaliana] gb|AAM65679.1| putative 40S ribosomal protein S19 [Arabidopsis thaliana] sp|Q9SGA6|RS191 ARATH 40S ribosomal protein S19-1	143	2E-15
					>emb|CAA10125.1| 40S ribosomal protein S19 [Cicer arietinum]	105	3E-15
CB885824	1.66E-03	Mo17<B73=F1	1.48	10	ns		
DV491151	1.66E-03	Mo17<F1<B73	1.44	9	>ref|XP_550001.1| putative nuclease I [Oryza sativa (japonica cultivar-group)]dbj|BAB03377.1| putative nuclease I [Oryza sativa (japonica cultivar-group)] dbj|BAD52548.1| putative nuclease I [Oryza sativa (japonica cultivar-group)]	308	1E-81
					>ref|NP 909100.1| putative bifunctional nuclease [Oryza sativa (japonicacultivar-group)]	310	3E-79
					>ref|NP 680734.1| endonuclease/ nucleic acid binding [Arabidopsis thaliana]	299	6E-56
					>ref|XP 474151.1| OSJNBa0060D06.10 [Oryza sativa (japonica cultivar-group)]emb|CAE03544.2| OSJNBa0060D06.10 [Oryza sativa (japonica cultivar-group)]	290	1E-54
					>gb|AAD00695.1| bifunctional nuclease [Zinnia elegans]	328	3E-53
BM334691	1.70E-03	B73<F1=Mo17	6.64	3	ns		
BM073302	1.70E-03	B73=Mo17<F1	1.34	12	>sp|P11428|SODC2 MAIZE Superoxide dismutase [Cu-Zn] 2gb|AAA33511.1| SOD2 protein gb|AAA33510.1| superoxide dismutase 2	151	7E-74
					>emb|CAB57992.1| superoxide dismutase-4AP [Zea mays]sp|P23345|SODC4 MAIZE Superoxide dismutase [Cu-Zn] 4A	152	1E-68
					>sp|P28757|SODC2_ORYSA Superoxide dismutase [Cu-Zn] 2gb|AAC14465.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00800.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)]	152	2E-68
					>gb|AAY56345.1| cytoplasmic copper/zinc-superoxide dismutase [Oryza sativa (indicacultivar-group)] sp|P28756|SODC1_ORYSA Superoxide dismutase [Cu-Zn] 1 gb|AAC14464.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00799.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)] prf||2111424A Cu/Zn superoxide dismutase	152	4E-68
					>sp|P23346|SODC5 MAIZE Superoxide dismutase [Cu-Zn] 4AP	152	4E-68

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
CB331619	1.75E-03	Mo17<B73=F1	1.38	10	>gb|ABA99572.1| hypothetical protein LOC Os12g37060 [Oryza sativa (japonicacultivar-group)]	214	1E-86
					>gb|ABA95272.1| hypothetical protein LOC Os11g44940 [Oryza sativa (japonicacultivar-group)]	211	2E-76
					>ref|NP 567130.1| unknown protein [Arabidopsis thaliana]	213	7E-72
					>gb|AAN46755.1| At3g62580/T12C14 280 [Arabidopsis thaliana]gb|AAL06485.1| AT3g62580/T12C14 280 [Arabidopsis thaliana]	206	5E-65
					>emb|CAB83108.1| putative protein [Arabidopsis thaliana]	156	6E-58
DV621027	1.75E-03	Mo17<B73=F1	1.32	10	>emb|CAI64401.1| thioredoxin h2 protein [Zea mays]	122	1E-56
					>pdb|1WMJ|A Chain A, Solution Structure Of Thioredoxin Type H From Oryza Sativa	130	1E-38
					>ref|XP_476912.1| Thioredoxin H-type (TRX-H) [Oryza sativa (japonica cultivar-group)]dbj|BAD30186.1| Thioredoxin H-type (TRX-H) [Oryza sativa (japonica cultivar-group)] dbj|BAC79928.1| Thioredoxin H-type (TRX-H) [Oryza sativa (japonica cultivar-group)] dbj|BAA04864.1| thioredoxin h [Oryza sativa (japonica cultivar-group)] sp|Q42443|TRXH_ORYSA Thioredoxin H-type (TRX-H) (Phloem sap 13 kDa protein 1) gb|AAB51522.1| thioredoxin h [Oryza sativa] dbj|BAA05546.1| thioredoxin h [Oryza sativa]	122	2E-38
					>gb|AAL67139.1| thioredoxin H [Triticum aestivum]	118	1E-36
					>gb|AAP72290.1| thioredoxin h isoform 1; HvTrxh1 [Hordeum vulgare subsp. vulgare]	118	4E-36
DV494132	1.76E-03	Mo17<B73=F1	1.21	11	>gb|AAT77924.1| expressed protein [Oryza sativa (japonica cultivar-group)]	479	2E-73
					>emb|CAB46038.1| hypothetical protein [Arabidopsis thaliana]emb|CAB78700.1| hypothetical protein [Arabidopsis thaliana]	335	6E-65
					>gb|AAO63356.1| At4g16580 [Arabidopsis thaliana]dbj|BAC42578.1| unknown protein [Arabidopsis thaliana]	300	6E-65
					>ref|NP 193391.3| catalytic [Arabidopsis thaliana]	467	6E-65
					>ref|NP_201473.1| catalytic [Arabidopsis thaliana]gb|AAN15547.1| putative protein [Arabidopsis thaliana] gb|AAM97071.1| putative protein [Arabidopsis thaliana] dbj|BAA97278.1| unnamed protein product [Arabidopsis thaliana] dbj|BAC41805.1| unknown protein [Arabidopsis thaliana]	414	2E-62
BG842068	1.76E-03	Mo17<B73=F1	1.77	10	ns		
DV493995	1.77E-03	B73<F1=Mo17	1.87	3	>ref|XP_474072.1| OSJNBb0079B02.14 [Oryza sativa (japonica cultivar-group)]emb|CAE05968.2| OSJNBa0063C18.9 [Oryza sativa (japonica cultivar-group)] emb|CAD41855.2| OSJNBb0079B02.14 [Oryza sativa (japonica cultivar-group)]	269	1E-74
					>ref|NP_201056.1| ATEB1B; microtubule binding [Arabidopsis thaliana]gb|AAM61163.1| microtubule-associated protein EB1-like protein [Arabidopsis thaliana] dbj|BAB11500.1| microtubule-associated protein EB1-like protein [Arabidopsis thaliana]	293	4E-46
					>ref|NP 190353.3| ATEB1A; microtubule binding [Arabidopsis thaliana]gb|AAP88341.1| At3g47690 [Arabidopsis thaliana]	276	4E-45
					>ref|NP_922172.1| putative microtubule-associated protein [Oryza sativa (japonicacultivar-group)] gb|AAM93680.1| putative microtubule-associated protein [Oryza sativa (japonica cultivar-group)] gb|AAP54459.1| microtubule-associated protein, putative [Oryza sativa (japonica cultivar-group)]	332	2E-31
					>ref|NP_201528.1| ATEB1C (MICROTUBULE END BINDING PROTEIN 1); microtubule binding[Arabidopsis thaliana] gb|AAM65311.1| microtubule-associated protein EB1-like protein [Arabidopsis thaliana] dbj|BAD43258.1| unknown protein [Arabidopsis thaliana] dbj|BAB09646.1| unnamed protein product [Arabidopsis thaliana]	329	6E-29
DV489577	1.78E-03	B73=F1<Mo17	4.56	4	>ref|XP_463448.1| P0512C01.22 [Oryza sativa (japonica cultivar-group)]dbj|BAB92368.1| phospholipase-like [Oryza sativa (japonica cultivar-group)] dbj|BAB61223.1| contains EST AU057376(S21389)~similar to Arabidopsis thaliana chromosome 5, F8F6.250~unknown protein [Oryza sativa (japonica cultivar-group)]	1044	9E-39
BG873965	1.79E-03	Mo17<B73=F1	1.38	11	>ref|XP_467968.1| putative flavonol synthase [Oryza sativa (japonica cultivar-group)]dbj|BAD17324.1| putative flavonol synthase [Oryza sativa (japonica cultivar-group)]	331	5E-52
					>emb|CAA80264.1| flavonol synthase [Petunia x hybrida]sp|Q07512|FLS PETHY Flavonol synthase/flavanone 3-hydroxylase (FLS)	348	2E-44
					>sp|Q9ZWQ9|FLS CITUN Flavonol synthase/flavanone 3-hydroxylase (FLS) (CitFLS)dbj|BAA36554.1| flavonol synthase [Citrus unshiu]	335	2E-44
					>dbj|BAD34463.1| flavonol synthase [Eustoma grandiflorum]	335	3E-44
					>dbj|BAC10995.1| flavonol synthase [Nierembergia sp. NB17]	346	4E-44
DV492988	1.79E-03	B73<F1=Mo17	1.51	3	>ref|XP 475843.1| putative protein kinase [Oryza sativa (japonica cultivar-group)]	559	6E-58
					>dbj|BAD94332.1| putative protein kinase [Arabidopsis thaliana]	328	3E-48
					>ref|NP_564946.1| kinase/ protein kinase [Arabidopsis thaliana]gb|AAG52037.1| putative protein kinase; 22015-24834 [Arabidopsis thaliana] gb|AAG51596.1| putative protein kinase; tRNA-Met; tRNA-Phe; tRNA-Ile [Arabidopsis thaliana] sp|Q9S713|STT7_ARATH Serine/threonine-protein kinase SNT7, chloroplast precursor (Stt7 homolog)	562	3E-48
DV491297	1.80E-03	B73<F1=Mo17	1.54	3	>gb|AAC49676.1| lethal leaf-spot 1 [Zea mays]	467	1E-74
					>ref|XP 470215.1| Putative cell death suppressor protein [Oryza sativa]gb|AAK98735.1| Putative cell death suppressor protein [Oryza sativa]	515	2E-64
					>gb|AAC49678.1| lethal leaf-spot 1 [Zea mays]	505	1E-62
					>gb|AAL32300.1| lethal leaf spot 1-like protein [Lycopersicon esculentum]	537	5E-55
					>gb|AAP13565.1| lethal leaf spot 1-like protein [Vigna unguiculata]	545	4E-48
CB605539	1.80E-03	Mo17<B73=F1	1.29	10	>ref|XP_476832.1| putative z-protein [Oryza sativa (japonica cultivar-group)]dbj|BAD30317.1| putative z-protein [Oryza sativa (japonica cultivar-group)] dbj|BAC83445.1| putative z-protein [Oryza sativa (japonica cultivar-group)]	244	1E-46
					>emb|CAI53895.2| putative receptor associated protein [Capsicum chinense]	242	9E-41

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

<table>
<tr><th>GenBank accession no.</th><th>Overall P value</th><th>Significant pattern</th><th>Fold change†</th><th>Sector‡</th><th>BLAST annotation*</th><th>Score</th><th>E value</th></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_171806.1| glutamate binding [Arabidopsis thaliana]gb|AAR24681.1| At1g03070 [Arabidopsis thaliana] dbj|BAD43212.1| putative glutamate/aspartate-binding peptide [Arabidopsis thaliana] gb|AAD25802.1| Belongs to the PF|01027 Uncharacterized protein family UPF0005 with 7 transmembrane domains. [Arabidopsis thaliana]</td><td>247</td><td>3E-39</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_469710.1| putative receptor-associated protein [Oryza sativa (japonicacultivar-group)] gb|AAK71568.1| putative receptor-associated protein [Oryza sativa (japonica cultivar-group)]</td><td>229</td><td>6E-39</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAV74230.1| At3g63310 [Arabidopsis thaliana]ref|NP_191890.1| glutamate binding [Arabidopsis thaliana] emb|CAB86432.1| putative protein [Arabidopsis thaliana] gb|AAX22267.1| At3g63310 [Arabidopsis thaliana]</td><td>239</td><td>6E-39</td></tr>
<tr><td>CB885610</td><td>1.82E-03</td><td>B73<F1=Mo17</td><td>1.6</td><td>3</td><td>>dbj|BAD52841.1| putative insulin degrading enzyme [Oryza sativa (japonicacultivar-group)]</td><td>973</td><td>6E-70</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP 463457.1| putative zinc protease [Oryza sativa (japonica cultivar-group)]</td><td>946</td><td>6E-70</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAD52843.1| putative insulin degrading enzyme [Oryza sativa (japonicacultivar-group)]</td><td>949</td><td>2E-67</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP 463460.1| putative zinc protease [Oryza sativa (japonica cultivar-group)]</td><td>945</td><td>2E-67</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_478770.1| putative insulin degrading enzyme [Oryza sativa (japonicacultivar-group)] dbj|BAC79700.1| putative insulin degrading enzyme [Oryza sativa (japonica cultivar-group)]</td><td>988</td><td>6E-44</td></tr>
<tr><td>DV493565</td><td>1.82E-03</td><td>B73<F1=Mo17</td><td>1.54</td><td>2</td><td>>gb|AAQ62068.1| Single myb histone 4 [Zea mays]</td><td>288</td><td>8E-52</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAL73044.1| histone H1-like protein [Zea mays]</td><td>288</td><td>1E-51</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAQ62066.1| single myb histone 3 [Zea mays]</td><td>285</td><td>9E-40</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAD44620.1| MYB28 protein [Oryza sativa (japonica cultivar-group)]</td><td>304</td><td>1E-22</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAD81933.1| DNA-binding protein MYB1-like [Oryza sativa (japonicacultivar-group)]</td><td>257</td><td>1E-22</td></tr>
<tr><td>DV549673</td><td>1.82E-03</td><td>Mo17<B73=F1</td><td>1.3</td><td>11</td><td>>dbj|BAD72286.1| putative 26S proteasome regulatory particle triple-A ATPasesubunit5a [Oryza sativa (japonica cultivar-group)]</td><td>429</td><td>e-104</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAD36042.1| 26S proteasome regulatory particle triple-A ATPase subunit5a [Oryzasativa (japonica cultivar-group)] dbj|BAB78492.1| 26S proteasome regulatory particle triple-A ATPase subunit5a [Oryza sativa (japonica cultivar-group)]</td><td>429</td><td>e-101</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>sp|P46465|PRS6A_ORYSA 26S protease regulatory subunit 6A homolog (TAT-binding proteinhomolog 1) (TBP-1) dbj|BAA04614.1| rice homologue of Tat binding protein [Oryza sativa (japonica cultivar-group)]</td><td>429</td><td>e-101</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA52445.1| Mg-dependent ATPase 1 [Lycopersicon esculentum]sp|P54776|PRS6A_LYCES 26S protease regulatory subunit 6A homolog (TAT-binding protein homolog 1) (TBP-1) (Mg(2+)-dependent ATPase 1) (LEMA-1)</td><td>423</td><td>5E-97</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAB21595.1| Tat binding protein like protein [Brassica rapa]</td><td>424</td><td>3E-96</td></tr>
<tr><td>DV495861</td><td>1.83E-03</td><td>B73=F1<Mo17</td><td>1.48</td><td>4</td><td>>gb|AAT85074.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]</td><td>94</td><td>8E-40</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAM67304.1| unknown [Arabidopsis thaliana]gb|AAO42828.1| At1g67350 [Arabidopsis thaliana] gb|AAG00242.1| F1N21.17 [Arabidopsis thaliana]</td><td>98</td><td>2E-32</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAS20982.1| unknown [Hyacinthus orientalis]</td><td>91</td><td>3E-32</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|ABC46709.1| RW1-like protein [Arachis hypogaea]</td><td>64</td><td>1E-20</td></tr>
<tr><td>CD573098</td><td>1.83E-03</td><td>Mo17<B73=F1</td><td>1.58</td><td>10</td><td>>ref|XP_468402.1| putative NADH dehydrogenase [Oryza sativa (japonicacultivar-group)] dbj|BAD22016.1| putative NADH dehydrogenase [Oryza sativa (japonica cultivar-group)] dbj|BAD21515.1| putative NADH dehydrogenase [Oryza sativa (japonica cultivar-group)]</td><td>408</td><td>3E-81</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAH91192.1| Ndufa9 protein [Rattus norvegicus]</td><td>370</td><td>3E-30</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP 508942.1| PREDICTED: NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9,39kDa [Pan troglodytes]</td><td>347</td><td>4E-30</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAH92896.1| hypothetical protein [Pongo pygmaeus]</td><td>377</td><td>6E-30</td></tr>
<tr><td>DV489661</td><td>1.84E-03</td><td>F1=Mo17<B73</td><td>1.6</td><td>9</td><td>>dbj|BAD91083.1| beta-D-galactosidase [Pyrus pyrifolia]</td><td>842</td><td>5E-36</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAF70824.1| putative beta-galactosidase [Lycopersicon esculentum]</td><td>852</td><td>1E-35</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAQ21371.2| beta-galactosidase [Sandersonia aurantiaca]</td><td>818</td><td>5E-35</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAC44501.1| beta-galactosidase [Fragaria x ananassa]</td><td>840</td><td>2E-34</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAD20774.2| beta-galactosidase [Raphanus sativus]</td><td>851</td><td>1E-33</td></tr>
<tr><td>BG840947</td><td>1.86E-03</td><td>F1=Mo17<B73</td><td>2.99</td><td>9</td><td>>ref|XP_450939.1| putative succinoaminoimidazolecarboximide ribonucleotide synthetase[Oryza sativa (japonica cultivar-group)] dbj|BAD17522.1| putative succinoaminoimidazolecarboximide ribonucleotide synthetase [Oryza sativa (japonica cultivar-group)]</td><td>403</td><td>9E-34</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAR06292.1| SAICAR synthetase [Nicotiana tabacum]</td><td>399</td><td>4E-29</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAL48317.1| succinoaminoimidazolecarboximide ribonucleotide synthetase [Vignaunguiculata]</td><td>402</td><td>1E-28</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_001030739.1| PUR7; phosphoribosylaminoimidazolesuccinocarboxamide synthase[Arabidopsis thaliana] ref|NP_188748.1| PUR7; phosphoribosylaminoimidazolesuccinocarboxamide synthase [Arabidopsis thaliana] gb|AAO22563.1| putative phosphoribosyamidoimidazole-succinocarboxamide synthase [Arabidopsis thaliana] dbj|BAB01454.1| 5'-phosphoribosyl-4-(N-succinocarboxamide)-5- ami noimidazole synthetase [Arabidopsis thaliana] sp|P38025|PUR7 ARATH Phosphoribosylaminoimidazole-succinocarboxamide synthase, chloroplast precursor (SAICAR synthetase)</td><td>411</td><td>1E-27</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAL85973.1| putative phosphoribosyamidoimidazole-succinocarboxamide synthase[Arabidopsis thaliana]</td><td>374</td><td>1E-27</td></tr>
</table>

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
BM379680	1.87E-03	B73=Mo17<F1	1.37	12	>sp|P11428|SODC2 MAIZE Superoxide dismutase [Cu-Zn] 2gb|AAA33511.1| SOD2 protein gb|AAA33510.1| superoxide dismutase 2	151	1E-43
					>emb|CAB57993.1| superoxide dismutase-4A [Zea mays]gb|AAB49913.1| superoxide dismutase 4A	152	2E-40
					>emb|CAB57992.1| superoxide dismutase-4AP [Zea mays]sp|P23345|SODC4 MAIZE Superoxide dismutase [Cu-Zn] 4A	152	2E-40
					>sp|P23346|SODC5 MAIZE Superoxide dismutase [Cu-Zn] 4AP	152	2E-40
					>gb|AAY56345.1| cytoplasmic copper/zinc-superoxide dismutase [Oryza sativa (indicacultivar-group)] sp|P28756|SODC1_ORYSA Superoxide dismutase [Cu-Zn] 1 gb|AAC14464.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00799.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)] prf||2111424A Cu/Zn superoxide dismutase	152	2E-39
CD484895	1.87E-03	B73<F1=Mo17	1.4	3	>emb|CAA69075.1| S-adenosylmethionine decarboxylase [Zea mays]sp|O24575|DCAM_MAIZE S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain]	400	3E-12
					>gb|AAO43185.1| S-adenosylmethionine decarboxylase leader [Narcissuspseudonarcissus]	51	2E-11
					>emb|CAD41510.3| OSJNBa0029H02.4 [Oryza sativa (japonica cultivar-group)]	450	2E-11
					>gb|AAR84407.1| S-adenosylmethionine decarboxylase uORF [Daucus carota]	53	6E-11
					>gb|AAC48988.1| putative	51	6E-11
CD058876	1.88E-03	B73<F1=Mo17	1.35	3	>gb|AAT42128.1| putative zinc finger protein ZF2 [Zea mays]	176	1E-29
					>gb|AAO46040.1| zinc finger transcription factor ZFP30 [Oryza sativa (japonicacultivar-group)]	166	4E-26
					>ref|XP_464544.1| zinc finger transcription factor ZFP30 [Oryza sativa (japonicacultivar-group)] ref|XP_507460.1| PREDICTED OJ1135_F06.29 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_506755.1| PREDICTED OJ1135_F06.29 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD16000.1| zinc finger transcription factor ZFP30 [Oryza sativa (japonica cultivar-group)] dbj|BAD15513.1| zinc finger transcription factor ZFP30 [Oryza sativa (japonica cultivar-group)]	166	4E-26
					>gb|AAZ94630.1| zinc finger protein-like protein [Gossypium hirsutum]	139	2E-22
					>ref|NP_197931.1| binding [Arabidopsis thaliana]gb|AAO63982.1| unknown protein [Arabidopsis thaliana] dbj|BAC43503.1| unknown protein [Arabidopsis thaliana]	170	2E-15
CD527324	1.89E-03	Mo17<B73=F1	1.68	10	>gb|ABA96028.1| expressed protein [Oryza sativa (japonica cultivar-group)]	438	2E-39
					>ref|NP_200323.1| unknown protein [Arabidopsis thaliana]gb|AAM14224.1| unknown protein [Arabidopsis thaliana] gb|AAL36095.1| unknown protein [Arabidopsis thaliana] dbj|BAB08581.1| unnamed protein product [Arabidopsis thaliana]	431	1E-31
					>gb|AAT45011.1| unknown [Xerophyta humilis]	343	1E-30
					>gb|AAL07213.1| unknown protein [Arabidopsis thaliana]	442	2E-29
					>ref|NP_567759.1| VTC2 (VITAMIN C DEFECTIVE 2) [Arabidopsis thaliana]gb|AAM13137.1| putative protein [Arabidopsis thaliana] gb|AAP31933.1| At4g26850 [Arabidopsis thaliana]	442	2E-29
CD510345	1.91E-03	B73<F1=Mo17	1.53	3	>gb|AAT94032.1| beta-tubulin [Oryza sativa (japonica cultivar-group)]dbj|BAC82429.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|Q76FS3|TBB6 ORYSA Tubulin beta-6 chain (Beta-6 tubulin)	444	6E-75
					>emb|CAA55022.1| beta tubulin [Oryza sativa (japonica cultivar-group)]	447	8E-75
					>emb|CAE52516.1| beta tubulin [Setaria viridis]	448	8E-75
					>ref|NP_915874.1| tubulin beta chain [Oryza sativa (japonica cultivar-group)]dbj|BAB92274.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] dbj|BAA06381.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|P45960|TBB4 ORYSA Tubulin beta-4 chain (Beta-4 tubulin)	447	8E-75
					>gb|AAA66495.1| beta-tubulin	447	8E-75
CB381181	1.91E-03	B73<F1=Mo17	1.46	3	>emb|CAE52516.1| beta tubulin [Setaria viridis]	448	e-109
					>ref|NP_915874.1| tubulin beta chain [Oryza sativa (japonica cultivar-group)]dbj|BAB92274.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] dbj|BAA06381.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|P45960|TBB4 ORYSA Tubulin beta-4 chain (Beta-4 tubulin)	447	e-109
					>sp|Q41783|TBB6 MAIZE Tubulin beta-6 chain (Beta-6 tubulin)gb|AAA20186.1| beta-6 tubulin	446	e-109
					>sp|Q41785|TBB8 MAIZE Tubulin beta-8 chain (Beta-8 tubulin)gb|AAA19709.1| beta-8 tubulin	445	e-109
					>ref|NP_912596.1| tubulin beta-4 chain [Oryza sativa (japonica cultivar-group)]dbj|BAB64211.1| putative beta-tubulin 4 [Oryza sativa (japonica cultivar-group)] sp|Q43594|TBB1 ORYSA Tubulin beta-1 chain (Beta-1 tubulin) dbj|BAB39951.1| putative tubulin beta-4 chain [Oryza sativa (japonica cultivar-group)]	447	e-109
CB331093	1.91E-03	F1=Mo17<B73	1.26	9	>gb|AAT76364.1| putative ribosomal protein L19 [Oryza sativa (japonicacultivar-group)] gb|AAP05800.1| putative ribosomal protein L19 [Oryza sativa (japonica cultivar-group)]	206	2E-66
					>gb|AAP80858.1| ribosomal protein L19 [Triticum aestivum]	209	1E-65
					>gb|AAT08672.1| ribosomal protein L19 [Hyacinthus orientalis]	203	1E-63
					>gb|AAR83877.1| 60S ribosomal protein L19 [Capsicum annuum]	232	5E-62
					>gb|ABC01909.1| 60S ribosomal protein L19-like protein [Solanum tuberosum]	209	5E-62
DV490929	1.92E-03	Mo17<B73=F1	1.44	10	>ref|NP 918362.1| putative Ca2+/H+-exchanging protein [Oryza sativa (japonicacultivar-group)]	424	4E-55
					>dbj|BAD87649.1| cation/proton exchanger 1a [Oryza sativa (japonica cultivar-group)]dbj|BAD87498.1| cation/proton exchanger 1a [Oryza sativa (japonica cultivar-group)] dbj|BAD06218.1| cation/proton exchanger 1a [Oryza sativa (japonica cultivar-group)] sp|Q769E5|CAX1A_ORYSA Vacuolar cation/proton exchanger 1a (Ca(2+)/H(+) exchanger 1a) (OsCAX1a)	451	4E-55

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|AAM03123.1| putative Ca2+/H+ exchanger [Oryza sativa]	354	5E-50
					>gb|AAF91350.1| calcium/proton exchanger CAX1-like protein [Zea mays]	418	3E-43
					>dbj|BAA25753.1| Ca2+/H+ exchanger [Vigna radiata]	444	7E-43
CD001096	1.93E-03	Mo17<B73=F1	1.22	10	>gb|AAM08320.1| small Ran-related GTP-binding protein [Triticum aestivum]gb|AAL30396.1| small Ras-related GTP-binding protein [Triticum aestivum]	221	5E-27
					>ref|XP_475914.1| GTP-binding nuclear protein RAN-B1 [Oryza sativa (japonicacultivar-group)] gb|AAT69585.1| GTP-binding nuclear protein RAN-B1 [Oryza sativa (japonica cultivar-group)] dbj|BAA81911.1| Ran [Oryza sativa (japonica cultivar-group)] dbj|BAB82438.1| small GTP-binding protein (Ran2) [Oryza sativa (japonica cultivar-group)]	221	5E-27
					>gb|AAD18006.1| Ran-related GTP binding protein [Zea mays]	170	4E-26
					>emb|CAC10213.1| GTP-binding protein [Cicer arietinum]	221	3E-25
					>gb|AAM12880.1| GTP-binding protein [Helianthus annuus]	221	3E-25
CD661795	1.95E-03	Mo17<B73=F1	1.29	10	>dbj|BAD45865.1| pseudouridylate synthase-like [Oryza sativa (japonicacultivar-group)]	495	1E-96
					>ref|NP_198390.2| pseudouridylate synthase/ tRNA-pseudouridine synthase [Arabidopsisthaliana] gb|AAP37871.1| At5g35400 [Arabidopsis thaliana] gb|AAO00765.1| putative protein [Arabidopsis thaliana]	420	9E-58
					>gb|AAC13601.1| contains similarity to pseudouridylate synthases [Arabidopsisthaliana]	364	3E-41
					>ref|ZP 00525390.1| tRNA pseudouridine synthase [Solibacter usitatus Ellin6076]gb|EAM55608.1| tRNA pseudouridine synthase [Solibacter usitatus Ellin6076]	256	1E-8
					>ref|ZP_00511188.1| tRNA pseudouridine synthase [Chlorobium limicola DSM 245]gb|EAM44258.1| tRNA pseudouridine synthase [Chlorobium limicola DSM 245]	243	1E-7
CB604876	1.95E-03	B73<F1=Mo17	1.44	3	>gb|AAT93971.1| putative chaperonin [Oryza sativa (japonica cultivar-group)]	535	3E-71
					>gb|AAK62448.1| putative chaperonin [Arabidopsis thaliana]	535	7E-67
					>gb|AAM61312.1| putative chaperonin [Arabidopsis thaliana]	535	7E-67
					>ref|NP_186902.1| ATP binding / protein binding [Arabidopsis thaliana]gb|AAF32460.1| putative chaperonin [Arabidopsis thaliana] gb|AAM47971.1| putative chaperonin [Arabidopsis thaliana] gb|AAL32807.1| putative chaperonin [Arabidopsis thaliana] gb|AAN65043.1| putative chaperonin [Arabidopsis thaliana]	535	7E-67
					>emb|CAC01806.1| TCP-1 chaperonin-like protein [Arabidopsis thaliana]	540	3E-64
CD651684	1.96E-03	Mo17<B73=F1	1.3	10	>gb|ABA93723.1| ribosomal protein S7 [Oryza sativa (japonica cultivar-group)]	199	1E-96
					>ref|NP_908322.1| putative 40S ribosomal protein S5 [Oryza sativa (japonicacultivar-group)] dbj|BAB64234.1| putative 40S ribosomal protein S5 [Oryza sativa (japonica cultivar-group)] dbj|BAB62621.1| putative 40S ribosomal protein S5 [Oryza sativa (japonica cultivar-group)]	200	3E-95
					>ref|NP_187800.1| ATRPS5A (RIBOSOMAL PROTEIN 5A); structural constituent of ribosome[Arabidopsis thaliana] ref|NP_850564.1| ATRPS5A (RIBOSOMAL PROTEIN 5A); structural constituent of ribosome [Arabidopsis thaliana] gb|AAF23210.1| putative 40S ribosomal protein S5 [Arabidopsis thaliana] gb|AAM14315.1| putative 40S ribosomal protein S5 [Arabidopsis thaliana] gb|AAK76520.1| putative 40S ribosomal protein S5 [Arabidopsis thaliana] gb|AAM64502.1| 40S ribosomal protein S5, putative [Arabidopsis thaliana] dbj|BAB03103.1| 40S ribosomal protein S5-like [Arabidopsis thaliana] sp|P51427|RS5B ARATH 40S ribosomal protein S5-2	207	2E-91
					>ref|NP_181264.1| ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome[Arabidopsis thaliana] ref|NP_001031502.1| ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome [Arabidopsis thaliana] gb|AAC98068.1| 40S ribosomal protein S5 [Arabidopsis thaliana] gb|AAM10231.1| 40S ribosomal protein S5 [Arabidopsis thaliana] gb|AAL24331.1| 40S ribosomal protein S5 [Arabidopsis thaliana] sp|Q9ZUT9|RS5A_ARATH 40S ribosomal protein S5-1	207	6E-91
					>emb|CAA06491.1| 40S ribosomal protein S5 [Cicer arietinum]sp|O65731|RS5 CICAR 40S ribosomal protein S5	197	1E-90
BG842495	2.01E-03	Mo17<B73=F1	1.47	10	>gb|AAG43835.1| protein phosphatase type-2C [Zea mays]	366	3E-44
					>dbj|BAD38120.1| putative protein phosphatase type-2C [Oryza sativa (japonicacultivar-group)]	368	4E-34
					>dbj|BAD28017.1| putative protein phosphatase type-2C [Oryza sativa (japonicacultivar-group)]	362	6E-32
					>ref|NP_194914.1| catalytic/ protein phosphatase type 2C [Arabidopsis thaliana]emb|CAB79904.1| protein phosphatase 2C-like protein [Arabidopsis thaliana] emb|CAB40756.1| protein phosphatase 2C-like protein [Arabidopsis thaliana] gb|AAM47332.1| AT4g31860/F11C18_60 [Arabidopsis thaliana] gb|AAL14406.1| AT4g31860/F11C18 60 [Arabidopsis thaliana]	357	6E-25
					>ref|NP_180079.1| catalytic/ protein phosphatase type 2C/ protein serine/threoninephosphatase [Arabidopsis thaliana] gb|AAM14148.1| putative protein phosphatase 2C [Arabidopsis thaliana] gb|AAK92810.1| putative protein phosphatase 2C [Arabidopsis thaliana] gb|AAD23006.1| putative protein phosphatase 2C [Arabidopsis thaliana] dbj|BAB84700.1| protein phosphatase 2C [Arabidopsis thaliana]	355	8E-24
BM073786	2.02E-03	Mo17<B73=F1	1.54	11	>emb|CAA10616.1| eukaryotic translation initiation factor 5 [Zea mays]	451	5E-54
					>emb|CAA67868.1| Eukaryotic initiation factor-5 [Zea mays]sp|P55876|IF5 MAIZE Eukaryotic translation initiation factor 5 (eIF-5)	451	4E-53
					>dbj|BAD54665.1| putative eukaryotic translation initiation factor 5 [Oryza sativa(japonica cultivar-group)]	450	3E-41
					>ref|XP_450545.1| putative eukaryotic translation initiation factor 5 [Oryza sativa(japonica cultivar-group)] dbj|BAD23595.1| putative eukaryotic translation initiation factor 5 [Oryza sativa (japonica cultivar-group)]	333	1E-40
					>ref|XP_450544.1| putative eukaryotic translation initiation factor 5 [Oryza sativa(japonica cultivar-group)] ref|XP_506649.1| PREDICTED P0706E03.4-1 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD23594.1| putative eukaryotic translation initiation factor 5 [Oryza sativa (japonica cultivar-group)]	450	1E-40
CB604524	2.03E-03	Mo17<B73=F1	1.29	11	>gb|AAR99579.1| 60S ribosomal protein L44 [Phalaenopsis hybrid cultivar]	105	4E-40

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_911994.1| putative 60S ribosomal protein L44 [Oryza sativa (japonicacultivar-group)] dbj|BAC15877.1| putative 60S ribosomal protein L44 [Oryza sativa (japonica cultivar-group)]	105	5E-40
					>gb|AAK94425.1| 60S ribosomal protein L144 [Brassica rapa subsp. pekinensis]	119	4E-39
					>ref|NP_188981.1| structural constituent of ribosome [Arabidopsis thaliana]ref|NP_193168.1| structural constituent of ribosome [Arabidopsis thaliana] emb|CAB10211.1| ribosomal protein [Arabidopsis thaliana] emb|CAB78474.1| ribosomal protein [Arabidopsis thaliana] gb|AAM10201.1| ribosomal protein [Arabidopsis thaliana] gb|AAL38297.1| ribosomal protein [Arabidopsis thaliana] gb|AAL32933.1| 60S ribosomal protein L44-like [Arabidopsis thaliana] gb|AAM63001.1| ribosomal protein [Arabidopsis thaliana] gb|AAM61725.1| ribosomal protein [Arabidopsis thaliana] dbj|BAB02283.1| 60S ribosomal protein L44-like [Arabidopsis thaliana] sp|O23290|RL44 ARATH 60S ribosomal protein L44 gb|AAN65080.1| 60S ribosomal protein L44-like [Arabidopsis thaliana]	105	3E-38
					>gb|AAA34366.1| ribosomal protein L41	105	3E-38
CB381454	2.03E-03	Mo17<B73=F1	1.37	10	>dbj|BAD32975.1| putative ubiquitin-conjugating enzyme family protein [Oryza sativa(japonica cultivar-group)] dbj|BAD33214.1| putative ubiquitin-conjugating enzyme family protein [Oryza sativa (japonica cultivar-group)]	148	3E-70
					>gb|ABB29951.1| ubiquitin-conjugating enzyme family protein-like [Solanumtuberosum] gb|ABA40444.1| ubiquitin-conjugating enzyme family protein-like protein [Solanum tuberosum]	146	2E-67
					>ref|NP_565834.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme[Arabidopsis thaliana] gb|AAM13381.1| putative ubiquitin-conjugating enzyme [Arabidopsis thaliana] gb|AAD21451.1| E2, ubiquitin-conjugating enzyme, putative [Arabidopsis thaliana] gb|AAL32838.1| putative ubiquitin-conjugating enzyme [Arabidopsis thaliana]	145	2E-66
					>ref|NP_566968.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme[Arabidopsis thaliana] emb|CAB43411.1| putative DNA-binding protein [Arabidopsis thaliana] gb|AAL66907.1| unknown protein [Arabidopsis thaliana] gb|AAK68786.1| Unknown protein [Arabidopsis thaliana] gb|AAM62830.1| E2, ubiquitin-conjugating enzyme, putative [Arabidopsis thaliana]	146	1E-65
					>gb|ABA26987.1| TO38-23 [Taraxacum officinale]	138	1E-65
CB331071	2.04E-03	Mo17<B73=F1	1.53	10	>ref|XP_475712.1| putative GTP-binding protein Rab7a [Oryza sativa (japonicacultivar-group)] gb|AAT01314.1| putative GTP-binding protein Rab7a [Oryza sativa (japonica cultivar-group)]	206	1E-93
					>sp|Q40787|RAB7 PENCL Ras-related protein Rab7 (Possible apospory-associated protein)gb|AAA85273.1| possible apospory-associated protein	206	1E-93
					>gb|AAO67728.1| small GTP binding protein [Oryza sativa (indica cultivar-group)]	206	3E-92
					>sp|O24461|RAB7 PRUAR Ras-related protein Rab7gb|AAB71504.1| Rab7 GTP binding protein [Prunus armeniaca]	207	2E-86
					>emb|CAA98171.1| RAB7D [Lotus corniculatus var. japonicus]	207	6E-86
BM072807	2.04E-03	Mo17<B73=F1	2.03	10	>ref|NP_918332.1| B1110C07.23 [Oryza sativa (japonica cultivar-group)]dbj|BAB90622.1| putative zinc finger transcription factor ZFP30 [Oryza sativa (japonica cultivar-group)]	139	2E-61
					>gb|AAZ94630.1| zinc finger protein-like protein [Gossypium hirsutum]	139	2E-33
					>ref|XP_464544.1| zinc finger transcription factor ZFP30 [Oryza sativa (japonicacultivar-group)] ref|XP_507460.1| PREDICTED OJ1135_F06.29 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_506755.1| PREDICTED OJ1135_F06.29 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD16000.1| zinc finger transcription factor ZFP30 [Oryza sativa (japonica cultivar-group)] dbj|BAD15513.1| zinc finger transcription factor ZFP30 [Oryza sativa (japonica cultivar-group)]	166	4E-31
					>gb|AAO46040.1| zinc finger transcription factor ZFP30 [Oryza sativa (japonicacultivar-group)]	166	2E-30
					>gb|AAD46926.1| putative zinc finger protein [Oryza sativa]	145	1E-29
DV490715	2.05E-03	B73<F1=Mo17	1.33	3	>ref|NP_915675.1| putative protein kinase SPK-3 [Oryza sativa (japonicacultivar-group)] dbj|BAB89813.1| serine/threonine protein kinase SAPK4 [Oryza sativa (japonica cultivar-group)] dbj|BAB64101.1| serine/threonine protein kinase SAPK4 [Oryza sativa (japonica cultivar-group)] dbj|BAD18000.1| serine/threonine protein kinase SAPK4 [Oryza sativa (japonica cultivar-group)] sp|Q5N942|SAPK4_ORYSA Serine/threonine-protein kinase SAPK4 (Osmotic stress/abscisic acid-activated protein kinase 4)	360	1E-69
					>dbj|BAD82014.1| serine/threonine protein kinase SAPK4-like protein [Oryza sativa(japonica cultivar-group)] dbj|BAD81709.1| serine/threonine protein kinase SAPK4-like protein [Oryza sativa (japonica cultivar-group)]	168	1E-58
					>ref|XP_472550.1| OSJNBa0084A10.11 [Oryza sativa (japonica cultivar-group)]dbj|BAD18003.1| serine/threonine protein kinase SAPK7 [Oryza sativa (japonica cultivar-group)] sp|Q7XQP4|SAPK7 ORYSA Serine/threonine-protein kinase SAPK7 (Osmotic stress/abscisic acid-activated protein kinase 7)	359	8E-58
					>emb|CAE03037.3| OSJNBa0084A10.12 [Oryza sativa (japonica cultivar-group)]	407	8E-58
					>gb|AAU43772.1| putative salt-inducible protein kinase [Zea mays]	364	1E-57
CB351711	2.07E-03	B73<F1=Mo17	1.52	2	>emb|CAA42530.1| histone H2B [Triticum aestivum]sp|P27807|H2B1 WHEAT Histone H2B	152	2E-43
					>ref|XP_483094.1| putative Histone H2B.2 [Oryza sativa (japonica cultivar-group)]dbj|BAD09673.1| putative Histone H2B.2 [Oryza sativa (japonica cultivar-group)]	150	8E-43
					>sp|P54348|H2B5 MAIZE Histone H2Bgb|AAB04688.1| histone H2B	154	8E-43
					>sp|P05621|H2B2 WHEAT Histone H2B.2	149	2E-42
					>ref|NP 909263.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]dbj|BAB44008.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	153	2E-42
CB350867	2.07E-03	Mo17<B73=F1	1.65	10	>ref|XP 472424.1| OJ991214 12.11 [Oryza sativa (japonica cultivar-group)]emb|CAE01522.1| OJ991214 12.11 [Oryza sativa (japonica cultivar-group)]	116	4E-25
					>ref|XP_475631.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAV43925.1| unknown protein [Oryza sativa (japonica cultivar-group)] gb|AAT93913.1| unknown protein [Oryza sativa (japonica cultivar-group)]	117	3E-24

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>emb|CAH59408.1| hypothetical protein [Plantago major]	118	6E-20
					>dbj|BAD82674.1| unknown protein [Oryza sativa (japonica cultivar-group)]	118	2E-19
					>ref|XP 472425.1| OJ991214 12.12 [Oryza sativa (japonica cultivar-group)]emb|CAE01523.2| OJ991214 12.12 [Oryza sativa (japonica cultivar-group)]	123	2E-18
CB380869	2.08E-03	Mo17<B73=F1	1.42	10	>emb|CAA67225.1| ribosomal protein S21 [Zea mays]sp|Q41852|RS21 MAIZE 40S ribosomal protein S21	81	5E-38
					>emb|CAA70852.1| 40S ribosomal subunit protein S21 [Zea mays]	81	7E-37
					>dbj|BAA02158.1| 40S subunit ribosomal protein [Oryza sativa (japonicacultivar-group)] sp|P35687|RS21 ORYSA 40S ribosomal protein S21	82	2E-34
					>ref|XP_469197.1| 40S subunit ribosomal protein [Oryza sativa (japonicacultivar-group)] gb|AAP44638.1| 40S subunit ribosomal protein [Oryza sativa (japonica cultivar-group)]	82	5E-34
					>gb|AAU89141.1| 40S ribosomal protein S21, putative [Oryza sativa (japonicacultivar-group)]	119	8E-33
CD001603	2.10E-03	Mo17<B73=F1	1.44	10	>gb|AAV44171.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]gb|AAV43799.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	435	7E-39
					>ref|NP_190735.1| transporter [Arabidopsis thaliana]emb|CAB63153.1| putative protein [Arabidopsis thaliana] gb|AAL31927.1| AT3g51670/T18N14_50 [Arabidopsis thaliana] gb|AAN73306.1| At3g51670/T18N14 50 [Arabidopsis thaliana] sp|Q9SCU1|PATL6 ARATH Patellin-6	409	4E-25
					>emb|CAB43521.1| hypothetical protein [Arabidopsis thaliana]	147	4E-25
					>gb|AAV59419.1| putative cellular retinaldehyde-binding/triple function [Oryzasativa (japonica cultivar-group)] ref|XP_475265.1| putative cellular retinaldehyde-binding/triple function [Oryza sativa (japonica cultivar-group)]	585	2E-15
					>emb|CAB95829.1| hypothetical protein [Cicer arietinum]	482	3E-14
CB886363	2.11E-03	Mo17<B73=F1	1.3	11	>gb|AAT42201.1| gibberellin-stimulated protein [Oryza sativa (japonicacultivar-group)]	110	3E-34
					>dbj|BAD54389.1| putative gibberellin induced protein 3 [Oryza sativa (japonicacultivar-group)] dbj|BAD53514.1| putative gibberellin induced protein 3 [Oryza sativa (japonica cultivar-group)]	84	3E-34
					>gb|AAW83819.1| GASA2-like protein [Pelargonium zonale]	117	8E-28
					>emb|CAD10105.1| Gip1-like protein [Petunia x hybrida]	105	1E-27
					>emb|CAD10106.1| Gip1-like protein [Petunia x hybrida]	104	2E-27
CB351684	2.12E-03	Mo17<B73=F1	1.3	10	>dbj|BAD68228.1| leucine-rich repeat protein [Oryza sativa (japonicacultivar-group)] gb|AAO85403.1| leucine-rich repeat protein [Oryza sativa] gb|AAO85402.1| leucine-rich repeat protein [Oryza sativa]	213	1E-84
					>gb|AAO17321.1| floral organ regulator 1 [Oryza sativa (japonica cultivar-group)]	213	1E-81
					>gb|AAP23944.1| leucine-rich repeat protein [x Citrofortunella mitis]	228	1E-74
					>ref|NP_197608.1| protein binding [Arabidopsis thaliana]gb|AAM10104.1| unknown protein [Arabidopsis thaliana] gb|AAP13376.1| At5g21090 [Arabidopsis thaliana] gb|AAG40341.1| AT5g21090 [Arabidopsis thaliana] gb|AAK48970.1| Unknown protein [Arabidopsis thaliana] gb|AAO73897.1| leucine rich repeat protein (LRP), putative [Arabidopsis thaliana] gb|AAO00877.1| Unknown protein [Arabidopsis thaliana]	218	2E-72
					>emb|CAA64565.1| LRR protein [Lycopersicon esculentum]	221	3E-71
CD001573	2.16E-03	Mo17<B73=F1	1.4	11	>emb|CAB90214.1| putative elongation factor 1 beta [Hordeum vulgare subsp. vulgare]	226	6E-40
					>gb|AAR15081.1| translational elongation factor 1 subunit Bbeta [Pisum sativum]	231	4E-39
					>ref|XP_479153.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)]ref|XP_506463.1| PREDICTED P0616D06.117 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC16499.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)] dbj|BAA04903.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)] sp|Q40680|EF1D ORYSA Elongation factor 1-delta (EF-1-delta) (Elongation factor 1B-beta) (eEF-1B beta)	229	2E-38
					>gb|AAU89237.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)]dbj|BAA34599.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)] dbj|BAA34598.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)]	226	2E-38
					>gb|ABA81875.1| putative elongation factor 1B alpha-subunit0like [Solanumtuberosum] gb|ABA40427.1| unknown [Solanum tuberosum]	227	5E-38
DV943290	2.16E-03	B73=Mo17<F1	1.41	1	>ref|XP_463248.1| calcineurin B protein [Oryza sativa (japonica cultivar-group)]gb|AAR01663.1| calcineurin B protein [Oryza sativa (japonica cultivar-group)] gb|ABA54178.1| calcineurin B-like protein 3 [Oryza sativa (japonica cultivar-group)] gb|AAL31695.1| putative calcineurin B-like protein [Oryza sativa]	225	3E-51
					>gb|AAM91028.2| calcineurin B [Pisum sativum]gb|AAW73072.1| calcineurin B-like protein [Pisum sativum]	225	5E-51
					>gb|ABA54177.1| calcineurin B-like protein 2 [Oryza sativa (japonicacultivar-group)]	225	1E-49
					>gb|AAX20387.1| calcineurin B-like protein 3 [Gossypium hirsutum]	226	2E-49
					>ref|NP_200410.1| CBL2; calcium ion binding [Arabidopsis thaliana]gb|AAM98114.1| At5g55990/MDA7_3 [Arabidopsis thaliana] gb|AAK96497.1| AT5g55990/MDA7_3 [Arabidopsis thaliana] dbj|BAB09281.1| calcineurin B-like protein 2 [Arabidopsis thaliana] gb|AAC26009.1| calcineurin B-like protein 2 [Arabidopsis thaliana] sp|Q8LAS7|CNBL2 ARATH Calcineurin B-like protein 2 (SOS3-like calcium-binding protein 1)	226	2E-49
BM074404	2.16E-03	Mo17<B73=F1	3.33	10	>gb|AAL76334.1| putative G-box binding protein [Oryza sativa]dbj|BAD45657.1| G-box binding protein-like [Oryza sativa (japonica cultivar-group)] gb|AAB65433.1| HvB12D homolog [Oryza sativa]	89	5E-22
					>emb|CAA70936.1| B12Dg1 [Hordeum vulgare subsp. vulgare]emb|CAA54065.1| HvB12D [Hordeum vulgare subsp. vulgare]	87	3E-21
					>gb|AAD22104.1| B12D protein [Ipomoea batatas]	90	4E-17
					>ref|XP_477421.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]dbj|BAC84633.1| putative B12D protein [Oryza sativa (japonica cultivar-group)] dbj|BAD31625.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]	98	4E-15

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_190397.1| unknown protein [Arabidopsis thaliana]emb|CAB51061.1| B12D-like protein [Arabidopsis thaliana] gb|AAL91215.1| B12D-like protein [Arabidopsis thaliana] gb|AAN65070.1| B12D-like protein [Arabidopsis thaliana] pir||T13003 hypothetical protein T24C20.20 - Arabidopsis thaliana	88	4E-14
DV489637	2.16E-03	Mo17<B73=F1	1.76	10	>sp|Q43199|APT1 WHEAT Adenine phosphoribosyltransferase 1 (APRT)gb|AAA80609.1| adenine phosphoribosyltransferase form 1	181	7E-53
					>dbj|BAB08003.1| Adenine phosphoribosyltransferase [Hordeum vulgare subsp. vulgare]	181	9E-53
					>gb|ABA99757.1| adenine phosphoribosyltransferase, putative [Oryza sativa (japonicacultivar-group)]	240	5E-50
					>gb|AAP85303.1| adenine phosphoribosyltransferase [Brassica napus]	204	1E-47
					>gb|ABB86271.1| adenine phosphoribosyltransferase-like [Solanum tuberosum]	182	2E-46
BM073281	2.18E-03	F1=Mo17<B73	1.58	9	>ref|XP_463908.1| ubiquitin-conjugating enzyme [Oryza sativa (japonicacultivar-group)] dbj|BAD07595.1| ubiquitin-conjugating enzyme [Oryza sativa (japonica cultivar-group)] dbj|BAD08135.1| ubiquitin-conjugating enzyme [Oryza sativa (japonica cultivar-group)]	148	3E-50
					>gb|AAL99225.1| ubiquitin-conjugating enzyme E2 [Gossypium raimondii]gb|AAL99224.1| ubiquitin-conjugating enzyme E2 [Gossypium thurberi]	148	4E-48
					>gb|AAF24583.1| F22C12.2 [Arabidopsis thaliana]	146	6E-48
					>gb|AAL99223.1| ubiquitin-conjugating enzyme E2 [Gossypium arboreum]	148	6E-48
					>ref|NP_001031228.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme[Arabidopsis thaliana] ref|NP_564828.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme [Arabidopsis thaliana] gb|AAM91500.1| At1g64230/F22C12_17 [Arabidopsis thaliana] gb|AAM11574.1| ubiquitin conjugating enzyme UBC9A [Arabidopsis thaliana] gb|AAK60309.1| At1g64230/F22C12_17 [Arabidopsis thaliana] gb|AAY44867.1| ubiquitinating enzyme [Arabidopsis thaliana]	148	6E-48
DV490850	2.20E-03	Mo17<B73=F1	9.32	10	>ref|NP_922639.1| putative pectin acetylesterase [Oryza sativa (japonicacultivar-group)] gb|AAG13483.1| putative pectin acetylesterase [Oryza sativa (japonica cultivar-group)] gb|AAP54926.1| pectin acetylesterase, putative [Oryza sativa (japonica cultivar-group)]	394	3E-32
					>gb|AAG50747.1| pectinacetylesterase precursor, putative [Arabidopsis thaliana]	417	1E-22
					>gb|AAM74495.1| At1g57590/T8L23 6 [Arabidopsis thaliana]	423	1E-22
					>ref|NP 176072.3| carboxylic ester hydrolase [Arabidopsis thaliana]	444	1E-22
					>ref|NP_182216.1| carboxylic ester hydrolase [Arabidopsis thaliana]gb|AAC34238.1| putative pectinesterase [Arabidopsis thaliana] gb|AAK96575.1| At2g46930/F14M4.24 [Arabidopsis thaliana]	416	3E-21
DV621305	2.22E-03	B73<F1=Mo17	1.38	3	>ref|XP 481935.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD03782.1| unknown protein [Oryza sativa (japonica cultivar-group)]	534	2E-40
					>dbj|BAD82496.1| unknown protein [Oryza sativa (japonica cultivar-group)]	489	6E-34
					>ref|NP 917044.1| similar to Arabidopsis thaliana chromosome 1, At1g15060 [Oryzasativa (japonica cultivar-group)]	595	6E-34
					>emb|CAA03956.1| unnamed protein product [Hordeum vulgare subsp. vulgare]	108	7E-32
					>dbj|BAD44209.1| unknown protein [Arabidopsis thaliana]	394	2E-29
CB605123	2.23E-03	B73<F1=Mo17	1.44	3	>gb|AAO86709.1| tonoplast water channel [Zea mays]gb|AAC09245.1| tonoplast intrinsic protein; ZmTIP1 [Zea mays]	250	2E-57
					>emb|CAA56553.1| gamma-TIP-like protein [Hordeum vulgare subsp. vulgare]	250	3E-55
					>gb|AAD10494.1| gamma-type tonoplast intrinsic protein [Triticum aestivum]	250	3E-55
					>ref|XP_470213.1| Tonoplast intrinsic protein [Oryza sativa]gb|AAK98737.1| Tonoplast intrinsic protein [Oryza sativa] dbj|BAA05017.1| gamma-Tip [Oryza sativa] sp|P50156|TIP11 ORYSA Probable aquaporin TIP1.1 (Tonoplast intrinsic protein 1.1) (OsTIP1.1) (rTIP1)	250	3E-54
					>gb|AAX14478.1| putative tonoplast intrinsic protein [Gossypium hirsutum]	137	1E-50
CD650982	2.25E-03	Mo17<B73=F1	1.28	10	>dbj|BAD73480.1| putative ribosomal protein L37a [Oryza sativa (japonicacultivar-group)]	92	5E-47
					>ref|XP_475898.1| putative 60S ribosomal protein L37a [Oryza sativa (japonicacultivar-group)] gb|AAT58714.1| putative 60S ribosomal protein L37a [Oryza sativa (japonica cultivar-group)]	95	2E-46
					>ref|NP 916930.1| putative 60S ribosomal protein L37a [Oryza sativa (japonicacultivar-group)]	122	2E-46
					>emb|CAI48073.1| 60S ribosomal protein L37a [Capsicum chinense]	92	1E-45
					>emb|CAA10493.1| ribosomal protein L37A [Pseudotsuga menziesii]sp|Q9ZRS8|RL37A PSEMZ 60S ribosomal protein L37a	92	3E-45
BM073678	2.25E-03	F1=Mo17<B73	1.56	9	>gb|AAN77294.1| Unknown protein [Oryza sativa (japonica cultivar-group)]	91	2E-11
DV489748	2.26E-03	F1=Mo17<B73	1.5	9	ns		
CB381614	2.27E-03	Mo17<B73=F1	1.36	11	>ref|XP 482545.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD09833.1| unknown protein [Oryza sativa (japonica cultivar-group)]	250	2E-36
					>ref|NP 173724.2| unknown protein [Arabidopsis thaliana]gb|AAT68719.1| hypothetical protein At1g23110 [Arabidopsis thaliana]	248	3E-35
					>gb|AAX23759.1| hypothetical protein At1g23110 [Arabidopsis thaliana]	248	2E-34
					>gb|AAM66974.1| unknown [Arabidopsis thaliana]	244	1E-33
					>ref|NP_565005.1| unknown protein [Arabidopsis thaliana]gb|AAL85049.1| unknown protein [Arabidopsis thaliana] gb|AAK93674.1| unknown protein [Arabidopsis thaliana] gb|AAD55506.1| Unknown protein [Arabidopsis thaliana]	244	1E-33
CD670257	2.27E-03	Mo17<B73=F1	1.57	10	>ref|XP_477253.1| putative Sec13p [Oryza sativa (japonica cultivar-group)]dbj|BAD31963.1| putative Sec13p [Oryza sativa (japonica cultivar-group)] dbj|BAC82934.1| putative Sec13p [Oryza sativa (japonica cultivar-group)]	315	4E-70
					>ref|NP_909967.1| putative coat protein complex II (COPII) component [Oryza sativa(japonica cultivar-group)] gb|AAP46251.1| putative protein-transport protein [Oryza sativa (japonica cultivar-group)] gb|AAO39855.1| putative coat protein complex II (COPII) component [Oryza sativa (japonica cultivar-group)]	301	8E-63

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_180566.1| nucleotide binding [Arabidopsis thaliana]gb|AAM70557.1| At2g30050/F23F1.3 [Arabidopsis thaliana] gb|AAM14986.1| putative protein transport protein SEC13 [Arabidopsis thaliana] gb|AAC16967.1| putative protein transport protein SEC13 [Arabidopsis thaliana] gb|AAL06565.1| At2g30050/F23F1.3 [Arabidopsis thaliana]	302	2E-50
					>ref|NP_186783.1| nucleotide binding [Arabidopsis thaliana]ref|NP_001030616.1| nucleotide binding [Arabidopsis thaliana] gb|AAF03492.1| putative protein transport protein SEC13 [Arabidopsis thaliana] gb|AAL34253.1| putative transport protein SEC13 [Arabidopsis thaliana] gb|AAK44077.1| putative transport protein SEC13 [Arabidopsis thaliana]	302	3E-50
					>gb|AAM65095.1| putative protein transport protein SEC13 [Arabidopsis thaliana]	302	6E-49
DV489676	2.28E-03	Mo17<B73=F1	6.36	10	>ref|XP_473874.1| OSJNBa0070C17.22 [Oryza sativa (japonica cultivar-group)]emb|CAE05215.3| OSJNBa0070C17.22 [Oryza sativa (japonica cultivar-group)]	438	1E-25
DV491736	2.29E-03	Mo17<B73=F1	1.61	11	>dbj|BAD73259.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD73143.1| unknown protein [Oryza sativa (japonica cultivar-group)]	266	8E-32
					>ref|NP_918653.1| P0520B06.19 [Oryza sativa (japonica cultivar-group)]	258	8E-32
					>ref|NP_192449.1| unknown protein [Arabidopsis thaliana]ref|NP_001031586.1| unknown protein [Arabidopsis thaliana] emb|CAB81082.1| putative protein [Arabidopsis thaliana] gb|AAQ62419.1| At4g05400 [Arabidopsis thaliana] dbj|BAD43333.1| putative protein [Arabidopsis thaliana]	250	1E-20
					>ref|NP_193846.1| unknown protein [Arabidopsis thaliana]emb|CAB79114.1| hypothetical protein [Arabidopsis thaliana] emb|CAA17533.1| hypothetical protein [Arabidopsis thaliana]	228	2E-19
DV494333	2.31E-03	B73=Mo17<F1	1.34	12	>dbj|BAC78592.1| pre-mRNA splicing factor [Oryza sativa (japonica cultivar-group)]	232	3E-15
					>gb|ABA99674.1| RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain), putative[Oryza sativa (japonica cultivar-group)]	263	3E-15
					>ref|XP_464852.1| putative pre-mRNA splicing factor [Oryza sativa (japonicacultivar-group)] ref|XP_506764.1| PREDICTED OJ1113_G05.32 gene product [Oryza sativa (japonica cultivar-group)] gb|AAG43284.2| pre-mRNA splicing factor [Oryza sativa] dbj|BAD19762.1| putative pre-mRNA splicing factor [Oryza sativa (japonica cultivar-group)] dbj|BAD19168.1| putative pre-mRNA splicing factor [Oryza sativa (japonica cultivar-group)]	265	1E-14
					>gb|AAX95358.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	384	2E-6
					>gb|AAX95271.1| RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain), putative[Oryza sativa (japonica cultivar-group)] gb|ABA95508.1| RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain), putative [Oryza sativa (japonica cultivar-group)]	502	2E-6
CD670200	2.33E-03	Mo17<B73=F1	1.29	10	>ref|NP_909904.1| putative clathrin assembly protein [Oryza sativa]gb|AAL35902.1| clathrin assembly protein AP19-like protein [Oryza sativa] gb|AAK72894.1| putative clathrin assembly protein [Oryza sativa]	182	2E-85
					>gb|AAB39510.1| AP-1 Golgi-related complex component; clathrin coated vesicles;clathrin assembly protein	161	5E-81
					>ref|NP_565415.1| AP19 [Arabidopsis thaliana]gb|AAM61683.1| clathrin assembly small subunit protein AP19 [Arabidopsis thaliana] gb|AAB86515.1| clathrin assembly protein AP19, small subunit [Arabidopsis thaliana]	161	7E-80
					>ref|NP_195267.1| unknown protein [Arabidopsis thaliana]emb|CAB80258.1| clathrin assembly protein AP19 homolog [Arabidopsis thaliana] emb|CAA18728.1| clathrin assembly protein AP19 homolog [Arabidopsis thaliana] gb|AAM64317.1| clathrin assembly protein AP19 homolog [Arabidopsis thaliana] gb|AAO50497.1| putative clathrin assembly protein AP19 homolog [Arabidopsis thaliana] dbj|BAC43580.1| putative clathrin assembly protein AP19 [Arabidopsis thaliana] gb|AAB96889.1| clathrin assembly protein AP19 homolog [Arabidopsis thaliana]	162	2E-79
					>gb|AAB96888.1| clathrin assembly protein AP19 homolog [Arabidopsis thaliana]gb|AAB96887.1| clathrin assembly protein AP19 [Arabidopsis thaliana]	161	3E-79
CB329753	2.34E-03	B73=Mo17<F1	1.35	12	>sp|P23346|SODC5 MAIZE Superoxide dismutase [Cu-Zn] 4AP	152	4E-77
					>emb|CAB57992.1| superoxide dismutase-4AP [Zea mays]sp|P23345|SODC4 MAIZE Superoxide dismutase [Cu-Zn] 4A	152	4E-76
					>emb|CAB57993.1| superoxide dismutase-4A [Zea mays]gb|AAB49913.1| superoxide dismutase 4A	152	5E-75
					>sp|P28757|SODC2_ORYSA Superoxide dismutase [Cu-Zn] 2gb|AAC14465.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00800.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)]	152	8E-71
					>gb|AAY56345.1| cytoplasmic copper/zinc-superoxide dismutase [Oryza sativa (indicacultivar-group)] sp|P28756|SODC1_ORYSA Superoxide dismutase [Cu-Zn] 1 gb|AAC14464.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00799.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)] prf||2111424A Cu/Zn superoxide dismutase	152	9E-70
DV493630	2.34E-03	B73<F1=Mo17	2.21	3	>ref|XP_506961.1| PREDICTED P0516G10.12-1 gene product [Oryza sativa (japonicacultivar-group)] ref|XP_467707.1| putative proline-rich protein APG [Oryza sativa (japonica cultivar-group)] dbj|BAD15755.1| putative proline-rich protein APG [Oryza sativa (japonica cultivar-group)]	383	1E-36
					>gb|ABA99589.1| GDSL-like Lipase/Acylhydrolase, putative [Oryza sativa (japonicacultivar-group)]	402	2E-35
					>dbj|BAD61697.1| GDSL-lipase-like [Oryza sativa (japonica cultivar-group)]	381	2E-28
					>dbj|BAD28139.1| putative anter-specific proline-rich protein APG [Oryza sativa(japonica cultivar-group)] dbj|BAD28305.1| putative anter-specific proline-rich protein APG [Oryza sativa (japonica cultivar-group)]	362	4E-27
					>ref|XP_463902.1| putative GDSL-motif lipase/hydrolase protein [Oryza sativa(japonica cultivar-group)] dbj|BAD08129.1| putative GDSL-motif lipase/hydrolase protein [Oryza sativa (japonica cultivar-group)]	378	3E-26
DV621336	2.35E-03	B73=F1<Mo17	1.34	4	>gb|AAO72607.1| putative ubiquitin-specific protease [Oryza sativa (japonicacultivar-group)]	842	9E-33
					>dbj|BAD72518.1| putative ubiquitin-specific protease 23 [Oryza sativa (japonicacultivar-group)]	874	9E-33
					>dbj|BAD72517.1| putative ubiquitin-specific protease 23 [Oryza sativa (japonicacultivar-group)]	899	9E-33
					>dbj|BAD11338.1| BRI1-KD interacting protein 110 [Oryza sativa (japonicacultivar-group)]	517	9E-33
					>ref|XP_468249.1| putative hematopoietic-specific IL-2 deubiquitinating enzyme [Oryzasativa (japonica cultivar-group)] dbj|BAD19267.1| putative hematopoietic-specific IL-2 deubiquitinating enzyme [Oryza sativa (japonica cultivar-group)]	1185	4E-19

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
DV495488	2.36E-03	Mo17<B73=F1	1.57	11	ns		
DV551158	2.38E-03	B73<F1=Mo17	1.65	3	>emb|CAA49199.1| alanine aminotransferase [Panicum miliaceum]sp|P34106|ALA2_PANMI Alanine aminotransferase 2 (GPT) (Glutamic--pyruvic transaminase 2) (Glutamic--alanine transaminase 2) (ALAAT-2)	482	4E-17
					>gb|AAC62456.1| alanine aminotransferase [Zea mays]	482	6E-16
					>ref|NP_921266.1| putative alanine aminotransferase [Oryza sativa (japonicacultivar-group)] gb|AAK52114.1| Putative alanine aminotransferase [Oryza sativa (japonica cultivar-group)]	484	6E-15
					>gb|ABB47494.1| alanine aminotransferase [Oryza sativa (japonica cultivar-group)]dbj|BAA77261.1| alanine aminotransferase [Oryza sativa] dbj|BAA77260.1| alanine aminotransferase [Oryza sativa]	483	6E-15
					>emb|CAA81231.1| alanine aminotransferase [Hordeum vulgare subsp. vulgare]sp|P52894|ALA2_HORVU Alanine aminotransferase 2 (GPT) (Glutamic--pyruvic transaminase 2) (Glutamic--alanine transaminase 2) (ALAAT-2)	482	1E-14
DV491016	2.38E-03	Mo17<B73=F1	1.6	10	>ref|XP_466921.1| putative ubiquitin-conjugating enzyme E2 [Oryza sativa (japonicacultivar-group)] dbj|BAD25314.1| putative ubiquitin-conjugating enzyme E2 [Oryza sativa (japonica cultivar-group)] dbj|BAD25096.1| putative ubiquitin-conjugating enzyme E2 [Oryza sativa (japonica cultivar-group)]	157	2E-74
					>ref|NP_001031939.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme[Arabidopsis thaliana] ref|NP_568476.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme [Arabidopsis thaliana] gb|AAM60888.1| E2, ubiquitin-conjugating enzyme, putative [Arabidopsis thaliana] gb|AAY44861.1| ubiquitinating enzyme [Arabidopsis thaliana]	157	2E-71
					>ref|XP_643940.1| hypothetical protein DDB0167874 [Dictyostelium discoideum]gb|AAO51851.1| similar to Arabidopsis thaliana (Mouse-ear cress). E2, ubiquitin-conjugating enzyme, putative [Dictyostelium discoideum] gb|EAL70049.1| hypothetical protein DDB0167874 [Dictyostelium discoideum]	149	2E-46
					>gb|AAN16047.1| ubiquitin-conjugating enzyme E2 [Pavlova lutheri]	166	5E-45
					>emb|CAI74825.1| ubiquitin-conjugating enzyme e2, putative [Theileria annulata]ref|XP_952557.1| ubiquitin-conjugating enzyme E2 [Theileria annulata strain Ankara]	157	6E-43
CB240136	2.42E-03	F1=Mo17<B73	1.36	9	ns		
DV491385	2.42E-03	Mo17<B73=F1	3.81	10	>ref|NP_915308.1| putative GDSL-motif lipase/hydrolase [Oryza sativa (japonicacultivar-group)] dbj|BAB68101.1| putative family II lipase EXL1 [Oryza sativa (japonica cultivar-group)]	350	6E-63
					>ref|XP_475407.1| putative GDSL-motif lipase/hydrolase [Oryza sativa (japonicacultivar-group)] gb|AAT47006.1| putative GDSL-motif lipase/hydrolase [Oryza sativa (japonica cultivar-group)]	360	7E-34
					>gb|AAM64923.1| proline-rich protein, putative [Arabidopsis thaliana]	360	7E-34
					>ref|NP_176139.1| RXF26; carboxylic ester hydrolase/ hydrolase, acting on ester bonds[Arabidopsis thaliana] gb|AAG50646.1| proline-rich protein, putative [Arabidopsis thaliana] dbj|BAB83874.1| prolin-rich protein [Arabidopsis thaliana]	360	7E-34
					>dbj|BAA88267.1| RXF26 [Arabidopsis thaliana]	360	2E-33
BM075185	2.42E-03	Mo17<B73=F1	2.03	10	ns		
CB833451	2.44E-03	Mo17<B73=F1	1.21	10	>gb|AAU10802.1| 'putative endo-1,3;1,4-beta-D-glucanase' [Oryza sativa (japonicacultivar-group)]	240	2E-54
					>gb|AAU10803.1| 'putative endo-1,3;1,4-beta-D-glucanase' [Oryza sativa (japonicacultivar-group)]	239	1E-48
					>ref|NP_566731.1| hydrolase [Arabidopsis thaliana]gb|AAK48958.1| Unknown protein [Arabidopsis thaliana]	239	7E-41
					>dbj|BAB02775.1| unnamed protein product [Arabidopsis thaliana]	232	7E-41
					>gb|AAN65058.1| Unknown protein [Arabidopsis thaliana]	239	7E-41
BM079816	2.44E-03	Mo17<B73=F1	1.56	10	ns		
BG841386	2.45E-03	Mo17<B73=F1	1.69	10	>dbj|BAD52953.1| unknown protein [Oryza sativa (japonica cultivar-group)]	783	9E-9
					>dbj|BAD52952.1| unknown protein [Oryza sativa (japonica cultivar-group)]	895	9E-9
					>ref|NP_916345.1| P0490D09.22 [Oryza sativa (japonica cultivar-group)]	1194	9E-9
DV621246	2.46E-03	B73=F1<Mo17	1.41	4	>ref|XP_474777.1| OSJNBa0040D17.13 [Oryza sativa (japonica cultivar-group)]emb|CAE04544.2| OSJNBa0040D17.13 [Oryza sativa (japonica cultivar-group)]	964	2E-90
					>ref|NP_921690.1| putative ABC transporter [Oryza sativa (japonica cultivar-group)]	908	1E-65
					>gb|ABB47709.1| ABC transporter, putative [Oryza sativa (japonica cultivar-group)]gb|ABB47708.1| ABC transporter, putative [Oryza sativa (japonica cultivar-group)]	897	1E-65
					>gb|AAX95832.1| ABC transporter-like protein [Oryza sativa (japonica cultivar-group)]	1101	3E-64
					>gb|AAX92830.1| hypothetical protein LOC_Os11g22350 [Oryza sativa (japonicacultivar-group)] gb|ABA93154.1| hypothetical protein LOC_Os11g22350 [Oryza sativa (japonica cultivar-group)]	1073	3E-64
BM078695	2.51E-03	Mo17<B73=F1	1.32	11	>gb|AAV31238.1| putative 26S proteasome non-ATPase regulatory subunit 14 [Oryzasativa (japonica cultivar-group)]	307	2E-50
					>ref|NP_912909.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]dbj|BAA88535.1| putative Pad1 [Oryza sativa (japonica cultivar-group)] dbj|BAB78489.1| 26S proteasome regulatory particle non-ATPase subunit11 [Oryza sativa (japonica cultivar-group)]	307	8E-50
					>ref|NP_197745.1| unknown protein [Arabidopsis thaliana]gb|AAP86672.1| 26S proteasome subunit RPN11 [Arabidopsis thaliana] gb|AAP86671.1| 26S proteasome subunit RPN11a [Arabidopsis thaliana] gb|AAP86670.1| 26S proteasome subunit RPN11A [Arabidopsis thaliana] gb|AAM14268.1| putative 26S proteasome, non-ATPase regulatory subunit [Arabidopsis thaliana] gb|AAL49768.1| putative 26S proteasome, non-ATPase regulatory subunit [Arabidopsis thaliana] dbj|BAA97246.1| 26S proteasome, non-ATPase regulatory subunit [Arabidopsis thaliana] sp|Q9LT08|PSDE_ARATH 26S proteasome non-ATPase regulatory subunit 14 (26S proteasome regulatory subunit rpn11)	308	5E-47

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|AAM64349.1| 26S proteasome non-ATPase regulatory subunit [Arabidopsis thaliana]	308	5E-47
					>ref|XP 780027.1| PREDICTED: similar to proteasome (prosome, macropain) 26S subunit,non-ATPase, 14 isoform 1 [Strongylocentrotus purpuratus]	311	1E-32
DV622044	2.52E-03	B73<F1=Mo17	1.54	3	>ref|XP 480594.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]dbj|BAD05323.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	128	7E-36
					>ref|XP 469591.1| expressed protein [Oryza sativa (japonica cultivar-group)]gb|AAR01643.1| expressed protein [Oryza sativa (japonica cultivar-group)]	95	1E-35
					>ref|NP 568055.1| unknown protein [Arabidopsis thaliana]	86	2E-25
					>gb|AAM62578.1| unknown [Arabidopsis thaliana]	86	4E-25
					>ref|NP_187208.1| unknown protein [Arabidopsis thaliana]gb|AAR92313.1| At3g05570 [Arabidopsis thaliana] gb|AAF26140.1| unknown protein [Arabidopsis thaliana] gb|AAR24155.1| At3g05570 [Arabidopsis thaliana]	90	1E-23
CA829827	2.53E-03	Mo17<B73=F1	1.34	10	>gb|ABB02647.1| unknown [Solanum tuberosum]gb|ABA46758.1| unknown [Solanum tuberosum]	130	2E-66
					>ref|NP_973783.1| RPS15A (RIBOSOMAL PROTEIN S15A); structural constituent of ribosome[Arabidopsis thaliana] ref|NP_172256.1| RPS15A (RIBOSOMAL PROTEIN S15A); structural constituent of ribosome [Arabidopsis thaliana] ref|NP_200793.1| structural constituent of ribosome [Arabidopsis thaliana] gb|AAN31818.1| putative cytoplasmic ribosomal protein S15a [Arabidopsis thaliana] gb|AAG48810.1| putative ribosomal protein S15 [Arabidopsis thaliana] gb|AAL34202.1| putative cytoplasmic ribosomal protein S15a [Arabidopsis thaliana] gb|AAK93717.1| putative ribosomal protein S15 [Arabidopsis thaliana] gb|AAK59661.1| putative cytoplasmic ribosomal protein S15a [Arabidopsis thaliana] gb|AAK25994.1| putative ribosomal protein S15 [Arabidopsis thaliana] gb|AAM10251.1| similar to 40S ribosomal protein S15A [Arabidopsis thaliana] gb|AAM10034.1| similar to 40S ribosomal protein S15A [Arabidopsis thaliana] gb|AAK68770.1| Putative 40S ribosomal protein S15A [Arabidopsis thaliana] gb|AAK62367.1| 40S ribosomal protein S15A [Arabidopsis thaliana]	130	2E-66
					>emb|CAA42599.1| r-protein BnS15a [Brassica napus]sp|Q00332|RS15A BRANA 40S ribosomal protein S15a (PPCB8)	130	6E-66
					>dbj|BAA89231.1| wrp15a [Citrullus lanatus]	130	1E-65
					>ref|NP_190190.1| structural constituent of ribosome [Arabidopsis thaliana]emb|CAB90931.1| cytoplasmic ribosomal protein S15a-like [Arabidopsis thaliana] gb|AAM14312.1| putative cytoplasmic ribosomal protein S15a [Arabidopsis thaliana] gb|AAK76511.1| putative cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]	130	2E-65
DV942741	2.54E-03	F1=Mo17<B73	1.76	9	>gb|AAV64237.1| putative alanine aminotransferase [Zea mays]	516	6E-47
					>gb|AAV64199.1| putative alanine aminotransferase [Zea mays]	516	1E-46
					>ref|XP_479171.1| putative alanine aminotransferase [Oryza sativa (japonicacultivar-group)] dbj|BAC79995.1| putative alanine aminotransferase [Oryza sativa (japonica cultivar-group)] dbj|BAC79866.1| putative alanine aminotransferase [Oryza sativa (japonica cultivar-group)]	486	2E-45
					>emb|CAA49199.1| alanine aminotransferase [Panicum miliaceum]sp|P34106|ALA2_PANMI Alanine aminotransferase 2 (GPT) (Glutamic--pyruvic transaminase 2) (Glutamic--alanine transaminase 2) (ALAAT-2)	482	4E-41
					>gb|AAK59591.2| putative alanine aminotransferase [Arabidopsis thaliana]	532	4E-40
CD484747	2.55E-03	Mo17<B73=F1	1.37	10	>ref|XP_464690.1| Elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]dbj|BAD17615.1| Elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)] sp|Q9ZRI7|EF1G ORYSA Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) dbj|BAA34206.1| elongation factor 1B gamma [Oryza	418	5E-86
					>gb|AAO72574.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]	409	1E-85
					>ref|XP_464689.1| putative elongation factor 1-gamma [Oryza sativa (japonicacultivar-group)] dbj|BAD17614.1| putative elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]	414	1E-85
					>gb|AAO72563.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]	413	8E-85
					>dbj|BAD61932.1| putative elongation factor 1 gamma [Oryza sativa (japonicacultivar-group)] dbj|BAD61828.1| putative elongation factor 1 gamma [Oryza sativa (japonica cultivar-group)]	416	8E-85
DV492787	2.55E-03	B73<F1=Mo17	1.78	3	>dbj|BAD45275.1| putative 24 kDa seed maturation protein [Oryza sativa (japonicacultivar-group)]	265	3E-38
					>gb|ABB51093.1| reticulon [Hordeum vulgare]	204	5E-38
					>dbj|BAD27895.1| putative 24 kDa seed maturation protein [Oryza sativa (japonicacultivar-group)]	230	8E-36
					>ref|NP_913448.1| P0492F05.25 [Oryza sativa (japonica cultivar-group)]dbj|BAB32723.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAB92114.1| unknown protein [Oryza sativa (japonica cultivar-group)]	279	7E-26
					>ref|NP_192861.1| unknown protein [Arabidopsis thaliana]emb|CAB81223.1| putative protein [Arabidopsis thaliana] emb|CAB51406.1| putative protein [Arabidopsis thaliana] gb|AAK59408.1| unknown protein [Arabidopsis thaliana] gb|AAL14401.1| AT4g11220/F8L21_10 [Arabidopsis thaliana] gb|AAK82535.1| AT4g11220/F8L21 10 [Arabidopsis thaliana] gb|AAM64366.1| unknown [Arabidopsis thaliana] gb|AAN86201.1| unknown protein [Arabidopsis thaliana]	271	1E-24
DV495145	2.56E-03	Mo17<B73=F1	1.46	11	ns		
DV494154	2.57E-03	B73<F1=Mo17	1.74	2	>gb|AAF13094.1| unknown protein [Arabidopsis thaliana]gb|AAF21186.1| unknown protein [Arabidopsis thaliana]	196	3E-26
					>ref|NP_566319.1| unknown protein [Arabidopsis thaliana]ref|NP_850538.1| unknown protein [Arabidopsis thaliana] gb|AAL47395.1| unknown protein [Arabidopsis thaliana] gb|AAL16180.1| At3g07760/F17A17.10 [Arabidopsis thaliana] gb|AAK96782.1| Unknown protein [Arabidopsis thaliana] gb|AAM66036.1| unknown [Arabidopsis thaliana]	125	3E-26
					>gb|ABA99120.1| AC009176 putative heat-shock protein [Oryza sativa (japonicacultivar-group)]	1210	4E-7
CD527707	2.60E-03	Mo17<B73=F1	1.43	10	>gb|AAU44063.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	207	1E-52
					>dbj|BAD87014.1| RING zinc finger protein-like [Oryza sativa (japonicacultivar-group)]	197	4E-48
					>ref|NP 916004.1| OSJNBb0021A09.3 [Oryza sativa (japonica cultivar-group)]	238	4E-48

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_182139.1| protein binding / ubiquitin-protein ligase/ zinc ion binding[Arabidopsis thaliana] gb|AAC62890.1| hypothetical protein [Arabidopsis thaliana] gb|AAL69457.1| At2g46160/T3F17.19 [Arabidopsis thaliana] sp|O82353|ATL2M ARATH RING-H2 finger protein ATL2M	214	2E-38
					>ref|NP_191714.1| protein binding / ubiquitin-protein ligase/ zinc ion binding[Arabidopsis thaliana] emb|CAB71085.1| putative protein [Arabidopsis thaliana] dbj|BAD95337.1| hypothetical protein [Arabidopsis thaliana] gb|AAM51602.1| AT3g61550/F2A19_150 [Arabidopsis thaliana] gb|AAL16112.1| AT3g61550/F2A19 150 [Arabidopsis thaliana] sp|Q9M313|ATL3K ARATH RING-H2 finger protein ATL3K	212	3E-36
BM338902	2.61E-03	Mo17<B73=F1	4.53	10	>gb|AAT94020.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAT93960.1| unknown protein [Oryza sativa (japonica cultivar-group)]	316	5E-12
CB604485	2.63E-03	Mo17<B73=F1	1.54	11	ns		
CD573493	2.65E-03	Mo17<B73=F1	1.28	10	>gb|AAV36518.1| vacuolar ATPase subunit c isoform [Pennisetum glaucum]gb|AAL08022.1| vacuolar H+-ATPase 16 kDa proteolipid subunit c [Pennisetum glaucum]	165	2E-44
					>gb|AAK91135.1| V-ATPase subunit c [Porteresia coarctata]gb|ABA95923.1| V-type ATPase, C subunit [Oryza sativa (japonica cultivar-group)]	165	2E-44
					>gb|AAX93004.1| V-type ATPase, C subunit, putative [Oryza sativa (japonicacultivar-group)] sp|Q40635|VATL_ORYSA Vacuolar ATP synthase 16 kDa proteolipid subunit gb|ABA91617.1| V-type ATPase, C subunit, putative [Oryza sativa (japonica cultivar-group)] gb|AAA68175.1| H+-ATPase	165	2E-44
					>gb|AAU44174.1| putative vacuolar ATP synthase 16 kDa proteolipid subunit [Oryzasativa (japonica cultivar-group)]	166	6E-44
					>ref|XP_466150.1| putative Vacuolar ATP synthase 16 kDa proteolipid subunit [Oryzasativa (japonica cultivar-group)] dbj|BAD33262.1| putative Vacuolar ATP synthase 16 kDa proteolipid subunit [Oryza sativa (japonica cultivar-group)] dbj|BAD16200.1| putative Vacuolar ATP synthase 16 kDa proteolipid subunit [Oryza sativa (japonica cultivar-group)]	167	6E-44
BM338817	2.66E-03	Mo17<B73=F1	9.79	10	ns		
BG840897	2.67E-03	F1=Mo17<B73	1.57	9	>ref|XP_468227.1| putative tumor differentially expressed protein 1 [Oryza sativa(japonica cultivar-group)] ref|XP_507542.1| PREDICTED OJ1249_F12.26 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_507541.1| PREDICTED OJ1249_F12.26 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_507023.1| PREDICTED OJ1249_F12.26 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD19186.1| putative tumor differentially expressed protein 1 [Oryza sativa (japonica cultivar-group)] dbj|BAD19654.1| putative tumor differentially expressed protein 1 [Oryza sativa (japonica cultivar-group)]	414	3E-41
					>ref|NP_173069.1| unknown protein [Arabidopsis thaliana]gb|AAF18512.1| Contains similarity to gb|AF181686 membrane protein TMS1d from Drosophila melanogaster. ESTs gb|R64994, gb|AI994832, gb|Z47674 come from this gene. [Arabidopsis thaliana]	412	8E-37
					>ref|XP_468965.1| putative membrane protein [Oryza sativa (japonica cultivar-group)]gb|AAO73245.1| putative membrane protein [Oryza sativa (japonica cultivar-group)]	417	5E-28
					>gb|AAF30310.1| hypothetical protein [Arabidopsis thaliana]	315	8E-26
					>dbj|BAD94992.1| hypothetical protein [Arabidopsis thaliana]	57	8E-26
BM334653	2.68E-03	F1=Mo17<B73	1.39	9	>emb|CAA68419.1| ribulose 1,5-bisphosphate carboxylase/oxygenase [Zea mays]	169	2E-9
					>emb|CAA29784.1| ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor [Zea mays]sp|P05348|RBS_MAIZE Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) dbj|BAA00120.1| ribulose 1,5-bisphosphate carboxylase small subunit [Zea mays] prf||1312317A ribulosebisphosphate carboxylase	170	2E-9
					>emb|CAA70416.1| rubisco small subunit [Zea mays]	170	1E-8
					>gb|AAF06100.1| ribulose 1,5-bisphosphate carboxylase small chain precursor[Manihot esculenta]	184	3E-6
					>gb|AAF06101.1| ribulose 1,5-bisphosphate carboxylase small chain precursor[Manihot esculenta] gb|AAF06098.1| ribulose 1,5-bisphosphate carboxylase small chain precursor [Manihot esculenta]	184	3E-6
CB815525	2.69E-03	F1=Mo17<B73	1.89	9	>emb|CAA82751.1| protein kinase C inhibitor [Zea mays]sp|P42856|ZB14 MAIZE 14 kDa zinc-binding protein (Protein kinase C inhibitor) (PKCI)	128	4E-51
					>sp|P42855|ZB14 BRAJU 14 kDa zinc-binding protein (Protein kinase C inhibitor) (PKCI)gb|AAA18397.1| putative protein kinase C inhibitor	113	2E-43
					>emb|CAB88052.1| protein kinase C inhibitor-like protein [Arabidopsis thaliana]gb|AAK76535.1| putative protein kinase C inhibitor [Arabidopsis thaliana] gb|AAM63920.1| protein kinase C inhibitor-like protein [Arabidopsis thaliana]	129	5E-43
					>ref|NP 567038.1| protein kinase C binding / zinc ion binding [Arabidopsis thaliana]gb|AAN86189.1| putative protein kinase C inhibitor [Arabidopsis thaliana]	147	5E-43
					>gb|ABC75370.1| Histidine triad (HIT) protein [Medicago truncatula]	182	2E-38
CD001379	2.72E-03	Mo17<B73=F1	1.32	10	>ref|XP_468756.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)] ref|XP_468752.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] gb|AAP20855.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] gb|AAP20842.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] sp|P40978|RS19 ORYSA 40S ribosomal protein S19	146	1E-70
					>gb|AAW34237.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	144	6E-68
					>gb|AAW34236.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	166	4E-67
					>gb|AAW34240.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	122	2E-60
					>gb|ABB87116.1| 40S ribosomal protein S19-like [Solanum tuberosum]	143	4E-60
DV550717	2.73E-03	B73<F1=Mo17	1.69	2	>ref|XP_464513.1| putative BRI1-KD interacting protein [Oryza sativa (japonicacultivar-group)] dbj|BAD15848.1| putative BRI1-KD interacting protein [Oryza sativa (japonica cultivar-group)]	395	3E-37
					>dbj|BAD11346.1| BRI1-KD interacting protein 118 [Oryza sativa (japonicacultivar-group)]	334	3E-37
					>dbj|BAD36112.1| BRI1-KD interacting protein 118-like [Oryza sativa (japonicacultivar-group)]	145	1E-28
					>dbj|BAD36111.1| putative BRI1-KD interacting protein 118 [Oryza sativa (japonicacultivar-group)]	372	1E-28

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

<table>
<thead>
<tr><th>GenBank accession no.</th><th>Overall P value</th><th>Significant pattern</th><th>Fold change†</th><th>Sector‡</th><th>BLAST annotation*</th><th>Score</th><th>E value</th></tr>
</thead>
<tbody>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_567893.1| unknown protein [Arabidopsis thaliana]gb|AAM44942.1| unknown protein [Arabidopsis thaliana] gb|AAK59686.1| unknown protein [Arabidopsis thaliana]</td><td>437</td><td>2E-20</td></tr>
<tr><td>CD568511</td><td>2.74E-03</td><td>Mo17<B73=F1</td><td>1.28</td><td>10</td><td>>ref|XP_483494.1| nuclear transport factor 2 (NTF-2) [Oryza sativa (japonicacultivar-group)] dbj|BAD11649.1| nuclear transport factor 2 (NTF-2) [Oryza sativa (japonica cultivar-group)] sp|Q9XJ54|NTF2_ORYSA Nuclear transport factor 2 (NTF-2) dbj|BAA81910.1| nuclear transport factor 2 (NTF2) [Oryza sativa (japonica cultivar-group)]</td><td>122</td><td>6E-42</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_174118.1| protein transporter [Arabidopsis thaliana]gb|AAG51491.1| nuclear transport factor 2, putative [Arabidopsis thaliana] sp|Q9C7F5|NTF2_ARATH Nuclear transport factor 2 (NTF-2)</td><td>126</td><td>5E-33</td></tr>
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<tr><td>CB617229</td><td>2.74E-03</td><td>B73=Mo17<F1</td><td>1.3</td><td>12</td><td>>sp|P11428|SODC2 MAIZE Superoxide dismutase [Cu-Zn] 2gb|AAA33511.1| SOD2 protein gb|AAA33510.1| superoxide dismutase 2</td><td>151</td><td>2E-84</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAP85303.1| adenine phosphoribosyltransferase [Brassica napus]</td><td>204</td><td>4E-48</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|ABB86271.1| adenine phosphoribosyltransferase-like [Solanum tuberosum]</td><td>182</td><td>4E-47</td></tr>
<tr><td>BM333081</td><td>2.81E-03</td><td>Mo17<B73=F1</td><td>1.69</td><td>10</td><td>ns</td><td></td><td></td></tr>
<tr><td>DV549655</td><td>2.82E-03</td><td>B73<F1=Mo17</td><td>1.37</td><td>3</td><td>>dbj|BAD73106.1| RNA-binding protein -like [Oryza sativa (japonica cultivar-group)]dbj|BAD73038.1| RNA-binding protein -like [Oryza sativa (japonica cultivar-group)]</td><td>308</td><td>2E-8</td></tr>
<tr><td>DV622390</td><td>2.82E-03</td><td>B73<F1=Mo17</td><td>1.49</td><td>3</td><td>>dbj|BAD81289.1| unknown protein [Oryza sativa (japonica cultivar-group)]</td><td>487</td><td>9E-65</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP 913512.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]</td><td>210</td><td>2E-62</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP 188244.2| nucleic acid binding [Arabidopsis thaliana]</td><td>449</td><td>3E-48</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAB01263.1| unnamed protein product [Arabidopsis thaliana]</td><td>419</td><td>1E-46</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAD81288.1| unknown protein [Oryza sativa (japonica cultivar-group)]</td><td>225</td><td>1E-43</td></tr>
<tr><td>CD568965</td><td>2.83E-03</td><td>Mo17<B73=F1</td><td>1.29</td><td>10</td><td>>ref|XP_468402.1| putative NADH dehydrogenase [Oryza sativa (japonicacultivar-group)] dbj|BAD22016.1| putative NADH dehydrogenase [Oryza sativa (japonica cultivar-group)] dbj|BAD21515.1| putative NADH dehydrogenase [Oryza sativa (japonica cultivar-group)]</td><td>408</td><td>1E-80</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_565469.1| unknown protein [Arabidopsis thaliana]gb|AAT68351.1| hypothetical protein At2g20360 [Arabidopsis thaliana] gb|AAK93749.1| putative NADH-ubiquinone oxireductase [Arabidopsis thaliana] gb|AAK59545.1| putative NADH-ubiquinone oxireductase [Arabidopsis thaliana] gb|AAD21752.2| putative NADH-ubiquinone oxireductase [Arabidopsis thaliana] gb|AAX23820.1| hypothetical protein At2g20360 [Arabidopsis thaliana]</td><td>402</td><td>9E-67</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAL41318.1| NADH-ubiquinone oxidoreductase [Agrobacterium tumefaciens str. C58]ref|NP_531002.1| NADH-ubiquinone oxidoreductase [Agrobacterium tumefaciens str. C58]</td><td>326</td><td>6E-18</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAK86111.1| AGR C 511p [Agrobacterium tumefaciens str. C58]ref|NP 353326.1| hypothetical protein AGR C 511 [Agrobacterium tumefaciens str. C58]</td><td>354</td><td>6E-18</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|EAN07479.1| NADH dehydrogenase (ubiquinone) 1 alpha subcomplex [Mesorhizobiumsp. BNC1] ref|ZP_00611528.1| NADH dehydrogenase (ubiquinone) 1 alpha subcomplex [Mesorhizobium sp. BNC1]</td><td>323</td><td>8E-18</td></tr>
<tr><td>CD484299</td><td>2.86E-03</td><td>F1=Mo17<B73</td><td>1.36</td><td>9</td><td>>ref|XP 472335.1| OSJNBa0039C07.4 [Oryza sativa (japonica cultivar-group)]emb|CAE05148.2| OSJNBa0039C07.4 [Oryza sativa (japonica cultivar-group)]</td><td>888</td><td>2E-10</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>sp|P35100|CLPA_PEA ATP-dependent Clp protease ATP-binding subunit clpA homolog,chloroplast precursor gb|AAA33680.1| nuclear encoded precursor to chloroplast protein</td><td>922</td><td>9E-10</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAD02267.1| ClpC protease [Spinacia oleracea]</td><td>891</td><td>3E-9</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|ABA96309.1| Clp amino terminal domain, putative [Oryza sativa (japonicacultivar-group)]</td><td>1407</td><td>3E-9</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>sp|P31542|CLPAB_LYCES ATP-dependent Clp protease ATP-binding subunit clpA homolog CD4B,chloroplast precursor gb|AAA34161.1| ATP-dependent protease (CD4B)</td><td>923</td><td>3E-9</td></tr>
<tr><td>BG840952</td><td>2.87E-03</td><td>Mo17<B73=F1</td><td>1.56</td><td>10</td><td>>dbj|BAD28236.1| putative ASR2 [Oryza sativa (japonica cultivar-group)]</td><td>105</td><td>3E-7</td></tr>
</tbody>
</table>

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>gb|AAD00255.1| similar to Solanum tuberosum ci21A gene product encoded by thesequence presented in GenBank Accession Number U76610	108	8E-7
					>gb|AAD00254.1| cold inducible; similar to other osmotic stress induced geneproducts including: Tomato abscisic stress ripening protein 1 encoded by GenBank Accession Number L08255, Solanum lycopersicum ABA- and ripening-induced protein encoded by GenBank Accession Number L20756 and to Solanum chacoense abscisic stress ripening protein encoded by GenBank Accession Number U12439 [Solanum tuberosum]	109	2E-6
					>gb|ABB55381.1| fruit-ripening protein-like [Solanum tuberosum]	109	2E-6
					>gb|AAP37981.1| ASR2 [Lycopersicon peruvianum var. humifusum]	112	7E-6
BM078784	2.87E-03	Mo17<B73=F1	1.23	10	>gb|ABA91282.1| expressed protein [Oryza sativa (japonica cultivar-group)]	312	4E-21
					>gb|ABA95707.1| expressed protein [Oryza sativa (japonica cultivar-group)]	312	4E-21
					>gb|AAN60225.1| unknown [Arabidopsis thaliana]	321	2E-9
					>gb|AAM67353.1| unknown [Arabidopsis thaliana]	203	2E-9
					>ref|NP_566456.3| unknown protein [Arabidopsis thaliana]gb|AAL15206.1| unknown protein [Arabidopsis thaliana] gb|AAK59532.1| unknown protein [Arabidopsis thaliana] gb|AAP06824.1| unknown protein [Arabidopsis thaliana] gb|AAP04171.1| unknown protein [Arabidopsis thaliana]	321	3E-9
DV489988	2.87E-03	B73<F1=Mo17	2.26	2	>gb|AAL99610.1| cytosolic aldehyde dehydrogenase RF2D [Zea mays]	466	2E-49
					>gb|AAL99611.1| cytosolic aldehyde dehydrogenase RF2D [Zea mays]	511	2E-49
					>ref|NP_917473.1| putative cytosolic aldehyde dehydrogenase [Oryza sativa (japonicacultivar-group)] dbj|BAB55808.1| putative cytosolic aldehyde dehydrogenase RF2D [Oryza sativa (japonica cultivar-group)]	507	4E-45
					>emb|CAD70189.1| aldehyde dehydrogenase [Bixa orellana]	504	1E-39
					>gb|AAL99608.1| cytosolic aldehyde dehydrogenase RF2C [Zea mays]	502	2E-38
BM336709	2.89E-03	F1=Mo17<B73	1.44	9	>gb|AAG34825.1| glutathione S-transferase GST 17 [Zea mays]	213	4E-96
					>ref|XP_466275.1| putative glutathione s-transferase [Oryza sativa (japonicacultivar-group)] dbj|BAD15813.1| putative glutathione s-transferase [Oryza sativa (japonica cultivar-group)] dbj|BAD15586.1| putative glutathione s-transferase [Oryza sativa (japonica cultivar-group)]	237	6E-75
					>gb|AAS83978.1| glutathione S-transferase [Oryza sativa (japonica cultivar-group)]	241	2E-74
					>gb|AAX95838.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]gb|AAX92930.1| maleylacetoacetate isomerase [Oryza sativa (japonica cultivar-group)] gb|ABA92395.1| maleylacetoacetate isomerase [Oryza sativa (japonica cultivar-group)]	240	2E-58
					>emb|CAD31225.1| glutathione s-transferase [Oryza sativa (japonica cultivar-group)]	185	1E-56
DV551313	2.90E-03	B73<F1=Mo17	1.37	2	>dbj|BAD82281.1| putative microtubule bundling polypeptide TMBP200 [Oryza sativa(japonica cultivar-group)] dbj|BAD82707.1| putative microtubule bundling polypeptide TMBP200 [Oryza sativa (japonica cultivar-group)]	1997	3E-32
					>dbj|BAB88648.1| microtubule bundling polypeptide TMBP200 [Nicotiana tabacum]	2029	2E-28
					>dbj|BAD93861.1| similar to ch-TOG protein from Homo sapiens [Arabidopsis thaliana]	434	2E-27
					>gb|AAD15450.2| similar to ch-TOG protein from Homo sapiens [Arabidopsis thaliana]	1611	2E-27
					>ref|NP_565811.2| MOR1 (MICROTUBULE ORGANIZATION 1) [Arabidopsis thaliana]gb|AAM94170.1| MOR1/GEM1 [Arabidopsis thaliana] gb|AAK59871.1| microtubule organization 1 protein [Arabidopsis thaliana]	1978	2E-27
CB251987	2.91E-03	Mo17<B73=F1	1.33	10	>dbj|BAD46697.1| putative hASNA-I [Oryza sativa (japonica cultivar-group)]	361	3E-11
					>dbj|BAD94314.1| arsA homolog (hASNA-I) [Arabidopsis thaliana]	71	7E-6
BM337350	2.93E-03	Mo17<B73=F1	5.06	10	ns		
CD001277	2.93E-03	B73<F1=Mo17	1.18	3	>ref|NP_187148.2| metal ion binding [Arabidopsis thaliana]	397	9E-19
CB350721	2.94E-03	B73<F1=Mo17	1.49	3	>emb|CAD41688.1| OSJNBb0015D13.13 [Oryza sativa (japonica cultivar-group)]	319	2E-62
					>gb|AAZ08319.1| putative xyloglucan endotransglycosylase/hydrolase [Eucalyptusglobulus]	158	9E-39
					>gb|AAS77347.1| sadtomato protein [Capsicum annuum]	201	2E-38
					>gb|AAZ08349.1| xyloglucan endotransglycosylase/hydrolase 16 protein [Lycopersiconesculentum]	266	1E-36
					>gb|AAV92081.1| xyloglucan endotransglycosylase/hydrolase [Brassica rapa]	281	3E-33
DV490053	2.95E-03	Mo17<B73=F1	2.32	10	>gb|AAP80670.1| early nodule-specific-like protein ENOD8 gene [Triticum aestivum]	166	6E-61
					>ref|XP_550346.1| putative early nodule-specific-like protein ENOD8 [Oryza sativa(japonica cultivar-group)] dbj|BAD67642.1| putative early nodule-specific-like protein ENOD8 [Oryza sativa (japonica cultivar-group)]	227	8E-61
					>ref|NP_194612.2| S-adenosylmethionine-dependent methyltransferase [Arabidopsisthaliana] gb|AAO64787.1| At4g28830 [Arabidopsis thaliana]	208	5E-51
					>emb|CAB81471.1| putative protein [Arabidopsis thaliana]emb|CAA22969.1| putative protein [Arabidopsis thaliana]	138	1E-35
					>gb|EAA06478.2| ENSANGP00000019387 [Anopheles gambiae str. PEST]ref|XP_310965.2| ENSANGP00000019387 [Anopheles gambiae str. PEST]	215	1E-28
AW067012	2.98E-03	B73<F1=Mo17	8.34	3	ns		
CD568618	2.99E-03	B73<F1=Mo17	1.34	3	>gb|AAU43984.1| unknown protein [Oryza sativa (japonica cultivar-group)]	613	4E-79
					>dbj|BAD82224.1| putative SEC14 protein [Oryza sativa (japonica cultivar-group)]dbj|BAD81782.1| putative SEC14 protein [Oryza sativa (japonica cultivar-group)]	671	1E-58
					>ref|NP_917103.1| putative SEC14 - like protein [Oryza sativa (japonicacultivar-group)]	492	2E-58

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>emb|CAB80580.1| SEC14-like protein [Arabidopsis thaliana]emb|CAB43632.1| SEC14-like protein [Arabidopsis thaliana]	617	1E-56
					>gb|AAM91428.1| AT4g39170/T22F8_70 [Arabidopsis thaliana]gb|AAK59767.1| AT4g39170/T22F8_70 [Arabidopsis thaliana]	583	1E-56
CB381307	3.02E-03	B73=Mo17<F1	1.34	12	>ref|XP_468112.1| putative 20 kDa chaperonin, chloroplast [Oryza sativa (japonicacultivar-group)] dbj|BAD19442.1| putative 20 kDa chaperonin, chloroplast [Oryza sativa (japonica cultivar-group)]	195	7E-47
					>ref|XP_468113.1| putative 20 kDa chaperonin, chloroplast [Oryza sativa (japonicacultivar-group)] ref|XP_507011.1| PREDICTED OJ1369_G08.10-2 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD19441.1| putative 20 kDa chaperonin, chloroplast [Oryza sativa (japonica cultivar-group)]	255	7E-47
					>dbj|BAD36628.1| putative chaperonin 21 precursor [Oryza sativa (japonicacultivar-group)] dbj|BAD35232.1| putative chaperonin 21 precursor [Oryza sativa (japonica cultivar-group)]	216	3E-46
					>dbj|BAD35228.1| putative chaperonin 21 precursor [Oryza sativa (japonicacultivar-group)]	252	3E-46
					>gb|AAT80889.1| chloroplast chaperonin 21 [Vitis vinifera]	125	6E-43
DV490284	3.04E-03	B73<F1=Mo17	1.55	3	>ref|XP_473572.1| OSJNBa0019K04.6 [Oryza sativa (japonica cultivar-group)]emb|CAD41659.3| OSJNBa0019K04.6 [Oryza sativa (japonica cultivar-group)]	725	6E-46
					>dbj|BAD29367.1| SPX (SYG1/Pho81/XPR1) domain-containing protein-like [Oryza sativa(japonica cultivar-group)] dbj|BAD29241.1| SPX (SYG1/Pho81/XPR1) domain-containing protein-like [Oryza sativa (japonica cultivar-group)]	697	7E-42
					>ref|NP_192918.1| unknown protein [Arabidopsis thaliana]emb|CAB78224.1| putative protein [Arabidopsis thaliana] emb|CAB44319.1| putative protein [Arabidopsis thaliana]	707	4E-38
					>gb|AAL08230.1| AT4g22990/F7H19_170 [Arabidopsis thaliana]	699	3E-37
					>ref|NP_567674.1| unknown protein [Arabidopsis thaliana]	699	3E-37
DV551091	3.05E-03	B73<F1=Mo17	2.24	3	>gb|AAN78327.1| ATP-dependent Clp protease ATP-binding subunit precursor [Oryzasativa (indica cultivar-group)]	938	2E-82
					>ref|XP_466044.1| ATP-dependent Clp protease ATP-binding subunit precursor [Oryzasativa (japonica cultivar-group)] dbj|BAD25404.1| ATP-dependent Clp protease ATP-binding subunit precursor [Oryza sativa (japonica cultivar-group)]	938	5E-81
					>ref|XP_472386.1| OJ000315_02.14 [Oryza sativa (japonica cultivar-group)]emb|CAE05369.1| OJ000315_02.14 [Oryza sativa (japonica cultivar-group)]	877	5E-66
					>ref|NP_568750.1| ERD1 (EARLY RESPONSIVE TO DEHYDRATION 1); ATP binding / ATPase/nucleoside-triphosphatase/ nucleotide binding / protein binding [Arabidopsis thaliana] gb|AAM91802.1| putative ATP-dependent Clp protease ATP-binding subunit ClpD, ERD1 protein precursor [Arabidopsis thaliana] gb|AAK59617.1| putative ATP-dependent Clp protease ATP-binding subunit ClpD, ERD1 protein precursor [Arabidopsis thaliana] dbj|BAA04506.1| ERD1 protein [Arabidopsis thaliana] sp|P42762|ERD1_ARATH ERD1 protein, chloroplast precursor	945	2E-49
					>ref|ZP_00110397.1| COG0542: ATPases with chaperone activity, ATP-binding subunit [Nostocpunctiforme PCC 73102]	822	1E-39
CB329503	3.07E-03	Mo17<B73=F1	1.36	10	>ref|XP_474269.1| OSJNBa0043A12.6 [Oryza sativa (japonica cultivar-group)]emb|CAE02801.1| OSJNBa0043A12.6 [Oryza sativa (japonica cultivar-group)]	148	2E-20
					>gb|AAM08126.1| elicitor and UV light related transcription factor [Oryza sativa]	147	2E-20
					>gb|AAU82109.1| ubiquitin-conjugating enzyme [Triticum aestivum]	148	1E-19
					>dbj|BAB89354.1| ubiquitin-conjugating enzyme OsUBC5a [Oryza sativa (japonicacultivar-group)]	147	2E-19
					>ref|NP_915993.1| ubiquitin conjugating enzyme [Oryza sativa (japonicacultivar-group)] ref|NP_915996.1| ubiquitin conjugating enzyme [Oryza sativa (japonica cultivar-group)] dbj|BAB93374.1| ubiquitin conjugating enzyme [Oryza sativa (japonica cultivar-group)] dbj|BAB93371.1| ubiquitin conjugating enzyme [Oryza sativa (japonica cultivar-group)]	148	4E-19
DV490204	3.07E-03	B73<F1=Mo17	1.5	2	>dbj|BAD33496.1| 26S proteasome regulatory subunit-like protein [Oryza sativa(japonica cultivar-group)]	213	2E-39
					>ref|NP_568872.1| protein binding [Arabidopsis thaliana]gb|AAM65312.1| 26S proteasome regulatory subunit p27, putative [Arabidopsis thaliana] gb|AAO63310.1| At5g57950 [Arabidopsis thaliana] dbj|BAC43064.1| unknown protein [Arabidopsis thaliana]	227	8E-26
					>dbj|BAB08865.1| unnamed protein product [Arabidopsis thaliana]	275	1E-20
					>emb|CAG08436.1| unnamed protein product [Tetraodon nigroviridis]	212	7E-15
					>gb|AAH41532.1| MGC53232 protein [Xenopus laevis]	213	2E-13
CD661753	3.08E-03	F1=Mo17<B73	1.46	9	>ref|XP_472193.1| OSJNBb0006N15.8 [Oryza sativa (japonica cultivar-group)]emb|CAE04591.2| OSJNBb0006N15.8 [Oryza sativa (japonica cultivar-group)]	123	5E-51
					>ref|XP_507485.1| PREDICTED OJ1126_B06.24 gene product [Oryza sativa (japonicacultivar-group)] ref|XP_465859.1| putative 60S ribosomal protein L35 [Oryza sativa (japonica cultivar-group)] ref|XP_506809.1| PREDICTED OJ1126_B06.24 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD22912.1| putative 60S ribosomal protein L35 [Oryza sativa (japonica cultivar-group)] dbj|BAD23213.1| putative 60S ribosomal protein L35 [Oryza sativa (japonica cultivar-group)]	123	8E-50
					>ref|NP_195881.1| structural constituent of ribosome [Arabidopsis thaliana]emb|CAB85998.1| ribosomal protein L35-like [Arabidopsis thaliana] gb|AAQ22651.1| At5g02610 [Arabidopsis thaliana] sp|Q9LZ41|RL354_ARATH 60S ribosomal protein L35-4 pir||T48282 ribosomal protein L35-like - Arabidopsis thaliana	123	5E-47
					>ref|NP_181471.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAL34210.1| putative 60S ribosomal protein L35 [Arabidopsis thaliana] gb|AAK59609.1| putative 60S ribosomal protein L35 [Arabidopsis thaliana] gb|AAC27830.1| 60S ribosomal protein L35 [Arabidopsis thaliana] gb|AAM61292.1| 60S ribosomal protein L35 [Arabidopsis thaliana] pir||T00549 60S ribosomal protein L35 [imported] - Arabidopsis thaliana sp|O80626|RL352_ARATH 60S ribosomal protein L35-1	123	6E-46
					>ref|NP_187561.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAM64363.1| putative 60S ribosomal protein L35 [Arabidopsis thaliana] gb|AAF23282.1| putative 60S ribosomal protein L35 [Arabidopsis thaliana] gb|AAO50471.1| putative 60S ribosomal protein L35 [Arabidopsis thaliana] gb|AAO42195.1| putative 60S ribosomal protein L35 [Arabidopsis thaliana] sp|Q9SF53|RL351_ARATH 60S ribosomal protein L35-2	123	1E-45

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<table>
<tr><th>GenBank accession no.</th><th>Overall P value</th><th>Significant pattern</th><th>Fold change†</th><th>Sector‡</th><th>BLAST annotation*</th><th>Score</th><th>E value</th></tr>
<tr><td>DV495837</td><td>3.08E-03</td><td>B73<F1=Mo17</td><td>1.35</td><td>3</td><td>>ref|XP_464376.1| receptor protein kinase PERK1-like protein [Oryza sativa (japonicacultivar-group)] ref|XP_506736.1| PREDICTED OJ1115_B01.27 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD15446.1| receptor protein kinase PERK1-like protein [Oryza sativa (japonica cultivar-group)] dbj|BAD15416.1| receptor protein kinase PERK1-like protein [Oryza sativa (japonica cultivar-group)]</td><td>377</td><td>1E-32</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_550361.1| putative receptor protein kinase PERK1 [Oryza sativa (japonicacultivar-group)] dbj|BAD67868.1| putative receptor protein kinase PERK1 [Oryza sativa (japonica cultivar-group)] dbj|BAD67605.1| putative receptor protein kinase PERK1 [Oryza sativa (japonica cultivar-group)]</td><td>367</td><td>7E-18</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_564609.3| ATP binding / kinase/ protein kinase/ protein serine/threoninekinase/ protein-tyrosine kinase [Arabidopsis thaliana] gb|AAM63304.1| somatic embryogenesis receptor-like kinase, putative [Arabidopsis thaliana]</td><td>350</td><td>2E-11</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAD55610.1| Contains PF|00069 Eukaryotic protein kinase domain. ESTsgb|W43822, gb|T20475 and gb|AA586152 come from this gene. [Arabidopsis thaliana]</td><td>347</td><td>2E-11</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAM65900.1| protein kinase, putative [Arabidopsis thaliana]</td><td>361</td><td>7E-10</td></tr>
<tr><td>DV622388</td><td>3.09E-03</td><td>F1=Mo17<B73</td><td>1.23</td><td>9</td><td>>dbj|BAD53489.1| putative decoy [Oryza sativa (japonica cultivar-group)]</td><td>248</td><td>8E-49</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_172914.1| DECOY [Arabidopsis thaliana]gb|AAN46785.1| At1g14620/T5E21_15 [Arabidopsis thaliana] gb|AAM83228.1| At1g14620/T5E21_15 [Arabidopsis thaliana]</td><td>233</td><td>9E-38</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAF63174.1| T5E21.12 [Arabidopsis thaliana]</td><td>254</td><td>1E-34</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAB48039.1| decoy [Arabidopsis thaliana]gb|AAB51588.1| decoy [Arabidopsis thaliana]</td><td>210</td><td>5E-22</td></tr>
<tr><td>DV549373</td><td>3.09E-03</td><td>Mo17<B73=F1</td><td>2.4</td><td>11</td><td>>ref|NP_917838.1| putative chloroplast 50S ribosomal protein L31 [Oryza sativa(japonica cultivar-group)] dbj|BAB90423.1| chloroplast 50S ribosomal protein L31-like [Oryza sativa (japonica cultivar-group)] dbj|BAB90722.1| chloroplast 50S ribosomal protein L31-like [Oryza sativa (japonica cultivar-group)]</td><td>135</td><td>4E-30</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAC77927.1| similar to chloroplast 50S ribosomal protein L31 [Medicago sativa]</td><td>133</td><td>5E-8</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_565109.1| EMB2184; structural constituent of ribosome [Arabidopsis thaliana]gb|AAL15224.1| putative chloroplast 50S ribosomal protein L31 [Arabidopsis thaliana] gb|AAK44041.1| putative chloroplast 50S ribosomal protein L31 [Arabidopsis thaliana] gb|AAM65248.1| chloroplast 50S ribosomal protein L31, putative [Arabidopsis thaliana] gb|AAG13073.1| Unknown protein [Arabidopsis thaliana]</td><td>144</td><td>6E-6</td></tr>
<tr><td>CB381605</td><td>3.10E-03</td><td>B73<F1=Mo17</td><td>1.62</td><td>3</td><td>ns</td><td></td><td></td></tr>
<tr><td>CD484257</td><td>3.11E-03</td><td>Mo17<B73=F1</td><td>1.44</td><td>11</td><td>>ref|NP_921134.1| putative hydrolase [Oryza sativa (japonica cultivar-group)]gb|AAM08665.1| Putative hydrolase [Oryza sativa (japonica cultivar-group)] gb|AAM08532.1| Putative hydrolase [Oryza sativa] gb|AAP53421.1| hydrolase, alpha/beta fold family, putative [Oryza sativa (japonica cultivar-group)]</td><td>401</td><td>2E-87</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP 470785.1| putative hydrolase [Oryza sativa (japonica cultivar-group)]gb|AAR06364.1| putative hydrolase [Oryza sativa (japonica cultivar-group)]</td><td>333</td><td>2E-50</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAM61205.1| putative hydrolase [Arabidopsis thaliana]</td><td>328</td><td>5E-36</td></tr>
<tr><td>DV489819</td><td>3.12E-03</td><td>B73=F1<Mo17</td><td>1.69</td><td>5</td><td>>dbj|BAD88223.1| putative MtN3 [Oryza sativa (japonica cultivar-group)]</td><td>243</td><td>2E-19</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_566493.1| unknown protein [Arabidopsis thaliana]gb|AAL47411.1| AT3g14770/T21E2_2 [Arabidopsis thaliana] gb|AAL06889.1| AT3g14770/T21E2_2 [Arabidopsis thaliana] dbj|BAB02642.1| MtN3-like protein [Arabidopsis thaliana]</td><td>236</td><td>2E-13</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAD82209.1| MtN3-like [Oryza sativa (japonica cultivar-group)]dbj|BAD81867.1| MtN3-like [Oryza sativa (japonica cultivar-group)]</td><td>230</td><td>6E-10</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAV25007.1| unknow protein [Oryza sativa (japonica cultivar-group)]</td><td>261</td><td>3E-8</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_915057.1| P0018C10.36 [Oryza sativa (japonica cultivar-group)]dbj|BAC06235.1| putative MtN3 [Oryza sativa (japonica cultivar-group)] dbj|BAB90353.1| putative MtN3 [Oryza sativa (japonica cultivar-group)]</td><td>273</td><td>3E-8</td></tr>
<tr><td>CB280807</td><td>3.12E-03</td><td>B73=Mo17<F1</td><td>1.25</td><td>12</td><td>>gb|AAB82138.1| proteasome component [Oryza sativa]</td><td>261</td><td>2E-18</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAT78811.1| proteasome subunit alpha type 2 [Oryza sativa (japonicacultivar-group)] sp|Q9LSU2|PSA2_ORYSA Proteasome subunit alpha type 2 (20S proteasome alpha subunit B) (20S proteasome subunit alpha-2) dbj|BAA96830.1| alpha 2 subunit of 20S proteasome [Oryza sativa (japonica cultivar-group)]</td><td>235</td><td>7E-17</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_507513.1| PREDICTED OJ1626_B09.4 gene product [Oryza sativa (japonicacultivar-group)] ref|XP_466922.1| alpha 2 subunit of 20S proteasome [Oryza sativa (japonica cultivar-group)] ref|XP_507512.1| PREDICTED OJ1626_B09.4 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_506877.1| PREDICTED OJ1626_B09.4 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD25097.1| alpha 2 subunit of 20S proteasome [Oryza sativa (japonica cultivar-group)]</td><td>235</td><td>2E-16</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_001031057.1| PAB1; endopeptidase/ peptidase/ threonine endopeptidase[Arabidopsis thaliana] ref|NP_173096.1| PAB1; endopeptidase/ peptidase/ threonine endopeptidase [Arabidopsis thaliana] emb|CAA73619.1| multicatalytic endopeptidase [Arabidopsis thaliana] gb|AAG48830.1| putative multicatalytic endopeptidase [Arabidopsis thaliana] gb|AAM66950.1| multicatalytic endopeptidase [Arabidopsis thaliana] gb|AAD34699.1| Identical to gb|Y13176 Arabidopsis thaliana mRNA for proteasome subunit prc3. ESTs gb|H36972, gb|T22551 and gb|T13800 come from this gene sp|O23708|PSA2A_ARATH Proteasome subunit alpha type 2-A (20S proteasome alpha subunit B) (Proteasome component 3) gb|AAC32056.1| 20S proteasome subunit PAB1 [Arabidopsis thaliana]</td><td>235</td><td>1E-12</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAN18089.1| At1g16470/F3O9 27 [Arabidopsis thaliana]gb|AAK95291.1| At1g16470/F3O9 27 [Arabidopsis thaliana]</td><td>99</td><td>1E-12</td></tr>
<tr><td>BM348046</td><td>3.14E-03</td><td>Mo17<B73=F1</td><td>1.36</td><td>10</td><td>>ref|NP_190556.2| ATARLA1C; GTP binding [Arabidopsis thaliana]gb|AAM48037.1| ADP-ribosylation factor-like protein [Arabidopsis thaliana] gb|AAL62421.1| ADP-RIBOSYLATION FACTOR -like protein [Arabidopsis thaliana]</td><td>184</td><td>9E-24</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_568553.1| ATARLA1A; GTP binding [Arabidopsis thaliana]gb|AAM47962.1| ADP-ribosylation factor-like protein [Arabidopsis thaliana] gb|AAL32736.1| ADP-ribosylation factor-like protein [Arabidopsis thaliana] gb|AAM62503.1| ADP-ribosylation factor-like protein [Arabidopsis thaliana]</td><td>184</td><td>1E-23</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_467635.1| putative ADP-ribosylation factor [Oryza sativa (japonicacultivar-group)] dbj|BAD16140.1| putative ADP-ribosylation factor [Oryza sativa (japonica cultivar-group)]</td><td>184</td><td>1E-23</td></tr>
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Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

<table>
<tr><th>GenBank accession no.</th><th>Overall P value</th><th>Significant pattern</th><th>Fold change[†]</th><th>Sector[‡]</th><th>BLAST annotation*</th><th>Score</th><th>E value</th></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_569051.1| ATARLA1D; GTP binding [Arabidopsis thaliana]gb|AAL47331.1| ADP-ribosylation factor-like protein [Arabidopsis thaliana] gb|AAK96715.1| ADP-ribosylation factor-like protein [Arabidopsis thaliana] gb|AAM65030.1| ADP-ribosylation factor-like protein [Arabidopsis thaliana]</td><td>184</td><td>2E-22</td></tr>
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<tr><td>DV495862</td><td>3.15E-03</td><td>B73<F1=Mo17</td><td>1.54</td><td>2</td><td>>gb|AAM47577.1| putative mitochondrial carrier protein [Sorghum bicolor]</td><td>323</td><td>1E-18</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAG48999.1| putative mitochondrial carrier protein [Hordeum vulgare subsp.vulgare]</td><td>322</td><td>2E-17</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAL74183.1| putative mitochondrial carrier protein [Triticum monococcum]</td><td>322</td><td>2E-17</td></tr>
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<tr><td>BG840791</td><td>3.15E-03</td><td>B73<F1=Mo17</td><td>1.53</td><td>3</td><td>>dbj|BAD82103.1| putative helix-loop-helix protein 1A [Oryza sativa (japonicacultivar-group)]</td><td>387</td><td>5E-20</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP 563749.1| DNA binding / transcription factor [Arabidopsis thaliana]gb|AAN41354.1| unknown protein [Arabidopsis thaliana]</td><td>362</td><td>9E-14</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP 177394.1| unknown protein [Arabidopsis thaliana]gb|AAG52586.1| hypothetical protein; 14673-17893 [Arabidopsis thaliana]</td><td>758</td><td>3E-15</td></tr>
<tr><td>CB816337</td><td>3.21E-03</td><td>Mo17<B73=F1</td><td>1.39</td><td>10</td><td>>gb|AAO72563.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]</td><td>413</td><td>1E-80</td></tr>
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<tr><td>BM341324</td><td>3.23E-03</td><td>Mo17<B73=F1</td><td>1.39</td><td>10</td><td>>ref|XP_473045.1| OSJNBa0067K08.22 [Oryza sativa (japonica cultivar-group)]emb|CAD41243.2| OSJNBa0067K08.22 [Oryza sativa (japonica cultivar-group)] dbj|BAB12275.1| cytochrome c oxidase subunit 6b [Oryza sativa (japonica cultivar-group)] dbj|BAB12339.1| cytochrome c oxidase subunit 6b [Oryza sativa (japonica cultivar-group)]</td><td>77</td><td>3E-36</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAM92706.1| putative cytochrome c oxidase subunit [Triticum aestivum]</td><td>157</td><td>1E-34</td></tr>
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<tr><td>CB331687</td><td>3.24E-03</td><td>Mo17<B73=F1</td><td>1.36</td><td>10</td><td>ns</td><td></td><td></td></tr>
<tr><td>DV493876</td><td>3.30E-03</td><td>B73<F1=Mo17</td><td>1.37</td><td>2</td><td>>ref|XP_476668.1| putative glycine-rich protein [Oryza sativa (japonicacultivar-group)] dbj|BAC84718.1| putative glycine-rich protein [Oryza sativa (japonica cultivar-group)]</td><td>280</td><td>1E-10</td></tr>
<tr><td>DV492863</td><td>3.31E-03</td><td>B73<F1=Mo17</td><td>1.49</td><td>3</td><td>>gb|AAL33650.1| HMG-like nucleosome/chromatin assembly factor D [Zea mays]</td><td>126</td><td>2E-46</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAM93217.1| nucleasome/chromatin assembly factor D protein NFD101 [Zea mays]emb|CAA70045.1| HMGd1 [Zea mays]</td><td>126</td><td>5E-46</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAD33893.1| putative HMGd1 [Oryza sativa (japonica cultivar-group)]</td><td>127</td><td>1E-41</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAB61215.1| DNA-binding protein [Nicotiana tabacum]</td><td>142</td><td>3E-32</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAC50019.1| high mobility group protein 2 HMG2 [Ipomoea nil]</td><td>146</td><td>6E-31</td></tr>
</table>

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
CB605341	3.33E-03	Mo17<B73=F1	1.31	10	>ref|XP_468756.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)] ref|XP_468752.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] gb|AAP20855.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] gb|AAP20842.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] sp|P40978|RS19 ORYSA 40S ribosomal protein S19	146	1E-74
					>gb|AAW34237.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	144	7E-72
					>gb|AAW34236.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	166	4E-71
					>gb|AAW34240.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	122	2E-64
					>gb|ABB87116.1| 40S ribosomal protein S19-like [Solanum tuberosum]	143	3E-61
BG841557	3.34E-03	Mo17<B73=F1	1.5	10	>gb|ABB47793.1| pol polyprotein, putative [Oryza sativa (japonica cultivar-group)]	116	5E-53
					>ref|NP 922007.1| putative pol polyprotein [Oryza sativa (japonica cultivar-group)]gb|AAG13579.1| putative pol polyprotein [Oryza sativa]	105	3E-47
					>dbj|BAD87130.1| magmas-like protein [Oryza sativa (japonica cultivar-group)]dbj|BAD87219.1| magmas-like protein [Oryza sativa (japonica cultivar-group)]	113	3E-42
					>ref|NP 914245.1| P0401G10.24 [Oryza sativa (japonica cultivar-group)]	264	1E-41
					>ref|NP_567078.1| TXR1 (THAXTOMIN A RESISTANT 1) [Arabidopsis thaliana]gb|AAM63549.1| thaxtomin resistance protein TXR1 [Arabidopsis thaliana] gb|AAL06797.1| AT3g59280/F25L23 140 [Arabidopsis thaliana] gb|AAK55724.1| AT3g59280/F25L23 140 [Arabidopsis thaliana]	116	2E-37
BM073916	3.34E-03	F1=Mo17<B73	5.01	9	ns		
DV491092	3.35E-03	B73=F1<Mo17	1.39	5	>ref|XP_450956.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD22260.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAD19750.1| unknown protein [Oryza sativa (japonica cultivar-group)]	189	3E-13
					>ref|XP_483015.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD09300.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAD10699.1| unknown protein [Oryza sativa (japonica cultivar-group)]	191	5E-9
CB331768	3.36E-03	Mo17<B73=F1	1.49	10	>ref|XP 463045.1| expressed protein [Oryza sativa (japonica cultivar-group)]gb|AAS07181.1| expressed protein [Oryza sativa (japonica cultivar-group)]	91	6E-13
					>emb|CAJ13713.1| hypothetical protein [Capsicum chinense]	96	1E-11
					>ref|NP_850005.1| unknown protein [Arabidopsis thaliana]gb|AAK00397.1| unknown protein [Arabidopsis thaliana] gb|AAG41478.1| unknown protein [Arabidopsis thaliana] gb|AAL06786.1| At2g20820/F5H14.21 [Arabidopsis thaliana] gb|AAG40023.1| At2g20820 [Arabidopsis thaliana] gb|AAK55709.1| At2g20820/F5H14.21 [Arabidopsis thaliana]	93	3E-9
BM073171	3.38E-03	Mo17<B73	1.45	9	>gb|AAM65603.1| transmembrane protein, putative [Arabidopsis thaliana]	230	3E-32
					>ref|NP_173923.1| unknown protein [Arabidopsis thaliana]gb|AAG50804.1| transmembrane protein, putative [Arabidopsis thaliana] gb|AAO42430.1| putative transmembrane protein [Arabidopsis thaliana] gb|AAO22664.1| putative transmembrane protein [Arabidopsis thaliana]	230	3E-32
					>ref|NP_177032.1| unknown protein [Arabidopsis thaliana]dbj|BAC43336.1| putative transmembrane protein [Arabidopsis thaliana] gb|AAD49978.1| Is a member of PF|01169 Uncharacterized (transmembrane domain) protein family. [Arabidopsis thaliana]	228	3E-32
					>emb|CAJ07116.1| membrane protein, putative [Leishmania major]	252	1E-18
					>gb|AAH89176.1| Unknown (protein for MGC:98993) [Xenopus laevis]	242	2E-18
CB334551	3.38E-03	F1=Mo17<B73	1.41	9	>gb|AAX92922.1| Kelch motif, putative [Oryza sativa (japonica cultivar-group)]gb|ABA92301.1| Kelch motif, putative [Oryza sativa (japonica cultivar-group)]	383	9E-16
CB351515	3.39E-03	Mo17<B73=F1	1.46	10	>gb|AAV28627.1| putative 60S ribosomal protein L31 [Zea mays]	124	4E-43
					>ref|XP_483237.1| putative 60S ribosomal protein L31 [Oryza sativa (japonicacultivar-group)] dbj|BAD10170.1| putative 60S ribosomal protein L31 [Oryza sativa (japonica cultivar-group)] dbj|BAD08833.1| putative 60S ribosomal protein L31 [Oryza sativa (japonica cultivar-group)]	122	8E-43
					>dbj|BAD61612.1| putative 60S ribosomal protein L31 [Oryza sativa (japonicacultivar-group)]	124	1E-42
					>ref|XP_467485.1| putative 60S ribosomal protein L31 [Oryza sativa (japonicacultivar-group)] dbj|BAD12898.1| putative 60S ribosomal protein L31 [Oryza sativa (japonica cultivar-group)]	123	2E-42
					>gb|AAV92213.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii]gb|AAV92212.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92211.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92210.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92209.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92208.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92207.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92206.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92205.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92204.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92203.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92202.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92201.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii]	113	1E-40
DV494470	3.41E-03	Mo17<B73=F1	1.54	10	>ref|XP_482379.1| putative RNA binding protein [Oryza sativa (japonicacultivar-group)] ref|XP_507581.1| PREDICTED OSJNBa0007M04.13 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_507230.1| PREDICTED OSJNBa0007M04.13 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC99692.1| putative RNA binding protein [Oryza sativa (japonica cultivar-group)]	214	3E-80
					>emb|CAE00870.1| TA8 protein [Oryza sativa (japonica cultivar-group)]	197	3E-72
					>gb|AAL76994.1| RNA binding protein [Elaeis oleifera]	218	4E-67
					>gb|ABB87134.1| RNA binding protein-like protein [Solanum tuberosum]	217	8E-66
					>ref|NP_196080.1| RNA binding / nucleic acid binding [Arabidopsis thaliana]emb|CAB85566.1| rna binding protein-like [Arabidopsis thaliana] gb|AAM67546.1| putative RNA binding protein [Arabidopsis thaliana] gb|AAL36178.1| putative rna binding protein [Arabidopsis thaliana] gb|AAL06954.1| AT5g04600/T32M21 200 [Arabidopsis thaliana] gb|AAK55702.1| AT5g04600/T32M21 200 [Arabidopsis thaliana]	222	3E-56

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
DV551199	3.42E-03	Mo17<B73	1.42	9	>gb|AAO72563.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]	413	7E-87
					>dbj|BAD61932.1| putative elongation factor 1 gamma [Oryza sativa (japonicacultivar-group)] dbj|BAD61828.1| putative elongation factor 1 gamma [Oryza sativa (japonica cultivar-group)]	416	7E-87
					>ref|XP_464690.1| Elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]dbj|BAD17615.1| Elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)] sp|Q9ZRI7|EF1G ORYSA Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) dbj|BAA34206.1| elongation factor 1B gamma [Oryza	418	5E-86
					>gb|AAO72574.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]	409	1E-85
					>ref|XP_464689.1| putative elongation factor 1-gamma [Oryza sativa (japonicacultivar-group)] dbj|BAD17614.1| putative elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]	414	1E-85
CD058927	3.44E-03	B73<F1=Mo17	1.98	3	>ref|XP_469890.1| putative aurora-related kinase [Oryza sativa (japonicacultivar-group)] gb|AAP50960.1| putative aurora-related kinase [Oryza sativa (japonica cultivar-group)] dbj|BAE00023.1| Aurora kinase [Oryza sativa (japonica cultivar-group)]	279	1E-82
					>ref|NP_182073.1| ATP binding / protein kinase/ protein serine/threonine kinase/protein-tyrosine kinase [Arabidopsis thaliana] emb|CAH69534.1| aurora-like kinase 3 [Arabidopsis thaliana] dbj|BAE00021.1| Aurora kinase [Arabidopsis thaliana] gb|AAC06151.1| putative protein kinase [Arabidopsis thaliana] gb|AAL69469.1| At2g45490/F17K2.2 [Arabidopsis thaliana]	288	6E-62
					>ref|NP_195009.1| kinase/ protein serine/threonine kinase [Arabidopsis thaliana]emb|CAB80000.1| putative serine/threonine protein kinase [Arabidopsis thaliana] emb|CAH69532.1| aurora-like kinase 1 [Arabidopsis thaliana] dbj|BAD95178.1| putative serine/threonine protein kinase [Arabidopsis thaliana] dbj|BAE00019.1| Aurora kinase [Arabidopsis thaliana]	294	3E-56
					>gb|AAM64506.1| putative serine/threonine protein kinase [Arabidopsis thaliana]	294	6E-56
					>emb|CAH69533.1| aurora-like kinase 2 [Arabidopsis thaliana]gb|AAR07517.1| At2g25880 [Arabidopsis thaliana] dbj|BAE00020.1| Aurora kinase [Arabidopsis thaliana] gb|AAC42257.1| putative protein kinase [Arabidopsis thaliana]	282	2E-55
DV490811	3.46E-03	Mo17<B73=F1	1.83	10	>gb|ABA99041.1| F-box protein family, putative [Oryza sativa (japonicacultivar-group)]	399	8E-60
					>dbj|BAB03143.1| ankyrin-like protein [Arabidopsis thaliana]	1100	1E-20
					>gb|AAG51006.1| hypothetical protein; 96168-94294 [Arabidopsis thaliana]	455	6E-20
					>gb|AAM63646.1| unknown [Arabidopsis thaliana]	422	8E-20
					>ref|NP 566421.1| unknown protein [Arabidopsis thaliana]gb|AAN71924.1| putative F-box protein family [Arabidopsis thaliana]	422	8E-20
DV495228	3.47E-03	B73=F1<Mo17	1.79	4	ns		
CA829886	3.49E-03	Mo17<B73=F1	1.26	10	>ref|XP_450550.1| apospory-associated protein C-like [Oryza sativa (japonicacultivar-group)] dbj|BAD23600.1| apospory-associated protein C-like [Oryza sativa (japonica cultivar-group)]	319	2E-74
					>ref|NP_201454.1| aldose 1-epimerase [Arabidopsis thaliana]gb|AAN15356.1| apospory-associated protein C-like protein [Arabidopsis thaliana] gb|AAM53269.1| apospory-associated protein C-like protein [Arabidopsis thaliana] dbj|BAB10929.1| apospory-associated protein C-like [Arabidopsis thaliana]	307	8E-48
					>gb|AAF34174.1| apospory-associated protein C; APOC [Chlamydomonas reinhardtii]	338	2E-37
					>ref|XP_480917.1| putative Aldose 1-epimerase [Oryza sativa (japonicacultivar-group)] dbj|BAD05576.1| putative Aldose 1-epimerase [Oryza sativa (japonica cultivar-group)] dbj|BAD05401.1| putative Aldose 1-epimerase [Oryza sativa (japonica cultivar-group)]	337	1E-18
					>ref|XP 473781.1| OSJNBa0041A02.19 [Oryza sativa (japonica cultivar-group)]emb|CAE01826.2| OSJNBa0041A02.19 [Oryza sativa (japonica cultivar-group)]	325	2E-18
CB381648	3.51E-03	F1=Mo17<B73	1.24	9	>emb|CAA48638.1| cyclophilin [Zea mays]sp|P21569|CYPH_MAIZE Peptidyl-prolyl cis-trans isomerase (PPIase) (Rotamase) (Cyclophilin) (Cyclosporin A-binding protein) gb|AAA63403.1| cyclophilin	172	1E-86
					>ref|XP_463914.1| peptidylprolyl isomerase Cyp2 [Oryza sativa (japonicacultivar-group)] ref|XP_506694.1| PREDICTED OSJNBb0088N06.23 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD07601.1| peptidylprolyl isomerase Cyp2 [Oryza sativa (japonica cultivar-group)] dbj|BAD08141.1| peptidylprolyl isomerase Cyp2 [Oryza sativa (japonica cultivar-group)] gb|AAA57045.1| cyclophilin 2	172	3E-75
					>gb|AAK49427.1| cyclophilin A-2 [Triticum aestivum]gb|AAS17067.1| cyclophilin A [Triticum aestivum]	171	4E-75
					>gb|AAK49428.1| cyclophilin A-3 [Triticum aestivum]gb|AAK49426.1| cyclophilin A-1 [Triticum aestivum]	171	6E-75
					>gb|AAA57046.1| cyclophilin 2	172	1E-74
CB605143	3.52E-03	Mo17<B73=F1	1.28	10	>gb|AAV44197.1| putative beta-N-acetylhexosaminidase [Oryza sativa (japonicacultivar-group)] gb|AAU44085.1| putative beta-N-acetylhexosaminidase [Oryza sativa (japonica cultivar-group)]	541	2E-53
					>emb|CAB75760.1| beta-N-acetylhexosaminidase-like protein [Arabidopsis thaliana]	557	1E-45
					>gb|AAN41320.1| putative beta-N-acetylhexosaminidase [Arabidopsis thaliana]gb|AAM61367.1| beta-N-acetylhexosaminidase-like protein [Arabidopsis thaliana]	445	1E-45
					>ref|NP 567017.2| beta-N-acetylhexosaminidase/ hydrolase, hydrolyzing O-glycosylcompounds [Arabidopsis thaliana]	541	1E-45
					>dbj|BAD87534.1| putative beta-N-acetylhexosaminidase [Oryza sativa (japonicacultivar-group)]	526	9E-34
CD527140	3.54E-03	Mo17<B73=F1	1.33	10	>ref|XP_478414.1| putative translational inhibitor protein [Oryza sativa (japonicacultivar-group)] dbj|BAC20708.1| putative translational inhibitor protein [Oryza sativa (japonica cultivar-group)] dbj|BAD31311.1| putative translational inhibitor protein [Oryza sativa (japonica cultivar-group)]	180	2E-58
					>dbj|BAD00048.1| perchloric acid soluble translation inhibitor protein homolog[Gentiana triflora] dbj|BAC66487.1| translation-inhibitor protein [Gentiana triflora]	188	2E-54
					>ref|NP_188674.1| endoribonuclease [Arabidopsis thaliana]gb|AAK53030.1| AT3g20390/MQC12_15 [Arabidopsis thaliana] gb|AAL31178.1| AT3g20390/MQC12 15 [Arabidopsis thaliana] gb|AAM63246.1| translational inhibitor protein, putative [Arabidopsis thaliana]	187	7E-53
					>dbj|BAB02821.1| unnamed protein product [Arabidopsis thaliana]	143	7E-53

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>emb|CAE56534.1| Hypothetical protein CBG24261 [Caenorhabditis briggsae]	172	1E-32
CB604473	3.54E-03	B73<F1=Mo17	1.38	2	>dbj|BAD53747.1| putative T complex protein [Oryza sativa (japonica cultivar-group)]	535	4E-69
					>prf||2206327A T complex protein	534	1E-66
					>gb|AAD11431.1| T-complex protein 1 epsilon subunit [Mesembryanthemum crystallinum]	418	3E-65
					>emb|CAA53397.1| t complex polypeptide 1 [Avena sativa]sp|P54411|TCPE2_AVESA T-complex protein 1 subunit epsilon (TCP-1-epsilon) (CCT-epsilon) (TCP-K36)	535	7E-65
					>emb|CAA53396.1| T complex polypeptide 1 [Avena sativa]sp|P40412|TCPE1_AVESA T-complex protein 1 subunit epsilon (TCP-1-epsilon) (CCT-epsilon) (TCP-K19)	535	7E-65
CB380842	3.55E-03	F1=Mo17<B73	1.25	9	>gb|ABA98950.1| expressed protein [Oryza sativa (japonica cultivar-group)]	880	2E-71
					>ref|NP 180698.1| ATP binding / damaged DNA binding [Arabidopsis thaliana]gb|AAD26479.1| unknown protein [Arabidopsis thaliana]	918	4E-35
					>gb|AAC97219.1| hypothetical protein [Arabidopsis thaliana]	1107	4E-19
					>gb|AAM62704.1| unknown [Arabidopsis thaliana]	463	4E-19
					>ref|NP_565422.1| unknown protein [Arabidopsis thaliana]gb|AAO64123.1| unknown protein [Arabidopsis thaliana] gb|AAO42121.1| unknown protein [Arabidopsis thaliana] pir||A84555 hypothetical protein At2g17670 [imported] - Arabidopsis thaliana	463	4E-19
CD001778	3.57E-03	Mo17<B73=F1	1.45	10	>ref|NP 921446.1| unknown protein [Oryza sativa (japonica cultivar-group)]	713	1E-25
					>gb|AAP80664.1| S28 ribosomal protein [Triticum aestivum]	86	7E-22
					>emb|CAA04565.1| rpS28 [Hordeum vulgare subsp. vulgare]	65	4E-21
					>emb|CAA57636.1| small subunit ribosomal protein S28 [Zea mays]sp|P46302|RS28 MAIZE 40S ribosomal protein S28	65	6E-21
					>emb|CAA10103.1| ribosomal protein S28 [Prunus persica]emb|CAA10102.1| ribosomal protein S28 [Prunus persica] emb|CAA10101.1| ribosomal protein S28 [Prunus persica]	65	2E-19
DV491600	3.57E-03	B73<F1=Mo17	1.53	3	ns		
CB351568	3.58E-03	Mo17<B73=F1	3.45	10	>ref|XP_464072.1| RNA recognition motif (RRM)-containing protein-like [Oryza sativa(japonica cultivar-group)] dbj|BAD10531.1| RNA recognition motif (RRM)-containing protein-like [Oryza sativa (japonica cultivar-group)]	552	2E-85
					>gb|AAM98125.1| unknown protein [Arabidopsis thaliana]	748	6E-44
					>ref|NP 200621.1| nucleic acid binding [Arabidopsis thaliana]dbj|BAB11005.1| unnamed protein product [Arabidopsis thaliana]	748	6E-44
					>ref|NP_913805.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]dbj|BAD05411.1| hypothetical protein [Oryza sativa (japonica cultivar-group)] dbj|BAC22576.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	146	2E-7
					>emb|CAH90090.1| hypothetical protein [Pongo pygmaeus]	1167	4E-7
BM073657	3.59E-03	F1=Mo17<B73	1.79	9	>emb|CAA73068.1| serine/threonine kinase [Sorghum bicolor]	440	5E-19
					>emb|CAA73067.1| serine/threonine kinase [Sorghum bicolor]	440	1E-16
					>gb|ABA91407.1| serine/threonine kinase SNFL1, putative [Oryza sativa (japonicacultivar-group)]	454	3E-16
					>dbj|BAD95889.1| Ser/Thr protein kinase [Lotus corniculatus var. japonicus]	441	2E-12
					>ref|XP_479600.1| putative serine/threonine kinase [Oryza sativa (japonicacultivar-group)] dbj|BAD30291.1| putative serine/threonine kinase [Oryza sativa (japonica cultivar-group)] dbj|BAC10350.1| putative serine/threonine kinase [Oryza sativa (japonica cultivar-group)]	445	5E-11
CD651115	3.59E-03	B73<F1=Mo17	1.23	2	>ref|XP_469436.1| beta-glucosidase (with alternative splicing) [Oryza sativa(japonica cultivar-group)] gb|AAX95519.1| Putative Glycosyl hydrolase family 1 protein [Oryza sativa (japonica cultivar-group)] gb|AAS07254.1| beta-glucosidase (with alternative splicing) [Oryza sativa (japonica cultivar-group)]	504	8E-63
					>gb|AAA84906.2| beta-glucosidase [Oryza sativa]	504	8E-63
					>gb|AAX95520.1| Putative Glycosyl hydrolase family 1 protein [Oryza sativa(japonica cultivar-group)]	603	5E-52
					>ref|XP_469438.1| putative beta-glucosidase [Oryza sativa (japonica cultivar-group)]gb|AAS07251.1| putative beta-glucosidase [Oryza sativa (japonica cultivar-group)]	568	5E-52
					>dbj|BAD73293.1| putative beta-glucosidase [Oryza sativa (japonica cultivar-group)]	516	7E-48
BM079585	3.59E-03	F1=Mo17<B73	1.67	9	>gb|ABA99330.1| expressed protein [Oryza sativa (japonica cultivar-group)]	197	3E-18
					>ref|NP_192227.1| unknown protein [Arabidopsis thaliana]gb|AAD14446.1| predicted protein of unknown function [Arabidopsis thaliana] emb|CAB77803.1| predicted protein of unknown function [Arabidopsis thaliana] gb|AAM66022.1| unknown [Arabidopsis thaliana]	185	8E-10
CD651681	3.62E-03	Mo17<B73=F1	1.25	11	>ref|XP_483755.1| putative 60S ribosomal protein L10A (RPL10aC) [Oryza sativa(japonica cultivar-group)] dbj|BAD09090.1| putative 60S ribosomal protein L10A (RPL10aC) [Oryza sativa (japonica cultivar-group)]	216	3E-88
					>dbj|BAD28853.1| putative ribosomal protein L10a [Oryza sativa (japonicacultivar-group)]	216	7E-86
					>gb|AAW50982.1| ribosomal protein L10A [Triticum aestivum]	216	2E-84
					>ref|NP_563813.2| structural constituent of ribosome [Arabidopsis thaliana]gb|AAM47861.1| putative ribosomal protein L10 [Arabidopsis thaliana] gb|AAL38253.1| putative ribosomal protein L10 [Arabidopsis thaliana] sp|Q8VZB9|R10AA ARATH 60S ribosomal protein L10a-1	216	7E-83

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>ref|NP_850104.1| structural constituent of ribosome [Arabidopsis thaliana]ref|NP_565654.1| structural constituent of ribosome [Arabidopsis thaliana] gb|AAL07257.1| putative 60S ribosomal protein L10A [Arabidopsis thaliana] gb|AAK25856.1| putative 60S ribosomal protein L10A [Arabidopsis thaliana] gb|AAM15190.1| 60S ribosomal protein L10A [Arabidopsis thaliana] gb|AAC73045.2| 60S ribosomal protein L10A [Arabidopsis thaliana] gb|AAL91152.1| 60S ribosomal protein L10A [Arabidopsis thaliana] gb|AAP13370.1| At2g27530 [Arabidopsis thaliana] sp|P59230|R10AB_ARATH 60S ribosomal protein L10a-2	216	2E-82
BM267999	3.63E-03	Mo17<B73=F1	1.3	10	>ref|NP_001031228.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme[Arabidopsis thaliana] ref|NP_564828.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme [Arabidopsis thaliana] gb|AAM91500.1| At1g64230/F22C12_17 [Arabidopsis thaliana] gb|AAM11574.1| ubiquitin conjugating enzyme UBC9A [Arabidopsis thaliana] gb|AAK60309.1| At1g64230/F22C12_17 [Arabidopsis thaliana] gb|AAY44867.1| ubiquitinating enzyme [Arabidopsis thaliana]	148	1E-71
					>ref|XP_464900.1| ubiquitin-conjugating enzyme OsUBC5b [Oryza sativa (japonicacultivar-group)] dbj|BAD20047.1| ubiquitin-conjugating enzyme OsUBC5b [Oryza sativa (japonica cultivar-group)] dbj|BAB89355.1| ubiquitin-conjugating enzyme OsUBC5b [Oryza sativa (japonica cultivar-group)]	148	2E-71
					>gb|AAA64427.1| ubiquitin conjugating enzyme	148	7E-71
					>gb|AAR83891.1| ubiquitin-conjugating enzyme 8 [Capsicum annuum]gb|ABB54487.1| ubiquitin-conjugating enzyme E2 [Capsicum annuum]	148	7E-71
					>ref|NP_568788.1| UBC10; ubiquitin conjugating enzyme/ ubiquitin-like activatingenzyme [Arabidopsis thaliana] ref|NP_851181.1| UBC10; ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme [Arabidopsis thaliana] emb|CAA78715.1| ubiquitin conjugating enzyme [Arabidopsis thaliana] gb|AAM44985.1| putative E2, ubiquitin-conjugating enzyme UBC10 [Arabidopsis thaliana] gb|AAG41454.1| putative E2, ubiquitin-conjugating enzyme UBC10 [Arabidopsis thaliana] gb|AAM91074.1| AT5g53300/K19E1_10 [Arabidopsis thaliana] gb|AAL57693.1| AT5g53300/K19E1_10 [Arabidopsis thaliana] gb|AAK62621.1| AT5g53300/K19E1_10 [Arabidopsis thaliana] gb|AAG40357.1| AT5g53300 [Arabidopsis thaliana] gb|AAG40069.1| AT5g53300 [Arabidopsis thaliana] dbj|BAB09792.1| ubiquitin-conjugating enzyme E2-17 kD 10 (ubiquitin-protein ligase 10) (ubiquitin carrier protein 10) [Arabidopsis thaliana] gb|AAY44850.1| ubiquitinating enzyme [Arabidopsis thaliana] sp|P35133|UBC10_ARATH Ubiquitin-conjugating enzyme E2-17 kDa 10/12 (Ubiquitin-protein ligase 10/12) (Ubiquitin carrier protein 10/12) gb|AAA32895.1| ubiquitin conjugating enzyme	148	7E-71
AI692097	3.65E-03	Mo17<B73=F1	2.01	10	>emb|CAA56313.1| putative pp70 ribosomal protein S6 kinase [Avena sativa]	480	2E-52
					>ref|XP_479548.1| putative S6 ribosomal protein kinase [Oryza sativa (japonicacultivar-group)] dbj|BAC80008.1| putative S6 ribosomal protein kinase [Oryza sativa (japonica cultivar-group)]	310	4E-44
					>emb|CAB89082.1| S6 ribosomal protein kinase [Asparagus officinalis]	454	8E-42
					>gb|AAQ93804.1| ribosomal protein S6 kinase [Zea mays]	488	3E-38
					>ref|NP_850543.1| ATPK19; kinase [Arabidopsis thaliana]ref|NP_187484.1| ATPK19; kinase [Arabidopsis thaliana] gb|AAK17162.1| putative ribosomal-protein S6 kinase (ATPK19) [Arabidopsis thaliana] gb|AAG51345.1| putative ribosomal-protein S6 kinase (ATPK19); 61330-59548 [Arabidopsis thaliana] sp|Q39030|KPK19_ARATH Serine/threonine-protein kinase AtPK19 (Ribosomal-protein S6 kinase homolog)	471	2E-35
AI734703	3.67E-03	Mo17<B73=F1	1.43	10	>dbj|BAD81915.1| putative geranylgeranylated protein NTGP1 [Oryza sativa (japonicacultivar-group)]	216	1E-42
					>gb|AAT37501.1| putative SNARE protein [Hevea brasiliensis]	199	4E-39
					>dbj|BAD87240.1| putative NTGP1 [Oryza sativa (japonica cultivar-group)]	214	9E-39
					>gb|AAQ84317.1| fiber NTGP1-related protein [Gossypium barbadense]	199	4E-38
					>ref|NP_200614.1| YKT61 [Arabidopsis thaliana]gb|AAM91499.1| AT5g58060/k21l19_40 [Arabidopsis thaliana] gb|AAK60295.1| AT5g58060/k21l19_40 [Arabidopsis thaliana] gb|AAG40392.1| AT5g58060 [Arabidopsis thaliana] dbj|BAB10997.1| ATGP1 [Arabidopsis thaliana] sp|Q9ZRD6|YKT61_ARATH VAMP-like protein YKT61 (AtYKT61) (Geranylgeranylated protein 1) (AtGP1) gb|AAD00112.1| ATGP1 [Arabidopsis thaliana]	199	4E-38
DV621106	3.68E-03	B73<F1=Mo17	1.42	3	>ref|XP_464257.1| dentin sialophosphoprotein precursor-like [Oryza sativa (japonicacultivar-group)] dbj|BAD25712.1| dentin sialophosphoprotein precursor-like [Oryza sativa (japonica cultivar-group)] dbj|BAD26250.1| dentin sialophosphoprotein precursor-like [Oryza sativa (japonica cultivar-group)]	389	2E-32
					>ref|NP_909810.1| dentin sialophosphoprotein precursor-like protein [Oryza sativa(japonica cultivar-group)] gb|AAM19018.1| hypothetical protein [Oryza sativa (japonica cultivar-group)] gb|AAN65039.1| dentin sialophosphoprotein precursor-like protein [Oryza sativa (japonica cultivar-group)]	494	1E-15
					>gb|AAM13918.1| unknown protein [Arabidopsis thaliana]	337	6E-14
					>ref|NP_172151.2| unknown protein [Arabidopsis thaliana]	481	6E-14
					>ref|NP_001031449.1| unknown protein [Arabidopsis thaliana]ref|NP_180640.2| unknown protein [Arabidopsis thaliana] gb|AAU45205.1| At2g30820 [Arabidopsis thaliana] gb|AAS49046.1| At2g30820 [Arabidopsis thaliana]	421	8E-14
BM079958	3.68E-03	Mo17<B73=F1	3.67	10	>gb|AAS88577.1| terpene synthase 7 [Zea mays]	548	3E-22
					>ref|XP_471998.1| OSJNBb0085H11.9 [Oryza sativa (japonica cultivar-group)]emb|CAE03960.2| OSJNBb0085H11.9 [Oryza sativa (japonica cultivar-group)]	504	1E-21
					>ref|XP_471978.1| OSJNBb0062B06.7 [Oryza sativa (japonica cultivar-group)]emb|CAE04049.2| OSJNBb0062B06.7 [Oryza sativa (japonica cultivar-group)]	500	3E-21
					>ref|XP_471996.1| OSJNBb0085H11.7 [Oryza sativa (japonica cultivar-group)]emb|CAE03958.2| OSJNBb0085H11.7 [Oryza sativa (japonica cultivar-group)]	481	7E-21
					>ref|XP_471997.1| OSJNBb0085H11.8 [Oryza sativa (japonica cultivar-group)]emb|CAE03959.2| OSJNBb0085H11.8 [Oryza sativa (japonica cultivar-group)]	474	9E-21
CD661986	3.69E-03	B73=Mo17<F1	1.59	12	>gb|AAA87042.1| putative 32.7 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72097.1| 32 kDa protein [Hordeum vulgare]	304	2E-19
					>gb|AAB72098.1| 32 kDa protein [Hordeum vulgare]	306	7E-19
					>gb|AAA87041.1| putative 32.6 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72096.1| 32 kDa protein [Hordeum vulgare]	304	7E-19
					>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	2E-18
					>gb|ABA96669.1| jakalin homolog [Oryza sativa (japonica cultivar-group)]	258	1E-17

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
CD651745	3.70E-03	B73=F1<Mo17	1.32	4	>tpg|DAA05104.1| TPA: TPA exp: WRKY transcription factor 39 [Oryza sativa (indicacultivar-group)]	361	1E-17
					>dbj|BAD27888.1| putative WRKY transcription factor [Oryza sativa (japonicacultivar-group)]	361	1E-17
					>ref|NP_568777.1| WRKY27; transcription factor [Arabidopsis thaliana]gb|AAL13041.1| WRKY transcription factor 27 [Arabidopsis thaliana] dbj|BAB10431.1| unnamed protein product [Arabidopsis thaliana] sp|Q9FLX8|WRK27 ARATH Probable WRKY transcription factor 27 (WRKY DNA-binding protein 27)	348	1E-7
					>gb|AAO23325.1| WRKY transcription factor 22 [Capsella rubella]gb|AAO23324.1| WRKY transcription factor 22 [Capsella rubella]	302	6E-7
					>ref|NP_192034.1| WRKY22; transcription factor [Arabidopsis thaliana]emb|CAB80934.1| putative DNA-binding protein [Arabidopsis thaliana] gb|AAL85135.1| putative DNA-binding protein [Arabidopsis thaliana] gb|AAK76583.1| putative DNA-binding protein [Arabidopsis thaliana] gb|AAL35285.1| WRKY transcription factor 22 [Arabidopsis thaliana] gb|AAB61016.1| similar to SPF1 DNA-binding protein [Arabidopsis thaliana] sp|O04609|WRK22_ARATH WRKY transcription factor 22 (WRKY DNA-binding protein 22)	298	6E-7
CB334689	3.72E-03	F1=Mo17<B73	1.37	9	>ref|XP 464007.1| putative ATP synthase [Oryza sativa (japonica cultivar-group)]dbj|BAD07747.1| putative ATP synthase [Oryza sativa (japonica cultivar-group)]	240	4E-74
					>gb|AAT36616.1| mitochondrial ATP synthase precursor [Triticum aestivum]	238	9E-74
					>emb|CAA52349.1| putative ATP synthase subunit [Glycine max]	179	9E-50
					>ref|NP_179778.1| unknown protein [Arabidopsis thaliana]gb|AAL85043.1| putative ATP synthase [Arabidopsis thaliana] gb|AAK76694.1| putative ATP synthase [Arabidopsis thaliana] gb|AAD20405.1| putative ATP synthase [Arabidopsis thaliana] sp|Q9SJ12|ATP7_ARATH Probable ATP synthase 24 kDa subunit, mitochondrial precursor	240	1E-48
					>ref|NP 850018.1| unknown protein [Arabidopsis thaliana]	220	1E-48
DV549348	3.73E-03	F1=Mo17<B73	1.33	9	>ref|NP 921446.1| unknown protein [Oryza sativa (japonica cultivar-group)]	713	1E-26
					>gb|AAP80664.1| S28 ribosomal protein [Triticum aestivum]	86	1E-20
					>emb|CAA04565.1| rpS28 [Hordeum vulgare subsp. vulgare]	65	7E-20
					>emb|CAA57636.1| small subunit ribosomal protein S28 [Zea mays]sp|P46302|RS28 MAIZE 40S ribosomal protein S28	65	1E-19
					>emb|CAA10103.1| ribosomal protein S28 [Prunus persica]emb|CAA10102.1| ribosomal protein S28 [Prunus persica] emb|CAA10101.1| ribosomal protein S28 [Prunus persica]	65	3E-18
CD527497	3.74E-03	Mo17<B73=F1	1.29	10	ns		
AW585290	3.75E-03	B73=F1<Mo17	1.53	5	ns		
CB815806	3.78E-03	Mo17<B73=F1	1.38	10	>ref|XP 476772.1| putative root hairless 1 [Oryza sativa (japonica cultivar-group)]dbj|BAC83617.1| putative root hairless 1 [Oryza sativa (japonica cultivar-group)]	367	1E-53
					>gb|AAC69460.1| ROOT HAIRLESS 1 [Arabidopsis thaliana]	355	1E-21
					>ref|NP_564526.1| RHL1 (ROOT HAIRLESS 1) [Arabidopsis thaliana]gb|AAM91453.1| At1g48380/F11A17_7 [Arabidopsis thaliana] gb|AAL15337.1| At1g48380/F11A17_7 [Arabidopsis thaliana] gb|AAD49759.1| Identical to root hairless 1 (RHL1) from Arabidopsis thaliana gb|Z29767. EST gb|AI995014 comes from this gene gb|AAC23500.1| ROOT HAIRLESS 1 [Arabidopsis thaliana]	355	1E-21
BG873845	3.78E-03	Mo17<B73=F1	1.49	10	>ref|NP 915654.1| P0677H08.7 [Oryza sativa (japonica cultivar-group)]dbj|BAB89792.1| membrane protein COV-like [Oryza sativa (japonica cultivar-group)]	259	1E-56
					>gb|AAV59306.1| unknown protein [Oryza sativa (japonica cultivar-group)]ref|XP 475304.1| unknown protein [Oryza sativa (japonica cultivar-group)]	260	2E-51
					>gb|AAM64375.1| unknown [Arabidopsis thaliana]	261	4E-44
					>ref|NP_564483.1| LCV2 [Arabidopsis thaliana]gb|AAG50825.1| unknown protein [Arabidopsis thaliana] dbj|BAD44523.1| unknown protein [Arabidopsis thaliana] dbj|BAD44455.1| unknown protein [Arabidopsis thaliana]	261	4E-44
					>ref|NP_565465.1| LCV1 [Arabidopsis thaliana]gb|AAM91311.1| unknown protein [Arabidopsis thaliana] gb|AAD24400.2| expressed protein [Arabidopsis thaliana] gb|AAL62439.1| unknown protein [Arabidopsis thaliana] gb|AAM61503.1| unknown [Arabidopsis thaliana]	256	1E-40
BM338943	3.80E-03	Mo17<B73=F1	1.51	10	>dbj|BAD35914.1| tubulin-specific chaperone C-like [Oryza sativa (japonicacultivar-group)] dbj|BAD35569.1| tubulin-specific chaperone C-like [Oryza sativa (japonica cultivar-group)]	581	2E-35
					>ref|XP_464449.1| tubulin-specific chaperone C-like protein [Oryza sativa (japonicacultivar-group)] ref|XP_506744.1| PREDICTED OJ1225_F07.5-1 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD25242.1| tubulin-specific chaperone C-like protein [Oryza sativa (japonica cultivar-group)]	579	4E-35
					>ref|NP 973669.1| unknown protein [Arabidopsis thaliana]gb|AAU95425.1| At2g42230 [Arabidopsis thaliana] gb|AAU05480.1| At2g42230 [Arabidopsis thaliana]	568	5E-28
					>ref|NP_567059.1| unknown protein [Arabidopsis thaliana]gb|AAL36073.1| AT3g57890/T10K17_100 [Arabidopsis thaliana] gb|AAK96632.1| AT3g57890/T10K17 100 [Arabidopsis thaliana]	573	7E-28
					>emb|CAB67617.1| putative protein [Arabidopsis thaliana]	570	2E-23
CB833986	3.84E-03	B73<F1=Mo17	1.42	3	>sp|Q41785|TBB8 MAIZE Tubulin beta-8 chain (Beta-8 tubulin)gb|AAA19709.1| beta-8 tubulin	445	1E-88
					>ref|NP_912596.1| tubulin beta-4 chain [Oryza sativa (japonica cultivar-group)]dbj|BAB64211.1| putative beta-tubulin 4 [Oryza sativa (japonica cultivar-group)] sp|Q43594|TBB1 ORYSA Tubulin beta-1 chain (Beta-1 tubulin) dbj|BAB39951.1| putative tubulin beta-4 chain [Oryza sativa (japonica cultivar-group)]	447	1E-88
					>emb|CAA52720.1| beta-5 tubulin [Zea mays]sp|Q43697|TBB5 MAIZE Tubulin beta-5 chain (Beta-5 tubulin)	445	1E-88
					>sp|Q9ZRA8|TBB5 WHEAT Tubulin beta-5 chain (Beta-5 tubulin)gb|AAD10492.1| beta-tubulin 5 [Triticum aestivum]	447	1E-88
					>sp|Q9ZPN7|TBB4 ELEIN Tubulin beta-4 chain (Beta-4 tubulin)gb|AAD20181.1| beta-tubulin 4 [Eleusine indica]	446	1E-88
CB816036	3.88E-03	B73=F1<Mo17	1.37	4	>ref|NP_912768.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]dbj|BAD06873.1| replication protein A 14kDa [Oryza sativa (japonica cultivar-group)] dbj|BAA84607.1| unknown protein [Oryza sativa (japonica cultivar-group)]	106	2E-26
					>ref|NP 567560.2| unknown protein [Arabidopsis thaliana]gb|AAS88756.1| At4g18590 [Arabidopsis thaliana] gb|AAS76692.1| At4g18590 [Arabidopsis thaliana]	106	3E-18

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation[*]	Score	E value
					>emb|CAB78861.1| pollen-specific protein-like [Arabidopsis thaliana]emb|CAA16739.1| pollen-specific protein - like [Arabidopsis thaliana]	842	4E-16
					>ref|NP_190831.1| unknown protein [Arabidopsis thaliana]emb|CAB89224.1| putative protein [Arabidopsis thaliana]	107	4E-15
CD568491	3.89E-03	B73<F1=Mo17	1.24	3	>gb|ABA95281.1| U2 snRNP auxilliary factor, large subunit, splicing factor,putative [Oryza sativa (japonica cultivar-group)]	613	3E-43
					>gb|AAY84880.1| U2AF large subunit [Triticum aestivum]	543	2E-42
					>gb|AAM98156.1| putative U2 snRNP auxiliary factor [Arabidopsis thaliana]	589	2E-33
					>gb|AAG51641.1| putative U2 snRNP auxiliary factor; 19096-22891 [Arabidopsisthaliana]	568	2E-33
					>ref|NP_176287.3| RNA binding / nucleic acid binding [Arabidopsis thaliana]	589	2E-33
CB605071	3.90E-03	Mo17<B73=F1	1.61	10	>dbj|BAD19416.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD36049.1| unknown protein [Oryza sativa (japonica cultivar-group)]	122	1E-11
CB605414	3.92E-03	Mo17<B73=F1	1.48	10	>ref|XP_465375.1| putative diaminopimelate decarboxylase [Oryza sativa (japonicacultivar-group)] dbj|BAD16980.1| putative diaminopimelate decarboxylase [Oryza sativa (japonica cultivar-group)]	490	9E-42
					>emb|CAB87661.1| diaminopimelate decarboxylase-like protein [Arabidopsis thaliana]	496	6E-40
					>emb|CAB62550.1| diaminopimelate decarboxylase [Arabidopsis thaliana]	145	6E-40
					>ref|NP_568252.1| diaminopimelate decarboxylase [Arabidopsis thaliana]gb|AAM98306.1| At5g11880/F14F18_50 [Arabidopsis thaliana] gb|AAK83608.1| AT5g11880/F14F18_50 [Arabidopsis thaliana]	489	6E-40
					>ref|NP_188056.1| diaminopimelate decarboxylase [Arabidopsis thaliana]gb|AAM67531.1| putative diaminopimelate decarboxylase [Arabidopsis thaliana] gb|AAK92758.1| putative diaminopimelate decarboxylase [Arabidopsis thaliana] gb|AAL55653.1| diaminopimelate decarboxylase [Arabidopsis thaliana] gb|AAM65955.1| putative diaminopimelate decarboxylase [Arabidopsis thaliana]	484	6E-40
DV491329	3.94E-03	Mo17<B73=F1	1.34	10	>gb|AAO72599.1| putative 2-dehydro-3-deoxyphosphooctonate aldolase [Oryza sativa(japonica cultivar-group)]	340	e-105
					>emb|CAA74645.1| 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum sativum]emb|CAA74644.1| 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum sativum] sp|O50044|KDSA_PEA 2-dehydro-3-deoxyphosphooctonate aldolase (Phospho-2-dehydro-3-deoxyoctonate aldolase) (3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase) (KDO-8-phosphate synthetase) (KDO 8-P synthase) (KDOPS)	290	e-101
					>ref|NP_974176.1| KDSA; 3-deoxy-8-phosphooctulonate synthase [Arabidopsis thaliana]ref|NP_001031300.1| KDSA; 3-deoxy-8-phosphooctulonate synthase [Arabidopsis thaliana] ref|NP_178068.1| KDSA; 3-deoxy-8-phosphooctulonate synthase [Arabidopsis thaliana] ref|NP_849906.1| KDSA; 3-deoxy-8-phosphooctulonate synthase [Arabidopsis thaliana] gb|AAK50087.1| At1g79500/T8K14_8 [Arabidopsis thaliana] gb|AAD30227.1| Strong similarity to gb|Y14272 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase from Pisum sativum. ESTs gb|AA067485 and gb|AI100551 come from this gene. [Arabidopsis thaliana] sp|Q9AV97|KDSA_ARATH 2-dehydro-3-deoxyphosphooctonate aldolase (Phospho-2-dehydro-3-deoxyoctonate aldolase) (3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase) (KDO-8-phosphate synthetase) (KDO 8-P synthase) (KDOPS) (AtkdsA)	290	3E-98
					>gb|AAM47465.1| AT5g09730/F17I14_80 [Arabidopsis thaliana]	290	3E-98
					>dbj|BAB41014.1| 2-dehydro-3-deoxyphosphooctonate aldolase [Arabidopsis thaliana]	290	1E-97
BM339889	3.95E-03	Mo17<B73=F1	1.34	11	>dbj|BAD53672.1| protodermal factor-like [Oryza sativa (japonica cultivar-group)]	186	2E-9
CD650941	3.97E-03	B73<F1=Mo17	1.49	3	>ref|XP_469890.1| putative aurora-related kinase [Oryza sativa (japonicacultivar-group)] gb|AAP50960.1| putative aurora-related kinase [Oryza sativa (japonica cultivar-group)] dbj|BAE00023.1| Aurora kinase [Oryza sativa (japonica cultivar-group)]	279	9E-61
					>ref|NP_182073.1| ATP binding / protein kinase/ protein serine/threonine kinase/protein-tyrosine kinase [Arabidopsis thaliana] emb|CAH69534.1| aurora-like kinase 3 [Arabidopsis thaliana] dbj|BAE00021.1| Aurora kinase [Arabidopsis thaliana] gb|AAC06151.1| putative protein kinase [Arabidopsis thaliana] gb|AAL69469.1| At2g45490/F17K2.2 [Arabidopsis thaliana]	288	3E-47
					>ref|NP_195009.1| kinase/ protein serine/threonine kinase [Arabidopsis thaliana]emb|CAB80000.1| putative serine/threonine protein kinase [Arabidopsis thaliana] emb|CAH69532.1| aurora-like kinase 1 [Arabidopsis thaliana] dbj|BAD95178.1| putative serine/threonine protein kinase [Arabidopsis thaliana] dbj|BAE00019.1| Aurora kinase [Arabidopsis thaliana]	294	9E-45
					>gb|AAM64506.1| putative serine/threonine protein kinase [Arabidopsis thaliana]	294	9E-45
					>emb|CAH69533.1| aurora-like kinase 2 [Arabidopsis thaliana]gb|AAR07517.1| At2g25880 [Arabidopsis thaliana] dbj|BAE00020.1| Aurora kinase [Arabidopsis thaliana] gb|AAC42257.1| putative protein kinase [Arabidopsis thaliana]	282	1E-43
CB816779	3.97E-03	Mo17<B73=F1	1.34	10	>ref|XP_483414.1| putative ribosomal protein L32 [Oryza sativa (japonicacultivar-group)] dbj|BAC75414.1| putative ribosomal protein L32 [Oryza sativa (japonica cultivar-group)]	133	4E-56
					>emb|CAH55765.1| ribosomal L32 [Oryza sativa (indica cultivar-group)]	133	3E-53
					>gb|AAZ32896.1| ribosomal protein L32 [Medicago sativa]	133	5E-51
					>gb|AAR83884.1| ly200 protein [Capsicum annuum]	133	2E-50
					>gb|ABB02639.1| ly200-like protein [Solanum tuberosum]gb|ABA40471.1| ly200-like protein [Solanum tuberosum]	133	6E-50
CD569015	3.97E-03	F1=Mo17<B73	6.71	9	>ref|XP_470471.1| putative chloroplastic RNA-binding protein, with alternative splicingisoforms [Oryza sativa (japonica cultivar-group)] gb|AAS01974.1| putative chloroplastic RNA-binding protein, with alternative splicing isoforms [Oryza sativa (japonica cultivar-group)]	884	8E-76
					>ref|NP_172989.1| unknown protein [Arabidopsis thaliana]gb|AAG54007.1| unknown protein [Arabidopsis thaliana] dbj|BAC43292.1| unknown protein [Arabidopsis thaliana] gb|AAD39665.1| ESTs gb|T22508, gb|H36196 and gb|AI100134 come from this gene. [Arabidopsis thaliana]	147	8E-65
					>emb|CAG14986.1| hypothetical protein [Cicer arietinum]	139	4E-63
BM337640	4.00E-03	F1<B73=Mo17	5.16	7	>gb|AAL16980.1| 15kD beta zein [Zea mays]	178	8E-44

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					>gb|AAA33543.1| zein protein	180	5E-41
					>gb|AAA33522.1| zein protein precursor	180	5E-41
					>sp|P06673|ZEB1 MAIZE Zein-beta precursor (16 kDa) (Zein 2) (Clone 15A3)gb|AAA33521.1| 15 kDa zein protein	180	1E-40
					>emb|CAG30668.1| beta-kafirin [Sorghum bicolor]	191	3E-16
CB381316	4.01E-03	Mo17<B73=F1	1.58	10	>dbj|BAD81138.1| unc-84 homolog B -like [Oryza sativa (japonica cultivar-group)]	455	2E-48
					>gb|AAV67831.1| unknown protein [Oryza sativa (japonica cultivar-group)]ref|XP_476245.1| unknown protein [Oryza sativa (japonica cultivar-group)] gb|AAV43967.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAC78599.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	453	4E-36
					>ref|NP_566380.2| unknown protein [Arabidopsis thaliana]gb|AAF19576.1| hypothetical protein [Arabidopsis thaliana] gb|AAP04030.1| unknown protein [Arabidopsis thaliana] dbj|BAC42710.1| unknown protein [Arabidopsis thaliana]	455	9E-33
					>gb|AAM65947.1| unknown [Arabidopsis thaliana]	285	3E-32
					>ref|NP_196118.1| unknown protein [Arabidopsis thaliana]gb|AAM47476.1| AT5g04990/MUG13_15 [Arabidopsis thaliana] gb|AAL08289.1| AT5g04990/MUG13_15 [Arabidopsis thaliana] dbj|BAB11521.1| unnamed protein product [Arabidopsis thaliana]	471	1E-28
DV551200	4.01E-03	B73<F1=Mo17	1.56	2	>gb|AAX96059.1| dna-directed rna polymerase ii 8.2 kda polypeptide (ec2.7.7.6)(rpb10) (rp10) (abc10) [Oryza sativa (japonica cultivar-group)] gb|ABA91866.1| dna-directed rna polymerase ii 8.2 kda polypeptide [Oryza sativa (japonica cultivar-group)]	74	3E-33
					>ref|NP_849640.1| DNA-directed RNA polymerase [Arabidopsis thaliana]gb|AAM61374.1| RNA polymerase II subunit (hsRPB10), putative [Arabidopsis thaliana] dbj|BAC42977.1| putative RNA polymerase II subunit hsRPB10 [Arabidopsis thaliana]	71	2E-31
					>sp|Q39290|RPB10_BRANA DNA-directed RNA polymerase II 8.2 kDa polypeptide (RPB10) (RP10)(ABC10) gb|AAA21279.1| RNA polymerase II subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139	71	3E-31
					>ref|NP_176363.1| DNA-directed RNA polymerase [Arabidopsis thaliana]gb|AAD21426.1| Putative RNA polymerase II subunit Rpb10 [Arabidopsis thaliana] sp|Q9SYA6|RPB10 ARATH DNA-directed RNA polymerase II 8.2 kDa polypeptide (RPB10) (RP10) (ABC10)	71	3E-30
					>ref|XP_790633.1| PREDICTED: similar to DNA-directed RNA polymerase II 7.6 kDapolypeptide (RPB10) (RPB7.6) (RPABC5) [Strongylocentrotus purpuratus]	76	2E-26
CB411000	4.02E-03	Mo17<B73=F1	1.25	11	>ref|XP_469890.1| putative aurora-related kinase [Oryza sativa (japonicacultivar-group)] gb|AAP50960.1| putative aurora-related kinase [Oryza sativa (japonica cultivar-group)] dbj|BAE00023.1| Aurora kinase [Oryza sativa (japonica cultivar-group)]	279	1E-99
					>ref|NP_182073.1| ATP binding / protein kinase/ protein serine/threonine kinase/protein-tyrosine kinase [Arabidopsis thaliana] emb|CAH69534.1| aurora-like kinase 3 [Arabidopsis thaliana] dbj|BAE00021.1| Aurora kinase [Arabidopsis thaliana] gb|AAC06151.1| putative protein kinase [Arabidopsis thaliana] gb|AAL69469.1| At2g45490/F17K2.2 [Arabidopsis thaliana]	288	1E-76
					>ref|NP_195009.1| kinase/ protein serine/threonine kinase [Arabidopsis thaliana]emb|CAB80000.1| putative serine/threonine protein kinase [Arabidopsis thaliana] emb|CAH69532.1| aurora-like kinase 1 [Arabidopsis thaliana] dbj|BAD95178.1| putative serine/threonine protein kinase [Arabidopsis thaliana] dbj|BAE00019.1| Aurora kinase [Arabidopsis thaliana]	294	3E-68
					>gb|AAM64506.1| putative serine/threonine protein kinase [Arabidopsis thaliana]	294	7E-68
					>emb|CAH69533.1| aurora-like kinase 2 [Arabidopsis thaliana]gb|AAR07517.1| At2g25880 [Arabidopsis thaliana] dbj|BAE00020.1| Aurora kinase [Arabidopsis thaliana] gb|AAC42257.1| putative protein kinase [Arabidopsis thaliana]	282	2E-67
CB886589	4.04E-03	Mo17<B73=F1	1.31	11	>emb|CAA67225.1| ribosomal protein S21 [Zea mays]sp|Q41852|RS21 MAIZE 40S ribosomal protein S21	81	4E-38
					>emb|CAA70852.1| 40S ribosomal subunit protein S21 [Zea mays]	81	6E-37
					>dbj|BAA02158.1| 40S subunit ribosomal protein [Oryza sativa (japonicacultivar-group)] sp|P35687|RS21 ORYSA 40S ribosomal protein S21	82	2E-34
					>ref|XP_469197.1| 40S subunit ribosomal protein [Oryza sativa (japonicacultivar-group)] gb|AAP44638.1| 40S subunit ribosomal protein [Oryza sativa (japonica cultivar-group)]	82	5E-34
					>gb|AAU89141.1| 40S ribosomal protein S21, putative [Oryza sativa (japonicacultivar-group)]	119	7E-33
CB331516	4.04E-03	Mo17<B73=F1	1.34	10	>gb|AAR87233.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]gb|AAT78768.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	145	5E-22
					>dbj|BAB21526.1| mitochondrial ATP synthase 6 KD subunit [Oryza sativa (japonicacultivar-group)]	58	3E-21
					>ref|NP_680457.1| unknown protein [Arabidopsis thaliana]ref|NP_190227.1| unknown protein [Arabidopsis thaliana] emb|CAB62034.1| putative protein [Arabidopsis thaliana] gb|AAM19926.1| AT3g46430/F18L15_150 [Arabidopsis thaliana] gb|AAM10121.1| unknown protein [Arabidopsis thaliana] gb|AAL36060.1| AT3g46430/F18L15_150 [Arabidopsis thaliana] gb|AAL32914.1| Unknown protein [Arabidopsis thaliana] dbj|BAC43026.1| unknown protein [Arabidopsis thaliana] dbj|BAC42332.1| unknown protein [Arabidopsis thaliana]	55	3E-20
CB381093	4.05E-03	Mo17<B73=F1	1.26	10	ns		
BM074085	4.07E-03	B73<F1=Mo17	1.46	3	ns		
CB605200	4.08E-03	Mo17<B73=F1	1.37	10	>emb|CAA63903.1| heat shock protein 17.9 [Pennisetum glaucum]	159	5E-49
					>ref|NP_912354.1| putative class I low-molecular-weight heat shock protein [Oryzasativa (japonica cultivar-group)] dbj|BAC78583.1| heat shock protein 18 [Oryza sativa (japonica cultivar-group)] gb|AAK54445.1| class I low-molecular-weight heat shock protein 17.9 [Oryza sativa] gb|AAP06878.1| putative class I low-molecular-weight heat shock protein [Oryza sativa (japonica cultivar-group)]	161	4E-48
					>ref|NP_912359.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAP06883.1| unknown protein [Oryza sativa (japonica cultivar-group)]	161	2E-46
					>ref|NP_912358.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAP06882.1| unknown protein [Oryza sativa (japonica cultivar-group)] gb|AAC78392.1| low molecular mass heat shock protein Oshsp17.3 [Oryza sativa]	154	3E-45
					>gb|AAM28293.1| class-1 LMW heat shock protein [Ananas comosus]	156	7E-45

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
DV489868	4.08E-03	B73=F1<Mo17	2.24	4	>ref|XP_550452.1| putative MYB29 protein [Oryza sativa (japonica cultivar-group)]dbj|BAD67706.1| putative MYB29 protein [Oryza sativa (japonica cultivar-group)]	298	2E-48
					>dbj|BAD45449.1| MYB29 protein [Oryza sativa (japonica cultivar-group)]	166	1E-24
					>emb|CAD44621.1| MYB29 protein [Oryza sativa (japonica cultivar-group)]	107	2E-24
					>gb|AAZ20444.1| MYBR5 [Malus x domestica]	323	1E-23
					>ref|NP_851177.1| DNA binding / transcription factor [Arabidopsis thaliana]emb|CAI77451.1| myb transcription factor LHY-CCA1-like2 [Arabidopsis thaliana] gb|AAM65227.1| contains similarity to MYB-related DNA-binding protein [Arabidopsis thaliana]	330	3E-22
AW076397	4.08E-03	Mo17<B73=F1	1.4	10	>ref|XP 475676.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAT44270.1| unknown protein [Oryza sativa (japonica cultivar-group)]	374	4E-7
					>ref|NP 922097.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]gb|AAN05005.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	297	4E-6
					>gb|ABA99826.1| DNA binding protein, putative [Oryza sativa (japonicacultivar-group)]	407	6E-6
DV490225	4.11E-03	Mo17<B73=F1	1.25	11	>ref|XP_468271.1| putative 60S ribosomal protein L39 [Oryza sativa (japonicacultivar-group)] dbj|BAD19088.1| putative 60S ribosomal protein L39 [Oryza sativa (japonica cultivar-group)]	118	3E-24
					>ref|XP_468273.1| 60S RIBOSOMAL PROTEIN L39 [Oryza sativa (japonica cultivar-group)]dbj|BAD19090.1| 60S RIBOSOMAL PROTEIN L39 [Oryza sativa (japonica cultivar-group)] emb|CAA64728.1| ribosomal protein L39 [Zea mays] sp|P51425|RL39_MAIZE 60S ribosomal protein L39 sp|P51426|RL39_ORYSA 60S ribosomal protein L39	51	1E-23
					>dbj|BAD72572.1| 60S ribosomal protein L39 [Oryza sativa (japonica cultivar-group)]dbj|BAD72315.1| 60S ribosomal protein L39 [Oryza sativa (japonica cultivar-group)]	51	4E-23
					>gb|AAW50988.1| ribosomal protein L39 [Triticum aestivum]	51	1E-22
					>ref|NP_567886.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAQ65098.1| At2g25210 [Arabidopsis thaliana] gb|AAL15360.1| AT4g31981/F13D4.162 [Arabidopsis thaliana] gb|AAK49624.1| F13D4.162/F13D4.162 [Arabidopsis thaliana] dbj|BAC42854.1| unknown protein [Arabidopsis thaliana] sp|P51424|RL39 ARATH 60S ribosomal protein L39	51	5E-21
BG841520	4.14E-03	Mo17<B73=F1	1.7	10	>ref|NP_915433.1| putative triosephosphate isomerase [Oryza sativa (japonicacultivar-group)] dbj|BAB93230.1| putative triosephosphate isomerase [Oryza sativa (japonica cultivar-group)]	255	2E-64
					>ref|XP_462797.1| putative triosephosphate isomerase [Oryza sativa (japonicacultivar-group)] dbj|BAB21144.1| putative triosephosphate isomerase [Oryza sativa (japonica cultivar-group)] dbj|BAB43989.1| putative triosephosphate isomerase [Oryza sativa (japonica cultivar-group)] sp|P48494|TPIS_ORYSA Triosephosphate isomerase, cytosolic (TIM) (Triose-phosphate isomerase) gb|AAA18541.1| triosephosphate isomerase	253	2E-59
					>gb|AAB81110.1| triosephosphate isomerase 1 [Zea mays]sp|P12863|TPIS_MAIZE Triosephosphate isomerase, cytosolic (TIM) (Triose-phosphate isomerase) dbj|BAA00009.1| triosephosphate isomerase [Zea mays]	253	3E-58
					>emb|CAA81487.1| triosephosphate isomerase [Secale cereale]sp|P46226|TPIS_SECCE Triosephosphate isomerase, cytosolic (TIM) (Triose-phosphate isomerase) prf||2109226A triosephosphate isomerase	253	2E-57
					>gb|ABA46792.1| triosphosphate isomerase-like protein [Solanum tuberosum]	257	2E-57
DV491652	4.15E-03	Mo17<B73	1.52	9	>gb|AAO26580.1| glyoxalase II [Brassica juncea]	335	1E-20
					>gb|AAM34273.1| glyoxalase II [Pennisetum glaucum]	336	1E-20
					>gb|AAL14249.1| glyoxalase II [Oryza sativa]dbj|BAD33825.1| glyoxalase II [Oryza sativa (japonica cultivar-group)]	336	1E-20
					>ref|NP_849599.1| hydroxyacylglutathione hydrolase [Arabidopsis thaliana]gb|AAM91233.1| glyoxalase II isozyme, putative [Arabidopsis thaliana] gb|AAM20436.1| glyoxalase II isozyme, putative [Arabidopsis thaliana]	330	2E-15
					>ref|NP 563760.1| hydroxyacylglutathione hydrolase [Arabidopsis thaliana]gb|AAM62972.1| glyoxalase II isozyme, putative [Arabidopsis thaliana]	331	2E-15
DV491301	4.17E-03	Mo17<B73=F1	1.37	11	>ref|XP_467761.1| putative ATPase [Oryza sativa (japonica cultivar-group)]dbj|BAD16127.1| putative ATPase [Oryza sativa (japonica cultivar-group)] dbj|BAD15543.1| putative ATPase [Oryza sativa (japonica cultivar-group)]	406	5E-41
					>gb|AAF02825.1| putative ATPase [Arabidopsis thaliana]	386	6E-37
					>ref|NP 187646.2| ATP binding [Arabidopsis thaliana]	411	6E-37
					>ref|NP 200881.2| ATP binding [Arabidopsis thaliana]gb|AAV43781.1| At5g60730 [Arabidopsis thaliana] gb|AAU84673.1| At5g60730 [Arabidopsis thaliana]	391	2E-33
					>dbj|BAB09846.1| arsenite translocating ATPase-like protein [Arabidopsis thaliana]	417	2E-33
CA829982	4.17E-03	Mo17<B73=F1	1.21	10	>gb|ABA94602.1| ribosomal protein S4 [Oryza sativa (japonica cultivar-group)]	192	5E-17
					>gb|ABA94601.1| ribosomal protein S4 [Oryza sativa (japonica cultivar-group)]gb|ABA94599.1| ribosomal protein S4 [Oryza sativa (japonica cultivar-group)]	195	5E-17
					>gb|ABA94598.1| ribosomal protein S4 [Oryza sativa (japonica cultivar-group)]	158	5E-17
					>emb|CAG47084.1| 40S ribosomal protein S9 [Catharanthus roseus]	197	1E-15
					>ref|NP_198801.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAM65655.1| 40S ribosomal protein S9-like [Arabidopsis thaliana] dbj|BAB10209.1| 40S ribosomal protein S9 [Arabidopsis thaliana]	197	3E-15
CB380716	4.19E-03	F1=Mo17<B73	1.28	9	>ref|XP_480842.1| putative 60S ribosomal protein L7 [Oryza sativa (japonicacultivar-group)] dbj|BAD03800.1| putative 60S ribosomal protein L7 [Oryza sativa (japonica cultivar-group)]	245	1E-82
					>gb|AAW50989.1| ribosomal protein L7 [Triticum aestivum]	244	1E-81

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>ref|XP_473801.1| OSJNBb0015N08.13 [Oryza sativa (japonica cultivar-group)]emb|CAE03885.2| OSJNBb0015N08.13 [Oryza sativa (japonica cultivar-group)] emb|CAE02124.2| OSJNBa0035M09.3 [Oryza sativa (japonica cultivar-group)]	250	7E-81
					>ref|NP_974305.1| structural constituent of ribosome / transcription regulator[Arabidopsis thaliana] ref|NP_974304.1| structural constituent of ribosome / transcription regulator [Arabidopsis thaliana] ref|NP_187967.1| structural constituent of ribosome / transcription regulator [Arabidopsis thaliana] gb|AAL76153.1| AT3g13580/K20M4_2 [Arabidopsis thaliana] gb|AAL06999.1| AT3g13580/K20M4_2 [Arabidopsis thaliana] gb|AAK64004.1| AT3g13580/K20M4_2 [Arabidopsis thaliana] dbj|BAB02600.1| 60S ribosomal protein L7 [Arabidopsis thaliana] sp|Q9LHP1|RL73 ARATH 60S ribosomal protein L7-3	244	1E-74
					>ref|NP_850411.1| structural constituent of ribosome / transcription regulator[Arabidopsis thaliana] gb|AAC23430.1| 60S ribosomal protein L7 [Arabidopsis thaliana] pir||T00692 60S ribosomal protein L7 [imported] - Arabidopsis thaliana	247	2E-74
DV621338	4.20E-03	Mo17<B73=F1	1.58	10	>dbj|BAD81308.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD81453.1| unknown protein [Oryza sativa (japonica cultivar-group)]	249	6E-23
					>ref|NP_920307.1| putative DNA binding protein [Oryza sativa (japonicacultivar-group)] gb|AAN09856.1| putative DNA binding protein [Oryza sativa (japonica cultivar-group)] gb|AAP52594.1| DNA binding protein, putative [Oryza sativa (japonica cultivar-group)]	454	1E-22
					>gb|ABA99343.1| hypothetical protein LOC Os12g35400 [Oryza sativa (japonicacultivar-group)]	780	3E-22
					>gb|AAT81738.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	1500	4E-22
					>gb|AAX95750.1| Eukaryotic protein of unknown function (DUF889), putative [Oryzasativa (japonica cultivar-group)]	1806	3E-21
CB833704	4.23E-03	Mo17<B73=F1	1.36	10	>gb|AAM08320.1| small Ran-related GTP-binding protein [Triticum aestivum]gb|AAL30396.1| small Ras-related GTP-binding protein [Triticum aestivum]	221	2E-17
					>ref|XP_475914.1| GTP-binding nuclear protein RAN-B1 [Oryza sativa (japonicacultivar-group)] gb|AAT69585.1| GTP-binding nuclear protein RAN-B1 [Oryza sativa (japonica cultivar-group)] dbj|BAA81911.1| Ran [Oryza sativa (japonica cultivar-group)] dbj|BAB82438.1| small GTP-binding protein (Ran2) [Oryza sativa (japonica cultivar-group)]	221	2E-17
					>gb|AAD18006.1| Ran-related GTP binding protein [Zea mays]	170	1E-16
					>emb|CAC10213.1| GTP-binding protein [Cicer arietinum]	221	1E-15
					>gb|AAM12880.1| GTP-binding protein [Helianthus annuus]	221	1E-15
CB380415	4.24E-03	Mo17<B73=F1	2.91	10	ns		
CD568714	4.24E-03	Mo17<B73=F1	1.33	10	>ref|XP_479153.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)]ref|XP_506463.1| PREDICTED P0616D06.117 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC16499.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)] dbj|BAA04903.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)] sp|Q40680|EF1D ORYSA Elongation factor 1-delta (EF-1-delta) (Elongation factor 1B-beta) (eEF-1B beta)	229	7E-41
					>emb|CAB90214.1| putative elongation factor 1 beta [Hordeum vulgare subsp. vulgare]	226	6E-40
					>gb|AAR15081.1| translational elongation factor 1 subunit Bbeta [Pisum sativum]	231	4E-39
					>gb|AAU89237.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)]dbj|BAA34599.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)] dbj|BAA34598.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)]	226	1E-38
					>gb|ABA81875.1| putative elongation factor 1B alpha-subunit0like [Solanumtuberosum] gb|ABA40427.1| unknown [Solanum tuberosum]	227	4E-38
BM351809	4.28E-03	B73<F1=Mo17	1.44	2	>ref|XP_475961.1| putative late embryogenesis abundant protein [Oryza sativa(japonica cultivar-group)] gb|AAT47056.1| 'putative late embryogenesis abundant protein, LEA14-A' [Oryza sativa (japonica cultivar-group)] gb|AAS16887.1| putative late embryogenesis abundant protein [Oryza sativa (japonica cultivar-group)]	151	2E-72
					>gb|AAV88599.1| late embryonic abundant-like protein [Pennisetum glaucum]	176	4E-62
					>ref|NP_917764.1| putative embryogenesis-abundant protein [Oryza sativa (japonicacultivar-group)] dbj|BAB19059.1| late embryogenesis-abundant protein Lea14-A-like [Oryza sativa (japonica cultivar-group)] dbj|BAB21097.1| late embryogenesis-abundant protein Lea14-A-like [Oryza sativa (japonica cultivar-group)]	180	1E-61
					>ref|NP_913440.1| putative late embryogenesis abundant protein LEA14-A [Oryza sativa(japonica cultivar-group)] dbj|BAB32715.1| putative late embryogenesis-abundant protein [Oryza sativa (japonica cultivar-group)] dbj|BAB92106.1| putative late embryogenesis-abundant protein [Oryza sativa (japonica cultivar-group)]	151	4E-52
					>emb|CAI65403.1| dehydrin [Triticum turgidum subsp. durum]	151	3E-51
DV495681	4.28E-03	F1=Mo17<B73	1.46	9	>gb|AAP80664.1| S28 ribosomal protein [Triticum aestivum]	86	8E-22
					>emb|CAA04565.1| rpS28 [Hordeum vulgare subsp. vulgare]	65	6E-20
					>emb|CAA57636.1| small subunit ribosomal protein S28 [Zea mays]sp|P46302|RS28 MAIZE 40S ribosomal protein S28	65	8E-20
					>emb|CAA10103.1| ribosomal protein S28 [Prunus persica]emb|CAA10102.1| ribosomal protein S28 [Prunus persica] emb|CAA10101.1| ribosomal protein S28 [Prunus persica]	65	2E-18
					>gb|AAM78552.1| ribosomal protein small subunit 28 [Helianthus annuus]	65	7E-18
CB885881	4.31E-03	B73<F1=Mo17	1.41	3	>emb|CAA33620.1| GAPDH [Zea mays]sp|P08735|G3PC MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 1	337	1E-17
					>emb|CAA30151.1| unnamed protein product [Zea mays]	337	1E-17
					>gb|AAQ55395.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp.spontaneum] gb|AAQ55392.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55390.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55388.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55383.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55382.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55376.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum]	245	3E-16

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|AAQ55397.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp.spontaneum] gb|AAQ55396.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55394.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55393.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55391.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55389.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55387.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55386.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55385.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55384.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55381.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55380.1| glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare subsp. spontaneum] gb|AAQ55379.1| glyceraldehyde-3-phosphate dehydrogenase	245	3E-16
					>emb|CAA42901.1| glyceraldehyde 3-phosphate dehydrogenase [Hordeum vulgare]sp|P26517|G3PX_HORVU Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	337	3E-16
CB604707	4.32E-03	B73=F1<Mo17	1.61	4	>ref|XP_483378.1| p53 binding protein-like [Oryza sativa (japonica cultivar-group)]dbj|BAD10450.1| p53 binding protein-like [Oryza sativa (japonica cultivar-group)] dbj|BAD08763.1| p53 binding protein-like [Oryza sativa (japonica cultivar-group)]	347	8E-8
					>ref|XP_483379.1| p53 binding protein-like [Oryza sativa (japonica cultivar-group)]dbj|BAD10449.1| p53 binding protein-like [Oryza sativa (japonica cultivar-group)] dbj|BAD08762.1| p53 binding protein-like [Oryza sativa (japonica cultivar-group)]	346	8E-8
DV621532	4.32E-03	B73=F1<Mo17	1.53	5	>gb|AAL75999.1| putative polyprotein [Zea mays]	2749	4E-56
					>ref|XP_471041.1| OSJNBb0050O03.4 [Oryza sativa (japonica cultivar-group)]emb|CAE01714.2| OSJNBb0050O03.4 [Oryza sativa (japonica cultivar-group)]	1199	2E-32
					>gb|ABA97942.1| retrotransposon protein, putative, unclassified [Oryza sativa(japonica cultivar-group)]	985	5E-32
					>ref|NP_919539.1| putative retroelement [Oryza sativa (japonica cultivar-group)]gb|AAM08521.1| Putative retroelement [Oryza sativa] gb|AAP51826.1| retrotransposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]	335	4E-31
					>emb|CAE05716.2| OSJNBb0065J09.12 [Oryza sativa (japonica cultivar-group)]	436	2E-30
CB816420	4.33E-03	B73=F1<Mo17	1.28	4	>ref|NP_922068.1| putative thioredoxin-like U5 small ribonucleoprotein particleprotein [Oryza sativa (japonica cultivar-group)] ref|XP_477037.1| putative dim1p [Oryza sativa (japonica cultivar-group)] gb|AAL59040.1| putative thioredoxin-like U5 small ribonucleoprotein particle protein [Oryza sativa] dbj|BAD31005.1| putative dim1p [Oryza sativa (japonica cultivar-group)] dbj|BAC79773.1| putative dim1p [Oryza sativa (japonica cultivar-group)] gb|AAP54355.1| thioredoxin-like U5 small ribonucleoprotein particle protein, putative [Oryza sativa (japonica cultivar-group)]	142	3E-69
					>gb|AAP85544.1| putative DIM-like protein [Glycine max]	137	9E-69
					>ref|NP_196446.1| YLS8; catalytic/ electron transporter [Arabidopsis thaliana]emb|CAC08329.1| putative protein [Arabidopsis thaliana] gb|AAK00362.1| unknown protein [Arabidopsis thaliana] gb|AAG41439.1| unknown protein [Arabidopsis thaliana] gb|AAK52991.1| AT5g08290/F8L15_20 [Arabidopsis thaliana] gb|AAL47418.1| AT5g08290/F8L15_20 [Arabidopsis thaliana] gb|AAG40036.1| AT5g08290 [Arabidopsis thaliana] dbj|BAB32888.1| Dim1 homolog [Arabidopsis thaliana]	142	2E-68
					>gb|AAM61612.1| putative thioredoxin-like U5 small ribonucleoprotein particleprotein [Arabidopsis thaliana]	142	9E-68
					>ref|XP_418903.1| PREDICTED: similar to dim1; dim1 (S. pombe) [Gallus gallus]ref|XP_615554.1| PREDICTED: similar to dim1 isoform 1 [Bos taurus] ref|XP_533363.2| PREDICTED: similar to dim1 isoform 1 [Canis familiaris]	142	1E-61
DV492982	4.34E-03	B73=Mo17<F1	1.32	12	>ref|NP_910927.2| putative translation elongation factor eEF-1 beta' chain [Oryzasativa (japonica cultivar-group)] ref|XP_506540.1| PREDICTED P0453E03.111 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC22427.2| putative translation elongation factor eEF-1 beta' chain [Oryza sativa (japonica cultivar-group)]	224	5E-40
					>gb|ABA81875.1| putative elongation factor 1B alpha-subunit0like [Solanumtuberosum] gb|ABA40427.1| unknown [Solanum tuberosum]	227	3E-39
					>gb|AAT40505.1| putative elongation factor [Solanum demissum]	227	4E-39
					>gb|ABA40463.1| elongation factor-like protein [Solanum tuberosum]	227	1E-38
					>ref|NP_179402.1| translation elongation factor [Arabidopsis thaliana]gb|AAD31355.1| putative elongation factor beta-1 [Arabidopsis thaliana] gb|AAM15146.1| putative elongation factor beta-1 [Arabidopsis thaliana] gb|AAM10130.1| putative elongation factor 1-beta [Arabidopsis thaliana] gb|AAL38335.1| putative elongation factor 1-beta [Arabidopsis thaliana] sp|Q9SI20|EF1D2_ARATH Elongation factor 1-delta 2 (EF-1-delta 2) (Elongation factor 1B-beta 2) (eEF-1B beta 2)	231	5E-38
CB816784	4.35E-03	Mo17<B73=F1	1.4	10	>ref|XP_468402.1| putative NADH dehydrogenase [Oryza sativa (japonicacultivar-group)] dbj|BAD22016.1| putative NADH dehydrogenase [Oryza sativa (japonica cultivar-group)] dbj|BAD21515.1| putative NADH dehydrogenase [Oryza sativa (japonica cultivar-group)]	408	4E-74
					>ref|NP_565469.1| unknown protein [Arabidopsis thaliana]gb|AAT68351.1| hypothetical protein At2g20360 [Arabidopsis thaliana] gb|AAK93749.1| putative NADH-ubiquinone oxireductase [Arabidopsis thaliana] gb|AAK59545.1| putative NADH-ubiquinone oxireductase [Arabidopsis thaliana] gb|AAD21752.2| putative NADH-ubiquinone oxireductase [Arabidopsis thaliana] gb|AAX23820.1| hypothetical protein At2g20360 [Arabidopsis thaliana]	402	3E-49
					>gb|AAH91192.1| Ndufa9 protein [Rattus norvegicus]	370	8E-28
					>ref|XP_508942.1| PREDICTED: NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9,39kDa [Pan troglodytes]	347	1E-27
					>emb|CAH92896.1| hypothetical protein [Pongo pygmaeus]	377	1E-27
CD651138	4.35E-03	B73=F1<Mo17	1.2	4	>gb|AAB33305.1| GF14-12=GRF2 product/14-3-3 protein homolog [Zea mays, XL80,Peptide, 261 aa] sp|Q01526|14332 MAIZE 14-3-3-like protein GF14-12	261	2E-82
					>gb|AAB33304.1| GF14-6 [Zea mays]sp|P49106|14331 MAIZE 14-3-3-like protein GF14-6	261	4E-82
					>ref|XP_472763.1| OSJNBa0072F16.20 [Oryza sativa (japonica cultivar-group)]emb|CAE76003.1| B1358B12.12 [Oryza sativa (japonica cultivar-group)] emb|CAE01538.2| OSJNBa0072F16.20 [Oryza sativa (japonica cultivar-group)] gb|AAB07456.1| GF14-b protein	262	9E-81

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>emb|CAB77673.1| 14-3-3-like protein [Oryza sativa]dbj|BAD29578.1| putative GF14-b protein [Oryza sativa (japonica cultivar-group)] dbj|BAD27625.1| putative GF14-b protein [Oryza sativa (japonica cultivar-group)]	262	2E-78
					>emb|CAA63658.1| Hv14-3-3b [Hordeum vulgare subsp. vulgare]sp|Q43470|1433B HORVU 14-3-3-like protein B (14-3-3B)	262	2E-78
CD650893	4.36E-03	F1=Mo17<B73	1.39	9	ns		
CD001782	4.36E-03	B73<F1=Mo17	1.47	2	>dbj|BAD54452.1| putative xyloglucan endotransglycosylase [Oryza sativa (japonicacultivar-group)]	290	1E-11
					>emb|CAA63662.1| xyloglucan endotransglycosylase (XET) [Hordeum vulgare subsp.vulgare]	292	8E-11
					>ref|NP_200564.1| TCH4 (TOUCH 4); hydrolase, acting on glycosyl bonds / hydrolase,hydrolyzing O-glycosyl compounds [Arabidopsis thaliana] gb|AAL38614.1| AT5g57560/MUA2_13 [Arabidopsis thaliana] gb|AAL05902.1| AT5g57560/MUA2_13 [Arabidopsis thaliana] gb|AAK96616.1| AT5g57560/MUA2_13 [Arabidopsis thaliana] gb|AAK56251.1| AT5g57560/MUA2_13 [Arabidopsis thaliana] dbj|BAB08791.1| TCH4 protein [Arabidopsis thaliana] sp|Q38857|XTH22_ARATH Xyloglucan endotransglucosylase/hydrolase protein 22 precursor (At-XTH22) (XTH-22) (Touch protein 4) gb|AAC05572.1| xyloglucan endotransglycosylase related protein [Arabidopsis thaliana] gb|AAA92363.1| TCH4 protein	284	1E-9
					>emb|CAC40807.1| Xet1 protein [Festuca pratensis]	291	3E-9
					>emb|CAA63663.1| xyloglucan endotransglycosylase (XET) [Hordeum vulgare subsp.vulgare]	286	3E-9
CD485141	4.37E-03	B73<F1=Mo17	1.37	3	>dbj|BAD28177.1| putative Chain C, Structure Of The Plant Transcriptional RegulatorPbf-2 [Oryza sativa (japonica cultivar-group)] dbj|BAD28032.1| putative Chain C, Structure Of The Plant Transcriptional Regulator Pbf-2 [Oryza sativa (japonica cultivar-group)]	228	8E-78
					>ref|NP_177282.2| unknown protein [Arabidopsis thaliana]gb|AAM67494.1| unknown protein [Arabidopsis thaliana] gb|AAL59932.1| unknown protein [Arabidopsis thaliana]	238	1E-45
					>gb|AAG51881.1| unknown protein; 79476-81015 [Arabidopsis thaliana]	237	1E-45
					>gb|AAF91282.1| DNA-binding protein p24 [Solanum tuberosum]	274	1E-34
					>pdb|1L3A|D Chain D, Structure Of The Plant Transcriptional Regulator Pbf-2	171	1E-34
AW355879	4.37E-03	B73<F1=Mo17	1.36	3	>gb|AAQ24341.1| O-methyltransferase [Zea mays]gb|AAQ24340.1| O-methyltransferase [Zea mays]	364	1E-51
					>gb|AAQ24360.1| O-methyltransferase [Zea mays]gb|AAQ24338.1| O-methyltransferase [Zea mays]	364	1E-51
					>gb|AAQ24369.1| O-methyltransferase [Zea mays]gb|AAQ24367.1| O-methyltransferase [Zea mays] gb|AAQ24352.1| O-methyltransferase [Zea mays] gb|AAQ24349.1| O-methyltransferase [Zea mays] gb|AAQ24337.1| O-methyltransferase [Zea mays]	364	1E-51
					>gb|AAQ24347.1| O-methyltransferase [Zea mays]gb|AAQ24346.1| O-methyltransferase [Zea mays] sp|Q06509|COMT1_MAIZE Caffeic acid 3-O-methyltransferase (S-adenosysl-L-methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOMT) gb|AAB03364.1| O-methyltransferase	364	1E-51
					>gb|AAQ24339.1| O-methyltransferase [Zea mays]	364	3E-51
BG841347	4.37E-03	Mo17<B73=F1	1.45	11	>ref|XP_483755.1| putative 60S ribosomal protein L10A (RPL10aC) [Oryza sativa(japonica cultivar-group)] dbj|BAD09090.1| putative 60S ribosomal protein L10A (RPL10aC) [Oryza sativa (japonica cultivar-group)]	216	6E-85
					>dbj|BAD28853.1| putative ribosomal protein L10a [Oryza sativa (japonicacultivar-group)]	216	2E-82
					>gb|AAW50982.1| ribosomal protein L10A [Triticum aestivum]	216	5E-81
					>ref|NP_563813.2| structural constituent of ribosome [Arabidopsis thaliana]gb|AAM47861.1| putative ribosomal protein L10 [Arabidopsis thaliana] gb|AAL38253.1| putative ribosomal protein L10 [Arabidopsis thaliana] sp|Q8VZB9|R10AA ARATH 60S ribosomal protein L10a-1	216	2E-79
					>ref|NP_850104.1| structural constituent of ribosome [Arabidopsis thaliana]ref|NP_565654.1| structural constituent of ribosome [Arabidopsis thaliana] gb|AAL07257.1| putative 60S ribosomal protein L10A [Arabidopsis thaliana] gb|AAK25856.1| putative 60S ribosomal protein L10A [Arabidopsis thaliana] gb|AAM15190.1| 60S ribosomal protein L10A [Arabidopsis thaliana] gb|AAC73045.2| 60S ribosomal protein L10A [Arabidopsis thaliana] gb|AAL91152.1| 60S ribosomal protein L10A [Arabidopsis thaliana] gb|AAP13370.1| At2g27530 [Arabidopsis thaliana] sp|P59230|R10AB ARATH 60S ribosomal protein L10a-2	216	5E-79
DV942867	4.37E-03	F1=Mo17<B73	2.2	8	ns		
DV621372	4.39E-03	Mo17<B73=F1	1.37	11	>sp|P23346|SODC5 MAIZE Superoxide dismutase [Cu-Zn] 4AP	152	2E-84
					>emb|CAB57992.1| superoxide dismutase-4AP [Zea mays]sp|P23345|SODC4 MAIZE Superoxide dismutase [Cu-Zn] 4A	152	1E-83
					>emb|CAB57993.1| superoxide dismutase-4A [Zea mays]gb|AAB49913.1| superoxide dismutase 4A	152	2E-82
					>sp|P28757|SODC2_ORYSA Superoxide dismutase [Cu-Zn] 2gb|AAC14465.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00800.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)]	152	3E-78
					>gb|AAY56345.1| cytoplasmic copper/zinc-superoxide dismutase [Oryza sativa (indicacultivar-group)] sp|P28756|SODC1_ORYSA Superoxide dismutase [Cu-Zn] 1 gb|AAC14464.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00799.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)] prf||2111424A Cu/Zn superoxide dismutase	152	3E-77
BM339253	4.39E-03	F1=Mo17<B73	1.31	9	>ref|XP_467824.1| putative FKBP-type peptidyl-prolyl cis-trans isomerase 3 [Oryzasativa (japonica cultivar-group)] ref|XP_507531.1| PREDICTED P0431B06.35 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_506974.1| PREDICTED P0431B06.35 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD15648.1| putative FKBP-type peptidyl-prolyl cis-trans isomerase 3 [Oryza sativa (japonica cultivar-group)]	230	5E-50
					>ref|NP 568067.1| FK506 binding / peptidyl-prolyl cis-trans isomerase [Arabidopsisthaliana] emb|CAB64721.1| FKBP like protein [Arabidopsis thaliana]	217	6E-41
					>dbj|BAD45876.1| putative peptidyl-prolyl cis-trans isomerase [Oryza sativa(japonica cultivar-group)]	218	5E-25

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_199380.1| FK506 binding / peptidyl-prolyl cis-trans isomerase [Arabidopsisthaliana] gb|AAM10279.1| AT5g45680/MRA19_7 [Arabidopsis thaliana] gb|AAL57682.1| AT5g45680/MRA19_7 [Arabidopsis thaliana] dbj|BAB09210.1| unnamed protein product [Arabidopsis thaliana] sp|Q9SCY2|FKB13_ARATH FKBP-type peptidyl-prolyl cis-trans isomerase 3, chloroplast precursor (PPIase) (Rotamase) (AtFKBP13) (FK506 binding protein 1)	208	1E-23
					>emb|CAD35362.1| FK506 binding protein 1 [Arabidopsis thaliana]	208	1E-23
CB329597	4.40E-03	F1=Mo17<B73	1.24	9	>gb|ABA94601.1| ribosomal protein S4 [Oryza sativa (japonica cultivar-group)]gb|ABA94599.1| ribosomal protein S4 [Oryza sativa (japonica cultivar-group)]	195	3E-95
					>gb|ABA94602.1| ribosomal protein S4 [Oryza sativa (japonica cultivar-group)]	192	7E-92
					>gb|ABA46767.1| unknown [Solanum tuberosum]	197	5E-90
					>emb|CAG47084.1| 40S ribosomal protein S9 [Catharanthus roseus]	197	7E-90
					>gb|AAU93594.1| putative ribosomal protein [Solanum demissum]	197	2E-89
DV621095	4.41E-03	B73<F1=Mo17	1.42	3	>ref|NP_922279.1| actin [Oryza sativa (japonica cultivar-group)]gb|AAK84456.1| actin [Oryza sativa (japonica cultivar-group)] gb|AAP54566.1| actin [Oryza sativa (japonica cultivar-group)] sp|P17298|ACT2 ORYSA Actin-2	377	1E-86
					>ref|NP_196543.1| ACT7 [Arabidopsis thaliana]gb|AAM20037.1| putative actin 2/7 protein [Arabidopsis thaliana] gb|AAL36336.1| putative ACTIN 2/7 protein [Arabidopsis thaliana] gb|AAM53337.1| actin 2/7 [Arabidopsis thaliana] gb|AAM47998.1| ACTIN 2/7 [Arabidopsis thaliana] gb|AAL32780.1| ACTIN 2/7 [Arabidopsis thaliana] dbj|BAB09402.1| ACTIN 2/7 [Arabidopsis thaliana] sp|P53492|ACT7_ARATH Actin-7 (Actin-2) gb|AAB52506.1| actin7 gb|AAA80356.1| actin-2	377	4E-85
					>gb|AAD03741.1| actin [Brassica napus]	377	6E-85
					>gb|AAX95100.1| actin [Oryza sativa (japonica cultivar-group)]gb|AAX95099.1| actin [Oryza sativa (japonica cultivar-group)] gb|AAX95098.1| actin [Oryza sativa (japonica cultivar-group)] gb|AAO62546.1| actin [Oryza sativa (japonica cultivar-group)] gb|ABA91668.1| actin [Oryza sativa (japonica cultivar-group)] gb|ABA91667.1| actin [Oryza sativa (japonica cultivar-group)] gb|ABA91666.1| actin [Oryza sativa (japonica cultivar-group)]	377	6E-85
					>gb|AAW63030.1| actin [Isatis tinctoria]	377	6E-85
CD484983	4.41E-03	F1=Mo17<B73	1.25	9	>gb|AAN04491.1| phosphoribosyl pyrophosphate synthetase [Saccharum hybrid cultivar]	328	7E-51
					>ref|XP_467457.1| putative phosphoribosyl pyrophosphate synthetase [Oryza sativa(japonica cultivar-group)] ref|XP_507525.1| PREDICTED OJ1479_B12.26 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_506937.1| PREDICTED OJ1479_B12.26 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD09159.1| putative phosphoribosyl pyrophosphate synthetase [Oryza sativa (japonica cultivar-group)] dbj|BAD07797.1| putative phosphoribosyl pyrophosphate synthetase [Oryza sativa (japonica cultivar-group)] sp|Q6ZFT5|KPRS4_ORYSA Ribose-phosphate pyrophosphokinase 4 (Phosphoribosyl pyrophosphate synthetase 4)	325	3E-47
					>ref|NP_181819.1| ribose phosphate diphosphokinase [Arabidopsis thaliana]emb|CAB43553.1| phosphoribosyl diphosphate synthase [Arabidopsis thaliana] gb|AAN15402.1| putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana] gb|AAM91605.1| putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana] gb|AAD21718.1| putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana] gb|AAM15296.1| putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana] gb|AAM64955.1| putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana] sp|Q680A5|KPRS4_ARATH Ribose-phosphate pyrophosphokinase 4 (Phosphoribosyl pyrophosphate synthetase 4)	337	5E-38
					>ref|NP_916715.1| putative phosphoribosyl pyrophosphate synthase [Oryza sativa(japonica cultivar-group)] dbj|BAB89498.1| putative phosphoribosyl pyrophosphate synthase [Oryza sativa (japonica cultivar-group)] sp|Q8S2E5|KPRS3_ORYSA Ribose-phosphate pyrophosphokinase 3 (Phosphoribosyl pyrophosphate synthetase 3)	409	6E-37
					>emb|CAB43602.1| phosphoribosyl pyrophosphate synthase isozyme 4 [Spinacia oleracea]sp|Q9XGA1|KPRS4_SPIOL Ribose-phosphate pyrophosphokinase 4 (Phosphoribosyl pyrophosphate synthetase 4)	318	6E-37
CD670329	4.42E-03	F1=Mo17<B73	1.59	9	ns		
DV491801	4.43E-03	B73<F1=Mo17	1.49	2	>ref|XP_480473.1| putative Aconitate hydratase [Oryza sativa (japonica cultivar-group)]dbj|BAD05751.1| putative Aconitate hydratase [Oryza sativa (japonica cultivar-group)]	898	9E-40
					>dbj|BAD94991.1| cytoplasmic aconitate hydratase [Arabidopsis thaliana]	328	7E-38
					>ref|NP_178634.2| RNA binding / aconitate hydratase/ hydro-lyase/ iron ion binding /lyase [Arabidopsis thaliana] gb|AAP68248.1| At2g05710 [Arabidopsis thaliana] gb|AAM97080.1| cytoplasmic aconitate hydratase [Arabidopsis thaliana]	990	7E-38
					>gb|AAD25640.1| cytoplasmic aconitate hydratase [Arabidopsis thaliana]	898	7E-38
					>dbj|BAE71240.1| putative cytoplasmic aconitate hydratase [Trifolium pratense]	316	2E-36
CB331027	4.43E-03	Mo17<B73=F1	1.36	10	>ref|XP_468756.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)] ref|XP_468752.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] gb|AAP20855.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] gb|AAP20842.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] sp|P40978|RS19 ORYSA 40S ribosomal protein S19	146	7E-75
					>gb|AAW34237.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	144	4E-72
					>gb|AAW34236.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	166	3E-71
					>gb|AAW34240.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	122	1E-64
					>gb|ABB87116.1| 40S ribosomal protein S19-like [Solanum tuberosum]	143	2E-61
CB816349	4.45E-03	B73<F1=Mo17	1.36	3	>ref|XP_472639.1| OSJNBa0058G03.7 [Oryza sativa (japonica cultivar-group)]emb|CAE02431.2| OSJNBa0058G03.7 [Oryza sativa (japonica cultivar-group)] emb|CAE02442.2| OSJNBa0027P08.4 [Oryza sativa (japonica cultivar-group)]	425	8E-39

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_174210.1| ATS9 (19S PROTEOSOME SUBUNIT 9) [Arabidopsis thaliana]gb|AAP86663.1| 26S proteasome subunit RPN6a [Arabidopsis thaliana] gb|AAP86662.1| 26S proteasome subunit RPN6a [Arabidopsis thaliana] gb|AAL07160.1| putative 19S proteosome subunit 9 [Arabidopsis thaliana] gb|AAK44018.1| putative 19S proteosome subunit 9 [Arabidopsis thaliana] gb|AAF88122.1| Similar to 26S proteasome subunits [Arabidopsis thaliana]	419	4E-20
					>gb|AAC34120.1| 19S proteosome subunit 9 [Arabidopsis thaliana]	421	4E-20
					>gb|AAP86661.1| 26S proteasome subunit RPN6a [Arabidopsis thaliana]	419	2E-19
					>gb|AAP86664.1| 26S proteasome subunit RPN6a [Arabidopsis thaliana]	399	4E-17
CD001199	4.45E-03	Mo17<B73=F1	1.26	10	>gb|ABA94601.1| ribosomal protein S4 [Oryza sativa (japonica cultivar-group)]gb|ABA94599.1| ribosomal protein S4 [Oryza sativa (japonica cultivar-group)]	195	4E-99
					>gb|ABA94602.1| ribosomal protein S4 [Oryza sativa (japonica cultivar-group)]	192	1E-95
					>emb|CAG47084.1| 40S ribosomal protein S9 [Catharanthus roseus]	197	6E-91
					>gb|ABA46767.1| unknown [Solanum tuberosum]	197	6E-91
					>gb|AAU93594.1| putative ribosomal protein [Solanum demissum]	197	2E-90
AW585293	4.49E-03	Mo17<B73=F1	1.38	10	>ref|XP_470037.1| putative 40S ribosomal protein S2 [Oryza sativa (japonicacultivar-group)] gb|AAP21434.1| putative 40S ribosomal protein S2 [Oryza sativa (japonica cultivar-group)]	274	2E-58
					>ref|XP_477083.1| putative 40S ribosomal protein S2 [Oryza sativa (japonicacultivar-group)] dbj|BAC83243.1| putative 40S ribosomal protein S2 [Oryza sativa (japonica cultivar-group)]	276	7E-56
					>emb|CAC27136.1| 40S ribosomal protein S2 [Picea abies]	232	3E-52
					>gb|AAM62944.1| 40S ribosomal protein S2 [Arabidopsis thaliana]	285	2E-50
					>ref|NP_181715.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAM91391.1| At2g41840/T11A7.6 [Arabidopsis thaliana] gb|AAC02764.1| 40S ribosomal protein S2 [Arabidopsis thaliana] gb|AAK82512.1| At2g41840/T11A7.6 [Arabidopsis thaliana] sp|P49688|RS2 ARATH 40S ribosomal protein S2	285	2E-50
DV490563	4.52E-03	B73<F1=Mo17	1.35	2	>ref|XP_470662.1| Putative phosphate/phosphoenolpyruvate translocator protein [Oryzasativa (japonica cultivar-group)] gb|AAO16996.1| Putative phosphate/phosphoenolpyruvate translocator protein [Oryza sativa (japonica cultivar-group)]	322	3E-7
					>dbj|BAD91177.1| plastidic phosphate translocator-like protein2 [Mesembryanthemumcrystallinum]	306	4E-7
					>ref|NP 187740.2| organic anion transporter [Arabidopsis thaliana]gb|AAU94370.1| At3g11320 [Arabidopsis thaliana]	308	2E-6
					>gb|AAG50965.1| integral membrane protein, putative; 85705-84183 [Arabidopsisthaliana]	344	2E-6
					>ref|NP_196201.2| organic anion transporter [Arabidopsis thaliana]gb|AAU45213.1| At5g05820 [Arabidopsis thaliana] gb|AAT70430.1| At5g05820 [Arabidopsis thaliana]	309	4E-6
CD484325	4.52E-03	Mo17<B73=F1	1.47	10	>ref|XP_475416.1| putative 40S ribosomal protein S26 [Oryza sativa (japonicacultivar-group)] gb|AAT01360.1| putative 40S ribosomal protein S26 [Oryza sativa (japonica cultivar-group)]	194	7E-32
					>dbj|BAD87076.1| putative ribosomal protein S26 [Oryza sativa (japonicacultivar-group)] dbj|BAD73505.1| putative ribosomal protein S26 [Oryza sativa (japonica cultivar-group)]	133	7E-32
					>sp|P49216|RS26 ORYSA 40S ribosomal protein S26 (S31)dbj|BAA07208.1| ribosomal protein S31 [Oryza sativa (japonica cultivar-group)]	133	6E-31
					>gb|AAD47346.1| ribosomal protein S26 [Pisum sativum]	130	3E-26
					>ref|NP_191193.1| structural constituent of ribosome [Arabidopsis thaliana]emb|CAB87433.1| 40S ribosomal protein S26 homolog [Arabidopsis thaliana] gb|AAM91494.1| AT3g56340/F18O21 300 [Arabidopsis thaliana] gb|AAK63990.1| AT3g56340/F18O21 300 [Arabidopsis thaliana]	130	3E-25
CB886120	4.55E-03	Mo17<B73=F1	1.44	10	>ref|XP 474251.1| OSJNBa0087O24.9 [Oryza sativa (japonica cultivar-group)]emb|CAE03586.1| OSJNBa0087O24.9 [Oryza sativa (japonica cultivar-group)]	309	3E-16
					>dbj|BAD35424.1| KH domain-containing protein / zinc finger protein-like [Oryzasativa (japonica cultivar-group)]	295	1E-12
					>ref|XP_464444.1| KH domain-containing protein-like [Oryza sativa (japonicacultivar-group)] dbj|BAD15406.1| KH domain-containing protein-like [Oryza sativa (japonica cultivar-group)]	300	2E-11
					>ref|NP_566412.1| nucleic acid binding / transcription factor [Arabidopsis thaliana]gb|AAM62964.1| unknown [Arabidopsis thaliana] gb|AAG51040.1| unknown protein; 15726-17646 [Arabidopsis thaliana]	248	1E-8
					>dbj|BAB01961.1| unnamed protein product [Arabidopsis thaliana]	231	1E-8
CB334565	4.58E-03	Mo17<B73=F1	1.28	10	>gb|AAV36518.1| vacuolar ATPase subunit c isoform [Pennisetum glaucum]gb|AAL08022.1| vacuolar H+-ATPase 16 kDa proteolipid subunit c [Pennisetum glaucum]	165	3E-49
					>gb|AAK91135.1| V-ATPase subunit c [Porteresia coarctata]gb|ABA95923.1| V-type ATPase, C subunit [Oryza sativa (japonica cultivar-group)]	165	3E-49
					>gb|AAX93004.1| V-type ATPase, C subunit, putative [Oryza sativa (japonicacultivar-group)] sp|Q40635|VATL_ORYSA Vacuolar ATP synthase 16 kDa proteolipid subunit gb|ABA91617.1| V-type ATPase, C subunit, putative [Oryza sativa (japonica cultivar-group)] gb|AAA68175.1| H+-ATPase	165	3E-49
					>ref|NP_177693.1| AVA-P; ATPase [Arabidopsis thaliana]gb|AAM19995.1| At1g75630/F10A5_17 [Arabidopsis thaliana] gb|AAL11568.1| At1g75630/F10A5_17 [Arabidopsis thaliana] gb|AAF87129.1| F10A5.17 [Arabidopsis thaliana] gb|AAD38803.1| vacuolar H+-pumping ATPase 16 kDa subunit c isoform 4 [Arabidopsis thaliana] sp|P59229|VATL4_ARATH Vacuolar ATP synthase 16 kDa proteolipid subunit 4 (V-ATPase 16 kDa proteolipid subunit 4) gb|AAA99936.1| vacuolar H+-pumping ATPase 16 kDa proteolipid	166	9E-49
					>sp|P23957|VATL AVESA Vacuolar ATP synthase 16 kDa proteolipid subunitgb|AAA32712.1| H+-ATPase	165	9E-49
CB886286	4.61E-03	B73<F1=Mo17	1.28	3	>gb|AAK56131.1| beta-expansin 8 [Zea mays]	286	2E-84

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>ref|NP_922683.1| beta-expansin EXPB4 [Oryza sativa (japonica cultivar-group)]gb|AAK55466.1| beta-expansin (EXPB4) [Oryza sativa (japonica cultivar-group)] gb|AAP54970.1| beta-expansin [Oryza sativa (japonica cultivar-group)]	286	9E-80
					>gb|AAF72985.1| beta-expansin [Oryza sativa]	286	2E-79
					>gb|AAS48880.1| expansin EXPB2 [Triticum aestivum]	278	3E-74
					>gb|AAK56125.1| beta-expansin 2 [Zea mays]	175	3E-73
DV622582	4.64E-03	Mo17<B73=F1	1.23	10	>ref|NP_908805.1| putative GTP-binding protein [Oryza sativa (japonicacultivar-group)] dbj|BAB67979.1| putative small GTP-binding protein Bsar1a [Oryza sativa (japonica cultivar-group)] dbj|BAB63877.1| putative small GTP-binding protein Bsar1a [Oryza sativa (japonica cultivar-group)]	193	8E-49
					>ref|NP_192117.1| ASAR1; GTP binding [Arabidopsis thaliana]emb|CAB80701.1| SAR1/GTP-binding secretory factor [Arabidopsis thaliana] gb|AAM20333.1| putative SAR1/GTP-binding secretory factor [Arabidopsis thaliana] gb|AAL38798.1| putative SAR1/GTP-binding secretory factor [Arabidopsis thaliana] gb|AAM67080.1| SAR1/GTP-binding secretory factor [Arabidopsis thaliana] gb|AAC78700.1| SAR1/GTP-binding secretory factor [Arabidopsis thaliana] gb|AAB57799.1| AGAA.4 [Arabidopsis thaliana] sp|O04834|SAR1A ARATH GTP-binding protein SAR1A gb|AAA99827.1| Sar1 homolog	193	2E-48
					>gb|AAC32610.1| ras-like small monomeric GTP-binding protein [Avena fatua]	193	5E-48
					>gb|ABA98928.1| ADP-ribosylation factor family [Oryza sativa (japonicacultivar-group)]	193	5E-48
					>ref|NP_912773.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]gb|AAT28677.1| GTP-binding protein [Oryza sativa (japonica cultivar-group)] dbj|BAA84612.1| putative small GTP-binding protein Bsar1a [Oryza sativa (japonica cultivar-group)]	193	3E-47
BM080488	4.64E-03	F1=Mo17<B73	2.2	9	>gb|AAT75262.1| putative DnaJ like protein [Oryza sativa (japonicacultivar-group)]	417	2E-44
					>emb|CAD29846.1| putative DnaJ protein [Oryza sativa (japonica cultivar-group)]	108	2E-44
					>gb|AAD51625.1| seed maturation protein PM37 [Glycine max]	417	2E-40
					>emb|CAA63965.1| DnaJ protein [Solanum tuberosum]	419	2E-39
					>gb|AAN87055.1| tuber-induction protein [Solanum tuberosum]	315	2E-39
CB604380	4.64E-03	B73<F1=Mo17	1.32	3	>gb|AAT68209.1| putative histone H2B [Cynodon dactylon]	98	3E-30
					>ref|XP_475912.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]gb|AAU44113.1| putative histone H2B [Oryza sativa (japonica cultivar-group)] gb|AAT69583.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	152	3E-30
					>ref|NP_915412.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]dbj|BAB93209.1| putative histone H2B [Oryza sativa (japonica cultivar-group)] dbj|BAB67889.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	139	3E-30
					>ref|NP 909298.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]dbj|BAB44055.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	155	3E-30
					>ref|NP 909263.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]dbj|BAB44008.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	153	3E-30
BM337948	4.67E-03	Mo17<B73=F1	1.64	10	>gb|AAV24911.1| unknown protein [Oryza sativa (japonica cultivar-group)]	259	2E-6
DV550289	4.68E-03	B73<F1=Mo17	1.24	3	>ref|XP 475481.1| putative SMC protein [Oryza sativa (japonica cultivar-group)]gb|AAT07581.1| putative SMC protein [Oryza sativa (japonica cultivar-group)]	1241	9E-8
					>emb|CAD32690.1| SMC4 protein [Oryza sativa]	1236	9E-8
					>ref|NP 199671.1| ATSMC3; ATP binding [Arabidopsis thaliana]dbj|BAB10693.1| chromosome condensation protein [Arabidopsis thaliana]	1241	9E-8
					>emb|CAD59406.1| SMC4 protein [Anopheles gambiae]	1376	4E-7
					>gb|EAA12256.2| ENSANGP00000018543 [Anopheles gambiae str. PEST]ref|XP 317674.2| ENSANGP00000018543 [Anopheles gambiae str. PEST]	1376	4E-7
BM073988	4.68E-03	B73<F1=Mo17	1.55	3	>ref|XP_466799.1| putative CER1 protein [Oryza sativa (japonica cultivar-group)]dbj|BAD21579.1| putative CER1 protein [Oryza sativa (japonica cultivar-group)] dbj|BAD21539.1| putative CER1 protein [Oryza sativa (japonica cultivar-group)]	619	4E-46
					>ref|XP 473150.1| OSJNBa0004N05.14 [Oryza sativa (japonica cultivar-group)]emb|CAE03390.2| OSJNBa0004N05.14 [Oryza sativa (japonica cultivar-group)]	597	4E-43
					>ref|NP_921941.1| putative CER1 [Oryza sativa (japonica cultivar-group)]gb|AAG21908.1| putative CER1 [Oryza sativa] gb|AAP54228.1| CER1, putative [Oryza sativa (japonica cultivar-group)]	621	2E-35
					>gb|AAC23640.1| CER1-like protein [Arabidopsis thaliana]	635	8E-31
					>ref|XP_468372.1| putative CER1 [Oryza sativa (japonica cultivar-group)]dbj|BAD22402.1| putative CER1 [Oryza sativa (japonica cultivar-group)] dbj|BAD21663.1| putative CER1 [Oryza sativa (japonica cultivar-group)]	635	2E-30
CD001874	4.68E-03	B73<F1=Mo17	1.5	3	ns		
CB331044	4.69E-03	Mo17<B73=F1	1.35	11	>gb|AAA72758.1| glutathione S-transferase	214	3E-29
					>gb|AAA33470.1| glutathione S-transferase Igb|AAA33469.1| glutathione S-transferase I prf||1303351A transferase,glutathione S	214	3E-29
					>emb|CAA29928.1| unnamed protein product [Zea mays]sp|P12653|GSTF1 MAIZE Glutathione S-transferase I (GST-I) (GST-29) (GST class-phi)	214	8E-29
					>pdb|1BYE|D Chain D, Glutathione S-Transferase I From Mais In Complex WithAtrazine Glutathione Conjugate pdb|1BYE|C Chain C, Glutathione S-Transferase I From Mais In Complex With Atrazine Glutathione Conjugate pdb|1BYE|B Chain B, Glutathione S-Transferase I From Mais In Complex With Atrazine Glutathione Conjugate pdb|1BYE|A Chain A, Glutathione S-Transferase I From Mais In Complex With Atrazine Glutathione Conjugate	213	3E-28
					>pdb|1AXD|B Chain B, Structure Of Glutathione S-Transferase-I Bound With TheLigand Lactoylglutathione pdb|1AXD|A Chain A, Structure Of Glutathione S-Transferase-I Bound With The Ligand Lactoylglutathione	209	3E-28
CD484958	4.69E-03	F1=Mo17<B73	1.3	9	ns		
BM074116	4.70E-03	F1=Mo17<B73	1.65	9	ns		
CB886468	4.71E-03	Mo17<B73=F1	1.31	10	ns		

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
CD001354	4.71E-03	F1=Mo17<B73	1.36	9	ns		
CB251998	4.72E-03	Mo17<B73=F1	1.33	10	>gb|AAL70108.1| putative aldehyde dehydrogenase MIS1 [Zea mays]	549	8E-79
					>gb|AAL70109.1| putative aldehyde dehydrogenase WIS1 [Triticum aestivum]	551	3E-73
					>gb|AAZ91463.1| delta-1-pyrroline-5-carboxylate dehydrogenase [Triticum turgidum]	551	9E-73
					>ref|XP_475772.1| putative aldehyde dehydrogenase [Oryza sativa (japonicacultivar-group)] gb|AAT39215.1| putative aldehyde dehydrogenase [Oryza sativa (japonica cultivar-group)]	513	3E-72
					>gb|AAL70106.1| putative aldehyde dehydrogenase BIS1 [Hordeum vulgare]gb|AAZ91461.1| delta-1-pyrroline-5-carboxylate dehydrogenase [Hordeum vulgare]	551	3E-72
DV621391	4.72E-03	B73<Mo17	1.32	3	>ref|XP_464088.1| putative cycloartenol synthase [Oryza sativa (japonicacultivar-group)] dbj|BAD10254.1| putative cycloartenol synthase [Oryza sativa (japonica cultivar-group)]	759	4E-63
					>gb|AAF03375.1| putative cycloartenol synthase [Oryza sativa]	757	4E-63
					>gb|AAT38891.1| cycloartenol synthase [Avena strigosa]	759	5E-63
					>gb|AAT38889.1| cycloartenol synthase [Avena longiglumis]	759	5E-63
					>gb|AAT38890.1| cycloartenol synthase [Avena prostrata]	759	9E-63
CB381008	4.73E-03	Mo17<B73=F1	1.34	11	ns		
DV490694	4.73E-03	F1=Mo17<B73	1.78	9	>dbj|BAD81765.1| Myb-like protein [Oryza sativa (japonica cultivar-group)]	584	5E-41
					>emb|CAD22534.1| transcription factor myb [Oryza sativa]	499	1E-39
					>gb|AAU44021.1| unknown protein [Oryza sativa (japonica cultivar-group)]	473	2E-25
					>gb|AAZ20428.1| MYB4 [Malus x domestica]	571	3E-8
					>emb|CAD98760.1| MYB transcription factor R3 type [Populus tremula x Populustremuloides]	530	1E-7
CD568529	4.75E-03	F1=Mo17<B73	1.24	9	>emb|CAB65537.1| Toc34-1 protein [Zea mays]	326	1E-32
					>emb|CAB77551.1| Toc34-2 protein [Zea mays]	326	1E-30
					>emb|CAA82196.1| chloroplast outer envelope protein 34 [Pisum sativum]sp|Q41009|TOC34_PEA Translocase of chloroplast 34 (34 kDa chloroplast outer envelope protein) (GTP-binding protein OEP34) (GTP-binding protein IAP34) gb|AAC25785.1| GTP-binding protein [Pisum sativum]	310	9E-27
					>ref|NP_850768.1| OEP34 [Arabidopsis thaliana]ref|NP_974732.1| OEP34 [Arabidopsis thaliana] ref|NP_196119.1| OEP34 [Arabidopsis thaliana] dbj|BAB11522.1| GTP-binding protein [Arabidopsis thaliana]	313	1E-25
					>emb|CAC17699.1| atToc34 protein [Arabidopsis thaliana]sp|Q38906|TOC34_ARATH Translocase of chloroplast 34 (34 kDa chloroplast outer envelope protein) (GTP-binding protein OEP34) (AtToc34) gb|AAD09203.1| GTP-binding protein [Arabidopsis thaliana]	313	1E-25
BM074494	4.76E-03	B73<F1=Mo17	1.27	2	>gb|AAL65396.1| putative aminotransferase [Oryza sativa]	231	5E-37
					>ref|XP_473880.1| OSJNBa0008M17.4 [Oryza sativa (japonica cultivar-group)]emb|CAE04333.2| OSJNBa0008M17.4 [Oryza sativa (japonica cultivar-group)] gb|AAQ14479.1| putative aminotransferase [Oryza sativa]	516	5E-37
					>ref|XP 473879.1| OSJNBa0008M17.3 [Oryza sativa (japonica cultivar-group)]emb|CAE04332.2| OSJNBa0008M17.3 [Oryza sativa (japonica cultivar-group)]	497	2E-36
					>ref|XP_480608.1| putative gamma-aminobutyrate transaminase subunit precursor isozyme3 [Oryza sativa (japonica cultivar-group)] dbj|BAD11549.1| putative gamma-aminobutyrate transaminase subunit precursor isozyme 3 [Oryza sativa (japonica cultivar-group)] dbj|BAD05337.1| putative gamma-aminobutyrate transaminase subunit precursor isozyme 3 [Oryza sativa (japonica cultivar-group)]	510	2E-36
					>ref|XP_463843.1| putative 4-aminobutyrate aminotransferase [Oryza sativa (japonicacultivar-group)] dbj|BAD07632.1| putative 4-aminobutyrate aminotransferase [Oryza sativa (japonica cultivar-group)]	483	2E-35
CB381312	4.76E-03	B73<F1=Mo17	1.37	3	>gb|AAP80858.1| ribosomal protein L19 [Triticum aestivum]	209	7E-46
					>gb|AAT76364.1| putative ribosomal protein L19 [Oryza sativa (japonicacultivar-group)] gb|AAP05800.1| putative ribosomal protein L19 [Oryza sativa (japonica cultivar-group)]	206	7E-46
					>gb|AAT08672.1| ribosomal protein L19 [Hyacinthus orientalis]	203	3E-44
					>gb|AAR83877.1| 60S ribosomal protein L19 [Capsicum annuum]	232	4E-43
					>gb|ABC01909.1| 60S ribosomal protein L19-like protein [Solanum tuberosum]	209	4E-43
CD573072	4.77E-03	Mo17<B73=F1	1.35	10	>gb|AAG34818.1| glutathione S-transferase GST 10 [Zea mays]	199	7E-87
					>gb|AAG32477.1| putative glutathione S-transferase OsGSTF3 [Oryza sativa (japonicacultivar-group)]	224	4E-78
					>ref|XP_470193.1| Putative glutathione S-transferase [Oryza sativa (japonicacultivar-group)] gb|AAN05495.1| Putative glutathione S-transferase [Oryza sativa (japonica cultivar-group)]	224	4E-78
					>gb|AAB65163.1| glutathione S-transferase, class-phi [Solanum commersonii]	213	3E-35
					>emb|CAA96431.1| glutathione S-transferase [Nicotiana plumbaginifolia]	203	1E-34
DV493710	4.79E-03	B73=F1<Mo17	1.38	4	>emb|CAD23418.1| m5 [Zea mays]gb|AAG43199.1| MADS box protein 1 [Zea mays]	232	5E-36
					>ref|XP_468582.1| Putative MADS box-like protein [Oryza sativa (japonicacultivar-group)] gb|AAS59820.1| MADS-box protein RMADS208 [Oryza sativa (japonica cultivar-group)] gb|AAN74833.1| Putative MADS box-like protein [Oryza sativa (japonica cultivar-group)]	151	9E-25
					>gb|AAQ01162.1| MADS box protein [Oryza sativa (japonica cultivar-group)]dbj|BAA81886.1| MADS box-like protein [Oryza sativa (japonica cultivar-group)]	230	9E-25
					>gb|AAM14668.1| ZAGL1 [Zea diploperennis]gb|AAM14647.1| ZAGL1 [Zea mays subsp. parviglumis]	60	8E-15

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|AAM14667.1| ZAGL1 [Zea mays]gb|AAM14666.1| ZAGL1 [Zea mays] gb|AAM14665.1| ZAGL1 [Zea mays] gb|AAM14664.1| ZAGL1 [Zea mays] gb|AAM14663.1| ZAGL1 [Zea mays] gb|AAM14662.1| ZAGL1 [Zea mays] gb|AAM14661.1| ZAGL1 [Zea mays] gb|AAM14660.1| ZAGL1 [Zea mays] gb|AAM14659.1| ZAGL1 [Zea mays] gb|AAM14658.1| ZAGL1 [Zea mays] gb|AAM14657.1| ZAGL1 [Zea mays] gb|AAM14656.1| ZAGL1 [Zea mays] gb|AAM14655.1| ZAGL1 [Zea mays] gb|AAM14653.1| ZAGL1 [Zea mays] gb|AAM14652.1| ZAGL1 [Zea mays] gb|AAM14650.1| ZAGL1 [Zea mays subsp. parviglumis] gb|AAM14645.1| ZAGL1 [Zea mays subsp. parviglumis] gb|AAM14642.1| ZAGL1 [Zea mays subsp. parviglumis] gb|AAM14640.1| ZAGL1 [Zea mays subsp. parviglumis] gb|AAM14639.1| ZAGL1 [Zea mays subsp. parviglumis] gb|AAM14638.1| ZAGL1 [Zea mays subsp. parviglumis] gb|AAM14637.1| ZAGL1 [Zea mays subsp. parviglumis]	60	8E-15
DV490950	4.79E-03	B73<F1=Mo17	1.32	3	>gb|AAT75247.1| expressed protein [Oryza sativa (japonica cultivar-group)]	474	5E-7
BM333787	4.83E-03	Mo17<B73=F1	2.7	10	>ref|NP_922019.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]gb|AAK21343.1| hypothetical protein [Oryza sativa (japonica cultivar-group)] gb|AAP54306.1| hypothetical protein LOC Os10g34030 [Oryza sativa (japonica cultivar-group)]	396	1E-32
					>gb|AAT08697.1| unknown [Hyacinthus orientalis]	99	7E-12
					>ref|NP_029430.1| unknown protein [Arabidopsis thaliana]gb|AAM16216.1| At2g28430/T1B3.5 [Arabidopsis thaliana] gb|AAD20683.1| expressed protein [Arabidopsis thaliana] gb|AAL25550.1| At2g28430/T1B3.5 [Arabidopsis thaliana]	85	4E-11
CB240083	4.85E-03	Mo17<B73=F1	1.46	11	>dbj|BAD81998.1| putative NEW1 domain containing protein isoform [Oryza sativa(japonica cultivar-group)]	424	2E-73
					>ref|XP_475303.1| 'unknown protein contains, zinc finger DHHC domain' [Oryza sativa(japonica cultivar-group)] gb|AAT58886.1| 'unknown protein contains, zinc finger DHHC domain' [Oryza sativa (japonica cultivar-group)]	889	4E-73
					>ref|NP_194194.1| metal ion binding [Arabidopsis thaliana]emb|CAB79373.1| putative protein [Arabidopsis thaliana] emb|CAA23000.1| putative protein [Arabidopsis thaliana]	374	4E-61
					>ref|XP_483525.1| putative DHHC-type zinc finger domain-containing protein [Oryzasativa (japonica cultivar-group)] dbj|BAD13105.1| putative DHHC-type zinc finger domain-containing protein [Oryza sativa (japonica cultivar-group)] dbj|BAD01220.1| putative DHHC-type zinc finger domain-containing protein [Oryza sativa (japonica cultivar-group)]	416	2E-52
					>ref|NP_199813.2| metal ion binding [Arabidopsis thaliana]gb|AAM20317.1| unknown protein [Arabidopsis thaliana] gb|AAL49807.1| unknown protein [Arabidopsis thaliana]	407	4E-52
CD001615	4.85E-03	Mo17<B73=F1	1.26	10	>ref|NP_568778.1| oxidoreductase, acting on NADH or NADPH [Arabidopsis thaliana]gb|AAL79599.1| AT5g52840/MXC20_6 [Arabidopsis thaliana] gb|AAL06910.1| AT5g52840/MXC20_6 [Arabidopsis thaliana] dbj|BAB10432.1| unnamed protein product [Arabidopsis thaliana] sp|Q9FLX7|NUFM_ARATH Probable NADH-ubiquinone oxidoreductase 18 kDa subunit, mitochondrial precursor (Complex I-18Kd) (CI-18Kd)	169	4E-41
					>gb|AAL32032.1| NADH-ubiquinone oxidoreductase [Retama raetam]	153	1E-39
					>ref|NP 680745.1| unknown protein [Arabidopsis thaliana]	115	4E-8
					>gb|AAU44524.1| hypothetical protein AT4G28005 [Arabidopsis thaliana]	112	5E-8
					>ref|XP 504293.1| hypothetical protein [Yarrowia lipolytica]emb|CAG79892.1| unnamed protein product [Yarrowia lipolytica CLIB122]	146	1E-6
DV491034	4.88E-03	B73<F1=Mo17	1.67	3	>dbj|BAD87057.1| putative NADP-dependent malic protein [Oryza sativa (japonicacultivar-group)]	388	6E-15
					>dbj|BAD87056.1| putative NADP-dependent malic protein [Oryza sativa (japonicacultivar-group)]	496	6E-15
					>dbj|BAB20887.2| NADP dependent malic enzyme [Oryza sativa (japonicacultivar-group)]	593	6E-15
					>ref|NP 916713.1| P0022F10.12 [Oryza sativa (japonica cultivar-group)]	593	6E-15
					>gb|AAF73006.1| NADP-dependent malic protein [Ricinus communis]	641	1E-12
DV491071	4.91E-03	F1=Mo17<B73	1.38	9	>gb|AAP80666.1| pyrophosphate-dependent phosphofructo-1-kinase [Triticum aestivum]	130	3E-59
					>ref|XP_550650.1| putative pyrophosphate-dependent phosphofructo-1-kinase [Oryzasativa (japonica cultivar-group)] dbj|BAD69066.1| putative pyrophosphate-dependent phosphofructo-1-kinase [Oryza sativa (japonica cultivar-group)] dbj|BAD69330.1| putative pyrophosphate-dependent phosphofructo-1-kinase [Oryza sativa (japonica cultivar-group)]	541	2E-57
					>ref|NP_568842.1| 6-phosphofructokinase [Arabidopsis thaliana]gb|AAK64113.1| putative pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana] gb|AAK25917.1| putative pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]	485	1E-45
					>dbj|BAB09881.1| pyrophosphate-dependent phosphofructo-1-kinase-like protein[Arabidopsis thaliana]	488	1E-45
					>gb|AAV44044.1| putative diphosphate-fructose-6-phosphate 1-phosphotransferase[Oryza sativa (japonica cultivar-group)] gb|AAU44054.1| putative diphosphate-fructose-6-phosphate 1-phosphotransferase [Oryza sativa (japonica cultivar-group)]	567	2E-43
CB886256	4.95E-03	B73<F1=Mo17	1.61	3	>ref|XP_467147.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD25738.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAD25775.1| unknown protein [Oryza sativa (japonica cultivar-group)]	283	8E-76
					>gb|AAM65994.1| unknown [Arabidopsis thaliana]	293	1E-51
					>dbj|BAB02931.1| unnamed protein product [Arabidopsis thaliana]	330	1E-51
					>ref|NP 566746.1| unknown protein [Arabidopsis thaliana]	293	1E-51
					>dbj|BAC43550.1| unknown protein [Arabidopsis thaliana]	293	4E-51
CB329476	5.03E-03	Mo17<B73=F1	1.33	10	>gb|AAL76334.1| putative G-box binding protein [Oryza sativa]dbj|BAD45657.1| G-box binding protein-like [Oryza sativa (japonica cultivar-group)] gb|AAB65433.1| HvB12D homolog [Oryza sativa]	89	4E-24
					>emb|CAA70936.1| B12Dg1 [Hordeum vulgare subsp. vulgare]emb|CAA54065.1| HvB12D [Hordeum vulgare subsp. vulgare]	87	5E-22

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>gb|AAD22104.1| B12D protein [Ipomoea batatas]	90	3E-18
					>ref|XP_477421.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]dbj|BAC84633.1| putative B12D protein [Oryza sativa (japonica cultivar-group)] dbj|BAD31625.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]	98	2E-16
					>ref|NP_190397.1| unknown protein [Arabidopsis thaliana]emb|CAB51061.1| B12D-like protein [Arabidopsis thaliana] gb|AAL91215.1| B12D-like protein [Arabidopsis thaliana] gb|AAN65070.1| B12D-like protein [Arabidopsis thaliana] pir||T13003 hypothetical protein T24C20.20 - Arabidopsis thaliana	88	2E-15
CD484410	5.06E-03	Mo17<B73=F1	1.38	11	>sp|P23346|SODC5 MAIZE Superoxide dismutase [Cu-Zn] 4AP	152	2E-66
					>emb|CAB57992.1| superoxide dismutase-4AP [Zea mays]sp|P23345|SODC4 MAIZE Superoxide dismutase [Cu-Zn] 4A	152	1E-65
					>emb|CAB57993.1| superoxide dismutase-4A [Zea mays]gb|AAB49913.1| superoxide dismutase 4A	152	2E-64
					>gb|AAB49912.1| superoxide dismutase 4	124	7E-64
					>sp|P28757|SODC2_ORYSA Superoxide dismutase [Cu-Zn] 2gb|AAC14465.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00800.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)]	152	1E-60
BM333867	5.14E-03	F1=Mo17<B73	1.37	9	>ref|NP_921492.1| putative epimerase/dehydratase [Oryza sativa (japonicacultivar-group)] dbj|BAD66930.1| GDP-mannose-3",5"-epimerase [Oryza sativa (japonica cultivar-group)] gb|AAM08784.1| Putative epimerase/dehydratase [Oryza sativa]	378	2E-59
					>gb|ABA94522.1| NAD dependent epimerase/dehydratase family [Oryza sativa (japonicacultivar-group)]	371	7E-56
					>ref|NP_198236.1| GDP-mannose 3,5-epimerase/ catalytic [Arabidopsis thaliana]gb|AAM51587.1| AT5g28840/F7P1_20 [Arabidopsis thaliana] gb|AAL15324.1| AT5g28840/F7P1_20 [Arabidopsis thaliana] gb|AAL15291.1| AT5g28840/F7P1_20 [Arabidopsis thaliana] sp|Q93VR3|GMANE_ARATH GDP-mannose 3,5-epimerase (GDP-Man 3,5-epimerase)	377	2E-53
					>pdb|2C5E|B Chain B, Gdp-Mannose-3', 5' -Epimerase (Arabidopsis Thaliana),K217a, With Gdp-Alpha-D-Mannose Bound In The Active Site. pdb|2C5E|A Chain A, Gdp-Mannose-3', 5' -Epimerase (Arabidopsis Thaliana), K217a, With Gdp-Alpha-D-Mannose Bound In The Active Site.	379	2E-53
					>pdb|2C5A|B Chain B, Gdp-Mannose-3', 5' -Epimerase (Arabidopsis Thaliana),Y174f, With Gdp-Beta-L-Galactose Bound In The Active Site pdb|2C5A|A Chain A, Gdp-Mannose-3', 5' -Epimerase (Arabidopsis Thaliana), Y174f, With Gdp-Beta-L-Galactose Bound In The Active Site	379	2E-53
CB351719	5.22E-03	F1=Mo17<B73	1.36	9	>ref|XP_506504.1| PREDICTED P0524G08.101 gene product [Oryza sativa (japonicacultivar-group)] ref|XP_479288.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAD31263.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAC16465.1| unknown protein [Oryza sativa (japonica cultivar-group)]	131	9E-30
					>ref|NP_566416.1| catalytic/ oxidoreductase, acting on NADH or NADPH [Arabidopsisthaliana] gb|AAL47381.1| unknown protein [Arabidopsis thaliana] gb|AAK96767.1| unknown protein [Arabidopsis thaliana] gb|AAG51074.1| unknown protein; 35018-33933 [Arabidopsis thaliana] dbj|BAB03135.1| unnamed protein product [Arabidopsis thaliana]	133	8E-24
BM072898	5.22E-03	Mo17<B73=F1	1.36	10	>ref|NP_910584.1| EST AU082567(S21715) corresponds to a region of the predictedgene.~Similar to S.tuberosum ubiquinol cytochrome c reductase. (X79275) [Oryza sativa (japonica cultivar-group)] ref|NP_910574.1| EST AU082567(S21715) corresponds to a region of the predicted gene.~Similar to S.tuberosum ubiquinol--cytochrome c reductase. (X79275) [Oryza sativa (japonica cultivar-group)] dbj|BAA95831.1| putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein [Oryza sativa (japonica cultivar-group)] dbj|BAA95821.1| putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein [Oryza sativa (japonica cultivar-group)]	72	4E-33
					>ref|NP_187697.1| ubiquinol-cytochrome-c reductase [Arabidopsis thaliana]gb|AAF19563.1| putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein (QP-C) [Arabidopsis thaliana] gb|AAN17451.1| putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein (QP-C) [Arabidopsis thaliana] gb|AAP21315.1| At3g10860 [Arabidopsis thaliana] gb|AAM64437.1| putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein (QP-C) [Arabidopsis thaliana]	72	2E-27
					>ref|NP_196156.1| ubiquinol-cytochrome-c reductase [Arabidopsis thaliana]gb|AAQ65099.1| At5g05370 [Arabidopsis thaliana] dbj|BAB09980.1| ubiquinol-cytochrome C reductase complex ubiquinone-binding protein [Arabidopsis thaliana]	72	6E-26
					>emb|CAA55862.1| ubiquinol--cytochrome c reductase [Solanum tuberosum]sp|P46269|UCRQ_SOLTU Ubiquinol-cytochrome c reductase complex ubiquinone-binding protein QP-C (Ubiquinol-cytochrome c reductase complex 8.2 kDa protein) prf||2107179A cytochrome c oxidase:SUBUNIT=8.2kD	72	3E-25
					>gb|AAP80673.1| cytochrome reductase [Triticum aestivum]	115	2E-11
CB816343	5.23E-03	Mo17<B73=F1	1.31	10	>gb|AAO72563.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]	413	2E-90
					>dbj|BAD61932.1| putative elongation factor 1 gamma [Oryza sativa (japonicacultivar-group)] dbj|BAD61828.1| putative elongation factor 1 gamma [Oryza sativa (japonica cultivar-group)]	416	2E-90
					>ref|XP_464690.1| Elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]dbj|BAD17615.1| Elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)] sp|Q9ZRI7|EF1G ORYSA Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) dbj|BAA34206.1| elongation factor 1B gamma [Oryza	418	2E-89
					>gb|AAO72574.1| elongation factor 1 gamma-like protein [Oryza sativa (japonicacultivar-group)]	409	3E-89
					>ref|XP_464689.1| putative elongation factor 1-gamma [Oryza sativa (japonicacultivar-group)] dbj|BAD17614.1| putative elongation factor 1-gamma [Oryza sativa (japonica cultivar-group)]	414	3E-89
CB605343	5.29E-03	Mo17<B73=F1	1.28	11	>gb|AAU44051.1| unknown protein [Oryza sativa (japonica cultivar-group)]	132	2E-35
					>ref|NP 196020.1| unknown protein [Arabidopsis thaliana]emb|CAB85520.1| putative protein [Arabidopsis thaliana]	116	6E-16
					>gb|AAM63612.1| unknown [Arabidopsis thaliana]	116	7E-16
BM078832	5.30E-03	B73<F1=Mo17	1.37	2	>dbj|BAD87534.1| putative beta-N-acetylhexosaminidase [Oryza sativa (japonicacultivar-group)]	526	2E-82
					>ref|NP 915111.1| beta-N-acetylhexosaminidase -like protein [Oryza sativa (japonicacultivar-group)]	496	2E-82

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|AAV32135.1| putative beta-N-acetylhexosaminidase [Oryza sativa (japonicacultivar-group)]	531	2E-79
					>gb|AAT77374.1| putative beta-N-acetylhexosaminidase [Oryza sativa (japonicacultivar-group)]	527	2E-79
					>ref|NP_176737.2| beta-N-acetylhexosaminidase [Arabidopsis thaliana]gb|AAN33206.1| At1g65600/F5I14_13 [Arabidopsis thaliana] gb|AAM91092.1| At1g65600/F5I14 13 [Arabidopsis thaliana]	535	1E-71
CD001179	5.34E-03	Mo17<B73	1.24	9	>ref|XP 474269.1| OSJNBa0043A12.6 [Oryza sativa (japonica cultivar-group)]emb|CAE02801.1| OSJNBa0043A12.6 [Oryza sativa (japonica cultivar-group)]	148	1E-65
					>gb|AAU82109.1| ubiquitin-conjugating enzyme [Triticum aestivum]	148	7E-65
					>gb|AAF24583.1| F22C12.2 [Arabidopsis thaliana]	146	7E-64
					>ref|NP_001031228.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme[Arabidopsis thaliana] ref|NP_564828.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme [Arabidopsis thaliana] gb|AAM91500.1| At1g64230/F22C12_17 [Arabidopsis thaliana] gb|AAM11574.1| ubiquitin conjugating enzyme UBC9A [Arabidopsis thaliana] gb|AAK60309.1| At1g64230/F22C12_17 [Arabidopsis thaliana] gb|AAY44867.1| ubiquitinating enzyme [Arabidopsis thaliana]	148	7E-64
					>gb|AAB88617.1| ubiquitin conjugating enzyme [Zea mays]	148	7E-64
CB604393	5.35E-03	B73<Mo17	1.34	3	>emb|CAE52515.1| alpha tubulin [Setaria viridis]	451	1E-72
					>emb|CAA33733.1| alpha2-tubulin [Zea mays]sp|P14641|TBA2 MAIZE Tubulin alpha-2 chain (Alpha-2 tubulin)	451	1E-72
					>emb|CAA33734.1| alpha1-tubulin [Zea mays]sp|P14640|TBA1 MAIZE Tubulin alpha-1 chain (Alpha-1 tubulin)	451	1E-72
					>emb|CAA10663.1| alpha-tubulin 3 [Hordeum vulgare subsp. vulgare]sp|Q9ZRR5|TBA3 HORVU Tubulin alpha-3 chain	451	1E-72
					>emb|CAA06619.1| alpha-tubulin 1 [Eleusine indica]	451	1E-72
CB604474	5.39E-03	Mo17<B73=F1	1.23	10	>dbj|BAD52963.1| putative 40S ribosomal protein S4 [Oryza sativa (japonicacultivar-group)]	265	1E-31
					>sp|O22424|RS4 MAIZE 40S ribosomal protein S4gb|AAB66899.1| ribosomal protein S4 type I [Zea mays]	265	1E-31
					>dbj|BAD28085.1| putative ribosomal protein S4 [Oryza sativa (japonicacultivar-group)]	265	2E-31
					>gb|AAB67831.1| ribsomal protein S4 [Zea mays]	265	3E-31
					>emb|CAA55882.1| ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]sp|P46299|RS4 GOSHI 40S ribosomal protein S4	262	8E-31
DV621173	5.40E-03	Mo17<B73=F1	1.44	10	>ref|XP_467668.1| RING zinc finger protein-like [Oryza sativa (japonicacultivar-group)] dbj|BAD15897.1| RING zinc finger protein-like [Oryza sativa (japonica cultivar-group)]	180	6E-48
					>ref|NP_176974.1| protein binding / ubiquitin-protein ligase/ zinc ion binding[Arabidopsis thaliana] gb|AAG52017.1| putative RING zinc finger protein; 27623-28978 [Arabidopsis thaliana]	343	3E-31
					>gb|AAM61051.1| putative RING zinc finger protein [Arabidopsis thaliana]	343	3E-31
					>ref|NP_849924.1| RIE1 (RING-FINGER PROTEIN FOR EMBRYOGENESIS); ubiquitin-proteinligase/ zinc ion binding [Arabidopsis thaliana] gb|AAN87884.1| RES protein [Arabidopsis thaliana]	359	6E-29
					>ref|XP 473541.1| OSJNBb0032E06.5 [Oryza sativa (japonica cultivar-group)]emb|CAE02249.2| OSJNBb0032E06.5 [Oryza sativa (japonica cultivar-group)]	324	8E-26
BM073183	5.41E-03	Mo17<B73=F1	2.5	10	>ref|NP 922709.1| putative ethylene-forming enzyme [Oryza sativa (japonicacultivar-group)] gb|AAL79785.1| putative ethylene-forming enzyme [Oryza sativa]	281	8E-21
					>ref|NP_922706.1| putative ethylene-forming enzyme [Oryza sativa (japonicacultivar-group)] gb|AAL79792.1| putative ethylene-forming enzyme [Oryza sativa] gb|AAP54993.1| ethylene-forming enzyme, putative [Oryza sativa (japonica cultivar-group)]	348	8E-21
					>ref|NP_922703.1| putative ethylene-forming enzyme [Oryza sativa (japonicacultivar-group)] gb|AAK55454.1| putative dioxygenase [Oryza sativa (japonica cultivar-group)] gb|AAL79801.1| putative ethylene-forming enzyme [Oryza sativa] gb|AAP54990.1| dioxygenase, putative [Oryza sativa (japonica cultivar-group)]	357	1E-20
					>gb|ABB47977.1| dioxygenase, putative [Oryza sativa (japonica cultivar-group)]	331	1E-20
					>ref|NP_922700.1| putative dioxygenase [Oryza sativa (japonica cultivar-group)]gb|AAK55463.1| putative dioxygenase [Oryza sativa (japonica cultivar-group)] gb|AAP54987.1| dioxygenase, putative [Oryza sativa (japonica cultivar-group)]	368	2E-20
CB331835	5.42E-03	F1=Mo17<B73	1.48	9	>ref|XP_493825.1| similar to Aquifex aeolicus section 65 of 109 of the completegenome; hypothetical protein. (AE000733) [Oryza sativa (japonica cultivar-group)] gb|AAO72591.1| unknown [Oryza sativa (japonica cultivar-group)] dbj|BAA85416.1| similar to Aquifex aeolicus section 65 of 109 of the complete genome; hypothetical protein. (AE000733) [Oryza sativa (japonica cultivar-group)]	1413	6E-79
					>gb|AAM22714.1| Unknown protein [Oryza sativa (japonica cultivar-group)]	162	5E-64
					>ref|NP_001032157.1| ATP binding / nucleoside-triphosphatase/ nucleotide binding[Arabidopsis thaliana] gb|AAU29477.1| At5g66005 [Arabidopsis thaliana] gb|AAT41788.1| At5g66005 [Arabidopsis thaliana] dbj|BAD95397.1| hypothetical protein [Arabidopsis thaliana]	192	8E-62
					>ref|NP 974998.1| ATP binding / nucleoside-triphosphatase/ nucleotide binding[Arabidopsis thaliana]	164	5E-52
					>ref|NP 974997.1| ATP binding [Arabidopsis thaliana]	147	2E-44
CA829409	5.42E-03	Mo17<F1	1.41	11	>sp|P23346|SODC5 MAIZE Superoxide dismutase [Cu-Zn] 4AP	152	3E-76
					>emb|CAB57992.1| superoxide dismutase-4AP [Zea mays]sp|P23345|SODC4 MAIZE Superoxide dismutase [Cu-Zn] 4A	152	8E-76
					>emb|CAB57993.1| superoxide dismutase-4A [Zea mays]gb|AAB49913.1| superoxide dismutase 4A	152	3E-74
					>sp|P28757|SODC2_ORYSA Superoxide dismutase [Cu-Zn] 2gb|AAC14465.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00800.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)]	152	4E-71

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|AAY56345.1| cytoplasmic copper/zinc-superoxide dismutase [Oryza sativa (indicacultivar-group)] sp|P28756|SODC1_ORYSA Superoxide dismutase [Cu-Zn] 1 gb|AAC14464.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00799.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)] prf||2111424A Cu/Zn superoxide dismutase	152	5E-71
DV621635	5.42E-03	B73=F1<Mo17	1.56	4	>ref|XP_467545.1| putative SNF5 homolog BSH (bsh) [Oryza sativa (japonicacultivar-group)] dbj|BAD13031.1| putative SNF5 homolog BSH (bsh) [Oryza sativa (japonica cultivar-group)]	171	4E-11
CB833653	5.42E-03	B73<F1=Mo17	1.34	3	>ref|NP_564283.1| unknown protein [Arabidopsis thaliana]gb|AAK62382.1| Unknown protein [Arabidopsis thaliana] dbj|BAC43139.1| unknown protein [Arabidopsis thaliana] gb|AAN65056.1| Unknown protein [Arabidopsis thaliana]	81	3E-9
					>gb|ABA98228.1| hypothetical protein LOC Os12g29340 [Oryza sativa (japonicacultivar-group)]	68	8E-6
BM336730	5.45E-03	F1=Mo17<B73	4.18	9	ns		
CD001350	5.45E-03	B73=Mo17<F1	1.24	12	>gb|AAM95942.1| nucleosome/chromatin assembly factor group D protein [Zea mays]emb|CAA41220.1| high mobility group protein [Zea mays] emb|CAB46752.1| HMGa protein [Zea mays] sp|P27347|MNB1B MAIZE DNA-binding protein MNB1B (HMG1-like protein)	157	7E-12
					>emb|CAA46876.1| DNA-binding protein [Zea mays]pir||T03640 high mobility group protein MNB1b - maize (fragment)	168	7E-12
					>gb|AAP21609.1| HMGB1 [Oryza sativa (indica cultivar-group)]gb|AAN28722.1| HMG1 protein [Oryza sativa (indica cultivar-group)] dbj|BAD61823.1| HMGB1 [Oryza sativa (japonica cultivar-group)] gb|AAC78104.1| high mobility group protein [Oryza sativa]	157	1E-10
					>emb|CAA77641.1| high mobility group protein [Triticum aestivum]sp|P40621|HMGL WHEAT HMG1/2-like protein	161	5E-10
					>emb|CAA90679.1| HMG1/2-like protein [Hordeum vulgare subsp. vulgare]	160	1E-9
CD661920	5.48E-03	B73=F1<Mo17	1.3	4	>gb|AAF13094.1| unknown protein [Arabidopsis thaliana]gb|AAF21186.1| unknown protein [Arabidopsis thaliana]	196	3E-58
					>ref|NP_566319.1| unknown protein [Arabidopsis thaliana]ref|NP_850538.1| unknown protein [Arabidopsis thaliana] gb|AAL47395.1| unknown protein [Arabidopsis thaliana] gb|AAL16180.1| At3g07760/F17A17.10 [Arabidopsis thaliana] gb|AAK96782.1| Unknown protein [Arabidopsis thaliana] gb|AAM66036.1| unknown [Arabidopsis thaliana]	125	3E-58
					>gb|ABA99120.1| AC009176 putative heat-shock protein [Oryza sativa (japonicacultivar-group)]	1210	2E-41
					>ref|XP 786852.1| PREDICTED: similar to SH3/ankyrin domain gene 2 [Strongylocentrotuspurpuratus]	1038	5E-6
DV490651	5.49E-03	B73=F1<Mo17	1.5	4	ns		
BM332447	5.50E-03	Mo17<B73=F1	1.84	10	ns		
CB886274	5.52E-03	Mo17<B73=F1	1.32	11	>sp|P23346|SODC5 MAIZE Superoxide dismutase [Cu-Zn] 4AP	152	4E-82
					>emb|CAB57992.1| superoxide dismutase-4AP [Zea mays]sp|P23345|SODC4 MAIZE Superoxide dismutase [Cu-Zn] 4A	152	3E-81
					>emb|CAB57993.1| superoxide dismutase-4A [Zea mays]gb|AAB49913.1| superoxide dismutase 4A	152	5E-80
					>sp|P28757|SODC2_ORYSA Superoxide dismutase [Cu-Zn] 2gb|AAC14465.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00800.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)]	152	7E-76
					>gb|AAY56345.1| cytoplasmic copper/zinc-superoxide dismutase [Oryza sativa (indicacultivar-group)] sp|P28756|SODC1_ORYSA Superoxide dismutase [Cu-Zn] 1 gb|AAC14464.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00799.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)] prf||2111424A Cu/Zn superoxide dismutase	152	8E-75
CB605284	5.52E-03	B73<Mo17	1.34	4	>ref|XP_474386.1| OSJNBb0017I01.27 [Oryza sativa (japonica cultivar-group)]emb|CAE03422.1| OSJNBa0032F06.5 [Oryza sativa (japonica cultivar-group)] emb|CAE05747.1| OSJNBb0017I01.27 [Oryza sativa (japonica cultivar-group)]	711	3E-38
					>ref|XP 474387.1| OSJNBa0032F06.8 [Oryza sativa (japonica cultivar-group)]emb|CAE03425.1| OSJNBa0032F06.8 [Oryza sativa (japonica cultivar-group)]	711	8E-37
					>dbj|BAB02367.1| unnamed protein product [Arabidopsis thaliana]	697	2E-28
					>ref|NP_566511.1| unknown protein [Arabidopsis thaliana]gb|AAK76591.1| unknown protein [Arabidopsis thaliana] gb|AAN71973.1| unknown protein [Arabidopsis thaliana]	700	2E-28
					>gb|AAF35404.1| hypothetical protein [Arabidopsis thaliana]	722	4E-25
CB604523	5.55E-03	F1=Mo17<B73	1.67	9	ns		
CB411042	5.57E-03	Mo17<B73=F1	1.27	11	>emb|CAA64683.1| osr40c1 [Oryza sativa]	348	7E-84
					>ref|NP_912421.1| Putative r40c1 protein - rice [Oryza sativa (japonicacultivar-group)] gb|AAN64997.1| Putative r40c1 protein - rice [Oryza sativa (japonica cultivar-group)]	373	7E-84
					>ref|XP 479572.1| putative r40c2 protein [Oryza sativa (japonica cultivar-group)]dbj|BAC83805.1| putative r40c2 protein [Oryza sativa (japonica cultivar-group)]	285	5E-74
					>ref|XP 479571.1| r40g2 protein [Oryza sativa (japonica cultivar-group)]dbj|BAC83804.1| r40g2 protein [Oryza sativa (japonica cultivar-group)]	343	5E-74
					>emb|CAA70174.1| osr40g2 [Oryza sativa (indica cultivar-group)]	343	8E-72
DV621595	5.59E-03	B73<Mo17	1.4	4	>gb|AAW56447.1| putative methyl-binding domain protein MBD115 [Zea mays]	364	8E-44
					>gb|AAM93219.1| methyl binding domain protein MBD109 [Zea mays]	400	1E-28
DV495706	5.60E-03	B73<Mo17	1.4	4	>ref|XP_470597.1| Putative methionyl-tRNA synthetase [Oryza sativa (japonicacultivar-group)] gb|AAN77311.1| Putative methionyl-tRNA synthetase [Oryza sativa (japonica cultivar-group)]	579	2E-18
					>gb|AAM91427.1| AT3g55400/T22E16 60 [Arabidopsis thaliana]gb|AAK32940.1| AT3g55400/T22E16 60 [Arabidopsis thaliana]	616	2E-11
					>ref|NP_191100.1| ATP binding / methionine-tRNA ligase/ tRNA ligase [Arabidopsisthaliana] emb|CAB75898.1| methionyl-tRNA synthetase (AtcpMetRS) [Arabidopsis thaliana]	616	2E-11

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

<table>
<tr><th>GenBank accession no.</th><th>Overall P value</th><th>Significant pattern</th><th>Fold change†</th><th>Sector‡</th><th>BLAST annotation*</th><th>Score</th><th>E value</th></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA74281.1| MEtRS [Arabidopsis thaliana]</td><td>616</td><td>5E-11</td></tr>
<tr><td>AI621867</td><td>5.61E-03</td><td>Mo17<B73=F1</td><td>2.85</td><td>11</td><td>>ref|XP_466595.1| mitochondrial transcription termination factor-like protein [Oryzasativa (japonica cultivar-group)] dbj|BAD22170.1| mitochondrial transcription termination factor-like protein [Oryza sativa (japonica cultivar-group)] dbj|BAD19344.1| mitochondrial transcription termination factor-like protein [Oryza sativa (japonica cultivar-group)]</td><td>271</td><td>5E-65</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP 567435.1| unknown protein [Arabidopsis thaliana]</td><td>444</td><td>2E-29</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAB10239.1| hypothetical protein [Arabidopsis thaliana]emb|CAB78502.1| hypothetical protein [Arabidopsis thaliana]</td><td>590</td><td>2E-29</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_178405.2| unknown protein [Arabidopsis thaliana]gb|AAT69165.1| hypothetical protein At2g03050 [Arabidopsis thaliana] gb|AAO37134.1| hypothetical protein [Arabidopsis thaliana]</td><td>283</td><td>8E-18</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAC32923.1| predicted by genefinder and genscan [Arabidopsis thaliana]</td><td>284</td><td>8E-18</td></tr>
<tr><td>CD670178</td><td>5.61E-03</td><td>Mo17<B73=F1</td><td>1.42</td><td>10</td><td>>ref|XP_478414.1| putative translational inhibitor protein [Oryza sativa (japonicacultivar-group)] dbj|BAC20708.1| putative translational inhibitor protein [Oryza sativa (japonica cultivar-group)] dbj|BAD31311.1| putative translational inhibitor protein [Oryza sativa (japonica cultivar-group)]</td><td>180</td><td>4E-58</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAD00048.1| perchloric acid soluble translation inhibitor protein homolog[Gentiana triflora] dbj|BAC66487.1| translation-inhibitor protein [Gentiana triflora]</td><td>188</td><td>6E-54</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_188674.1| endoribonuclease [Arabidopsis thaliana]gb|AAK53030.1| AT3g20390/MQC12_15 [Arabidopsis thaliana] gb|AAL31178.1| AT3g20390/MQC12 15 [Arabidopsis thaliana] gb|AAM63246.1| translational inhibitor protein, putative [Arabidopsis thaliana]</td><td>187</td><td>1E-52</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAB02821.1| unnamed protein product [Arabidopsis thaliana]</td><td>143</td><td>1E-52</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAE56534.1| Hypothetical protein CBG24261 [Caenorhabditis briggsae]</td><td>172</td><td>2E-32</td></tr>
<tr><td>DV622264</td><td>5.61E-03</td><td>B73=F1<Mo17</td><td>1.17</td><td>4</td><td>>gb|AAX95093.1| ubiquinol--cytochrome-c reductase, putative [Oryza sativa (japonicacultivar-group)] gb|ABA91661.1| ubiquinol--cytochrome-c reductase, putative [Oryza sativa (japonica cultivar-group)]</td><td>96</td><td>1E-16</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAM63085.1| putative ubiquinol--cytochrome-c reductase [Arabidopsis thaliana]</td><td>69</td><td>1E-15</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP 172964.1| ubiquinol-cytochrome-c reductase [Arabidopsis thaliana]</td><td>69</td><td>2E-15</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA55860.1| ubiquinol--cytochrome c reductase [Solanum tuberosum]sp|P48504|UCRH_SOLTU Ubiquinol-cytochrome c reductase complex 7.8 kDa protein (Mitochondrial hinge protein) (CR7)</td><td>69</td><td>2E-14</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAD28224.1| putative ubiquinol-cytochrome C reductase complex 7.8 kDa protein[Oryza sativa (japonica cultivar-group)] dbj|BAD28073.1| putative ubiquinol-cytochrome C reductase complex 7.8 kDa protein [Oryza sativa (japonica cultivar-group)]</td><td>69</td><td>1E-13</td></tr>
<tr><td>CD001524</td><td>5.70E-03</td><td>Mo17<B73</td><td>1.27</td><td>10</td><td>>ref|XP 474269.1| OSJNBa0043A12.6 [Oryza sativa (japonica cultivar-group)]emb|CAE02801.1| OSJNBa0043A12.6 [Oryza sativa (japonica cultivar-group)]</td><td>148</td><td>7E-41</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAU82109.1| ubiquitin-conjugating enzyme [Triticum aestivum]</td><td>148</td><td>7E-41</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAF24583.1| F22C12.2 [Arabidopsis thaliana]</td><td>146</td><td>2E-40</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_001031228.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme[Arabidopsis thaliana] ref|NP_564828.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme [Arabidopsis thaliana] gb|AAM91500.1| At1g64230/F22C12_17 [Arabidopsis thaliana] gb|AAM11574.1| ubiquitin conjugating enzyme UBC9A [Arabidopsis thaliana] gb|AAK60309.1| At1g64230/F22C12_17 [Arabidopsis thaliana] gb|AAY44867.1| ubiquitinating enzyme [Arabidopsis thaliana]</td><td>148</td><td>2E-40</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAR83898.1| ubiquitin-conjugating protein [Capsicum annuum]</td><td>119</td><td>3E-40</td></tr>
<tr><td>BM074058</td><td>5.76E-03</td><td>Mo17<B73=F1</td><td>1.43</td><td>11</td><td>>ref|NP 908404.1| putative co-repressor protein [Oryza sativa (japonicacultivar-group)]</td><td>1589</td><td>3E-21</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP 549870.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]dbj|BAD44866.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]</td><td>155</td><td>2E-20</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAD46525.1| unknown protein [Oryza sativa (japonica cultivar-group)]</td><td>115</td><td>1E-10</td></tr>
<tr><td>CB380927</td><td>5.77E-03</td><td>Mo17<B73</td><td>1.33</td><td>10</td><td>>gb|ABA97552.1| Ribosomal S3Ae family, putative [Oryza sativa (japonicacultivar-group)]</td><td>800</td><td>2E-61</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_464995.1| putative ribosomal protein S3a, cytosolic [Oryza sativa (japonicacultivar-group)] ref|XP_506775.1| PREDICTED OJ1115_D03.49 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD21711.1| putative ribosomal protein S3a, cytosolic [Oryza sativa (japonica cultivar-group)] dbj|BAD21513.1| putative ribosomal protein S3a, cytosolic [Oryza sativa (japonica cultivar-group)]</td><td>261</td><td>3E-61</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAC98779.1| S-phase-specific ribosomal protein [Oryza sativa]</td><td>261</td><td>7E-61</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAA05059.1| cyc07 [Oryza sativa]sp|P49397|RS3A ORYSA 40S ribosomal protein S3a (CYC07 protein)</td><td>262</td><td>7E-61</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAA89498.1| cyc07 [Daucus carota]</td><td>261</td><td>8E-58</td></tr>
<tr><td>CD058818</td><td>5.79E-03</td><td>Mo17<B73</td><td>1.83</td><td>10</td><td>>ref|XP_463020.1| putative Acyl-CoA-binding protein [Oryza sativa (japonicacultivar-group)] gb|AAR10857.1| putative Acyl-CoA-binding protein [Oryza sativa (japonica cultivar-group)]</td><td>155</td><td>2E-39</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_913999.1| putative Acyl-CoA binding protein (ACBP) [Oryza sativa (japonicacultivar-group)] dbj|BAC99898.1| putative Acyl-CoA binding protein (ACBP) [Oryza sativa (japonica cultivar-group)] dbj|BAC57826.1| putative Acyl-CoA binding protein (ACBP) [Oryza sativa (japonica cultivar-group)]</td><td>91</td><td>3E-39</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAB85987.1| Acyl-CoA-binding protein [Panax ginseng]</td><td>87</td><td>2E-38</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAP82942.1| acyl-CoA-binding protein [Tropaeolum majus]</td><td>90</td><td>7E-38</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAB56693.1| Acyl-CoA binding protein (ACBP) [Digitalis lanata]</td><td>92</td><td>3E-37</td></tr>
<tr><td>CD058861</td><td>5.82E-03</td><td>F1=Mo17<B73</td><td>1.39</td><td>9</td><td>>ref|XP 472755.1| OSJNBa0072F16.12 [Oryza sativa (japonica cultivar-group)]emb|CAD40987.2| OSJNBa0072F16.12 [Oryza sativa (japonica cultivar-group)]</td><td>183</td><td>4E-51</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA10984.1| hypothetical protein [Hordeum vulgare subsp. vulgare]sp|O48609|RRP3_HORVU Plastid-specific 30S ribosomal protein 3, chloroplast precursor (PSRP-3)</td><td>181</td><td>1E-47</td></tr>
</table>

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|AAF64163.1| plastid-specific ribosomal protein 3 precursor [Spinacia oleracea]sp|P82412|RRP3_SPIOL Plastid-specific 30S ribosomal protein 3, chloroplast precursor (PSRP-3)	179	2E-37
					>ref|NP_564934.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAO50623.1| unknown protein [Arabidopsis thaliana] gb|AAO42029.1| unknown protein [Arabidopsis thaliana] gb|AAD49984.1| ESTs gb|H37416, gb|T21163, gb|T76138 and gb|AA651329 come from this gene. [Arabidopsis thaliana] sp|Q9SX22|RRP31 ARATH Plastid-specific 30S ribosomal protein 3-1, chloroplast precursor (PSRP-3 1)	166	1E-34
					>gb|AAM63350.1| plastid-specific ribosomal protein 3 precursor [Arabidopsisthaliana]	166	1E-34
CB617112	5.84E-03	Mo17<B73=F1	1.43	10	>ref|XP 463045.1| expressed protein [Oryza sativa (japonica cultivar-group)]gb|AAS07181.1| expressed protein [Oryza sativa (japonica cultivar-group)]	91	7E-18
					>emb|CAJ13713.1| hypothetical protein [Capsicum chinense]	96	2E-16
					>ref|NP_850005.1| unknown protein [Arabidopsis thaliana]gb|AAK00397.1| unknown protein [Arabidopsis thaliana] gb|AAG41478.1| unknown protein [Arabidopsis thaliana] gb|AAL06786.1| At2g20820/F5H14.21 [Arabidopsis thaliana] gb|AAG40023.1| At2g20820 [Arabidopsis thaliana] gb|AAK55709.1| At2g20820/F5H14.21 [Arabidopsis thaliana]	93	3E-15
DV489865	5.85E-03	B73=Mo17<F1	1.29	1	>gb|AAT78818.1| expressed protein [Oryza sativa (japonica cultivar-group)]	290	2E-39
					>ref|XP 479197.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAC79910.1| unknown protein [Oryza sativa (japonica cultivar-group)]	288	6E-37
					>ref|NP_195696.1| unknown protein [Arabidopsis thaliana]emb|CAB80649.1| putative protein [Arabidopsis thaliana] emb|CAB38899.1| putative protein [Arabidopsis thaliana]	299	1E-21
					>ref|NP_849528.1| unknown protein [Arabidopsis thaliana]gb|AAM51361.1| unknown protein [Arabidopsis thaliana] gb|AAL36221.1| unknown protein [Arabidopsis thaliana]	298	1E-21
					>gb|AAM62782.1| unknown [Arabidopsis thaliana]	299	3E-21
CB617282	5.86E-03	Mo17<F1	1.24	12	ns		
DV622441	5.88E-03	B73=F1<Mo17	1.23	5	>ref|NP_973987.1| unknown protein [Arabidopsis thaliana]ref|NP_564513.1| unknown protein [Arabidopsis thaliana] gb|AAM45073.1| unknown protein [Arabidopsis thaliana] gb|AAL87252.1| unknown protein [Arabidopsis thaliana]	279	3E-31
					>gb|AAM65611.1| unknown [Arabidopsis thaliana]	251	3E-31
					>gb|AAF99798.1| T2E6.19 [Arabidopsis thaliana]	292	3E-31
					>ref|NP_199542.1| unknown protein [Arabidopsis thaliana]gb|AAO64931.1| At5g47310 [Arabidopsis thaliana] dbj|BAA97165.1| unnamed protein product [Arabidopsis thaliana]	245	3E-18
					>ref|NP 565243.1| unknown protein [Arabidopsis thaliana]gb|AAM65516.1| unknown [Arabidopsis thaliana]	227	4E-18
BM337880	5.88E-03	F1=Mo17<B73	3.26	8	ns		
DV490892	5.92E-03	B73<F1=Mo17	1.76	2	ns		
DV942831	5.93E-03	Mo17<B73=F1	2.06	10	>ref|XP_472941.1| OSJNBa0081L15.17 [Oryza sativa (japonica cultivar-group)]emb|CAD41394.2| OJ000223_09.7 [Oryza sativa (japonica cultivar-group)] emb|CAE03155.2| OSJNBa0081L15.17 [Oryza sativa (japonica cultivar-group)]	308	3E-28
					>gb|AAS78923.1| CDC48-interacting UBX-domain protein [Arabidopsis thaliana]ref|NP_566815.1| PUX1 (PLANT UBX DOMAIN-CONTAINING PROTEIN 1) [Arabidopsis thaliana] gb|AAM61610.1| unknown [Arabidopsis thaliana] dbj|BAD43047.1| unknown protein [Arabidopsis thaliana] dbj|BAB02126.1| unnamed protein product [Arabidopsis thaliana]	251	4E-8
BM339782	5.97E-03	F1=Mo17<B73	2.87	9	ns		
BM079789	5.99E-03	F1=Mo17<B73	1.41	9	>ref|XP_470786.1| putative metacaspase, having alternative splicing products [Oryzasativa (japonica cultivar-group)] gb|AAR06360.1| putative metacaspase, having alternative splicing products [Oryza sativa (japonica cultivar-group)]	149	5E-28
					>ref|XP_470787.1| putative metacaspase, having alternative splicing products [Oryzasativa (japonica cultivar-group)] gb|AAR06359.1| putative metacaspase, having alternative splicing products [Oryza sativa (japonica cultivar-group)]	368	5E-28
					>ref|XP 470796.1| putative metacaspase [Oryza sativa (japonica cultivar-group)]gb|AAR06365.1| putative metacaspase [Oryza sativa (japonica cultivar-group)]	369	7E-15
					>ref|XP 470792.1| putative metacaspase [Oryza sativa (japonica cultivar-group)]gb|AAR06374.1| putative metacaspase [Oryza sativa (japonica cultivar-group)]	400	3E-13
					>ref|NP_171719.2| LOL3 (LSD ONE LIKE 3); caspase/ cysteine-type endopeptidase[Arabidopsis thaliana] gb|AAP84706.1| metacaspase 1 [Arabidopsis thaliana] gb|AAP44514.1| metacaspase 1 [Arabidopsis thaliana]	367	4E-7
CB381505	5.99E-03	Mo17<B73=F1	1.31	10	ns		
CD661670	6.05E-03	B73<F1=Mo17	1.34	3	>gb|AAA20239.1| cyclin IaZm	420	2E-79
					>ref|NP 915872.1| putative cyclin Ia [Oryza sativa (japonica cultivar-group)]dbj|BAB92272.1| putative cyclin [Oryza sativa (japonica cultivar-group)]	449	2E-65
					>ref|XP 475474.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]gb|AAT69653.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	521	3E-55
					>dbj|BAE53367.1| cyclin B1 [Allium cepa]	487	2E-52
					>emb|CAB81558.1| cyclin B1 [Nicotiana tabacum]	425	3E-51
DV489769	6.06E-03	Mo17<B73=F1	1.39	10	ns		
BM073952	6.08E-03	Mo17<B73=F1	2.76	10	ns		
CB886178	6.11E-03	B73<Mo17	1.71	3	ns		
CB604605	6.12E-03	Mo17<B73=F1	1.39	10	>ref|XP 483345.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD09976.1| unknown protein [Oryza sativa (japonica cultivar-group)]	197	6E-58
					>ref|XP 483344.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD09975.1| unknown protein [Oryza sativa (japonica cultivar-group)]	241	6E-58

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_566574.1| S-adenosylmethionine-dependent methyltransferase/ catalytic[Arabidopsis thaliana] gb|AAM67530.1| unknown protein [Arabidopsis thaliana] gb|AAK93650.1| unknown protein [Arabidopsis thaliana]	239	2E-41
					>ref|NP_191650.2| S-adenosylmethionine-dependent methyltransferase/ catalytic/methyltransferase [Arabidopsis thaliana] gb|AAM67532.1| unknown protein [Arabidopsis thaliana] gb|AAL86352.1| unknown protein [Arabidopsis thaliana]	252	2E-32
					>dbj|BAB02741.1| unnamed protein product [Arabidopsis thaliana]	419	1E-30
DV494243	6.12E-03	Mo17<B73	1.49	10	>dbj|BAD35675.1| putative cinnamoyl-CoA reductase [Oryza sativa (japonicacultivar-group)]	321	3E-22
					>dbj|BAD35672.1| putative cinnamoyl-CoA reductase [Oryza sativa (japonicacultivar-group)]	321	9E-21
					>ref|NP_180917.1| cinnamoyl-CoA reductase [Arabidopsis thaliana]gb|AAN15374.1| putative cinnamoyl-CoA reductase [Arabidopsis thaliana] gb|AAM53272.1| putative cinnamoyl-CoA reductase [Arabidopsis thaliana] gb|AAB80681.1| putative cinnamoyl-CoA reductase [Arabidopsis thaliana] gb|AAM61149.1| putative cinnamoyl-CoA reductase [Arabidopsis thaliana]	321	4E-15
					>ref|NP_180918.1| cinnamoyl-CoA reductase [Arabidopsis thaliana]gb|AAP42731.1| At2g33600 [Arabidopsis thaliana] gb|AAM13142.1| putative cinnamoyl-CoA reductase [Arabidopsis thaliana] gb|AAB80683.1| putative cinnamoyl-CoA reductase [Arabidopsis thaliana]	321	1E-13
					>ref|NP_177773.1| cinnamoyl-CoA reductase [Arabidopsis thaliana]gb|AAG51951.1| putative cinnamoyl-CoA reductase; 27707-26257 [Arabidopsis thaliana]	317	4E-10
DV492157	6.12E-03	B73=F1<Mo17	1.57	4	>dbj|BAD54446.1| putative xyloglucan endotransglycosylase [Oryza sativa (japonicacultivar-group)] dbj|BAD53910.1| putative xyloglucan endotransglycosylase [Oryza sativa (japonica cultivar-group)]	293	2E-23
					>emb|CAC40807.1| Xet1 protein [Festuca pratensis]	291	4E-21
					>emb|CAA63663.1| xyloglucan endotransglycosylase (XET) [Hordeum vulgare subsp.vulgare]	286	3E-20
					>gb|AAT94297.1| endotransglucosylase/hydrolase XTH5 [Triticum aestivum]	287	3E-20
					>ref|NP_200564.1| TCH4 (TOUCH 4); hydrolase, acting on glycosyl bonds / hydrolase,hydrolyzing O-glycosyl compounds [Arabidopsis thaliana] gb|AAL38614.1| AT5g57560/MUA2_13 [Arabidopsis thaliana] gb|AAL05902.1| AT5g57560/MUA2_13 [Arabidopsis thaliana] gb|AAK96616.1| AT5g57560/MUA2_13 [Arabidopsis thaliana] gb|AAK56251.1| AT5g57560/MUA2_13 [Arabidopsis thaliana] dbj|BAB08791.1| TCH4 protein [Arabidopsis thaliana] sp|Q38857|XTH22_ARATH Xyloglucan endotransglucosylase/hydrolase protein 22 precursor (At-XTH22) (XTH-22) (Touch protein 4) gb|AAC05572.1| xyloglucan endotransglycosylase related protein [Arabidopsis thaliana] gb|AAA92363.1| TCH4 protein	284	1E-13
DV490786	6.12E-03	F1<B73=Mo17	4.13	7	>gb|ABA94217.1| hypothetical protein LOC_Os11g34320 [Oryza sativa (japonicacultivar-group)]	362	1E-35
					>emb|CAC35876.1| putative protein [Arabidopsis thaliana]	435	4E-24
					>ref|NP_680156.2| Ran GTPase binding / chromatin binding [Arabidopsis thaliana]gb|AAO63918.1| putative UVB-resistance protein UVR8 [Arabidopsis thaliana] dbj|BAC43467.1| unknown protein [Arabidopsis thaliana]	434	4E-24
DV621846	6.13E-03	B73<F1=Mo17	1.26	3	>dbj|BAD46415.1| putative ubiquitin carrier protein E2 [Oryza sativa (japonicacultivar-group)]	252	8E-50
					>ref|NP_568148.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme[Arabidopsis thaliana] gb|AAM51582.1| AT5g05080/MUG13_6 [Arabidopsis thaliana] gb|AAL16250.1| AT5g05080/MUG13_6 [Arabidopsis thaliana] gb|AAM65652.1| E2, ubiquitin-conjugating enzyme, putative [Arabidopsis thaliana] dbj|BAB11530.1| unnamed protein product [Arabidopsis thaliana] gb|AAY44862.1| ubiquitinating enzyme [Arabidopsis thaliana]	251	4E-33
					>gb|AAZ57342.1| HL01424p [Drosophila melanogaster]gb|AAZ57341.1| AT05212p [Drosophila melanogaster] ref|NP_573237.2| CG8188-PA, isoform A [Drosophila melanogaster] ref|NP_001033852.1| CG8188-PB, isoform B [Drosophila melanogaster] gb|ABC67190.1| CG8188-PB, isoform B [Drosophila melanogaster] gb|AAF48756.2| CG8188-PA, isoform A [Drosophila melanogaster]	209	5E-17
					>ref|NP_001016438.1| hypothetical protein LOC549192 [Xenopus tropicalis]	211	7E-17
					>gb|AAI06318.1| MGC52831 protein [Xenopus laevis]gb|AAH41263.1| MGC52831 protein [Xenopus laevis]	211	2E-16
BM347887	6.13E-03	F1=Mo17<B73	1.78	9	ns		
CB617151	6.15E-03	Mo17<B73=F1	1.31	11	>ref|XP_483414.1| putative ribosomal protein L32 [Oryza sativa (japonicacultivar-group)] dbj|BAC75414.1| putative ribosomal protein L32 [Oryza sativa (japonica cultivar-group)]	133	4E-61
					>emb|CAH55765.1| ribosomal L32 [Oryza sativa (indica cultivar-group)]	133	2E-58
					>gb|AAZ32896.1| ribosomal protein L32 [Medicago sativa]	133	1E-53
					>gb|AAR83884.1| ly200 protein [Capsicum annuum]	133	2E-53
					>gb|ABB02639.1| ly200-like protein [Solanum tuberosum]gb|ABA40471.1| ly200-like protein [Solanum tuberosum]	133	9E-53
CD661726	6.17E-03	B73=F1<Mo17	1.31	4	>gb|AAT85295.1| FYVE zinc finger containing protein [Oryza sativa (japonicacultivar-group)]	1094	2E-31
					>ref|XP_469219.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAP44653.1| unknown protein [Oryza sativa (japonica cultivar-group)]	1142	2E-31
					>ref|NP_176362.3| zinc ion binding [Arabidopsis thaliana]gb|AAR23716.1| At1g61690 [Arabidopsis thaliana] dbj|BAD93965.1| hypothetical protein [Arabidopsis thaliana]	1171	1E-12
					>gb|AAD21427.1| Hypothetical protein [Arabidopsis thaliana]	1188	1E-12
CB380604	6.24E-03	B73<F1=Mo17	1.28	3	>ref|XP_482960.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD09002.1| unknown protein [Oryza sativa (japonica cultivar-group)]	422	7E-34
CB334557	6.24E-03	Mo17<B73=F1	1.29	10	>sp|O48557|RL17 MAIZE 60S ribosomal protein L17gb|AAB88619.1| ribosomal protein L17 [Zea mays]	171	3E-69
					>ref|XP_450351.1| putative ribosomal protein L17 [Oryza sativa (japonicacultivar-group)] ref|XP_507427.1| PREDICTED P0523B07.46 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_506642.1| PREDICTED P0523B07.46 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD23752.1| putative ribosomal protein L17 [Oryza sativa (japonica cultivar-group)] dbj|BAD23438.1| putative ribosomal protein L17 [Oryza sativa (japonica cultivar-group)]	171	4E-64

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>ref|XP_483472.1| putative ribosomal protein L17 [Oryza sativa (japonicacultivar-group)] dbj|BAD09119.1| putative ribosomal protein L17 [Oryza sativa (japonica cultivar-group)] dbj|BAD09020.1| putative ribosomal protein L17 [Oryza sativa (japonica cultivar-group)]	171	4E-64
					>gb|AAG49551.1| ribosomal protein L17-1 [Poa secunda]	171	4E-61
					>emb|CAA44598.1| ribosomal protein L17-1 [Hordeum vulgare subsp. vulgare]sp|P35266|RL171_HORVU 60S ribosomal protein L17-1	170	8E-61
DV490317	6.26E-03	F1=Mo17<B73	1.49	9	>gb|AAD39434.2| CENPCA protein [Zea mays]	701	2E-36
					>gb|AAU04624.1| CENP-C [Sorghum propinquum]	758	1E-26
					>gb|AAU04627.1| CENP-C2 [Saccharum officinarum]	709	3E-26
					>gb|AAU04628.1| CENP-C1 [Saccharum officinarum]gb|AAU04626.1| CENP-C1 [Saccharum officinarum]	709	3E-26
					>gb|AAU04623.1| CENP-C [Sorghum bicolor]	694	3E-26
CA829657	6.28E-03	Mo17<B73=F1	1.26	11	>emb|CAA74307.1| calmodulin [Zea mays]emb|CAA46150.1| calmodulin [Oryza sativa] gb|AAD10246.1| calmodulin [Phaseolus vulgaris]	149	1E-79
					>emb|CAA54583.1| calmodulin [Zea mays]	149	3E-79
					>ref|XP_475464.1| putative calmodulin [Oryza sativa (japonica cultivar-group)]gb|AAT69643.1| putative calmodulin [Oryza sativa (japonica cultivar-group)] gb|AAL35328.1| calmodulin [Oryza sativa] gb|AAC36058.1| calmodulin [Oryza sativa]	149	3E-79
					>emb|CAA36644.1| unnamed protein product [Medicago sativa]gb|AAM81203.1| calmodulin 2 [Medicago truncatula] gb|AAA34238.1| calmodulin [Vigna radiata] gb|AAD10244.1| calmodulin [Phaseolus vulgaris] sp|P17928|CALM_MEDSA Calmodulin (CaM) gb|AAA34014.1| calmodulin gb|AAA34013.1| calmodulin prf||2121384C calmodulin prf||2121384A calmodulin	149	3E-79
					>ref|NP_912914.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]ref|XP_479602.1| calmodulin [Oryza sativa (japonica cultivar-group)] emb|CAA78287.1| calmodulin [Oryza sativa (indica cultivar-group)] emb|CAA70982.1| CaM protein [Cicer arietinum] gb|AAL35329.1| calmodulin [Oryza sativa] gb|AAB36130.1| auxin-regulated calmodulin; arCaM [Vigna radiata] dbj|BAA88540.1| calmodulin [Oryza sativa (japonica cultivar-group)] gb|AAA34237.1| calmodulin [Vigna radiata] dbj|BAD30293.1| calmodulin [Oryza sativa (japonica cultivar-group)] dbj|BAC10352.1| calmodulin [Oryza sativa (japonica cultivar-group)] sp|P62162|CALM_HORVU Calmodulin (CaM) sp|P62163|CALM2_SOYBN Calmodulin-2 (CaM-2) gb|AAC49587.1| calmodulin TaCaM4-1 gb|AAC49586.1| calmodulin TaCaM3-3 gb|AAC49585.1| calmodulin TaCaM3-2 gb|AAC49584.1| calmodulin TaCaM3-1 gb|AAC49580.1| calmodulin TaCaM1-3 gb|AAC49579.1| calmodulin TaCaM1-2 gb|AAC49578.1| calmodulin TaCaM1-1 gb|AAC36059.1| calmodulin [Oryza sativa] sp|P29612|CALM_ORYSA Calmodulin (CaM) gb|AAA33901.1| calmodulin gb|AAA32938.1| calmodulin prf||2121384B calmodulin gb|AAA03580.1| calmodulin prf||1604476A calmodulin	149	3E-79
DV550870	6.29E-03	B73<F1=Mo17	1.4	2	>gb|AAL83985.1| putative protein phosphatase 2C [Oryza sativa]	130	4E-6
					>ref|XP_465582.1| putative protein phosphatase 2C [Oryza sativa (japonicacultivar-group)] ref|XP_506802.1| PREDICTED P0403C01.30 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD19608.1| putative protein phosphatase 2C [Oryza sativa (japonica cultivar-group)] dbj|BAD19485.1| putative protein phosphatase 2C [Oryza sativa (japonica cultivar-group)]	518	4E-6
DV942323	6.30E-03	F1=Mo17<B73	2.2	8	>ref|XP_465161.1| putative nicotianamine aminotransferase A [Oryza sativa (japonicacultivar-group)] dbj|BAD23582.1| putative nicotianamine aminotransferase A [Oryza sativa (japonica cultivar-group)]	444	e-102
					>dbj|BAA87052.2| nicotianamine aminotransferase A [Hordeum vulgare subsp. vulgare]	461	6E-93
					>dbj|BAA87055.1| nicotianamine aminotransferase [Hordeum vulgare subsp. vulgare]	461	2E-92
					>dbj|BAA87054.1| nicotianamine aminotransferase [Hordeum vulgare subsp. vulgare]	551	2E-89
					>dbj|BAA87053.1| nicotianamine aminotransferase B [Hordeum vulgare subsp. vulgare]	551	2E-89
CB833932	6.31E-03	Mo17<B73	1.31	10	>emb|CAA12028.1| Glyoxalase I [Cicer arietinum]sp|O49818|LGUL_CICAR Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)	186	4E-81
					>gb|AAK06838.1| glyoxalase I [Avicennia marina]	184	5E-80
					>ref|NP_001030996.1| calmodulin binding / lactoylglutathione lyase [Arabidopsisthaliana]	235	6E-80
					>ref|NP_849609.1| calmodulin binding / lactoylglutathione lyase [Arabidopsisthaliana] ref|NP_172291.1| calmodulin binding / lactoylglutathione lyase [Arabidopsis thaliana] ref|NP_001030995.1| calmodulin binding / lactoylglutathione lyase [Arabidopsis thaliana] gb|AAT41850.1| At1g08110 [Arabidopsis thaliana] gb|AAN72031.1| glyoxalase I, putative [Arabidopsis thaliana] sp|Q8H0V3|LGUL_ARATH Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)	185	1E-78
					>emb|CAA73691.1| Glyoxalase I [Brassica juncea]sp|O04885|LGUL_BRAJU Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)	185	3E-78
CB334416	6.33E-03	F1=Mo17<B73	1.26	9	>ref|NP_567410.1| hydrolase/ pyrophosphatase [Arabidopsis thaliana]dbj|BAD93787.1| hypothetical protein [Arabidopsis thaliana] gb|AAM66934.1| putative HAM1 protein [Arabidopsis thaliana]	206	1E-81
					>ref|NP_921812.1| putative HAM-1-like protein [Oryza sativa (japonicacultivar-group)] gb|AAK54301.1| putative HAM1 protein [Oryza sativa (japonica cultivar-group)] gb|AAP54099.1| HAM1 protein, putative [Oryza sativa (japonica cultivar-group)]	191	2E-81
					>dbj|BAD94569.1| hypothetical protein [Arabidopsis thaliana]	206	3E-81
					>emb|CAB78414.1| putative protein [Arabidopsis thaliana]emb|CAB36836.1| putative protein [Arabidopsis thaliana]	231	8E-75
					>ref|XP_637700.1| hypothetical protein DDB0215619 [Dictyostelium discoideum]gb|EAL64198.1| hypothetical protein DDB0215619 [Dictyostelium discoideum]	194	2E-64
CD484263	6.35E-03	Mo17<B73=F1	1.32	10	ns		
DV621637	6.35E-03	B73=F1<Mo17	1.39	4	ns		

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
DV942972	6.41E-03	F1<B73=Mo17	1.67	6	ns		
BM349773	6.42E-03	Mo17<B73=F1	1.39	10	>gb|AAL99608.1| cytosolic aldehyde dehydrogenase RF2C [Zea mays]	502	2E-7
					>gb|AAL99609.1| cytosolic aldehyde dehydrogenase RF2C [Zea mays]	503	2E-7
					>ref|NP_917471.1| cytosolic aldehyde dehydrogenase [Oryza sativa (japonicacultivar-group)] dbj|BAB55806.1| putative aldehyde dehydrogenase (NAD+) [Oryza sativa (japonica cultivar-group)] dbj|BAA96794.1| cytosolic aldehyde dehydrogenase [Oryza sativa (japonica cultivar-group)]	502	9E-6
DV492751	6.48E-03	B73<F1=Mo17	1.58	3	>gb|AAO72624.1| putative mitochondrial carrier protein [Oryza sativa (japonicacultivar-group)]	213	9E-44
					>ref|NP_177564.2| binding [Arabidopsis thaliana]gb|AAO50551.1| putative mitochondrial carrier protein [Arabidopsis thaliana] dbj|BAC42286.1| putative mitochondrial carrier protein [Arabidopsis thaliana]	364	2E-31
					>gb|AAG52407.1| putative mitochondrial carrier protein; 35518-32968 [Arabidopsisthaliana]	367	8E-30
					>gb|EAL21751.1| hypothetical protein CNBC4530 [Cryptococcus neoformans var.neoformans B-3501A]	717	4E-10
					>gb|AAW42258.1| mitochondrial inner membrane protein, putative [Cryptococcusneoformans var. neoformans JEC21] ref|XP_569565.1| mitochondrial inner membrane protein [Cryptococcus neoformans var. neoformans JEC21]	698	4E-10
CD651167	6.49E-03	B73<F1=Mo17	1.6	3	>ref|XP 474303.1| OSJNBb0004A17.1 [Oryza sativa (japonica cultivar-group)]	492	1E-83
					>emb|CAE03599.2| OSJNBb0004A17.1 [Oryza sativa (japonica cultivar-group)]	496	1E-83
					>ref|XP 474302.1| OSJNBa0043A12.39 [Oryza sativa (japonica cultivar-group)]emb|CAE02834.1| OSJNBa0043A12.39 [Oryza sativa (japonica cultivar-group)]	487	1E-64
					>gb|AAK43885.1| putative protein kinase gb|AAD22129 [Arabidopsis thaliana]	497	6E-52
					>ref|NP_176759.1| amine oxidase/ oxidoreductase [Arabidopsis thaliana]gb|AAN15672.1| putative protein kinase gb|AAD22129 [Arabidopsis thaliana] gb|AAO85405.1| putative amine oxidase 2 [Arabidopsis thaliana]	497	6E-52
CD661724	6.53E-03	F1=Mo17<B73	1.33	9	>emb|CAA48638.1| cyclophilin [Zea mays]sp|P21569|CYPH_MAIZE Peptidyl-prolyl cis-trans isomerase (PPIase) (Rotamase) (Cyclophilin) (Cyclosporin A-binding protein) gb|AAA63403.1| cyclophilin	172	1E-86
					>ref|XP_463914.1| peptidylprolyl isomerase Cyp2 [Oryza sativa (japonicacultivar-group)] ref|XP_506694.1| PREDICTED OSJNBb0088N06.23 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD07601.1| peptidylprolyl isomerase Cyp2 [Oryza sativa (japonica cultivar-group)] dbj|BAD08141.1| peptidylprolyl isomerase Cyp2 [Oryza sativa (japonica cultivar-group)] gb|AAA57045.1| cyclophilin 2	172	3E-75
					>gb|AAK49427.1| cyclophilin A-2 [Triticum aestivum]gb|AAS17067.1| cyclophilin A [Triticum aestivum]	171	5E-75
					>gb|AAK49428.1| cyclophilin A-3 [Triticum aestivum]gb|AAK49426.1| cyclophilin A-1 [Triticum aestivum]	171	7E-75
					>gb|AAA57046.1| cyclophilin 2	172	2E-74
CD001172	6.54E-03	Mo17<B73=F1	1.32	10	>dbj|BAD87555.1| unknown protein [Oryza sativa (japonica cultivar-group)]	229	2E-51
					>ref|NP 915142.1| B1078G07.36 [Oryza sativa (japonica cultivar-group)]dbj|BAC06256.1| P0696G06.13 [Oryza sativa (japonica cultivar-group)]	356	3E-31
					>ref|NP_973568.1| unknown protein [Arabidopsis thaliana]ref|NP_565704.1| unknown protein [Arabidopsis thaliana] gb|AAM16185.1| At2g30700/T11J7.9 [Arabidopsis thaliana] gb|AAM14829.1| Expressed protein [Arabidopsis thaliana] gb|AAL06467.1| At2g30700/T11J7.9 [Arabidopsis thaliana]	199	1E-13
DV550262	6.57E-03	B73<F1=Mo17	1.38	2	>ref|NP_911519.1| ADP-ribosylation factor 1 [Oryza sativa (japonica cultivar-group)]ref|NP_911517.1| ADP-ribosylation factor 1 [Oryza sativa (japonica cultivar-group)] dbj|BAD31195.1| ADP-ribosylation factor 1 [Oryza sativa (japonica cultivar-group)] dbj|BAC45192.1| ADP-ribosylation factor 1 [Oryza sativa (japonica cultivar-group)] dbj|BAC06914.1| ADP-ribosylation factor 1 [Oryza sativa (japonica cultivar-group)] gb|AAB65432.1| ADP-ribosylation factor 1 [Oryza sativa]	181	3E-97
					>gb|AAF65512.1| ADP-ribosylation factor [Capsicum annuum]gb|AAR03592.1| ARF-like small GTPase [Brassica juncea]	181	4E-96
					>ref|NP_182239.1| ARF1 (ADP-RIBOSYLATION FACTOR 1); GTP binding [Arabidopsisthaliana] gb|AAM98296.1| At2g47170/T3D7.2 [Arabidopsis thaliana] gb|AAM15469.1| ADP-ribosylation factor 1 [Arabidopsis thaliana] gb|AAB63817.1| ADP-ribosylation factor 1 [Arabidopsis thaliana] gb|AAL75910.1| At2g47170/T3D7.2 [Arabidopsis thaliana] gb|AAM64892.1| ADP-ribosylation factor 1 [Arabidopsis thaliana] sp|P36397|ARF1_ARATH ADP-ribosylation factor 1 gb|AAA32729.1| ADP-ribosylation factor	181	4E-96
					>gb|ABA40455.1| ARF-like small GTPase-like protein [Solanum tuberosum]gb|ABC01907.1| ARF-like small GTPase-like protein [Solanum tuberosum]	181	4E-96
					group)]	181	7E-96
DV491472	6.58E-03	Mo17<B73	1.52	9	>sp|Q9LSU1|PSA5_ORYSA Proteasome subunit alpha type 5 (20S proteasome alpha subunit E)(20S proteasome subunit alpha-5) gb|ABA94696.1| proteasome subunit alpha type 5 [Oryza sativa (japonica cultivar-group)] dbj|BAA96832.1| alpha 5 subunit of 20S proteasome [Oryza sativa (japonica cultivar-group)]	237	6E-61
					>ref|NP_175788.1| PAE1; endopeptidase/ peptidase/ threonine endopeptidase[Arabidopsis thaliana] gb|AAM47935.1| 20S proteasome subunit PAE1 [Arabidopsis thaliana] gb|AAL62363.1| 20S proteasome subunit PAE1 [Arabidopsis thaliana] gb|AAM63255.1| Proteasome subunit alpha type 5-1 (20S proteasome alpha subunit E1) [Arabidopsis thaliana] gb|AAF02858.1| 20S proteasome subunit PAE1 [Arabidopsis thaliana] gb|AAC32060.1| 20S proteasome subunit PAE1 [Arabidopsis thaliana] sp|O81149|PSA5A ARATH Proteasome subunit alpha type 5-A (20S proteasome alpha subunit E-1)	237	2E-59
					>gb|AAF70292.1| 20S proteasome subunit [Glycine max]sp|Q9M4T8|PSA5_SOYBN Proteasome subunit alpha type 5 (20S proteasome alpha subunit E) (20S proteasome subunit alpha-5)	237	3E-59
					>ref|NP_188046.1| PAE2; endopeptidase/ peptidase/ threonine endopeptidase[Arabidopsis thaliana] gb|AAL33816.1| putative 20S proteasome subunit PAE2 [Arabidopsis thaliana] gb|AAK44060.1| putative 20S proteasome subunit PAE2 [Arabidopsis thaliana] dbj|BAB01035.1| 20S proteasome subunit PAE-like protein [Arabidopsis thaliana] gb|AAC32061.1| 20S proteasome subunit PAE2 [Arabidopsis thaliana] sp|Q42134|PSA5B_ARATH Proteasome subunit alpha type 5-B (20S proteasome alpha subunit E-2) (Proteasome component Z)	237	5E-59
					>emb|CAD10778.1| 20S proteasome subunit alpha V [Physcomitrella patens]	237	2E-51

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CA829351	6.58E-03	B73<F1=Mo17	1.27	3	>gb|AAK40307.1| putative methyl-binding domain protein MBD105 [Zea mays]	433	2E-58
					>gb|AAK40308.1| putative methyl-binding domain protein MBD106 [Zea mays]	428	3E-35
					>gb|ABA99897.1| methyl-binding domain protein MBD106, putative [Oryza sativa(japonica cultivar-group)]	303	3E-29
					>gb|AAW56447.1| putative methyl-binding domain protein MBD115 [Zea mays]	364	7E-8
					>gb|AAM93219.1| methyl binding domain protein MBD109 [Zea mays]	400	4E-6
DV550515	6.59E-03	Mo17<B73=F1	2.26	10	>ref|NP_912350.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAP06874.1| unknown protein [Oryza sativa (japonica cultivar-group)] gb|AAP06842.1| unknown protein [Oryza sativa (japonica cultivar-group)]	144	5E-58
					>gb|AAV59350.1| unknown protein [Oryza sativa (japonica cultivar-group)]ref|XP_475341.1| unknown protein [Oryza sativa (japonica cultivar-group)]	166	3E-27
					>ref|NP_195447.1| unknown protein [Arabidopsis thaliana]emb|CAB16754.1| putative protein [Arabidopsis thaliana] emb|CAB80396.1| putative protein [Arabidopsis thaliana] gb|AAL33781.1| unknown protein [Arabidopsis thaliana] gb|AAK44007.1| unknown protein [Arabidopsis thaliana] gb|AAL06813.1| AT4g37300/C7A10_60 [Arabidopsis thaliana] gb|AAK62646.1| AT4g37300/C7A10_60 [Arabidopsis thaliana]	173	1E-18
CB604338	6.60E-03	Mo17<B73=F1	1.2	11	>gb|AAM95942.1| nucleosome/chromatin assembly factor group D protein [Zea mays]emb|CAA41220.1| high mobility group protein [Zea mays] emb|CAB46752.1| HMGa protein [Zea mays] sp|P27347|MNB1B_MAIZE DNA-binding protein MNB1B (HMG1-like protein)	157	2E-17
					>emb|CAA46876.1| DNA-binding protein [Zea mays]pir||T03640 high mobility group protein MNB1b - maize (fragment)	168	2E-17
					>gb|AAP21609.1| HMGB1 [Oryza sativa (indica cultivar-group)]gb|AAN28722.1| HMG1 protein [Oryza sativa (indica cultivar-group)] dbj|BAD61823.1| HMGB1 [Oryza sativa (japonica cultivar-group)] gb|AAC78104.1| high mobility group protein [Oryza sativa]	157	3E-16
					>emb|CAA77641.1| high mobility group protein [Triticum aestivum]sp|P40621|HMGL_WHEAT HMG1/2-like protein	161	1E-15
					>emb|CAA90679.1| HMG1/2-like protein [Hordeum vulgare subsp. vulgare]	160	8E-15
CB604128	6.64E-03	Mo17<B73=F1	1.36	10	>dbj|BAA28170.1| phosphoenolpyruvate carboxylase [Zea mays]	960	9E-91
					>emb|CAA46267.1| phosphoenolpyruvate carboxylase [Sorghum bicolor]emb|CAA39197.1| phosphoenolpyruvate carboxylase [Sorghum bicolor] sp|P29195|CAPP1_SORBI Phosphoenolpyruvate carboxylase 1 (PEPCase 1) (PEPC 1) (CP21)	960	8E-89
					>gb|AAR84575.1| C3 phosphoenolpyruvate carboxylase [Setaria italica]	961	5E-88
					>gb|AAP06951.1| phosphoenolpyruvate carboxylase [Echinochloa crus-galli]	961	2E-87
					>dbj|BAD27732.1| putative phosphoenolpyruvate carboxylase [Oryza sativa (japonicacultivar-group)]	968	1E-86
DV495744	6.69E-03	B73<F1=Mo17	1.74	3	ns		
DV550664	6.72E-03	B73=F1<Mo17	1.51	4	>ref|XP_474333.1| OSJNBa0018M05.20 [Oryza sativa (japonica cultivar-group)]emb|CAE03245.2| OSJNBa0018M05.20 [Oryza sativa (japonica cultivar-group)]	721	e-118
					>ref|NP_174675.2| STT3B (STAUROSPORIN AND TEMPERATURE SENSITIVE 3-LIKE B);oligosaccharyl transferase [Arabidopsis thaliana] gb|AAG12524.1| Putative integral membrane protein [Arabidopsis thaliana]	735	e-111
					>gb|EAA06273.3| ENSANGP00000020753 [Anopheles gambiae str. PEST]ref|XP_310665.2| ENSANGP00000020753 [Anopheles gambiae str. PEST]	715	7E-85
					>ref|XP_392786.2| PREDICTED: similar to CG1518-PA [Apis mellifera]	705	8E-84
					>ref|NP_608425.1| CG1518-PA [Drosophila melanogaster]gb|AAF50861.1| CG1518-PA [Drosophila melanogaster]	713	1E-83
BM333923	6.72E-03	F1=Mo17<B73	1.53	9	>dbj|BAD69166.1| putative somatic embryogenesis protein kinase 1 [Oryza sativa(japonica cultivar-group)] dbj|BAB19337.1| putative somatic embryogenesis protein kinase 1 [Oryza sativa (japonica cultivar-group)]	640	7E-17
					>emb|CAB79770.1| receptor-like kinase homolog [Arabidopsis thaliana]	573	8E-16
					>dbj|BAB01326.1| receptor-like kinase [Arabidopsis thaliana]	630	4E-14
					>ref|NP_189183.2| ATP binding / protein kinase/ protein serine/threonine kinase/protein-tyrosine kinase [Arabidopsis thaliana] gb|AAL91629.1| AT3g25560/MWL2_18 [Arabidopsis thaliana] gb|AAO11535.1| At3g25560/MWL2_18 [Arabidopsis thaliana]	635	4E-14
					>gb|AAM65586.1| receptor protein kinase-like protein [Arabidopsis thaliana]	629	6E-14
DV490752	6.73E-03	Mo17<B73=F1	2.25	10	ns		
rld2	6.77E-03	B73<F1=Mo17	1.27	3	ns		
CB833668	6.81E-03	B73<Mo17	1.41	3	>ref|XP_472198.1| OSJNBb0006N15.13 [Oryza sativa (japonica cultivar-group)]emb|CAE04596.2| OSJNBb0006N15.13 [Oryza sativa (japonica cultivar-group)]	347	3E-51
					>ref|NP_973808.1| TIF3H1; translation initiation factor [Arabidopsis thaliana]	250	4E-40
					>ref|NP_563880.1| TIF3H1; translation initiation factor [Arabidopsis thaliana]gb|AAN31904.1| putative translation initiation factor [Arabidopsis thaliana] gb|AAM10108.1| unknown protein [Arabidopsis thaliana] gb|AAK96832.1| Unknown protein [Arabidopsis thaliana] gb|AAM64888.1| putative translation initiation factor [Arabidopsis thaliana] gb|AAD31329.1| Similar to gb|U54559 eIF3-p40 subunit from Homo sapiens and is a member of the PF|01398 Mov34 family. ESTs gb|N96623 and gb|N07519 come from this gene. [Arabidopsis thaliana] pir||B86242 hypothetical protein [imported] - Arabidopsis thaliana sp|Q9C5Z2|IF33_ARATH Eukaryotic translation initiation factor 3 subunit 3 (eIF-3 gamma) (eIF3 p38 subunit) (eIF3h)	337	4E-40
					>gb|AAG53614.1| eukaryotic initiation factor 3H1 subunit [Arabidopsis thaliana]	337	4E-40
					>gb|AAH87438.1| LOC496043 protein [Xenopus laevis]	334	7E-13
AY501430	6.82E-03	B73<F1=Mo17	1.27	3	>gb|AAR97952.1| rolled leaf1 [Zea mays]	840	0E+0
					>gb|AAR04340.1| homeodomain leucine-zipper protein Hox10 [Oryza sativa (japonicacultivar-group)]	839	0E+0
					>ref|XP_468564.1| Putative homeodomain-leucine zipper protein [Oryza sativa (japonicacultivar-group)] gb|AAN61485.1| Putative homeodomain-leucine zipper protein [Oryza sativa (japonica cultivar-group)]	857	0E+0

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

<table>
<tr><th>GenBank accession no.</th><th>Overall P value</th><th>Significant pattern</th><th>Fold change†</th><th>Sector‡</th><th>BLAST annotation*</th><th>Score</th><th>E value</th></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_922012.1| putative homeodomain leucine zipper protein [Oryza sativa (japonicacultivar-group)] gb|AAK21338.1| putative homeodomain-leucine zipper protein [Oryza sativa (japonica cultivar-group)] gb|ABB47795.1| homeodomain-leucine zipper protein, putative [Oryza sativa (japonica cultivar-group)] gb|AAP54299.1| homeodomain-leucine zipper protein, putative [Oryza sativa (japonica cultivar-group)]</td><td>840</td><td>0E+0</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAQ98963.1| homeodomain leucine-zipper protein Hox9 [Oryza sativa (japonicacultivar-group)]</td><td>840</td><td>0E+0</td></tr>
<tr><td>AI738263</td><td>6.83E-03</td><td>B73=F1<Mo17</td><td>1.68</td><td>4</td><td>>ref|XP_470035.1| putative endosperm C-24 sterol methyltransferase [Oryza sativa(japonica cultivar-group)] gb|AAP21419.1| putative endosperm C-24 sterol methyltransferase [Oryza sativa (japonica cultivar-group)]</td><td>330</td><td>1E-10</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAZ83345.1| 24-sterol C-methyltransferase [Gossypium hirsutum]</td><td>346</td><td>3E-9</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAB37769.1| delta-24-sterol methyltransferase [Triticum aestivum]</td><td>363</td><td>7E-9</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAB49338.1| delta-24-sterol methyltransferase [Triticum aestivum]</td><td>363</td><td>1E-8</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAB70886.1| endosperm C-24 sterol methyltransferase [Zea mays]</td><td>344</td><td>2E-8</td></tr>
<tr><td>BM339393</td><td>6.85E-03</td><td>Mo17<B73=F1</td><td>1.67</td><td>11</td><td>>ref|XP_507493.1| PREDICTED OJ1058_F07.21 gene product [Oryza sativa (japonicacultivar-group)] ref|XP_466627.1| putative glycine-rich protein [Oryza sativa (japonica cultivar-group)] ref|XP_506857.1| PREDICTED OJ1058_F07.21 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD19331.1| putative glycine-rich protein [Oryza sativa (japonica cultivar-group)]</td><td>250</td><td>1E-62</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP 473006.1| OSJNBb0091E11.5 [Oryza sativa (japonica cultivar-group)]emb|CAD41536.2| OSJNBb0091E11.5 [Oryza sativa (japonica cultivar-group)]</td><td>337</td><td>2E-39</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_850396.1| unknown protein [Arabidopsis thaliana]gb|AAM20106.1| unknown protein [Arabidopsis thaliana] gb|AAL38892.1| unknown protein [Arabidopsis thaliana]</td><td>274</td><td>4E-15</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAB64043.1| unknown protein [Arabidopsis thaliana]</td><td>174</td><td>4E-15</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_191523.1| unknown protein [Arabidopsis thaliana]emb|CAB75461.1| putative protein [Arabidopsis thaliana] gb|AAK62385.1| putative protein [Arabidopsis thaliana] gb|AAN65060.1| putative protein [Arabidopsis thaliana]</td><td>246</td><td>5E-12</td></tr>
<tr><td>BM075199</td><td>6.87E-03</td><td>Mo17<B73=F1</td><td>1.33</td><td>10</td><td>>ref|XP_477314.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAC83023.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAD31296.1| unknown protein [Oryza sativa (japonica cultivar-group)]</td><td>252</td><td>2E-21</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_173557.2| unknown protein [Arabidopsis thaliana]ref|NP_849694.1| unknown protein [Arabidopsis thaliana] gb|AAT71985.1| At1g21350 [Arabidopsis thaliana] gb|AAO22789.1| unknown protein [Arabidopsis thaliana]</td><td>151</td><td>1E-19</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP 973876.1| unknown protein [Arabidopsis thaliana]gb|AAF87891.1| Hypothetical protein [Arabidopsis thaliana]</td><td>252</td><td>1E-19</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAE18742.1| conserved hypothetical protein [Prochlorococcus marinus subsp.pastoris str. CCMP1986] ref|NP_892402.1| hypothetical protein PMM0283 [Prochlorococcus marinus subsp. pastoris str. CCMP1986]</td><td>197</td><td>2E-10</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|ABB49346.1| conserved hypothetical protein [Prochlorococcus marinus str. MIT9312] ref|YP_396782.1| hypothetical protein PMT9312_0285 [Prochlorococcus marinus str. MIT 9312]</td><td>197</td><td>1E-9</td></tr>
<tr><td>CB381444</td><td>6.87E-03</td><td>B73=Mo17<F1</td><td>1.26</td><td>12</td><td>>gb|AAQ17040.2| pollen 2-phosphoglycerate dehydrogenase 2 precursor [Cynodondactylon] gb|AAD04187.1| enolase [Zea mays] sp|P42895|ENO2_MAIZE Enolase 2 (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)</td><td>446</td><td>6E-92</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAP94211.1| enolase [Oryza sativa (japonica cultivar-group)]</td><td>446</td><td>1E-87</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_920013.1| putative enolase (2-phospho-D-glycerate hydroylase) [Oryza sativa(japonica cultivar-group)] gb|AAN04181.1| Putative enolase (2-phospho-D-glycerate hydroylase) [Oryza sativa (japonica cultivar-group)]</td><td>428</td><td>1E-87</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|ABB46862.1| enolase [Oryza sativa (japonica cultivar-group)]</td><td>461</td><td>1E-87</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|ABB46861.1| enolase [Oryza sativa (japonica cultivar-group)]</td><td>461</td><td>1E-87</td></tr>
<tr><td>DV490553</td><td>6.90E-03</td><td>Mo17<B73=F1</td><td>1.72</td><td>10</td><td>>gb|AAT76373.1| putative Mob1/phocein family protein [Oryza sativa (japonicacultivar-group)]</td><td>190</td><td>3E-40</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_463026.1| putative Mob1-like protein [Oryza sativa (japonica cultivar-group)]gb|AAR10852.1| putative Mob1-like protein [Oryza sativa (japonica cultivar-group)]</td><td>214</td><td>3E-40</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAP45180.1| unknown [Solanum bulbocastanum]</td><td>218</td><td>2E-39</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAP45162.1| putative Mob1/phocein family protein [Solanum bulbocastanum]</td><td>215</td><td>2E-39</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAP12863.1| At4g19050 [Arabidopsis thaliana]dbj|BAC42011.1| unknown protein [Arabidopsis thaliana]</td><td>215</td><td>4E-39</td></tr>
<tr><td>BM079918</td><td>6.91E-03</td><td>B73<F1=Mo17</td><td>1.69</td><td>3</td><td>ns</td><td></td><td></td></tr>
<tr><td>BM349041</td><td>6.92E-03</td><td>Mo17<B73=F1</td><td>1.31</td><td>10</td><td>>gb|AAK16543.1| 9S ribosomal protein [Zea mays]gb|AAK16544.1| 9S ribosomal protein [Zea mays]</td><td>221</td><td>6E-79</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAT85048.1| putative 9S ribosomal protein [Oryza sativa (japonicacultivar-group)] gb|AAR87317.1| ribosomal protein S9 [Oryza sativa (japonica cultivar-group)] dbj|BAA82395.1| ribosomal protein S9 [Oryza sativa (japonica cultivar-group)]</td><td>223</td><td>2E-72</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_177635.1| RPS9 (RIBOSOMAL PROTEIN S9); structural constituent of ribosome[Arabidopsis thaliana] gb|AAK06869.1| putative ribosomal protein S9 [Arabidopsis thaliana] gb|AAM14321.1| putative ribosomal protein S9 [Arabidopsis thaliana] gb|AAK76530.1| putative ribosomal protein S9 [Arabidopsis thaliana] gb|AAK73958.1| ATg74970/F25A4.6 [Arabidopsis thaliana] gb|AAM63421.1| ribosomal protein S9, putative [Arabidopsis thaliana] dbj|BAD44621.1| putative ribosomal protein S9 [Arabidopsis thaliana] dbj|BAD44560.1| putative ribosomal protein S9 [Arabidopsis thaliana] dbj|BAD44553.1| putative ribosomal protein S9 [Arabidopsis thaliana] dbj|BAD44536.1| putative ribosomal protein S9 [Arabidopsis thaliana] dbj|BAD44521.1| putative ribosomal protein S9 [Arabidopsis thaliana] dbj|BAD44517.1| putative ribosomal protein S9 [Arabidopsis thaliana] dbj|BAD44459.1| putative ribosomal protein S9 [Arabidopsis thaliana] dbj|BAD44131.1| putative ribosomal protein S9 [Arabidopsis thaliana] dbj|BAD43731.1| putative ribosomal protein S9 [Arabidopsis thaliana] dbj|BAD43658.1| putative ribosomal</td><td>208</td><td>5E-59</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAD44402.1| putative ribosomal protein S9 [Arabidopsis thaliana]</td><td>208</td><td>1E-58</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAD43279.1| putative ribosomal protein S9 [Arabidopsis thaliana]</td><td>208</td><td>1E-58</td></tr>
</table>

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
CB605313	6.96E-03	B73=Mo17<F1	1.31	12	>gb|AAF71261.2| beta-glucosidase aggregating factor precursor [Zea mays]	306	6E-22
					>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	9E-21
					>gb|ABA97248.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]gb|ABB51090.1| mannose-specific jacalin-related lectin [Oryza sativa (japonica cultivar-group)]	306	8E-20
					>gb|AAA87041.1| putative 32.6 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72096.1| 32 kDa protein [Hordeum vulgare]	304	1E-19
					>gb|AAA87042.1| putative 32.7 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72097.1| 32 kDa protein [Hordeum vulgare]	304	3E-19
AI857160	6.99E-03	Mo17<B73	2.81	10	>emb|CAC19854.1| Oxalyl-CoA decarboxylase [Arabidopsis thaliana]	572	3E-10
					>ref|NP_197240.1| pyruvate decarboxylase [Arabidopsis thaliana]emb|CAC01733.1| 2-hydroxyphytanoyl-CoA lyase-like protein [Arabidopsis thaliana] gb|AAN15603.1| 2-hydroxyphytanoyl-CoA lyase-like protein [Arabidopsis thaliana] gb|AAM20625.1| 2-hydroxyphytanoyl-CoA lyase-like protein [Arabidopsis thaliana]	572	3E-10
					>gb|AAP69814.1| putative oxalyl-CoA decarboxylase [Vitis vinifera]	163	7E-10
					>ref|XP 463271.1| putative oxalyl-CoA decarboxylase [Oryza sativa (japonicacultivar-group)]	577	3E-9
					>dbj|BAD69045.1| unknown protein [Oryza sativa (japonica cultivar-group)]	285	4E-9
CB334498	7.00E-03	B73=Mo17<F1	1.65	1	ns		
AI714933	7.03E-03	Mo17<B73=F1	1.63	10	>gb|ABA94623.1| Zinc finger, C3HC4 type, putative [Oryza sativa (japonicacultivar-group)]	325	1E-37
					>ref|NP_179802.2| protein binding / ubiquitin-protein ligase/ zinc ion binding[Arabidopsis thaliana] gb|AAO50515.1| unknown protein [Arabidopsis thaliana] gb|AAO42065.1| unknown protein [Arabidopsis thaliana]	324	1E-30
					>gb|AAD25813.1| hypothetical protein [Arabidopsis thaliana]	252	3E-23
					>gb|AAM65602.1| unknown [Arabidopsis thaliana]	320	1E-12
					>gb|AAB65494.1| hypothetical protein; 51018-49636 [Arabidopsis thaliana]	281	1E-12
CD670355	7.10E-03	Mo17<B73=F1	1.22	10	>ref|XP 482061.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD05314.1| unknown protein [Oryza sativa (japonica cultivar-group)]	196	2E-21
DV550932	7.12E-03	Mo17<B73	3.43	10	>dbj|BAD87907.1| putative glutamate carboxypeptidase [Oryza sativa (japonicacultivar-group)]	728	5E-97
					>dbj|BAD86951.1| putative glutamate carboxypeptidase [Oryza sativa (japonicacultivar-group)]	661	3E-92
					>ref|NP 197475.2| dipeptidase [Arabidopsis thaliana]gb|AAP37682.1| At5g19740 [Arabidopsis thaliana]	681	4E-84
					>ref|NP 916030.1| peptidase-like protein [Oryza sativa (japonica cultivar-group)]	621	2E-69
					>ref|XP_469932.1| putative glutamate carboxypeptidase [Oryza sativa (japonicacultivar-group)] gb|AAO24914.1| putative glutamate carboxypeptidase [Oryza sativa (japonica cultivar-group)]	772	5E-65
DV491634	7.12E-03	B73<Mo17	1.37	4	>gb|ABA93456.1| transposon protein, putative, CACTA, En/Spm sub-class [Oryza sativa(japonica cultivar-group)]	302	6E-34
					>gb|ABA93448.1| serine carboxypeptidase I, putative [Oryza sativa (japonicacultivar-group)]	168	2E-33
					>ref|NP_919459.1| putative serine carboxypeptidase [Oryza sativa (japonicacultivar-group)] gb|AAL73563.1| Putative serine carboxypeptidase [Oryza sativa (japonica cultivar-group)] gb|AAM08635.1| Putative serine carboxypeptidase [Oryza sativa]	432	1E-31
					>gb|ABB46564.1| Serine carboxypeptidase [Oryza sativa (japonica cultivar-group)]	460	1E-31
					>ref|XP 474646.1| OSJNBb0051N19.2 [Oryza sativa (japonica cultivar-group)]emb|CAE01973.2| OSJNBb0051N19.2 [Oryza sativa (japonica cultivar-group)]	467	1E-27
AI820131	7.14E-03	B73<F1=Mo17	1.54	2	>dbj|BAD36121.1| putative 26S proteasome regulatory particle triple-A ATPasesubunit4 [Oryza sativa (japonica cultivar-group)] dbj|BAD35613.1| putative 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa (japonica cultivar-group)]	401	4E-48
					>dbj|BAB78495.1| 26S proteasome regulatory particle triple-A ATPase subunit4b [Oryzasativa (japonica cultivar-group)]	377	4E-48
					>ref|XP_464508.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryzasativa (japonica cultivar-group)] dbj|BAD25481.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa (japonica cultivar-group)] dbj|BAD15843.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa (japonica cultivar-group)] dbj|BAB17625.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa (japonica cultivar-group)]	400	6E-48
					>gb|ABA40428.1| 26S proteasome AAA-ATPase subunit RPT4a-like protein [Solanumtuberosum] dbj|BAC23035.1| 26S proteasome AAA-ATPase subunit RPT4a [Solanum tuberosum]	398	5E-46
					>ref|NP_199115.1| RPT4A; ATPase [Arabidopsis thaliana]gb|AAL77741.1| AT5g43010/MBD2_21 [Arabidopsis thaliana] gb|AAK50085.1| AT5g43010/MBD2_21 [Arabidopsis thaliana] dbj|BAB09203.1| 26S proteasome AAA-ATPase subunit RPT4a [Arabidopsis thaliana] gb|AAF22524.1| 26S proteasome AAA-ATPase subunit RPT4a [Arabidopsis thaliana]	399	5E-45
DV492840	7.17E-03	Mo17<B73=F1	1.6	10	>ref|XP_467485.1| putative 60S ribosomal protein L31 [Oryza sativa (japonicacultivar-group)] dbj|BAD12898.1| putative 60S ribosomal protein L31 [Oryza sativa (japonica cultivar-group)]	123	2E-50
					>gb|AAV28627.1| putative 60S ribosomal protein L31 [Zea mays]	124	2E-48
					>dbj|BAD61612.1| putative 60S ribosomal protein L31 [Oryza sativa (japonicacultivar-group)]	124	9E-48
					>ref|XP_483237.1| putative 60S ribosomal protein L31 [Oryza sativa (japonicacultivar-group)] dbj|BAD10170.1| putative 60S ribosomal protein L31 [Oryza sativa (japonica cultivar-group)] dbj|BAD08833.1| putative 60S ribosomal protein L31 [Oryza sativa (japonica cultivar-group)]	122	3E-47
					>sp|P46290|RL31 NICGU 60S ribosomal protein L31gb|AAA80638.1| ribosomal protein L31	120	7E-43
CB281932	7.20E-03	Mo17<B73	1.53	10	>gb|AAQ17040.2| pollen 2-phosphoglycerate dehydrogenase 2 precursor [Cynodondactylon] gb|AAD04187.1| enolase [Zea mays] sp|P42895|ENO2_MAIZE Enolase 2 (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)	446	2E-59

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15 % FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|AAP94211.1| enolase [Oryza sativa (japonica cultivar-group)]	446	3E-57
					>gb|AAC49173.1| enolasesp|Q42971|ENO ORYSA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (OSE1)	446	9E-57
					>emb|CAA41115.1| enolase [Lycopersicon esculentum]sp|P26300|ENO LYCES Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)	444	2E-55
					>emb|CAA39454.1| enolase [Zea mays]sp|P26301|ENO1 MAIZE Enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)	446	1E-54
CB604505	7.21E-03	Mo17<B73=F1	1.26	10	>ref|XP_478036.1| DnaJ protein family-like protein [Oryza sativa (japonicacultivar-group)] dbj|BAC06950.1| DnaJ protein family-like protein [Oryza sativa (japonica cultivar-group)]	212	2E-66
					>ref|NP_181738.1| heat shock protein binding / unfolded protein binding [Arabidopsisthaliana] gb|AAM97104.1| unknown protein [Arabidopsis thaliana] gb|AAB63536.1| unknown protein [Arabidopsis thaliana] gb|AAN72139.1| unknown protein [Arabidopsis thaliana]	263	5E-17
					>gb|AAL87325.1| unknown protein [Arabidopsis thaliana]	254	5E-9
CB885611	7.21E-03	Mo17<B73	1.3	9	>sp|Q08069|RS8 MAIZE 40S ribosomal protein S8gb|AAB06330.1| ribosomal protein S8	221	3E-87
					>emb|CAE05511.1| OSJNBa0038P21.4 [Oryza sativa (japonica cultivar-group)]	221	7E-82
					>ref|XP_465742.1| putative 40S ribosomal protein S8 [Oryza sativa (japonicacultivar-group)] ref|XP_506804.1| PREDICTED P0483C08.42 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD21871.1| putative 40S ribosomal protein S8 [Oryza sativa (japonica cultivar-group)] dbj|BAD21876.1| putative 40S ribosomal protein S8 [Oryza sativa (japonica cultivar-group)]	220	1E-81
					>sp|P49199|RS8 ORYSA 40S ribosomal protein S8dbj|BAA07207.1| ribosomal protein S8 [Oryza sativa (japonica cultivar-group)]	220	2E-78
					>gb|ABA46755.1| unknown [Solanum tuberosum]	224	8E-78
CB886094	7.22E-03	B73<F1=Mo17	1.27	2	>ref|XP_467147.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD25738.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAD25775.1| unknown protein [Oryza sativa (japonica cultivar-group)]	283	2E-28
					>gb|AAM65994.1| unknown [Arabidopsis thaliana]	293	1E-12
					>dbj|BAB02931.1| unnamed protein product [Arabidopsis thaliana]	330	1E-12
					>dbj|BAC43550.1| unknown protein [Arabidopsis thaliana]	293	1E-12
					>ref|NP 566746.1| unknown protein [Arabidopsis thaliana]	293	1E-12
BM351785	7.24E-03	B73<F1=Mo17	1.47	3	>gb|AAT94032.1| beta-tubulin [Oryza sativa (japonica cultivar-group)]dbj|BAC82429.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|Q76FS3|TBB6 ORYSA Tubulin beta-6 chain (Beta-6 tubulin)	444	6E-48
					>gb|AAQ92664.1| beta-tubulin 3 [Gossypium hirsutum]sp|Q6VAF8|TBB3 GOSHI Tubulin beta-3 chain (Beta-3 tubulin)	430	6E-48
					>emb|CAA55022.1| beta tubulin [Oryza sativa (japonica cultivar-group)]	447	8E-48
					>emb|CAE52516.1| beta tubulin [Setaria viridis]	448	8E-48
					>ref|NP_915874.1| tubulin beta chain [Oryza sativa (japonica cultivar-group)]dbj|BAB92274.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] dbj|BAA06381.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|P45960|TBB4 ORYSA Tubulin beta-4 chain (Beta-4 tubulin)	447	8E-48
CB334412	7.24E-03	Mo17<B73=F1	1.4	11	>ref|XP_466921.1| putative ubiquitin-conjugating enzyme E2 [Oryza sativa (japonicacultivar-group)] dbj|BAD25314.1| putative ubiquitin-conjugating enzyme E2 [Oryza sativa (japonica cultivar-group)] dbj|BAD25096.1| putative ubiquitin-conjugating enzyme E2 [Oryza sativa (japonica cultivar-group)]	157	1E-81
					>ref|NP_001031939.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme[Arabidopsis thaliana] ref|NP_568476.1| ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme [Arabidopsis thaliana] gb|AAM60888.1| E2, ubiquitin-conjugating enzyme, putative [Arabidopsis thaliana] gb|AAY44861.1| ubiquitinating enzyme [Arabidopsis thaliana]	157	5E-78
					>gb|AAN16047.1| ubiquitin-conjugating enzyme E2 [Pavlova lutheri]	166	7E-48
					>ref|XP_643940.1| hypothetical protein DDB0167874 [Dictyostelium discoideum]gb|AAO51851.1| similar to Arabidopsis thaliana (Mouse-ear cress). E2, ubiquitin-conjugating enzyme, putative [Dictyostelium discoideum] gb|EAL70049.1| hypothetical protein DDB0167874 [Dictyostelium discoideum]	149	6E-47
					>emb|CAI74825.1| ubiquitin-conjugating enzyme e2, putative [Theileria annulata]ref|XP_952557.1| ubiquitin-conjugating enzyme E2 [Theileria annulata strain Ankara]	157	2E-44
CB885492	7.24E-03	B73<F1=Mo17	1.41	3	>emb|CAA33620.1| GAPDH [Zea mays]sp|P08735|G3PC MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 1	337	1E-94
					>emb|CAA30151.1| unnamed protein product [Zea mays]	337	1E-94
					>emb|CAA51676.1| glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zeamays] sp|Q09054|G3PD_MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 2 gb|AAA87880.1| glyceraldehyde-3-phosphate dehydrogenase gb|AAA87578.1| cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2	337	2E-92
					>emb|CAA42901.1| glyceraldehyde 3-phosphate dehydrogenase [Hordeum vulgare]sp|P26517|G3PX_HORVU Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	337	9E-91
					>ref|XP_479895.1| glyceraldehyde 3-phosphate dehydrogenase, cytosolic [Oryza sativa(japonica cultivar-group)] ref|XP_507107.1| PREDICTED OJ1163_G08.15 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD08850.1| glyceraldehyde 3-phosphate dehydrogenase, cytosolic [Oryza sativa (japonica cultivar-group)] sp|Q42977|G3PC ORYSA Glyceraldehyde-3-phosphate dehydrogenase, cytosolic (PP38)	337	4E-89
BG842957	7.32E-03	Mo17<B73=F1	1.53	11	>dbj|BAD27922.1| harpin-induced protein-like [Oryza sativa (japonicacultivar-group)] dbj|BAD28833.1| harpin-induced protein-like [Oryza sativa (japonica cultivar-group)]	224	4E-42
					>ref|XP_472430.1| OJ991214_12.17 [Oryza sativa (japonica cultivar-group)]emb|CAD40930.3| OSJNBa0033G16.4 [Oryza sativa (japonica cultivar-group)] emb|CAE01528.2| OJ991214 12.17 [Oryza sativa (japonica cultivar-group)]	220	1E-34

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>gb|AAX92937.1| Harpin-induced protein 1 (Hin1), putative [Oryza sativa (japonicacultivar-group)] gb|ABA91552.1| Harpin-induced protein 1, putative [Oryza sativa (japonica cultivar-group)]	210	1E-29
					>gb|ABA96522.1| Harpin-induced protein 1, putative [Oryza sativa (japonicacultivar-group)]	212	1E-28
					>ref|NP_680206.1| unknown protein [Arabidopsis thaliana]emb|CAC34513.1| NDR1/HIN1-like protein [Arabidopsis thaliana]	210	3E-21
CD527618	7.34E-03	Mo17<B73=F1	3.31	10	>emb|CAD45251.1| barley B recombinant [Hordeum vulgare]	350	9E-20
					>gb|AAS75867.1| barley B recombinant like-protein B [Oryza sativa (japonicacultivar-group)] gb|AAS75866.1| barley B recombinant like-protein B [Oryza sativa (japonica cultivar-group)] gb|AAS75865.1| barley B recombinant like-protein A [Oryza sativa (japonica cultivar-group)] gb|ABB46626.1| GAGA binding protein-like family, putative [Oryza sativa (japonica cultivar-group)] gb|ABB46625.1| GAGA binding protein-like family, putative [Oryza sativa (japonica cultivar-group)]	341	3E-8
					>ref|NP_919574.1| unknown protein [Oryza sativa (japonica cultivar-group)]ref|NP_919580.1| unknown protein [Oryza sativa (japonica cultivar-group)] gb|AAK52543.1| Unknown protein [Oryza sativa (japonica cultivar-group)] gb|AAK52537.1| Unknown protein [Oryza sativa (japonica cultivar-group)] gb|AAM44863.1| Unknown protein [Oryza sativa (japonica cultivar-group)] gb|AAP51867.1| hypothetical protein LOC_Os10g02510 [Oryza sativa (japonica cultivar-group)]	344	3E-8
					>ref|NP_919582.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAK52535.1| Unknown protein [Oryza sativa (japonica cultivar-group)] gb|AAS76677.1| barley B recombinant like protein C [Oryza sativa (japonica cultivar-group)] gb|AAS76676.1| barley B recombinant like protein C [Oryza sativa (japonica cultivar-group)] gb|AAP51869.1| GAGA binding protein-like family, putative [Oryza sativa (japonica cultivar-group)]	343	9E-7
CD568501	7.36E-03	B73<F1=Mo17	1.16	2	>ref|XP_481937.1| putative p23 co-chaperone [Oryza sativa (japonica cultivar-group)]ref|XP_507202.1| PREDICTED P0488B06.44 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD03808.1| putative p23 co-chaperone [Oryza sativa (japonica cultivar-group)] dbj|BAD03784.1| putative p23 co-chaperone [Oryza sativa (japonica cultivar-group)]	213	2E-23
					>ref|NP_192154.2| unknown protein [Arabidopsis thaliana]gb|AAN18096.1| At4g02450/T14P8_5 [Arabidopsis thaliana] gb|AAM83226.1| AT4g02450/T14P8_5 [Arabidopsis thaliana]	241	2E-11
					>emb|CAC16575.1| p23 co-chaperone [Arabidopsis thaliana]	241	2E-11
					>emb|CAB80738.1| putative protein [Arabidopsis thaliana]gb|AAC19287.1| T14P8.5 [Arabidopsis thaliana]	262	2E-11
					>gb|AAG41763.1| p23 [Brassica napus]	178	3E-8
DV489625	7.38E-03	B73=Mo17<F1	1.41	12	>ref|XP_469888.1| putative serine-threonine protein kinase [Oryza sativa (japonicacultivar-group)] gb|AAP50965.1| putative serine-threonine protein kinase [Oryza sativa (japonica cultivar-group)] dbj|BAD18004.1| serine/threonine protein kinase SAPK8 [Oryza sativa (japonica cultivar-group)] sp|Q7Y0B9|SAPK8_ORYSA Serine/threonine-protein kinase SAPK8 (Osmotic stress/abscisic acid-activated protein kinase 8)	371	1E-42
					>ref|XP_463160.1| putative protein kinase [Oryza sativa (japonica cultivar-group)]gb|AAR00606.1| putative protein kinase [Oryza sativa (japonica cultivar-group)] dbj|BAD18006.2| serine/threonine protein kinase SAPK10 [Oryza sativa (japonica cultivar-group)] sp|Q75H77|SAPKA_ORYSA Serine/threonine-protein kinase SAPK10 (Osmotic stress/abscisic acid-activated protein kinase 10)	362	7E-36
					>emb|CAB80112.1| protein kinase-like protein [Arabidopsis thaliana]emb|CAA19877.1| protein kinase-like protein [Arabidopsis thaliana]	357	6E-35
					>ref|NP_567945.1| OST1 (OPEN STOMATA 1); kinase/ protein kinase [Arabidopsisthaliana] emb|CAC87047.1| protein kinase [Arabidopsis thaliana] gb|AAM10100.1| protein kinase-like protein [Arabidopsis thaliana] gb|AAK96815.1| protein kinase - like protein [Arabidopsis thaliana]	362	6E-35
					>dbj|BAD18005.1| serine/threonine protein kinase SAPK9 [Oryza sativa (japonicacultivar-group)] sp|Q75V57|SAPK9_ORYSA Serine/threonine-protein kinase SAPK9 (Osmotic stress/abscisic acid-activated protein kinase 9) gb|ABA99733.1| protein kinase-like protein [Oryza sativa (japonica cultivar-group)]	361	6E-35
CB815998	7.39E-03	B73<F1=Mo17	1.24	2	>gb|AAT68209.1| putative histone H2B [Cynodon dactylon]	98	1E-34
					>ref|XP_475912.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]gb|AAU44113.1| putative histone H2B [Oryza sativa (japonica cultivar-group)] gb|AAT69583.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	152	1E-34
					>ref|NP_915412.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]dbj|BAB93209.1| putative histone H2B [Oryza sativa (japonica cultivar-group)] dbj|BAB67889.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	139	1E-34
					>ref|NP_909298.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]dbj|BAB44055.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	155	1E-34
					>ref|NP_909263.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]dbj|BAB44008.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	153	1E-34
DV622485	7.45E-03	B73<F1=Mo17	1.3	3	>gb|AAV59379.1| putative early-responsive to dehydration stress protein (ERD4)[Oryza sativa (japonica cultivar-group)] ref|XP_476028.1| putative early-responsive to dehydration stress protein (ERD4) [Oryza sativa (japonica cultivar-group)]	766	3E-9
					>dbj|BAD87679.1| putative ERD4 protein [Oryza sativa (japonica cultivar-group)]	768	7E-9
					>ref|NP_918121.1| OJ1029_F04.25 [Oryza sativa (japonica cultivar-group)]	646	7E-9
					>gb|AAF70851.1| F24O1.4 [Arabidopsis thaliana]	778	9E-9
					>ref|NP_176422.1| unknown protein [Arabidopsis thaliana]	769	9E-9
CD670441	7.48E-03	Mo17<B73=F1	1.33	11	>ref|XP_474251.1| OSJNBa0087O24.9 [Oryza sativa (japonica cultivar-group)]emb|CAE03586.1| OSJNBa0087O24.9 [Oryza sativa (japonica cultivar-group)]	309	3E-12
					>ref|XP_464444.1| KH domain-containing protein-like [Oryza sativa (japonicacultivar-group)] dbj|BAD15406.1| KH domain-containing protein-like [Oryza sativa (japonica cultivar-group)]	300	4E-10
					>dbj|BAD35424.1| KH domain-containing protein / zinc finger protein-like [Oryzasativa (japonica cultivar-group)]	295	1E-8
					>ref|NP_566412.1| nucleic acid binding / transcription factor [Arabidopsis thaliana]gb|AAM62964.1| unknown [Arabidopsis thaliana] gb|AAG51040.1| unknown protein; 15726-17646 [Arabidopsis thaliana]	248	5E-6
					>dbj|BAB01961.1| unnamed protein product [Arabidopsis thaliana]	231	5E-6

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
CB816140	7.50E-03	Mo17<B73	1.4	9	>ref|NP_922780.1| putative chloroplast chaperonin [Oryza sativa (japonicacultivar-group)] gb|AAL79700.1| putative chloroplast chaperonin [Oryza sativa] gb|AAP55067.1| chloroplast chaperonin, putative [Oryza sativa (japonica cultivar-group)]	140	1E-50
					>ref|NP_191580.1| ATP binding [Arabidopsis thaliana]emb|CAB75936.1| putative protein [Arabidopsis thaliana] gb|AAM65007.1| unknown [Arabidopsis thaliana] gb|AAO64777.1| At3g60210 [Arabidopsis thaliana]	138	3E-36
					>ref|NP_566022.1| CHL-CPN10 [Arabidopsis thaliana]gb|AAC27467.1| expressed protein [Arabidopsis thaliana] dbj|BAB55457.1| chloroplast chaperonin 10 [Arabidopsis thaliana]	139	2E-33
					>gb|AAL66945.1| unknown protein [Arabidopsis thaliana]gb|AAK62415.1| Unknown protein [Arabidopsis thaliana]	139	2E-33
					>ref|YP 477843.1| chaperonin, 10 kDa [Cyanobacteria bacterium Yellowstone B-Prime]	103	2E-8
CB885579	7.55E-03	B73<F1=Mo17	1.25	2	>ref|XP 473529.1| OSJNBa0005N02.3 [Oryza sativa (japonica cultivar-group)]emb|CAE02070.2| OSJNBa0005N02.3 [Oryza sativa (japonica cultivar-group)]	1101	6E-56
					>dbj|BAD27856.1| putative argonaute protein [Oryza sativa (japonica cultivar-group)]	1082	5E-55
					>ref|NP_175274.1| AGO1 (ARGONAUTE 1) [Arabidopsis thaliana]gb|AAN41341.1| putative leaf development protein Argonaute [Arabidopsis thaliana] gb|AAD49755.1| Identical to Argonaute protein from Arabidopsis thaliana gb|U91995. EST gb|AA720232 comes from this gene gb|AAC18440.1| Argonaute protein [Arabidopsis thaliana] sp|O04379|AGO1 ARATH Argonaute protein	1048	7E-54
					>ref|NP 849784.1| AGO1 (ARGONAUTE 1) [Arabidopsis thaliana]	1050	7E-54
					>gb|AAF79718.1| T1N15.2 [Arabidopsis thaliana]	1123	7E-54
CD001596	7.62E-03	Mo17<B73=F1	1.24	10	>dbj|BAA35120.1| NADH dependent Glutamate Synthase [Oryza sativa]	2166	6E-69
					>ref|NP 916947.1| NADH-dependent glutamate synthase [Oryza sativa (japonicacultivar-group)]	2157	2E-68
					>ref|XP_475886.1| putative glutamate synthase [Oryza sativa (japonicacultivar-group)] gb|AAT58702.1| putative glutamate synthase [Oryza sativa (japonica cultivar-group)]	609	2E-60
					>sp|Q03460|GLSN MEDSA Glutamate synthase [NADH], chloroplast precursor (NADH-GOGAT)gb|AAB46617.1| NADH-glutamate synthase [Medicago sativa]	2194	9E-54
					>gb|AAY99625.1| NADH-dependent glutamate synthase protein [Puccinellia tenuiflora]	165	1E-53
DV490270	7.62E-03	Mo17<B73=F1	4.67	10	ns		
BM073003	7.64E-03	Mo17<B73=F1	1.37	11	>gb|AAD39834.1| eukaryotic translation initiation factor 3 large subunit [Zea mays]sp|Q9XHR2|IF3A_MAIZE Eukaryotic translation initiation factor 3 subunit 10 (eIF-3 theta) (Eukaryotic translation initiation factor 3 large subunit) (eIF3a)	962	5E-28
					>ref|XP_549952.1| putative translation initiation factor [Oryza sativa (japonicacultivar-group)] emb|CAD24839.1| translation initiation factor 3 [Oryza sativa (japonica cultivar-group)] dbj|BAD52450.1| putative translation initiation factor [Oryza sativa (japonica cultivar-group)]	986	1E-9
					>ref|NP 909031.1| putative eukaryotic translation initiation factor 3 large subunit[Oryza sativa (japonica cultivar-group)]	984	1E-9
DV550547	7.68E-03	B73<F1=Mo17	1.49	3	>dbj|BAD35672.1| putative cinnamoyl-CoA reductase [Oryza sativa (japonicacultivar-group)]	321	4E-55
					>dbj|BAD35675.1| putative cinnamoyl-CoA reductase [Oryza sativa (japonicacultivar-group)]	321	6E-39
					>ref|NP_180917.1| cinnamoyl-CoA reductase [Arabidopsis thaliana]gb|AAN15374.1| putative cinnamoyl-CoA reductase [Arabidopsis thaliana] gb|AAM53272.1| putative cinnamoyl-CoA reductase [Arabidopsis thaliana] gb|AAB80681.1| putative cinnamoyl-CoA reductase [Arabidopsis thaliana] gb|AAM61149.1| putative cinnamoyl-CoA reductase [Arabidopsis thaliana]	321	3E-36
					>ref|NP_180918.1| cinnamoyl-CoA reductase [Arabidopsis thaliana]gb|AAP42731.1| At2g33600 [Arabidopsis thaliana] gb|AAM13142.1| putative cinnamoyl-CoA reductase [Arabidopsis thaliana] gb|AAB80683.1| putative cinnamoyl-CoA reductase [Arabidopsis thaliana]	321	3E-35
					>ref|NP 177773.1| cinnamoyl-CoA reductase [Arabidopsis thaliana]gb|AAG51951.1| putative cinnamoyl-CoA reductase; 27707-26257 [Arabidopsis thaliana]	317	3E-29
CD001273	7.72E-03	Mo17<F1	1.3	11	>ref|XP_469638.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAR07080.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAC78576.1| hypothetical protein [Oryza sativa (japonica cultivar-group)] gb|AAP03422.1| unknown protein [Oryza sativa (japonica cultivar-group)]	205	3E-80
					>gb|AAU93534.1| unknown protein [Zea mays]	286	6E-79
					>gb|AAT08729.1| CBS1 [Hyacinthus orientalis]	203	4E-71
					>ref|NP_196647.1| unknown protein [Arabidopsis thaliana]emb|CAB96841.1| putative protein [Arabidopsis thaliana] gb|AAK32857.1| AT5g10860/T30N20_130 [Arabidopsis thaliana] gb|AAL47413.1| AT5g10860/T30N20 130 [Arabidopsis thaliana] sp|Q9LEV3|UMP3 ARATH Protein At5g10860, mitochondrial precursor	206	2E-66
					>gb|AAL67493.1| senescence-associated putative protein [Narcissus pseudonarcissus]	109	1E-37
DV550057	7.74E-03	B73<Mo17	1.37	3	>ref|XP_506162.1| PREDICTED OJ1027_G06.13 gene product [Oryza sativa (japonicacultivar-group)] ref|XP_476646.1| putative ERD4 protein [Oryza sativa (japonica cultivar-group)] dbj|BAC82906.1| putative ERD4 protein [Oryza sativa (japonica cultivar-group)]	731	5E-88
					>gb|AAL47004.1| unknown [Davidia involucrata]	226	1E-65
					>dbj|BAD94517.1| ERD4 protein [Arabidopsis thaliana]	203	1E-56
					>ref|NP_564354.1| unknown protein [Arabidopsis thaliana]gb|AAL34230.1| unknown protein [Arabidopsis thaliana] gb|AAK59597.1| unknown protein [Arabidopsis thaliana] gb|AAG51102.1| unknown protein [Arabidopsis thaliana]	724	1E-56
					>dbj|BAB63915.1| ERD4 protein [Arabidopsis thaliana]	640	3E-56
CB815770	7.75E-03	B73=F1<Mo17	1.32	4	>emb|CAA86728.1| calcium-binding protein [Zea mays]emb|CAA61939.1| Calreticulin precursor [Zea mays] prf||2205314A calreticulin	421	2E-60
					>ref|XP_477252.1| putative Calreticulin precursor [Oryza sativa (japonicacultivar-group)] dbj|BAD31962.1| putative Calreticulin precursor [Oryza sativa (japonica cultivar-group)] dbj|BAC82933.1| putative Calreticulin precursor [Oryza sativa (japonica cultivar-group)]	429	4E-58

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>ref|XP_477251.1| putative Calreticulin precursor [Oryza sativa (japonicacultivar-group)] ref|XP_507358.1| PREDICTED OJ1058_C08.28-2 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_506239.1| PREDICTED OJ1058_C08.28-2 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD31961.1| putative Calreticulin precursor [Oryza sativa (japonica cultivar-group)] dbj|BAC82932.1| putative Calreticulin precursor [Oryza sativa (japonica cultivar-group)] sp|Q9SLY8|CRTC_ORYSA Calreticulin precursor	424	4E-58
					>dbj|BAA88900.1| calcium-binding protein [Oryza sativa]	424	4E-58
					>gb|AAW02798.1| calreticulin-like protein [Triticum aestivum]	415	1E-57
BM073517	7.77E-03	Mo17<B73=F1	1.28	10	>gb|AAT08725.1| histone H4 [Hyacinthus orientalis]	103	1E-24
					>emb|CAB01913.1| Histone H4 homologue [Sesbania rostrata]	103	1E-24
					>emb|CAA64985.1| histone H4 [Allium cepa]	58	1E-24
					>ref|NP_563793.1| DNA binding [Arabidopsis thaliana]ref|NP_850660.1| DNA binding [Arabidopsis thaliana] ref|NP_180441.1| HIS4 [Arabidopsis thaliana] ref|NP_568911.1| DNA binding [Arabidopsis thaliana] ref|NP_568918.1| DNA binding [Arabidopsis thaliana] ref|NP_190941.1| DNA binding [Arabidopsis thaliana] ref|NP_563797.1| DNA binding [Arabidopsis thaliana] ref|NP_850939.1| DNA binding [Arabidopsis thaliana] ref|NP_190179.1| DNA binding [Arabidopsis thaliana] ref|XP_475394.1| histone H4 [Oryza sativa (japonica cultivar-group)] ref|XP_475383.1| putative histone H4 [Oryza sativa (japonica cultivar-group)] ref|NP_912452.1| Unknown protein [Oryza sativa (japonica cultivar-group)] ref|XP_467181.1| histone H4 [Oryza sativa (japonica cultivar-group)] ref|NP_922551.1| histone H4 [Oryza sativa (japonica cultivar-group)] ref|NP_915374.1| putative histone H4 [Oryza sativa (japonica cultivar-group)] ref|NP_910647.1| histone H4 [Oryza sativa (japonica cultivar-group)] ref|XP_473659.1| OSJNBa0088A01.17 [Oryza sativa (japonica cultivar-group)] gb|AAU90170.1| histone H4 [Oryza sativa	103	1E-24
					>sp|P62786|H42_WHEAT Histone H4 variant TH091gb|AAA34292.1| histone H4	103	1E-24
CB329458	7.79E-03	Mo17<B73	1.45	10	>emb|CAD29296.1| plasma membrane H+ ATPase [Oryza sativa (japonica cultivar-group)]gb|ABA99607.1| plasma-membrane proton-efflux P-type ATPase [Oryza sativa (japonica cultivar-group)]	956	2E-75
					>ref|XP_476966.1| plasma membrane H+ ATPase [Oryza sativa (japonica cultivar-group)]emb|CAD29295.1| plasma membrane H+ ATPase [Oryza sativa (japonica cultivar-group)] dbj|BAC83861.1| plasma membrane H+ ATPase [Oryza sativa (japonica cultivar-group)]	957	3E-75
					>dbj|BAA06629.1| plasma membrane H+-ATPase [Oryza sativa (japonica cultivar-group)]	957	6E-75
					>gb|AAT81733.1| H-ATPase [Oryza sativa (japonica cultivar-group)]emb|CAD29294.1| plasma membrane H+ ATPase [Oryza sativa (japonica cultivar-group)]	956	9E-74
					>gb|AAA34096.1| plasma membrane H+ ATPase	440	1E-71
CD670361	7.80E-03	B73=F1<Mo17	1.26	4	>dbj|BAD36121.1| putative 26S proteasome regulatory particle triple-A ATPasesubunit4 [Oryza sativa (japonica cultivar-group)] dbj|BAD35613.1| putative 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa (japonica cultivar-group)]	401	6E-43
					>dbj|BAB78495.1| 26S proteasome regulatory particle triple-A ATPase subunit4b [Oryzasativa (japonica cultivar-group)]	377	6E-43
					>ref|XP_464508.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryzasativa (japonica cultivar-group)] dbj|BAD25481.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa (japonica cultivar-group)] dbj|BAD15843.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa (japonica cultivar-group)] dbj|BAB17625.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa (japonica cultivar-group)]	400	1E-42
					>gb|ABA40428.1| 26S proteasome AAA-ATPase subunit RPT4a-like protein [Solanumtuberosum] dbj|BAC23035.1| 26S proteasome AAA-ATPase subunit RPT4a [Solanum tuberosum]	398	7E-41
					>ref|NP_199115.1| RPT4A; ATPase [Arabidopsis thaliana]gb|AAL77741.1| AT5g43010/MBD2_21 [Arabidopsis thaliana] gb|AAK50085.1| AT5g43010/MBD2_21 [Arabidopsis thaliana] dbj|BAB09203.1| 26S proteasome AAA-ATPase subunit RPT4a [Arabidopsis thaliana] gb|AAF22524.1| 26S proteasome AAA-ATPase subunit RPT4a [Arabidopsis thaliana]	399	8E-40
BM080445	7.81E-03	Mo17<B73=F1	1.38	10	ns		
CD059002	7.83E-03	Mo17<B73=F1	1.29	11	>gb|AAF71261.2| beta-glucosidase aggregating factor precursor [Zea mays]	306	8E-22
					>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	1E-20
					>gb|ABA97248.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]gb|ABB51090.1| mannose-specific jacalin-related lectin [Oryza sativa (japonica cultivar-group)]	306	3E-20
					>gb|AAA87041.1| putative 32.6 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72096.1| 32 kDa protein [Hordeum vulgare]	304	2E-19
					>gb|ABA94721.1| Jacalin-like lectin domain, putative [Oryza sativa (japonicacultivar-group)]	734	2E-19
CB240027	7.90E-03	B73<Mo17	1.46	4	>ref|NP_909910.1| unknown protein [Oryza sativa]gb|AAK72889.1| unknown protein [Oryza sativa]	350	2E-46
					>ref|NP_188868.2| unknown protein [Arabidopsis thaliana]gb|AAK43988.1| unknown protein [Arabidopsis thaliana] dbj|BAD94071.1| hypothetical protein [Arabidopsis thaliana] dbj|BAD44059.1| unknown protein [Arabidopsis thaliana] dbj|BAD43970.1| unknown protein [Arabidopsis thaliana] dbj|BAD43746.1| unknown protein [Arabidopsis thaliana] dbj|BAD43192.1| unknown protein [Arabidopsis thaliana]	354	5E-37
					>dbj|BAB17274.1| unnamed protein product [Arabidopsis thaliana]	333	1E-31
					>ref|XP_472721.1| OSJNBa0006M15.17 [Oryza sativa (japonica cultivar-group)]emb|CAE02574.2| OSJNBa0006M15.17 [Oryza sativa (japonica cultivar-group)]	386	8E-16
					>ref|XP_475457.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAT69636.1| unknown protein [Oryza sativa (japonica cultivar-group)]	384	8E-15
BM080525	7.94E-03	F1=Mo17<B73	5.47	9	ns		
CB816344	7.95E-03	Mo17<B73=F1	1.3	11	>gb|ABA97248.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]gb|ABB51090.1| mannose-specific jacalin-related lectin [Oryza sativa (japonica cultivar-group)]	306	4E-29
					>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	3E-27

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15 % FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>gb|AAR20919.1| jasmonate-induced protein [Triticum aestivum]	304	4E-27
					>gb|AAA87041.1| putative 32.6 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72096.1| 32 kDa protein [Hordeum vulgare]	304	5E-27
					>gb|AAF71261.2| beta-glucosidase aggregating factor precursor [Zea mays]	306	6E-27
CD001188	8.00E-03	Mo17<B73=F1	1.44	10	>gb|AAV41384.1| WRKY DNA-binding protein [Oryza sativa (indica cultivar-group)]	263	2E-6
					>gb|ABA91247.1| wrky transcription factor 62, putative [Oryza sativa (japonicacultivar-group)]	280	2E-6
					>gb|ABA95640.1| hypothetical protein LOC Os12g02440 [Oryza sativa (japonicacultivar-group)]	217	2E-6
BM074340	8.02E-03	Mo17<B73=F1	1.52	10	>emb|CAA73691.1| Glyoxalase I [Brassica juncea]sp|O04885|LGUL_BRAJU Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)	185	2E-20
					>ref|NP_849609.1| calmodulin binding / lactoylglutathione lyase [Arabidopsisthaliana] ref|NP_172291.1| calmodulin binding / lactoylglutathione lyase [Arabidopsis thaliana] ref|NP_001030995.1| calmodulin binding / lactoylglutathione lyase [Arabidopsis thaliana] gb|AAT41850.1| At1g08110 [Arabidopsis thaliana] gb|AAN72031.1| glyoxalase I, putative [Arabidopsis thaliana] sp|Q8H0V3|LGUL_ARATH Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)	185	6E-20
					>ref|NP 001030996.1| calmodulin binding / lactoylglutathione lyase [Arabidopsisthaliana]	235	6E-20
					>gb|AAF79827.1| T6D22.20 [Arabidopsis thaliana]	196	6E-20
					>emb|CAA09177.1| glyoxalase I [Glycine max]	185	8E-20
DV549456	8.03E-03	B73=F1<Mo17	1.38	4	>dbj|BAB11740.1| TaWIN2 [Triticum aestivum]	259	1E-32
					>ref|XP_482989.1| putative TaWIN2 [Oryza sativa (japonica cultivar-group)]gb|AAO72644.1| TaWIN2-like protein [Oryza sativa (japonica cultivar-group)] gb|AAO72553.1| WIN2-like protein [Oryza sativa (japonica cultivar-group)] dbj|BAD10275.1| putative TaWIN2 [Oryza sativa (japonica cultivar-group)] dbj|BAD09765.1| putative TaWIN2 [Oryza sativa (japonica cultivar-group)]	264	1E-31
					>emb|CAE54082.1| 14-3-3 protein [Fagus sylvatica]	176	1E-31
					>gb|AAF76226.1| 14-3-3 protein [Populus x canescens]	262	2E-31
					>emb|CAA53700.1| 14-3-3 protein 32kDa endonuclease [Cucurbita pepo]prf||2107305A nuclear matrix endonuclease	275	2E-31
DV622317	8.03E-03	B73<F1=Mo17	1.34	3	group))]	653	5E-89
					>ref|NP_177656.2| FMN binding / catalytic/ electron transporter/ iron ion binding /oxidoreductase [Arabidopsis thaliana] gb|AAM45053.1| unknown protein [Arabidopsis thaliana] gb|AAL87267.1| unknown protein [Arabidopsis thaliana]	647	2E-71
					>gb|AAG12693.1| unknown protein; 42527-45275 [Arabidopsis thaliana]	654	2E-71
					>ref|XP 690774.1| PREDICTED: similar to radical S-adenosyl methionine and flavodoxindomains 1 [Danio rerio]	797	4E-49
					>emb|CAG12739.1| unnamed protein product [Tetraodon nigroviridis]	680	4E-48
CB334444	8.03E-03	B73=F1<Mo17	1.54	4	ns		
DV550130	8.04E-03	Mo17<B73=F1	1.3	10	>gb|AAC19375.1| acireductone dioxygenase 2 [Oryza sativa]	198	6E-90
					>gb|AAX55895.1| aci-reductone dioxygenase-like protein [Oryza sativa (japonicacultivar-group)]	198	1E-89
					>gb|AAN06863.1| Putative probable submergence induced, nickel-binding protein 2A[Oryza sativa (japonica cultivar-group)]	254	7E-88
					>dbj|BAB61039.1| iron-deficiency induced gene [Hordeum vulgare]	198	2E-86
					>ref|NP 921506.1| putative zinc finger protein ID1 [Oryza sativa (japonicacultivar-group)]	230	4E-79
DV550103	8.08E-03	F1=Mo17<B73	1.5	9	>ref|XP 473776.1| OSJNBa0041A02.14 [Oryza sativa (japonica cultivar-group)]emb|CAD41867.2| OSJNBa0041A02.14 [Oryza sativa (japonica cultivar-group)]	396	e-103
					>gb|AAM65412.1| pectin acetylesterase [Arabidopsis thaliana]	391	1E-81
					>ref|NP_567585.1| carboxylic ester hydrolase [Arabidopsis thaliana]gb|AAL47339.1| putative pectinacetylesterase protein [Arabidopsis thaliana] gb|AAK96722.1| putative pectinacetylesterase protein [Arabidopsis thaliana] gb|AAM64921.1| putative pectinacetylesterase protein [Arabidopsis thaliana]	391	1E-80
					>ref|NP_199341.1| carboxylic ester hydrolase [Arabidopsis thaliana]gb|AAL15296.1| AT5g45280/K9E15_6 [Arabidopsis thaliana] dbj|BAB10249.1| pectin acetylesterase [Arabidopsis thaliana]	391	1E-80
					>emb|CAA67728.1| pectinacetylesterase precursor [Vigna radiata var. radiata]	399	1E-79
BM337359	8.12E-03	F1<B73	3.42	8	>dbj|BAD82225.1| putative wound inducive gene [Oryza sativa (japonicacultivar-group)] dbj|BAD81783.1| putative wound inducive gene [Oryza sativa (japonica cultivar-group)]	331	1E-14
					>gb|AAS79233.1| rust resistance protein rp3-1 [Zea mays]	1258	9E-13
					>ref|XP_481915.1| putative wound inductive gene [Oryza sativa (japonicacultivar-group)] dbj|BAD03758.1| putative wound inductive gene [Oryza sativa (japonica cultivar-group)]	215	2E-10
					>ref|XP_481914.1| putative wound inductive gene [Oryza sativa (japonicacultivar-group)] ref|XP_507201.1| PREDICTED P0426E02.15-2 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD03757.1| putative wound inductive gene [Oryza sativa (japonica cultivar-group)]	325	2E-10
					>dbj|BAA95791.1| wound inducive gene [Nicotiana tabacum]	317	8E-6
CB251993	8.13E-03	Mo17<B73=F1	1.25	11	>ref|XP_476024.1| putative vacuolar ATP synthase subunit C [Oryza sativa (japonicacultivar-group)] gb|AAT44305.1| putative vacuolar ATP synthase subunit C [Oryza sativa (japonica cultivar-group)]	377	1E-6
DV491809	8.13E-03	B73<F1=Mo17	1.52	3	>ref|XP_466184.1| transcriptional coactivator p15 (PC4) family protein-like [Oryzasativa (japonica cultivar-group)] dbj|BAD33299.1| transcriptional coactivator p15 (PC4) family protein-like [Oryza sativa (japonica cultivar-group)]	101	4E-31

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_196487.1| KIWI; DNA binding / transcription coactivator [Arabidopsisthaliana] emb|CAC05451.1| putative transcriptional co-activator (KIWI) [Arabidopsis thaliana] gb|AAC08574.1| putative transcriptional co-activator [Arabidopsis thaliana] gb|AAO44011.1| At5g09250 [Arabidopsis thaliana] pir||T52113 probable transcription co-activator KIWI [imported] - Arabidopsis thaliana sp|O65154|KIWI ARATH RNA polymerase II transcriptional coactivator KIWI	107	3E-16
					>ref|NP_192830.1| KELP; DNA binding / transcription coactivator [Arabidopsisthaliana] emb|CAB81193.1| putative protein [Arabidopsis thaliana] emb|CAB40060.1| putative protein [Arabidopsis thaliana] gb|AAC08575.1| putative transcriptional co-activator [Arabidopsis thaliana] gb|AAM63108.1| putative transcriptional coactivator [Arabidopsis thaliana] gb|AAO64782.1| At4g10920 [Arabidopsis thaliana] gb|AAC33951.1| contains similarity to RNA polymerase II transcription cofactor p15 [Arabidopsis thaliana] pir||T52114 probable transcription co-activator KELP [imported] - Arabidopsis thaliana sp|O65155|KELP_ARATH RNA polymerase II transcriptional coactivator KELP	165	4E-10
					>dbj|BAB41214.1| putative transcriptional coactivator [Brassica rapa]	165	6E-10
					>ref|NP_916536.1| P0684B02.23 [Oryza sativa (japonica cultivar-group)]dbj|BAB86514.1| transcriptional coactivator-like [Oryza sativa (japonica cultivar-group)] dbj|BAB44036.1| transcriptional coactivator-like [Oryza sativa (japonica cultivar-group)]	184	2E-9
CB816361	8.22E-03	B73=F1<Mo17	1.29	4	>gb|AAK40308.1| putative methyl-binding domain protein MBD106 [Zea mays]	428	2E-56
					>gb|AAK40307.1| putative methyl-binding domain protein MBD105 [Zea mays]	433	1E-50
					>gb|ABA99897.1| methyl-binding domain protein MBD106, putative [Oryza sativa(japonica cultivar-group)]	303	3E-48
					>gb|AAW56447.1| putative methyl-binding domain protein MBD115 [Zea mays]	364	5E-35
					>gb|AAM93219.1| methyl binding domain protein MBD109 [Zea mays]	400	7E-33
CB351734	8.23E-03	Mo17<B73=F1	1.27	11	>dbj|BAD73292.1| putative ATP-dependent Clp protease, proteolytic subunit [Oryzasativa (japonica cultivar-group)]	308	3E-62
					>ref|NP 918617.1| putative ATP-dependent Clp protease [Oryza sativa (japonicacultivar-group)]	317	3E-62
					>dbj|BAA85451.1| S-locus protein 2 [Brassica rapa]	311	5E-51
					>emb|CAC80640.1| ClpP putative protein [Brassica napus]	313	1E-50
					>emb|CAB89185.1| ClpP [Brassica napus var. napus]	313	1E-50
CB334461	8.23E-03	B73=F1<Mo17	1.54	4	>ref|XP 474303.1| OSJNBb0004A17.1 [Oryza sativa (japonica cultivar-group)]	492	5E-18
					>emb|CAE03599.2| OSJNBb0004A17.1 [Oryza sativa (japonica cultivar-group)]	496	5E-18
					>ref|XP 474302.1| OSJNBa0043A12.39 [Oryza sativa (japonica cultivar-group)]emb|CAE02834.1| OSJNBa0043A12.39 [Oryza sativa (japonica cultivar-group)]	487	9E-14
					>gb|AAL75899.1| At2g43020/MFL8.12 [Arabidopsis thaliana]	490	4E-10
					>ref|NP_181830.1| amine oxidase/ oxidoreductase [Arabidopsis thaliana]gb|AAD22129.1| putative amine oxidase [Arabidopsis thaliana] gb|AAO85404.1| putative amine oxidase 1 [Arabidopsis thaliana]	490	4E-10
CD527790	8.24E-03	B73<F1=Mo17	1.29	3	>gb|AAX55895.1| aci-reductone dioxygenase-like protein [Oryza sativa (japonicacultivar-group)]	198	e-101
					>gb|AAC19375.1| acireductone dioxygenase 2 [Oryza sativa]	198	e-101
					>dbj|BAB61039.1| iron-deficiency induced gene [Hordeum vulgare]	198	1E-97
					>gb|AAN06863.1| Putative probable submergence induced, nickel-binding protein 2A[Oryza sativa (japonica cultivar-group)]	254	3E-97
					>gb|AAC05511.1| acireductone dioxygenase 1 [Oryza sativa]	199	2E-95
CD651132	8.29E-03	Mo17<B73=F1	1.29	11	>ref|NP_922859.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAL67597.1| unknown protein [Oryza sativa] gb|AAP55146.1| expressed protein [Oryza sativa (japonica cultivar-group)]	99	7E-34
					>ref|NP_564394.1| unknown protein [Arabidopsis thaliana]gb|AAM63599.1| unknown [Arabidopsis thaliana] gb|AAG60169.1| unknown protein [Arabidopsis thaliana] gb|AAO64124.1| unknown protein [Arabidopsis thaliana] gb|AAO42198.1| unknown protein [Arabidopsis thaliana]	100	2E-9
					>gb|AAF81326.1| Strong similarity to an unknown protein F19D11.4 gi|7485759 fromArabidopsis thaliana BAC F19D11 gb|AC005310. EST gb|AV535485 comes from this gene	647	2E-9
CB833491	8.31E-03	B73=F1<Mo17	5.56	4	>gb|AAO72686.1| putative myosin heavy chain [Oryza sativa (japonicacultivar-group)]	455	2E-32
					>gb|ABA99627.1| hypothetical protein LOC Os12g44340 [Oryza sativa (japonicacultivar-group)]	567	2E-32
					>dbj|BAD45984.1| myosin II heavy chain-like [Oryza sativa (japonica cultivar-group)]	608	6E-19
					>ref|XP_467670.1| putative myosin II heavy chain [Oryza sativa (japonicacultivar-group)] dbj|BAD15899.1| putative myosin II heavy chain [Oryza sativa (japonica cultivar-group)]	599	8E-19
					>gb|AAN33201.1| At1g68060/T23K23 9 [Arabidopsis thaliana]gb|AAM91095.1| At1g68060/T23K23 9 [Arabidopsis thaliana]	634	3E-18
BM074811	8.32E-03	Mo17<B73=F1	1.31	10	>sp|P27787|FER1_MAIZE Ferredoxin-1, chloroplast precursor (Ferredoxin I) (Fd I)gb|AAA33460.1| ferredoxin gb|AAA33459.1| ferredoxin prf||1907324B ferredoxin:ISOTYPE=I	150	5E-44
					>pdb|1GAQ|B Chain B, Crystal Structure Of The Complex Between Ferredoxin AndFerredoxin-Nadp+ Reductase	98	3E-33
					>sp|P27789|FER5 MAIZE Ferredoxin-5, chloroplast precursor (Ferredoxin V) (Fd V)gb|AAA33462.1| ferredoxin prf||1907324A ferredoxin:ISOTYPE=V	135	2E-29
					>ref|XP_479678.1| Ferredoxin I, chloroplast precursor [Oryza sativa (japonicacultivar-group)] ref|XP_507559.1| PREDICTED OJ1300_E01.1 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_507558.1| PREDICTED OJ1300_E01.1 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_507082.1| PREDICTED OJ1300_E01.1 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD08924.1| Ferredoxin I, chloroplast precursor [Oryza sativa (japonica cultivar-group)] sp|P11051|FER1_ORYSA Ferredoxin-1, chloroplast precursor (Ferredoxin I) (Anti-disease protein 1) pir||FERZ ferredoxin [2Fe-2S] I precursor - rice dbj|BAA06436.1| ferredoxin [Oryza sativa (japonica cultivar-group)]	139	4E-29

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|AAL77198.1| anti-disease protein 1 [Oryza sativa]	138	4E-29
BM080544	8.33E-03	Mo17<B73	1.9	9	ns		
BM350025	8.36E-03	F1=Mo17<B73	2.02	9	>ref|XP_466672.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD19228.1| unknown protein [Oryza sativa (japonica cultivar-group)]	156	5E-35
					>ref|NP_567794.1| unknown protein [Arabidopsis thaliana]gb|AAK93722.1| unknown protein [Arabidopsis thaliana] gb|AAK25999.1| unknown protein [Arabidopsis thaliana]	157	8E-17
					>gb|AAM64668.1| unknown [Arabidopsis thaliana]	157	8E-17
					>emb|CAB79604.1| putative protein [Arabidopsis thaliana]emb|CAB36771.1| putative protein [Arabidopsis thaliana]	358	5E-13
DV494450	8.37E-03	B73<F1=Mo17	1.36	3	>dbj|BAD46209.1| putative inosine-uridine nucleoside N-ribohydrolase [Oryza sativa(japonica cultivar-group)]	337	3E-52
					>ref|XP_483754.1| putative inosine-uridine nucleoside N-ribohydrolase [Oryza sativa(japonica cultivar-group)] dbj|BAD09089.1| putative inosine-uridine nucleoside N-ribohydrolase [Oryza sativa (japonica cultivar-group)]	324	2E-49
					>gb|AAT00629.1| putative inosine-uridine preferring nucleoside hydrolase [Zea mays]	325	3E-46
					>ref|NP_565843.1| hydrolase [Arabidopsis thaliana]gb|AAD21435.2| expressed protein [Arabidopsis thaliana] gb|AAL47407.1| At2g36310/F2H17.8 [Arabidopsis thaliana] gb|AAL06843.1| At2g36310/F2H17.8 [Arabidopsis thaliana] gb|AAM63615.1| unknown [Arabidopsis thaliana]	336	2E-41
					>ref|XP_468759.1| putative inosine-uridine preferring nucleoside hydrolase [Oryzasativa (japonica cultivar-group)] gb|AAP20832.1| putative inosine-uridine preferring nucleoside hydrolase [Oryza sativa (japonica cultivar-group)]	322	1E-17
BG840722	8.39E-03	F1=Mo17<B73	1.62	9	ns		
CD568656	8.40E-03	Mo17<B73	1.36	9	>ref|XP_475141.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAT58828.1| unknown protein [Oryza sativa (japonica cultivar-group)]	200	3E-18
					>ref|NP_914950.1| P0492G09.23 [Oryza sativa (japonica cultivar-group)]dbj|BAB64201.1| putative succinate dehydrogenase subunit 4 [Oryza sativa (japonica cultivar-group)]	211	1E-16
					>gb|AAK97388.1| succinate dehydrogenase subunit 4 [Oryza sativa]	226	1E-16
CB329592	8.42E-03	Mo17<B73	1.24	10	>emb|CAE04894.3| OSJNBa0042I15.16 [Oryza sativa (japonica cultivar-group)]sp|Q7XLX6|S1FA2 ORYSA DNA-binding protein S1FA2	80	1E-7
					>emb|CAE04896.3| OSJNBa0042I15.18 [Oryza sativa (japonica cultivar-group)]sp|P42553|S1FA1 ORYSA DNA-binding protein S1FA1	76	2E-6
CB350798	8.43E-03	F1=Mo17<B73	2.43	9	ns		
DV493666	8.44E-03	Mo17<B73=F1	1.39	11	>ref|XP_475712.1| putative GTP-binding protein Rab7a [Oryza sativa (japonicacultivar-group)] gb|AAT01314.1| putative GTP-binding protein Rab7a [Oryza sativa (japonica cultivar-group)]	206	4E-91
					>sp|Q40787|RAB7 PENCL Ras-related protein Rab7 (Possible apospory-associated protein)gb|AAA85273.1| possible apospory-associated protein	206	4E-91
					>gb|AAO67728.1| small GTP binding protein [Oryza sativa (indica cultivar-group)]	206	1E-89
					>sp|O24461|RAB7 PRUAR Ras-related protein Rab7gb|AAB71504.1| Rab7 GTP binding protein [Prunus armeniaca]	207	6E-83
					>emb|CAA98171.1| RAB7D [Lotus corniculatus var. japonicus]	207	2E-82
DV621398	8.48E-03	B73<Mo17	1.4	4	>ref|XP_482468.1| putative methylcrotonyl-CoA carboxylase beta chain, mitochondrialprecursor [Oryza sativa (japonica cultivar-group)] dbj|BAC99804.1| putative methylcrotonyl-CoA carboxylase beta chain, mitochondrial precursor [Oryza sativa (japonica cultivar-group)]	572	e-106
					>ref|NP_567950.1| MCCB (3-METHYLCROTONYL-COA CARBOXYLASE); biotin carboxylase[Arabidopsis thaliana] gb|AAN15703.1| Unknown protein [Arabidopsis thaliana] gb|AAF35259.1| 3-methylcrotonyl-CoA carboxylase nonbiotinylated subunit [Arabidopsis thaliana] gb|AAF35258.1| 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit [Arabidopsis thaliana] sp|Q9LDD8|MCCB_ARATH Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial precursor (3-Methylcrotonyl-CoA carboxylase 2) (MCCase beta subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase beta subunit)	587	3E-87
					>gb|AAK62371.1| Unknown protein [Arabidopsis thaliana]	587	3E-87
					>emb|CAB80120.1| putative protein [Arabidopsis thaliana]emb|CAA17569.1| putative protein [Arabidopsis thaliana] pir||T05433 hypothetical protein F28A23.210 - Arabidopsis thaliana	630	1E-82
					>ref|ZP_00776070.1| Propionyl-CoA carboxylase [Pseudoalteromonas atlantica T6c]gb|EAO67369.1| Propionyl-CoA carboxylase [Pseudoalteromonas atlantica T6c]	535	6E-80
DV491545	8.48E-03	F1=Mo17<B73	1.45	9	>ref|NP_566336.1| unknown protein [Arabidopsis thaliana]ref|NP_850544.1| unknown protein [Arabidopsis thaliana] gb|AAF07835.1| unknown protein [Arabidopsis thaliana] gb|AAM63170.1| unknown [Arabidopsis thaliana]	170	9E-45
					>gb|AAV43812.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAV43807.1| unknown protein [Oryza sativa (japonica cultivar-group)]	170	1E-44
					>ref|NP_198523.1| unknown protein [Arabidopsis thaliana]gb|AAQ65141.1| At5g37070 [Arabidopsis thaliana] dbj|BAD44258.1| putative protein [Arabidopsis thaliana] dbj|BAD43875.1| putative protein [Arabidopsis thaliana] dbj|BAB11359.1| unnamed protein product [Arabidopsis thaliana]	170	2E-44
					>ref|NP_195781.1| unknown protein [Arabidopsis thaliana]emb|CAB82277.1| putative protein [Arabidopsis thaliana] gb|AAM63344.1| unknown [Arabidopsis thaliana] sp|Q9M015|Y5161 ARATH Protein At5g01610	170	1E-43
					>ref|NP_918452.1| OSJNBb0049O23.18 [Oryza sativa (japonica cultivar-group)]dbj|BAB90059.1| hypothetical protein [Oryza sativa (japonica cultivar-group)] dbj|BAB64677.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	170	5E-43
CB250082	8.50E-03	Mo17<B73=F1	1.36	10	ns		
DV490400	8.52E-03	Mo17<B73=F1	1.28	11	>gb|AAC08009.1| DnaJ-related protein ZMDJ1 [Zea mays]	419	5E-34
					>gb|AAX95135.1| DnaJ protein, putative [Oryza sativa (japonica cultivar-group)]	416	8E-30
					>gb|AAU89194.1| DnaJ protein, putative [Oryza sativa (japonica cultivar-group)]gb|AAO72551.1| DNAJ-like protein [Oryza sativa (japonica cultivar-group)]	417	8E-30

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>dbj|BAA35121.1| DnaJ homolog [Salix gilgiana]	420	1E-25
					>gb|AAG24643.1| J2P [Daucus carota]gb|AAG24642.1| J1P [Daucus carota]	418	6E-25
BM073225	8.62E-03	Mo17<B73	2.17	9	>ref|XP_479158.1| unknown protein [Oryza sativa (japonica cultivar-group)]ref|XP_506466.1| PREDICTED P0616D06.125 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC16504.1| unknown protein [Oryza sativa (japonica cultivar-group)]	244	1E-16
					>ref|XP_470898.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAP03360.1| unknown protein [Oryza sativa (japonica cultivar-group)]	228	3E-13
					>dbj|BAD36140.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD36082.1| unknown protein [Oryza sativa (japonica cultivar-group)]	232	5E-6
BM337696	8.63E-03	B73=F1<Mo17	2.3	4	ns		
CD651121	8.64E-03	B73=Mo17<F1	1.47	12	>gb|AAF71261.2| beta-glucosidase aggregating factor precursor [Zea mays]	306	3E-35
					>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	2E-33
					>gb|ABA97248.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]gb|ABB51090.1| mannose-specific jacalin-related lectin [Oryza sativa (japonica cultivar-group)]	306	8E-33
					>gb|AAR20919.1| jasmonate-induced protein [Triticum aestivum]	304	2E-32
					>gb|AAB72098.1| 32 kDa protein [Hordeum vulgare]	306	9E-32
DV494140	8.69E-03	Mo17<B73=F1	1.33	10	>dbj|BAD45908.1| putative 50S ribosomal protein L24, chloroplast precursor [Oryzasativa (japonica cultivar-group)] dbj|BAD45549.1| putative 50S ribosomal protein L24, chloroplast precursor [Oryza sativa (japonica cultivar-group)]	190	4E-82
					>ref|NP_851190.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAP21381.1| At5g54600 [Arabidopsis thaliana] gb|AAM63859.1| 50S ribosomal protein L24, chloroplast precursor [Arabidopsis thaliana] dbj|BAB09339.1| 50S ribosomal protein L24, chloroplast precursor [Arabidopsis thaliana] gb|AAN72001.1| 50S ribosomal protein L24, chloroplast precursor [Arabidopsis thaliana] sp|P92959|RK24_ARATH 50S ribosomal protein L24, chloroplast precursor	198	2E-54
					>emb|CAA70851.1| plastid ribosomal protein [Arabidopsis thaliana]	198	5E-54
					>sp|Q02764|RK24_TOBAC 50S ribosomal protein L24, chloroplast precursor (CL24)gb|AAA34114.1| ribosomal protein L24 gb|AAA34086.1| ribosomal protein L24	187	7E-54
					>emb|CAA32185.1| unnamed protein product [Pisum sativum]sp|P11893|RK24_PEA 50S ribosomal protein L24, chloroplast precursor (CL24)	194	6E-53
DV621757	8.70E-03	B73<Mo17	1.36	4	>ref|XP_483641.1| putative GTPase-activating protein GYP7 (GAP for YPT7) [Oryzasativa (japonica cultivar-group)] ref|XP_507320.1| PREDICTED P0544G09.9 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD09932.1| putative GTPase-activating protein GYP7 (GAP for YPT7) [Oryza sativa (japonica cultivar-group)]	565	6E-90
					>dbj|BAD33761.1| putative GTPase activating protein [Oryza sativa (japonicacultivar-group)]	579	5E-89
					>gb|AAY56433.1| At3g49350 [Arabidopsis thaliana]	539	3E-80
					>ref|NP_190504.1| unknown protein [Arabidopsis thaliana]emb|CAB66414.1| GTPase activating-like protein [Arabidopsis thaliana] gb|AAG52193.1| putative GTPase activator protein of Rab-like small GTPases; 20638-18455 [Arabidopsis thaliana]	554	3E-80
					>ref|NP_199009.2| unknown protein [Arabidopsis thaliana]dbj|BAD44199.1| GTPase activator protein of Rab-like small GTPases-like protein [Arabidopsis thaliana]	549	3E-79
DV491599	8.71E-03	B73=F1<Mo17	1.61	5	>gb|AAQ89670.1| At2g22190 [Arabidopsis thaliana]gb|AAD23621.1| putative trehalose-6-phosphate phosphatase [Arabidopsis thaliana]	269	7E-32
					>ref|NP_179809.2| catalytic/ trehalose-phosphatase [Arabidopsis thaliana]dbj|BAD44683.1| putative trehalose-6-phosphate phosphatase [Arabidopsis thaliana]	354	7E-32
					>ref|XP_482349.1| putative trehalose-phosphatase [Oryza sativa (japonicacultivar-group)] dbj|BAC99626.1| putative trehalose-phosphatase [Oryza sativa (japonica cultivar-group)]	370	4E-31
					>ref|XP_467838.1| putative trehalose-6-phosphate phosphatase [Oryza sativa (japonicacultivar-group)] dbj|BAD15563.1| putative trehalose-6-phosphate phosphatase [Oryza sativa (japonica cultivar-group)]	367	1E-30
					>dbj|BAD37685.1| putative trehalose-phosphatase [Oryza sativa (japonicacultivar-group)]	510	7E-30
CD651123	8.76E-03	Mo17<B73=F1	1.34	10	>gb|AAF71261.2| beta-glucosidase aggregating factor precursor [Zea mays]	306	1E-35
					>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	1E-34
					>gb|ABA97248.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]gb|ABB51090.1| mannose-specific jacalin-related lectin [Oryza sativa (japonica cultivar-group)]	306	2E-34
					>gb|AAR20919.1| jasmonate-induced protein [Triticum aestivum]	304	3E-34
					>gb|AAA87041.1| putative 32.6 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72096.1| 32 kDa protein [Hordeum vulgare]	304	3E-34
CB603924	8.78E-03	B73=Mo17<F1	1.36	12	>gb|AAA87042.1| putative 32.7 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72097.1| 32 kDa protein [Hordeum vulgare]	304	2E-19
					>gb|AAB72098.1| 32 kDa protein [Hordeum vulgare]	306	7E-19
					>gb|AAA87041.1| putative 32.6 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72096.1| 32 kDa protein [Hordeum vulgare]	304	7E-19
					>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	2E-18
					>gb|ABA96669.1| jakalin homolog [Oryza sativa (japonica cultivar-group)]	258	1E-17
BM334438	8.80E-03	Mo17<B73	1.49	10	>gb|AAR99579.1| 60S ribosomal protein L44 [Phalaenopsis hybrid cultivar]	105	1E-38
					>ref|NP_911994.1| putative 60S ribosomal protein L44 [Oryza sativa (japonicacultivar-group)] dbj|BAC15877.1| putative 60S ribosomal protein L44 [Oryza sativa (japonica cultivar-group)]	105	1E-38

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>gb|AAK94425.1| 60S ribosomal protein L144 [Brassica rapa subsp. pekinensis]	119	3E-37
					>ref|NP_188981.1| structural constituent of ribosome [Arabidopsis thaliana]ref|NP_193168.1| structural constituent of ribosome [Arabidopsis thaliana] emb|CAB10211.1| ribosomal protein [Arabidopsis thaliana] emb|CAB78474.1| ribosomal protein [Arabidopsis thaliana] gb|AAM10201.1| ribosomal protein [Arabidopsis thaliana] gb|AAL38297.1| ribosomal protein [Arabidopsis thaliana] gb|AAL32933.1| 60S ribosomal protein L44-like [Arabidopsis thaliana] gb|AAM63001.1| ribosomal protein [Arabidopsis thaliana] gb|AAM61725.1| ribosomal protein [Arabidopsis thaliana] dbj|BAB02283.1| 60S ribosomal protein L44-like [Arabidopsis thaliana] sp|O23290|RL44 ARATH 60S ribosomal protein L44 gb|AAN65080.1| 60S ribosomal protein L44-like [Arabidopsis thaliana]	105	2E-36
					>gb|AAA34366.1| ribosomal protein L41	105	2E-36
BM334179	8.84E-03	F1=Mo17<B73	1.39	9	ns		
CB250116	8.84E-03	Mo17<B73=F1	1.3	10	>gb|AAB88876.1| putative auxin-repressed protein [Prunus armeniaca]	133	1E-15
					>gb|ABA40468.1| Drm3-like protein [Solanum tuberosum]	128	2E-15
					>ref|NP 849820.1| unknown protein [Arabidopsis thaliana]gb|AAG50916.1| unknown protein [Arabidopsis thaliana]	140	4E-14
					>ref|NP 564714.1| unknown protein [Arabidopsis thaliana]gb|AAM64319.1| putative auxin-repressed protein [Arabidopsis thaliana]	137	9E-14
					>gb|AAM62422.1| Drm4 [Pisum sativum]	129	2E-13
BM341452	8.85E-03	Mo17<B73=F1	3.58	10	>emb|CAA73067.1| serine/threonine kinase [Sorghum bicolor]	440	3E-10
					>gb|ABA91407.1| serine/threonine kinase SNFL1, putative [Oryza sativa (japonicacultivar-group)]	454	3E-10
					>gb|ABA95717.1| serine/threonine kinase SNFL1, putative [Oryza sativa (japonicacultivar-group)]	419	3E-10
					>gb|ABA95716.1| serine/threonine kinase SNFL1, putative [Oryza sativa (japonicacultivar-group)]	338	3E-10
					>emb|CAA73068.1| serine/threonine kinase [Sorghum bicolor]	440	2E-9
BM080538	8.85E-03	Mo17<B73=F1	1.37	10	>dbj|BAD87070.1| putative lipid transfer protein [Oryza sativa (japonicacultivar-group)] dbj|BAD73499.1| putative lipid transfer protein [Oryza sativa (japonica cultivar-group)]	120	5E-36
					>ref|NP 915262.1| putative lipid transfer protein [Oryza sativa (japonicacultivar-group)]	122	7E-35
					>emb|CAH69211.1| type 1 non specific lipid transfer protein precursor [Triticumaestivum] emb|CAH69198.1| type 1 non specific lipid transfer protein precursor [Triticum aestivum]	120	4E-33
					>emb|CAH69197.1| type 1 non specific lipid transfer protein precursor [Triticumaestivum]	121	4E-33
					>emb|CAH69196.1| type 1 non specific lipid transfer protein precursor [Triticumaestivum]	120	4E-33
DV621347	8.86E-03	B73<Mo17	1.29	3	>ref|XP_480940.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD05448.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAD05644.1| unknown protein [Oryza sativa (japonica cultivar-group)]	641	3E-71
					>gb|AAV85688.1| At5g57460 [Arabidopsis thaliana]ref|NP_200555.1| unknown protein [Arabidopsis thaliana] gb|AAS49053.1| At5g57460 [Arabidopsis thaliana] dbj|BAB08782.1| unnamed protein product [Arabidopsis thaliana]	646	8E-41
CB886607	8.87E-03	B73<F1=Mo17	1.21	2	>dbj|BAB69069.1| UDP-glucose pyrophosphorylase [Oryza sativa (japonicacultivar-group)]	469	2E-69
					>gb|AAO48422.1| UDP-glucose pyrophosphorylase [Bambusa oldhamii]	473	5E-69
					>emb|CAA62689.1| UDP-glucose pyrophosphorylase [Hordeum vulgare subsp. vulgare]sp|Q43772|UGPA_HORVU UTP--glucose-1-phosphate uridylyltransferase (UDP-glucose pyrophosphorylase) (UDPGP) (UGPase)	473	6E-69
					>gb|AAF19422.1| UDP-glucose pyrophosphorylase [Musa acuminata]sp|Q9SDX3|UGPA_MUSAC UTP--glucose-1-phosphate uridylyltransferase (UDP-glucose pyrophosphorylase) (UDPGP) (UGPase)	467	2E-66
					>gb|AAP86317.1| UDP-glucose pyrophosphorylase [Populus tremula x Populustremuloides]	470	2E-64
CB605443	8.87E-03	B73<F1=Mo17	1.28	3	>ref|XP_464508.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryzasativa (japonica cultivar-group)] dbj|BAD25481.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa (japonica cultivar-group)] dbj|BAD15843.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa (japonica cultivar-group)] dbj|BAB17625.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa (japonica cultivar-group)]	400	9E-44
					>dbj|BAD36121.1| putative 26S proteasome regulatory particle triple-A ATPasesubunit4 [Oryza sativa (japonica cultivar-group)] dbj|BAD35613.1| putative 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa (japonica cultivar-group)]	401	4E-39
					>ref|NP_175120.1| ATP binding / ATPase/ hydrolase/ nucleoside-triphosphatase/nucleotide binding [Arabidopsis thaliana] gb|AAM47992.1| 26S proteasome AAA-ATPase subunit RPT4a-like protein [Arabidopsis thaliana] gb|AAL32787.1| similar to 26S proteasome AAA-ATPase subunit RPT4a [Arabidopsis thaliana] gb|AAF69154.1| F27F5.8 [Arabidopsis thaliana]	399	7E-38
					>gb|ABA40428.1| 26S proteasome AAA-ATPase subunit RPT4a-like protein [Solanumtuberosum] dbj|BAC23035.1| 26S proteasome AAA-ATPase subunit RPT4a [Solanum tuberosum]	398	2E-36
					>ref|NP_199115.1| RPT4A; ATPase [Arabidopsis thaliana]gb|AAL77741.1| AT5g43010/MBD2_21 [Arabidopsis thaliana] gb|AAK50085.1| AT5g43010/MBD2_21 [Arabidopsis thaliana] dbj|BAB09203.1| 26S proteasome AAA-ATPase subunit RPT4a [Arabidopsis thaliana] gb|AAF22524.1| 26S proteasome AAA-ATPase subunit RPT4a [Arabidopsis thaliana]	399	3E-36
DV489995	8.91E-03	Mo17<B73=F1	1.32	10	>ref|XP_450589.1| putative protein-arginine N-methyltransferase [Oryza sativa(japonica cultivar-group)] dbj|BAD23315.1| putative protein-arginine N-methyltransferase [Oryza sativa (japonica cultivar-group)]	306	8E-70
					>ref|NP_194680.1| S-adenosylmethionine-dependent methyltransferase/ protein-arginineN-methyltransferase [Arabidopsis thaliana] emb|CAB79709.1| arginine methyltransferase (pam1) [Arabidopsis thaliana] emb|CAB45311.1| arginine methyltransferase (pam1) [Arabidopsis thaliana] gb|AAN12952.1| arginine methyltransferase pam1 [Arabidopsis thaliana] gb|AAM65371.1| arginine methyltransferase pam1 [Arabidopsis thaliana]	390	8E-62

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<table>
<tr><th>GenBank accession no.</th><th>Overall P value</th><th>Significant pattern</th><th>Fold change†</th><th>Sector‡</th><th>BLAST annotation*</th><th>Score</th><th>E value</th></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAL36326.1| putative arginine methyltransferase pam1 [Arabidopsis thaliana]</td><td>390</td><td>5E-61</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_179557.1| S-adenosylmethionine-dependent methyltransferase/ protein-arginineN-methyltransferase [Arabidopsis thaliana] gb|AAC62148.1| putative arginine N-methyltransferase [Arabidopsis thaliana] gb|AAP21299.1| At2g19670 [Arabidopsis thaliana]</td><td>366</td><td>2E-60</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA07570.1| arginine methyltransferase [Arabidopsis thaliana]</td><td>376</td><td>1E-55</td></tr>
<tr><td>CA829361</td><td>8.91E-03</td><td>B73=F1<Mo17</td><td>1.58</td><td>4</td><td>>emb|CAA68422.1| ribosomal protein L22 (AA 1-126) [Zea mays]</td><td>126</td><td>1E-40</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAT44634.1| ribosomal protein L22 [Saccharum hybrid cultivar SP-80-3280]emb|CAA60325.1| ribosomal protein L22 [Zea mays] dbj|BAD27332.1| ribosomal protein L22 [Saccharum officinarum] ref|YP_054669.1| ribosomal protein L22 [Saccharum officinarum] ref|NP_043063.1| ribosomal protein L22 [Zea mays] sp|P06589|RK22_MAIZE Chloroplast 50S ribosomal protein L22 ref|YP_024319.1| ribosomal protein L22 [Saccharum hybrid cultivar SP-80-3280] sp|Q6L3F9|RK22 SACHY Chloroplast 50S ribosomal protein L22 sp|Q6ENS4|RK22 SACOF Chloroplast 50S ribosomal protein L22</td><td>148</td><td>1E-40</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_481016.1| ribosomal protein L22 [Oryza sativa (japonica cultivar-group)]ref|XP_479425.1| Chloroplast 50S ribosomal protein L22 [Oryza sativa (japonica cultivar-group)] gb|AAS46148.1| ribosomal protein L22; rpl22 [Oryza sativa (japonica cultivar-group)] gb|AAS46211.1| ribosomal protein L22; grpl22 [Oryza sativa (japonica cultivar-group)] gb|AAS46083.1| ribosomal protein L22; rpl22 [Oryza sativa (indica cultivar-group)] emb|CAA33935.1| ribosomal protein L22 [Oryza sativa (japonica cultivar-group)] dbj|BAD31430.1| Chloroplast 50S ribosomal protein L22 [Oryza sativa (japonica cultivar-group)] dbj|BAD05515.1| ribosomal protein L22 [Oryza sativa (japonica cultivar-group)] dbj|BAC10088.1| Chloroplast 50S ribosomal protein L22 [Oryza sativa (japonica cultivar-group)] dbj|BAD26818.1| ribosomal protein L22 [Oryza nivara] dbj|BAD36258.1| ribosomal protein L22 [Oryza sativa (japonica cultivar-group)] dbj|BAD33781.1| ribosomal protein L22 [Oryza sativa (japonica cultivar-group)] ref|NP 039425.1| ribosomal protein L22 [Oryza sativa (japonica cultivar-group)] ref|YP 052789.1|</td><td>149</td><td>9E-39</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_114297.1| ribosomal protein L22 [Triticum aestivum]sp|Q95H48|RK22_WHEAT Chloroplast 50S ribosomal protein L22 dbj|BAB47073.1| ribosomal protein L22 [Triticum aestivum]</td><td>148</td><td>2E-37</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAT44676.1| ribosomal protein S19 [Saccharum hybrid cultivar SP-80-3280]gb|AAT44635.1| ribosomal protein S19 [Saccharum hybrid cultivar SP-80-3280] emb|CAC35460.1| ribosomal protein S19 [Zea mays] emb|CAA60374.1| ribosomal protein S19 [Zea mays] emb|CAA60326.1| ribosomal protein S19 [Zea mays] dbj|BAD27387.1| ribosomal protein S19 [Saccharum officinarum] dbj|BAD27333.1| ribosomal protein S19 [Saccharum officinarum] ref|YP_054723.1| ribosomal protein S19 [Saccharum officinarum] ref|YP_054670.1| ribosomal protein S19 [Saccharum officinarum] ref|NP_043113.1| ribosomal protein S19 [Zea mays] ref|NP_043064.1| ribosomal protein S19 [Zea mays] sp|P06588|RR19_MAIZE Chloroplast 30S ribosomal protein S19 ref|YP_024362.1| ribosomal protein S19 [Saccharum hybrid cultivar SP-80-3280] ref|YP_024320.1| ribosomal protein S19 [Saccharum hybrid cultivar SP-80-3280] sp|Q6L3B6|RR19_SACHY Chloroplast 30S ribosomal protein S19 sp|Q6ENS3|RR19 SACOF Chloroplast 30S ribosomal protein S19</td><td>93</td><td>2E-34</td></tr>
<tr><td>CB833930</td><td>8.93E-03</td><td>B73=F1<Mo17</td><td>1.31</td><td>4</td><td>>ref|XP 474231.1| OSJNBa0084K01.15 [Oryza sativa (japonica cultivar-group)]emb|CAE04843.2| OSJNBa0084K01.15 [Oryza sativa (japonica cultivar-group)]</td><td>451</td><td>1E-28</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAO14624.1| hypothetical protein [Prunus persica]</td><td>446</td><td>4E-14</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP 564096.1| nucleic acid binding [Arabidopsis thaliana]dbj|BAD95060.1| hypothetical protein [Arabidopsis thaliana]</td><td>413</td><td>3E-13</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAG12545.1| Hypothetical Protein [Arabidopsis thaliana]</td><td>420</td><td>3E-13</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_201428.1| nucleic acid binding [Arabidopsis thaliana]gb|AAO50704.1| unknown protein [Arabidopsis thaliana] dbj|BAB10706.1| unnamed protein product [Arabidopsis thaliana] dbj|BAC42293.1| unknown protein [Arabidopsis thaliana]</td><td>449</td><td>3E-6</td></tr>
<tr><td>DV622152</td><td>8.94E-03</td><td>B73=F1<Mo17</td><td>1.2</td><td>5</td><td>>dbj|BAD46209.1| putative inosine-uridine nucleoside N-ribohydrolase [Oryza sativa(japonica cultivar-group)]</td><td>337</td><td>7E-83</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_483754.1| putative inosine-uridine nucleoside N-ribohydrolase [Oryza sativa(japonica cultivar-group)] dbj|BAD09089.1| putative inosine-uridine nucleoside N-ribohydrolase [Oryza sativa (japonica cultivar-group)]</td><td>324</td><td>1E-76</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAT00629.1| putative inosine-uridine preferring nucleoside hydrolase [Zea mays]</td><td>325</td><td>1E-73</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_565843.1| hydrolase [Arabidopsis thaliana]gb|AAD21435.2| expressed protein [Arabidopsis thaliana] gb|AAL47407.1| At2g36310/F2H17.8 [Arabidopsis thaliana] gb|AAL06843.1| At2g36310/F2H17.8 [Arabidopsis thaliana] gb|AAM63615.1| unknown [Arabidopsis thaliana]</td><td>336</td><td>3E-66</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_468759.1| putative inosine-uridine preferring nucleoside hydrolase [Oryzasativa (japonica cultivar-group)] gb|AAP20832.1| putative inosine-uridine preferring nucleoside hydrolase [Oryza sativa (japonica cultivar-group)]</td><td>322</td><td>2E-38</td></tr>
<tr><td>CB833952</td><td>8.94E-03</td><td>Mo17<F1</td><td>1.36</td><td>12</td><td>>gb|AAC08009.1| DnaJ-related protein ZMDJ1 [Zea mays]</td><td>419</td><td>5E-71</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAX95135.1| DnaJ protein, putative [Oryza sativa (japonica cultivar-group)]</td><td>416</td><td>6E-71</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAU89194.1| DnaJ protein, putative [Oryza sativa (japonica cultivar-group)]gb|AAO72551.1| DNAJ-like protein [Oryza sativa (japonica cultivar-group)]</td><td>417</td><td>6E-71</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAT75262.1| putative DnaJ like protein [Oryza sativa (japonicacultivar-group)]</td><td>417</td><td>9E-65</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>sp|P43644|DNJH ATRNU DnaJ protein homolog ANJ1</td><td>417</td><td>1E-64</td></tr>
<tr><td>CB816061</td><td>8.98E-03</td><td>Mo17<B73=F1</td><td>1.25</td><td>10</td><td>>gb|AAC08009.1| DnaJ-related protein ZMDJ1 [Zea mays]</td><td>419</td><td>5E-35</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAX95135.1| DnaJ protein, putative [Oryza sativa (japonica cultivar-group)]</td><td>416</td><td>8E-31</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAU89194.1| DnaJ protein, putative [Oryza sativa (japonica cultivar-group)]gb|AAO72551.1| DNAJ-like protein [Oryza sativa (japonica cultivar-group)]</td><td>417</td><td>8E-31</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAA35121.1| DnaJ homolog [Salix gilgiana]</td><td>420</td><td>2E-26</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAG24643.1| J2P [Daucus carota]gb|AAG24642.1| J1P [Daucus carota]</td><td>418</td><td>6E-26</td></tr>
<tr><td>BM079379</td><td>8.99E-03</td><td>Mo17<B73</td><td>2.6</td><td>10</td><td>ns</td><td></td><td></td></tr>
<tr><td>AI629488</td><td>9.01E-03</td><td>B73<F1=Mo17</td><td>2.26</td><td>3</td><td>ns</td><td></td><td></td></tr>
<tr><td>BM336484</td><td>9.03E-03</td><td>Mo17<B73=F1</td><td>1.34</td><td>11</td><td>>gb|AAT12488.1| copper chaperone [Populus alba x Populus tremula var. glandulosa]</td><td>85</td><td>1E-31</td></tr>
</table>

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_564870.1| metal ion binding [Arabidopsis thaliana]gb|AAL76156.1| At1g66240/T6J19_6 [Arabidopsis thaliana] gb|AAK64002.1| At1g66240/T6J19_6 [Arabidopsis thaliana]	106	1E-30
					>ref|XP_480605.1| putative copper chaperone [Oryza sativa (japonica cultivar-group)]dbj|BAD11546.1| putative copper chaperone [Oryza sativa (japonica cultivar-group)] dbj|BAD05334.1| putative copper chaperone [Oryza sativa (japonica cultivar-group)]	81	2E-30
					>gb|AAP06757.1| copper chaperone [Lycopersicon esculentum]	81	2E-28
					>ref|NP_191183.1| CCH [Arabidopsis thaliana]emb|CAB87423.1| copper homeostasis factor [Arabidopsis thaliana] gb|AAK32872.1| AT3g56240/F18O21_200 [Arabidopsis thaliana] gb|AAL47423.1| AT3g56240/F18O21_200 [Arabidopsis thaliana] gb|AAM62878.1| copper homeostasis factor [Arabidopsis thaliana] gb|AAC33510.1| copper homeostasis factor [Arabidopsis thaliana]	121	4E-28
DV550016	9.08E-03	Mo17<B73=F1	1.57	10	>gb|AAU44176.1| unknown protein [Oryza sativa (japonica cultivar-group)]	230	1E-45
					>ref|NP_849977.1| heat shock protein binding / unfolded protein binding [Arabidopsisthaliana] gb|AAM97127.1| unknown protein [Arabidopsis thaliana] gb|AAN65042.1| unknown protein [Arabidopsis thaliana]	268	3E-21
					>ref|XP 474436.1| OSJNBa0070M12.14 [Oryza sativa (japonica cultivar-group)]emb|CAD41937.2| OSJNBa0070M12.14 [Oryza sativa (japonica cultivar-group)]	274	2E-17
					>ref|NP_181738.1| heat shock protein binding / unfolded protein binding [Arabidopsisthaliana] gb|AAM97104.1| unknown protein [Arabidopsis thaliana] gb|AAB63536.1| unknown protein [Arabidopsis thaliana] gb|AAN72139.1| unknown protein [Arabidopsis thaliana]	263	2E-11
					>gb|AAL87325.1| unknown protein [Arabidopsis thaliana]	254	6E-11
CD670384	9.10E-03	Mo17<B73=F1	1.34	10	>sp|Q08069|RS8 MAIZE 40S ribosomal protein S8gb|AAB06330.1| ribosomal protein S8	221	7E-82
					>emb|CAE05511.1| OSJNBa0038P21.4 [Oryza sativa (japonica cultivar-group)]	221	1E-75
					>ref|XP_465742.1| putative 40S ribosomal protein S8 [Oryza sativa (japonicacultivar-group)] ref|XP_506804.1| PREDICTED P0483C08.42 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD21871.1| putative 40S ribosomal protein S8 [Oryza sativa (japonica cultivar-group)] dbj|BAD21876.1| putative 40S ribosomal protein S8 [Oryza sativa (japonica cultivar-group)]	220	4E-75
					>sp|P49199|RS8 ORYSA 40S ribosomal protein S8dbj|BAA07207.1| ribosomal protein S8 [Oryza sativa (japonica cultivar-group)]	220	5E-72
					>gb|ABA46755.1| unknown [Solanum tuberosum]	224	4E-71
CA998707	9.16E-03	Mo17<B73=F1	1.3	10	>gb|AAO00695.1| hypothetical protein OSJNBa0096G08.1 [Oryza sativa (japonicacultivar-group)]	114	3E-16
					>ref|NP 922396.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]gb|AAM92300.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	289	3E-16
					>gb|ABB47904.1| expressed protein [Oryza sativa (japonica cultivar-group)]	291	3E-16
					>dbj|BAD44327.1| unknown protein [Arabidopsis thaliana]dbj|BAD43126.1| unknown protein [Arabidopsis thaliana]	185	1E-6
					>ref|NP_200024.1| unknown protein [Arabidopsis thaliana]ref|NP_001032060.1| unknown protein [Arabidopsis thaliana] dbj|BAB11059.1| unnamed protein product [Arabidopsis thaliana]	275	1E-6
BM075631	9.27E-03	F1=Mo17<B73	1.49	9	>ref|XP 473516.1| OSJNBa0017B10.7 [Oryza sativa (japonica cultivar-group)]emb|CAE03092.2| OSJNBa0017B10.7 [Oryza sativa (japonica cultivar-group)]	852	3E-29
					>ref|NP_195281.1| unknown protein [Arabidopsis thaliana]emb|CAB80272.1| hypothetical protein [Arabidopsis thaliana] emb|CAA20026.1| hypothetical protein [Arabidopsis thaliana]	917	7E-10
BM073507	9.28E-03	F1<B73=Mo17	1.9	7	ns		
CB886579	9.29E-03	Mo17<B73=F1	1.44	10	>ref|NP_922190.1| putative leaf protein [Oryza sativa (japonica cultivar-group)]gb|AAM93671.1| putative leaf protein [Oryza sativa (japonica cultivar-group)] gb|AAP54477.1| leaf protein, putative [Oryza sativa (japonica cultivar-group)]	513	1E-28
					>ref|NP 922187.1| putative leaf protein [Oryza sativa (japonica cultivar-group)]gb|AAM93695.1| putative leaf protein [Oryza sativa (japonica cultivar-group)]	372	8E-28
					>ref|NP_922189.1| putative leaf protein [Oryza sativa (japonica cultivar-group)]gb|AAM93669.1| putative leaf protein [Oryza sativa (japonica cultivar-group)] gb|AAP54476.1| leaf protein, putative [Oryza sativa (japonica cultivar-group)]	545	8E-28
					>gb|ABB47839.1| leaf protein, putative [Oryza sativa (japonica cultivar-group)]	341	8E-28
					>ref|NP_179663.1| unknown protein [Arabidopsis thaliana]gb|AAT99801.1| At2g20710 [Arabidopsis thaliana] gb|AAD20924.1| hypothetical protein [Arabidopsis thaliana]	490	1E-6
CD001612	9.33E-03	Mo17<B73=F1	1.39	11	>sp|P23346|SODC5 MAIZE Superoxide dismutase [Cu-Zn] 4AP	152	1E-84
					>emb|CAB57992.1| superoxide dismutase-4AP [Zea mays]sp|P23345|SODC4 MAIZE Superoxide dismutase [Cu-Zn] 4A	152	9E-84
					>emb|CAB57993.1| superoxide dismutase-4A [Zea mays]gb|AAB49913.1| superoxide dismutase 4A	152	1E-82
					>sp|P28757|SODC2_ORYSA Superoxide dismutase [Cu-Zn] 2gb|AAC14465.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00800.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)]	152	2E-78
					>gb|AAY56345.1| cytoplasmic copper/zinc-superoxide dismutase [Oryza sativa (indicacultivar-group)] sp|P28756|SODC1_ORYSA Superoxide dismutase [Cu-Zn] 1 gb|AAC14464.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00799.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)] prf||2111424A Cu/Zn superoxide dismutase	152	2E-77
DV494176	9.34E-03	Mo17<F1	1.41	11	>ref|NP 911778.1| myosin-like protein [Oryza sativa (japonica cultivar-group)]dbj|BAC57340.1| myosin-like protein [Oryza sativa (japonica cultivar-group)]	309	2E-28
					>ref|XP 470354.1| myosin-like protein [Oryza sativa (japonica cultivar-group)]gb|AAO41145.1| myosin-like protein [Oryza sativa (japonica cultivar-group)]	216	1E-26
					>ref|XP_477099.1| myosin-like protein [Oryza sativa (japonica cultivar-group)]dbj|BAC82964.1| myosin-like protein [Oryza sativa (japonica cultivar-group)] dbj|BAC57288.1| myosin-like protein [Oryza sativa (japonica cultivar-group)]	383	3E-15
					>ref|NP 973593.1| unknown protein [Arabidopsis thaliana]	212	4E-12

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
CB331806	9.35E-03	Mo17<B73	1.26	10	>ref|XP_473801.1| OSJNBb0015N08.13 [Oryza sativa (japonica cultivar-group)]emb|CAE03885.2| OSJNBb0015N08.13 [Oryza sativa (japonica cultivar-group)] emb|CAE02124.2| OSJNBa0035M09.3 [Oryza sativa (japonica cultivar-group)]	250	3E-67
					>ref|XP_480842.1| putative 60S ribosomal protein L7 [Oryza sativa (japonicacultivar-group)] dbj|BAD03800.1| putative 60S ribosomal protein L7 [Oryza sativa (japonica cultivar-group)]	245	3E-66
					>gb|AAW50989.1| ribosomal protein L7 [Triticum aestivum]	244	2E-60
					>ref|NP_974305.1| structural constituent of ribosome / transcription regulator[Arabidopsis thaliana] ref|NP_974304.1| structural constituent of ribosome / transcription regulator [Arabidopsis thaliana] ref|NP_187967.1| structural constituent of ribosome / transcription regulator [Arabidopsis thaliana] gb|AAL76153.1| AT3g13580/K20M4_2 [Arabidopsis thaliana] gb|AAL06999.1| AT3g13580/K20M4_2 [Arabidopsis thaliana] gb|AAK64004.1| AT3g13580/K20M4_2 [Arabidopsis thaliana] dbj|BAB02600.1| 60S ribosomal protein L7 [Arabidopsis thaliana] sp|Q9LHP1|RL73 ARATH 60S ribosomal protein L7-3	244	1E-56
					>ref|NP_178234.1| structural constituent of ribosome / transcription regulator[Arabidopsis thaliana] gb|AAL85059.1| putative ribosomal protein L7 [Arabidopsis thaliana] gb|AAK76668.1| putative ribosomal protein L7 [Arabidopsis thaliana] gb|AAD14525.1| putative ribosomal protein L7 [Arabidopsis thaliana] gb|AAM10260.1| 60S ribosomal protein L7 [Arabidopsis thaliana] gb|AAM61692.1| putative ribosomal protein L7 [Arabidopsis thaliana] gb|AAK43861.1| 60S ribosomal protein L7 [Arabidopsis thaliana] sp|P60040|RL71 ARATH 60S ribosomal protein L7-1	242	3E-56
DV622665	9.36E-03	B73=F1<Mo17	1.18	4	>gb|AAM67260.1| alcohol dehydrogenase-like protein [Arabidopsis thaliana]	384	1E-54
					>emb|CAB79166.1| alcohol dehydrogenase like protein [Arabidopsis thaliana]emb|CAA18114.1| alcohol dehydrogenase like protein [Arabidopsis thaliana]	378	4E-54
					>ref|NP 567645.1| oxidoreductase/ zinc ion binding [Arabidopsis thaliana]ref|NP 974589.1| oxidoreductase/ zinc ion binding [Arabidopsis thaliana]	389	4E-54
					>ref|NP_912567.1| Putative alcohol dehydrogenase [Oryza sativa (japonicacultivar-group)] gb|AAN64150.1| Putative alcohol dehydrogenase [Oryza sativa (japonica cultivar-group)]	360	5E-54
					>ref|NP_914761.1| putative alcohol dehydrogenase [Oryza sativa (japonicacultivar-group)] dbj|BAC10189.1| putative alcohol dehydrogenase [Oryza sativa (japonica cultivar-group)]	390	2E-53
DV550879	9.36E-03	B73=F1<Mo17	1.6	4	ns		
DV491984	9.46E-03	Mo17<B73	1.5	9	>ref|NP_912805.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]dbj|BAA85219.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]	1197	1E-44
					>dbj|BAB07978.1| putative glycine-rich protein 2 [Oryza sativa (japonicacultivar-group)] sp|Q9LGE6|LSM4_ORYSA Probable U6 snRNA-associated Sm-like protein LSm4	147	1E-44
					>gb|ABB02633.1| glycine rich protein-like [Solanum tuberosum]gb|ABB87115.1| glycine rich protein-like [Solanum tuberosum]	147	5E-42
					>gb|AAM65462.1| glycine rich protein-like [Arabidopsis thaliana]	129	2E-41
					>ref|NP 198124.1| EMB1644 [Arabidopsis thaliana]	129	2E-41
BM073198	9.46E-03	F1=Mo17<B73	1.89	9	ns		
CD484517	9.52E-03	Mo17<B73=F1	2.35	11	>ref|XP 794816.1| PREDICTED: similar to H3 histone, family 2 isoform 2[Strongylocentrotus purpuratus]	145	1E-28
					>emb|CAF98785.1| unnamed protein product [Tetraodon nigroviridis]	188	4E-28
					>ref|XP 854287.1| PREDICTED: similar to histone 1, H2ai (predicted) [Canisfamiliaris]	156	4E-28
					>gb|AAV65112.1| histone 3 [Camellia sinensis]	136	5E-28
					>gb|AAX92952.1| histone H3 - maize [Oryza sativa (japonica cultivar-group)]gb|ABA91537.1| histone H3 [Oryza sativa (japonica cultivar-group)]	168	5E-28
CD568461	9.56E-03	B73=F1<Mo17	1.47	4	>emb|CAA74653.1| plastid RNA polymerase sigma factor [Sorghum bicolor]	500	2E-67
					>gb|AAC78468.1| RNA polymerase sigma factor 2 [Zea mays]	349	5E-67
					>gb|AAC78467.1| RNA polymerase sigma factor 1 [Zea mays]	398	1E-65
					>emb|CAA10725.1| chloroplast sigma factor [Triticum aestivum]	461	9E-65
					>ref|XP_480220.1| putative plastid RNA polymerase sigma factor [Oryza sativa(japonica cultivar-group)] dbj|BAC99906.1| putative plastid RNA polymerase sigma factor [Oryza sativa (japonica cultivar-group)]	342	1E-64
DV550134	9.59E-03	B73=F1<Mo17	1.82	4	>gb|AAT44693.1| photosystem I P700 apoprotein A2 [Saccharum hybrid cultivarSP-80-3280] dbj|BAD27292.1| PSI P700 apoprotein A2 [Saccharum officinarum] ref|YP_054630.1| PSI P700 apoprotein A2 [Saccharum officinarum] sp|Q6ENW4|PSAB_SACOF Photosystem I P700 chlorophyll a apoprotein A2 (PsaB) (PSI-B) sp|Q6L399|PSAB_SACHY Photosystem I P700 chlorophyll a apoprotein A2 (PsaB) (PSI-B) ref|YP_024379.1| photosystem I P700 apoprotein A2 [Saccharum hybrid cultivar SP-80-3280]	734	e-116
					>emb|CAD28720.1| PSI P700 apoprotein A2 [Calycanthus floridus var. glaucus]ref|NP_862753.1| photosystem I P700 apoprotein A2 [Calycanthus floridus var. glaucus] sp|Q7YJX3|PSAB CALFE Photosystem I P700 chlorophyll a apoprotein A2 (PsaB) (PSI-B)	734	e-115
					>gb|ABC73627.1| photosystem I P700 apoprotein A2 [Gossypium hirsutum]	734	e-115
					>emb|CAA60285.1| PSI P700 apoprotein A2 [Zea mays]ref|NP_043024.1| photosystem I P700 apoprotein A2 [Zea mays] sp|P04967|PSAB_MAIZE Photosystem I P700 chlorophyll a apoprotein A2 (PsaB) (PSI-B)	735	e-115
					>gb|AAA84486.1| P700 chlorophyll a-protein PSI-A2	735	e-115
DV622534	9.60E-03	Mo17<B73	1.51	9	>gb|AAV28627.1| putative 60S ribosomal protein L31 [Zea mays]	124	5E-46
					>ref|XP_467485.1| putative 60S ribosomal protein L31 [Oryza sativa (japonicacultivar-group)] dbj|BAD12898.1| putative 60S ribosomal protein L31 [Oryza sativa (japonica cultivar-group)]	123	1E-45

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15 % FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|XP_483237.1| putative 60S ribosomal protein L31 [Oryza sativa (japonicacultivar-group)] dbj|BAD10170.1| putative 60S ribosomal protein L31 [Oryza sativa (japonica cultivar-group)] dbj|BAD08833.1| putative 60S ribosomal protein L31 [Oryza sativa (japonica cultivar-group)]	122	1E-45
					>dbj|BAD61612.1| putative 60S ribosomal protein L31 [Oryza sativa (japonicacultivar-group)]	124	2E-45
					>gb|AAV92213.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii]gb|AAV92212.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92211.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92210.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92209.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92208.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92207.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92206.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92205.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92204.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92203.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92202.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii] gb|AAV92201.1| 60S ribosomal protein L31a [Pseudotsuga menziesii var. menziesii]	113	9E-43
CB239957	9.66E-03	Mo17<B73=F1	1.26	10	>ref|XP_469336.1| unknown protein [Oryza sativa]dbj|BAC78563.1| hypothetical protein [Oryza sativa (japonica cultivar-group)] gb|AAK14411.1| unknown protein [Oryza sativa]	138	8E-34
					>ref|NP_201245.1| unknown protein [Arabidopsis thaliana]gb|AAL34219.1| unknown protein [Arabidopsis thaliana] gb|AAK59405.1| unknown protein [Arabidopsis thaliana] dbj|BAB09871.1| unnamed protein product [Arabidopsis thaliana]	144	2E-27
					>gb|AAS21010.1| unknown [Hyacinthus orientalis]	150	2E-22
					>ref|NP_196519.1| unknown protein [Arabidopsis thaliana]gb|AAO39889.1| At5g09570 [Arabidopsis thaliana] dbj|BAC43288.1| unknown protein [Arabidopsis thaliana] emb|CAB89373.1| putative protein [Arabidopsis thaliana]	139	2E-22
					>ref|NP 001032137.1| unknown protein [Arabidopsis thaliana]	162	4E-14
DV490002	9.67E-03	F1=Mo17<B73	1.35	9	>ref|NP_915688.1| putative zinc finger protein [Oryza sativa (japonicacultivar-group)] dbj|BAB64114.1| putative transparent testa 1 [Oryza sativa (japonica cultivar-group)] dbj|BAB86538.1| putative zinc finger protein [Oryza sativa (japonica cultivar-group)]	522	7E-59
					>gb|AAM65531.1| zinc finger protein, putative [Arabidopsis thaliana]	499	5E-22
					>ref|NP_174697.1| nucleic acid binding / transcription factor/ zinc ion binding[Arabidopsis thaliana] ref|NP_849746.1| nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana] gb|AAG51898.1| zinc finger protein, putative; 58191-56692 [Arabidopsis thaliana]	499	5E-22
					>ref|NP 001031140.1| nucleic acid binding / zinc ion binding [Arabidopsis thaliana]	350	5E-22
					>ref|XP_470361.1| putative zinc finger protein [Oryza sativa (japonicacultivar-group)] gb|AAO41119.1| putative zinc finger protein [Oryza sativa (japonica cultivar-group)]	385	1E-14
CD651773	9.73E-03	F1=Mo17<B73	1.28	9	>ref|XP_468402.1| putative NADH dehydrogenase [Oryza sativa (japonicacultivar-group)] dbj|BAD22016.1| putative NADH dehydrogenase [Oryza sativa (japonica cultivar-group)] dbj|BAD21515.1| putative NADH dehydrogenase [Oryza sativa (japonica cultivar-group)]	408	2E-74
					>ref|NP_565469.1| unknown protein [Arabidopsis thaliana]gb|AAT68351.1| hypothetical protein At2g20360 [Arabidopsis thaliana] gb|AAK93749.1| putative NADH-ubiquinone oxireductase [Arabidopsis thaliana] gb|AAK59545.1| putative NADH-ubiquinone oxireductase [Arabidopsis thaliana] gb|AAD21752.2| putative NADH-ubiquinone oxireductase [Arabidopsis thaliana] gb|AAX23820.1| hypothetical protein At2g20360 [Arabidopsis thaliana]	402	1E-62
					>gb|EAN07479.1| NADH dehydrogenase (ubiquinone) 1 alpha subcomplex [Mesorhizobiumsp. BNC1] ref|ZP_00611528.1| NADH dehydrogenase (ubiquinone) 1 alpha subcomplex [Mesorhizobium sp. BNC1]	323	1E-16
					>ref|ZP 00627083.1| oxidoreductase [Nitrobacter hamburgensis X14]gb|EAN59795.1| oxidoreductase [Nitrobacter hamburgensis X14]	322	8E-16
					>ref|ZP_00845998.1| putative NADH dehydrogenase (ubiquinone) 1 alpha subcomplex[Rhodopseudomonas palustris BisB18] gb|EAP12165.1| putative NADH dehydrogenase (ubiquinone) 1 alpha subcomplex [Rhodopseudomonas palustris BisB18]	349	2E-15
BG841395	9.74E-03	Mo17<B73	1.37	9	>ref|XP_472942.1| OSJNBa0081L15.18 [Oryza sativa (japonica cultivar-group)]emb|CAE02006.2| OJ000223_09.8 [Oryza sativa (japonica cultivar-group)] emb|CAE03156.2| OSJNBa0081L15.18 [Oryza sativa (japonica cultivar-group)]	505	1E-38
					>ref|XP_466575.1| putative glucose-6-phosphate dehydrogenase [Oryza sativa (japonicacultivar-group)] dbj|BAD22150.1| putative glucose-6-phosphate dehydrogenase [Oryza sativa (japonica cultivar-group)]	517	1E-37
					>gb|AAL79959.1| glucose-6-phosphate dehydrogenase [Oryza sativa (japonicacultivar-group)]	505	2E-37
					>dbj|BAA97664.1| glucose-6-phosphate dehydrogenase [Triticum aestivum]	509	1E-36
					>dbj|BAA97663.1| glucose-6-phosphate dehydrogenase [Triticum aestivum]	513	1E-36
CB351715	9.78E-03	Mo17<B73=F1	1.2	10	>ref|XP_475153.1| putative nascent polypeptide associated complex alpha chain [Oryzasativa (japonica cultivar-group)] gb|AAT58840.1| putative nascent polypeptide associated complex alpha chain [Oryza sativa (japonica cultivar-group)] dbj|BAC78570.1| nascent polypeptide associated complex alpha chain [Oryza sativa (japonica cultivar-group)]	205	2E-55
					>gb|AAT41858.1| At5g13850 [Arabidopsis thaliana]sp|Q6ICZ8|NACA3_ARATH Nascent polypeptide-associated complex alpha subunit-like protein 3 (NAC-alpha-like protein 3) (Alpha-NAC-like protein 3)	204	2E-53
					>ref|NP_187845.1| unknown protein [Arabidopsis thaliana]gb|AAM16178.1| AT3g12390/T2E22_130 [Arabidopsis thaliana] gb|AAK82495.1| AT3g12390/T2E22_130 [Arabidopsis thaliana] gb|AAG51031.1| nascent polypeptide associated complex alpha chain, putative; 85450-84199 [Arabidopsis thaliana] dbj|BAB03146.1| unnamed protein product [Arabidopsis thaliana] sp|Q9LHG9|NACA1_ARATH Nascent polypeptide-associated complex alpha subunit-like protein 1 (NAC-alpha-like protein 1) (Alpha-NAC-like protein 1)	203	3E-53
					>gb|AAF27917.1| nascent polypeptide associated complex alpha chain [Pinus taeda]sp|Q9M612|NACA_PINTA Nascent polypeptide-associated complex alpha subunit-like protein (NAC-alpha-like protein) (Alpha-NAC-like protein)	205	5E-53

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>ref|NP_914976.1| putative nascent polypeptide associated complex alpha chain [Oryzasativa (japonica cultivar-group)] dbj|BAB90246.1| putative nascent polypeptide associated complex alpha chain [Oryza sativa (japonica cultivar-group)] dbj|BAB89723.1| putative nascent polypeptide associated complex alpha chain [Oryza sativa (japonica cultivar-group)]	202	9E-53
BM333546	9.85E-03	Mo17<B73=F1	1.3	10	>gb|AAU90153.1| unknown protein [Oryza sativa (japonica cultivar-group)]	126	2E-14
					>ref|NP_181349.1| PSRP4 (PLASTID-SPECIFIC RIBOSOMAL PROTEIN 4); structuralconstituent of ribosome [Arabidopsis thaliana] gb|AAC27163.1| 30S ribosomal protein S31 [Arabidopsis thaliana] gb|AAL31104.1| At2g38140/F16M14.7 [Arabidopsis thaliana] gb|AAK97685.1| At2g38140/F16M14.7 [Arabidopsis thaliana] gb|AAM67339.1| 30S ribosomal protein S31 [Arabidopsis thaliana] gb|AAF64153.1| plastid-specific ribosomal protein 4 precursor [Arabidopsis thaliana]	118	5E-6
CB815844	9.86E-03	Mo17<B73	1.21	9	>ref|XP_475453.1| putative 60S ribosomal protein L24 [Oryza sativa (japonicacultivar-group)] gb|AAT01333.1| putative 60S ribosomal protein L24 [Oryza sativa (japonica cultivar-group)]	161	1E-57
					>dbj|BAD82702.1| putative 60S ribosomal protein L24 [Oryza sativa (japonicacultivar-group)]	162	7E-57
					>emb|CAA63960.1| L24 ribosomal protein [Hordeum vulgare subsp. vulgare]sp|P50888|RL24 HORVU 60S ribosomal protein L24	162	1E-55
					>ref|NP_911528.1| putative 60S ribosomal protein L24 [Oryza sativa (japonicacultivar-group)] dbj|BAD30738.1| putative 60S ribosomal protein L24 [Oryza sativa (japonica cultivar-group)] dbj|BAC06922.1| putative 60S ribosomal protein L24 [Oryza sativa (japonica cultivar-group)]	160	6E-54
					>gb|AAG13986.1| 60S ribosomal protein L24 [Prunus avium]sp|Q9FUL4|RL24 PRUAV 60S ribosomal protein L24	186	3E-53
DV490318	9.92E-03	B73=F1<Mo17	1.53	4	ns		
DV491097	9.93E-03	B73=F1<Mo17	1.4	4	>ref|XP 478168.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAC80068.1| unknown protein [Oryza sativa (japonica cultivar-group)]	302	2E-24
					>ref|NP 199935.2| unknown protein [Arabidopsis thaliana]gb|AAY27063.1| At5g51220 [Arabidopsis thaliana]	281	4E-10
DV621900	9.93E-03	B73=F1<Mo17	1.25	4	ns		
CB605196	9.94E-03	B73<F1=Mo17	1.27	3	>ref|XP_470662.1| Putative phosphate/phosphoenolpyruvate translocator protein [Oryzasativa (japonica cultivar-group)] gb|AAO16996.1| Putative phosphate/phosphoenolpyruvate translocator protein [Oryza sativa (japonica cultivar-group)]	322	7E-40
					>ref|NP 187740.2| organic anion transporter [Arabidopsis thaliana]gb|AAU94370.1| At3g11320 [Arabidopsis thaliana]	308	2E-35
					>gb|AAG50965.1| integral membrane protein, putative; 85705-84183 [Arabidopsisthaliana]	344	2E-35
					>dbj|BAD91177.1| plastidic phosphate translocator-like protein2 [Mesembryanthemumcrystallinum]	306	1E-34
					>ref|NP_196201.2| organic anion transporter [Arabidopsis thaliana]gb|AAU45213.1| At5g05820 [Arabidopsis thaliana] gb|AAT70430.1| At5g05820 [Arabidopsis thaliana]	309	2E-33
BM080160	9.96E-03	Mo17<F1	1.27	11	>ref|NP_912352.1| putative LIM-domain protein [Oryza sativa (japonicacultivar-group)] gb|AAP06876.1| putative LIM-domain protein [Oryza sativa (japonica cultivar-group)]	196	4E-52
					>gb|AAL38006.1| LIM domain protein [Gossypium hirsutum]	189	1E-47
					>emb|CAA71891.1| LIM-domain SF3 protein [Nicotiana tabacum]gb|AAD56951.1| LIM domain protein WLIM2 [Nicotiana tabacum]	189	1E-46
					>ref|NP_001030870.1| zinc ion binding [Arabidopsis thaliana]ref|NP_680133.2| zinc ion binding [Arabidopsis thaliana] ref|NP_001030868.1| zinc ion binding [Arabidopsis thaliana] ref|NP_001030869.1| zinc ion binding [Arabidopsis thaliana] ref|NP_191136.1| zinc ion binding [Arabidopsis thaliana] emb|CAB81602.1| transcription factor L2 [Arabidopsis thaliana] gb|AAM14188.1| putative transcription factor L2 [Arabidopsis thaliana] gb|AAL36280.1| putative transcription factor L2 [Arabidopsis thaliana] gb|AAM60942.1| transcription factor L2 [Arabidopsis thaliana]	199	7E-44
					>gb|AAK49580.1| transcription factor L2 [Arabidopsis thaliana]	148	7E-44
DV491411	9.99E-03	B73=F1<Mo17	4.08	4	>ref|XP_479018.1| putative rRNA methylase [Oryza sativa (japonica cultivar-group)]dbj|BAC83213.1| putative rRNA methylase [Oryza sativa (japonica cultivar-group)]	343	5E-25
					>ref|NP 197043.1| RNA binding / RNA methyltransferase [Arabidopsis thaliana]emb|CAB89349.1| rRNA methylase-like protein [Arabidopsis thaliana]	350	9E-16
					>gb|AAR88654.1| rRNA methylase-like protein [Viscum album]	368	2E-14
					>ref|YP 445016.1| rRNA methylase [Salinibacter ruber DSM 13855]gb|ABC44820.1| rRNA methylase [Salinibacter ruber DSM 13855]	247	3E-6
					>emb|CAE79110.1| putative RNA methylase [Bdellovibrio bacteriovorus HD100]ref|NP 968117.1| putative RNA methylase [Bdellovibrio bacteriovorus HD100]	238	9E-6
CB834100	1.00E-02	Mo17<B73=F1	1.25	10	>emb|CAA59798.1| O-acetylserine (thiol) lyase; cysteine synthase [Zea mays]sp|P80608|CYSK_MAIZE Cysteine synthase (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) (CSase) (OAS-TL)	325	8E-66
					>sp|P38076|CYSK_WHEAT Cysteine synthase (O-acetylserine sulfhydrylase) (O-acetylserine(Thiol)-lyase) (CSase A) (OAS-TL A) dbj|BAA02438.1| O-acetylserine (thiol) lyase [Triticum aestivum]	325	1E-62
					>gb|ABA99438.1| cysteine synthase A [Oryza sativa (japonica cultivar-group)]	330	1E-61
					>gb|AAD23907.1| cysteine synthase [Oryza sativa]	321	3E-61
					>sp|Q9XEA6|CYSK1 ORYSA Cysteine synthase (O-acetylserine sulfhydrylase) (O-acetylserine(Thiol)-lyase) (CSase) (OAS-TL)	321	3E-61
DV494228	1.00E-02	Mo17<F1	1.52	12	>ref|XP_482149.1| putative transformer-SR ribonucleoprotein [Oryza sativa (japonicacultivar-group)] dbj|BAD05836.1| putative transformer-SR ribonucleoprotein [Oryza sativa (japonica cultivar-group)] dbj|BAD05420.1| putative transformer-SR ribonucleoprotein [Oryza sativa (japonica cultivar-group)]	279	8E-45
					>gb|AAY84876.1| alternative splicing regulator [Triticum aestivum]	250	7E-40
					>emb|CAA70700.1| transformer-SR ribonucleoprotein [Nicotiana tabacum]	235	8E-31
					>dbj|BAD62534.1| putative transformer-SR ribonucleoprotein [Oryza sativa (japonicacultivar-group)] dbj|BAD61690.1| putative transformer-SR ribonucleoprotein [Oryza sativa (japonica cultivar-group)]	273	8E-31

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>ref|NP_912347.1| putative transformer serine/arginine-rich ribonucleoprotein [Oryzasativa (japonica cultivar-group)] gb|AAP06839.1| putative transformer serine/arginine-rich ribonucleoprotein [Oryza sativa (japonica cultivar-group)]	324	9E-30
DV550737	1.00E-02	Mo17<B73=F1	1.5	11	>ref|XP_450411.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD26204.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAD26132.1| unknown protein [Oryza sativa (japonica cultivar-group)]	176	9E-24
					>ref|XP 472777.1| OSJNBa0060P14.7 [Oryza sativa (japonica cultivar-group)]emb|CAD41036.1| OSJNBa0060P14.7 [Oryza sativa (japonica cultivar-group)]	119	5E-9
					>ref|XP 472812.1| OSJNBa0016O02.17 [Oryza sativa (japonica cultivar-group)]emb|CAE06007.3| OSJNBa0016O02.17 [Oryza sativa (japonica cultivar-group)]	122	2E-8
					>dbj|BAD29340.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]dbj|BAD17466.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	117	2E-8
					>dbj|BAD29339.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]dbj|BAD17465.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	119	3E-8
CB886176	1.00E-02	Mo17<B73=F1	1.35	10	>gb|ABA98987.1| expressed protein [Oryza sativa (japonica cultivar-group)]	106	2E-43
					>gb|AAM64270.1| unknown [Arabidopsis thaliana]	104	4E-30
					>ref|NP 568115.1| unknown protein [Arabidopsis thaliana]	104	2E-29
					>gb|AAX55666.1| 11 kDa salivary protein [Phlebotomus ariasi]	114	1E-6
					>gb|EAA15151.2| ENSANGP00000010639 [Anopheles gambiae str. PEST]ref|XP 319892.2| ENSANGP00000010639 [Anopheles gambiae str. PEST]	108	2E-6
BM268642	1.01E-02	Mo17<B73=F1	2.14	11	>gb|AAO47712.1| transcription factor MADS57 [Oryza sativa (japonicacultivar-group)]	241	1E-23
					>ref|XP_467621.1| transcription factor MADS57 [Oryza sativa (japonicacultivar-group)] dbj|BAD15933.1| transcription factor MADS57 [Oryza sativa (japonica cultivar-group)]	237	1E-23
					>gb|AAO72601.1| MADS box protein-like protein [Oryza sativa (japonicacultivar-group)]	241	5E-23
					>emb|CAB09793.1| ANR1 , MADS-box protein [Arabidopsis thaliana]	234	8E-23
					>ref|NP_179033.1| ANR1; DNA binding / transcription factor [Arabidopsis thaliana]gb|AAD25638.1| putative MADS-box protein ANR1 [Arabidopsis thaliana] gb|AAO64796.1| At2g14210 [Arabidopsis thaliana]	234	8E-23
CD651663	1.01E-02	Mo17<B73=F1	1.37	10	ns		
CB334593	1.01E-02	B73<F1=Mo17	1.63	3	>ref|XP_463936.1| putative NADPH-dependent mannose 6-phosphate reductase [Oryzasativa (japonica cultivar-group)] dbj|BAD07953.1| putative NADPH-dependent mannose 6-phosphate reductase [Oryza sativa (japonica cultivar-group)]	319	6E-59
					>ref|XP 506697.1| PREDICTED P0575F10.14 gene product [Oryza sativa (japonicacultivar-group)]	375	6E-59
					>gb|AAP80625.1| NADPH-dependent mannose 6-phosphate reductase [Triticum aestivum]	274	2E-57
					>gb|AAM64779.1| putative NADPH dependent mannose 6-phosphate reductase [Arabidopsisthaliana]	309	2E-55
					>ref|NP_179721.1| oxidoreductase [Arabidopsis thaliana]gb|AAM13238.1| putative NADPH-dependent mannose 6-phosphate reductase [Arabidopsis thaliana] gb|AAM15409.1| putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana] gb|AAD23673.1| putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana] gb|AAN65130.1| putative NADPH-dependent mannose 6-phosphate reductase [Arabidopsis thaliana]	309	2E-55
BM350305	1.01E-02	Mo17<F1	1.36	11	ns		
DV495001	1.01E-02	Mo17<B73=F1	1.29	11	>ref|NP_910584.1| EST AU082567(S21715) corresponds to a region of the predictedgene.~Similar to S.tuberosum ubiquinol cytochrome c reductase. (X79275) [Oryza sativa (japonica cultivar-group)] ref|NP_910574.1| EST AU082567(S21715) corresponds to a region of the predicted gene.~Similar to S.tuberosum ubiquinol--cytochrome c reductase. (X79275) [Oryza sativa (japonica cultivar-group)] dbj|BAA95831.1| putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein [Oryza sativa (japonica cultivar-group)] dbj|BAA95821.1| putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein [Oryza sativa (japonica cultivar-group)]	72	5E-34
					>ref|NP_187697.1| ubiquinol-cytochrome-c reductase [Arabidopsis thaliana]gb|AAF19563.1| putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein (QP-C) [Arabidopsis thaliana] gb|AAN17451.1| putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein (QP-C) [Arabidopsis thaliana] gb|AAP21315.1| At3g10860 [Arabidopsis thaliana] gb|AAM64437.1| putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein (QP-C) [Arabidopsis thaliana]	72	7E-28
					>ref|NP_196156.1| ubiquinol-cytochrome-c reductase [Arabidopsis thaliana]gb|AAQ65099.1| At5g05370 [Arabidopsis thaliana] dbj|BAB09980.1| ubiquinol-cytochrome C reductase complex ubiquinone-binding protein [Arabidopsis thaliana]	72	2E-26
					>emb|CAA55862.1| ubiquinol--cytochrome c reductase [Solanum tuberosum]sp|P46269|UCRQ_SOLTU Ubiquinol-cytochrome c reductase complex ubiquinone-binding protein QP-C (Ubiquinol-cytochrome c reductase complex 8.2 kDa protein) prf||2107179A cytochrome c oxidase:SUBUNIT=8.2kD	72	4E-26
					>gb|AAP80673.1| cytochrome reductase [Triticum aestivum]	115	4E-12
DV551022	1.01E-02	B73<F1=Mo17	1.39	2	>ref|NP_180259.1| ATPase, coupled to transmembrane movement of substances [Arabidopsisthaliana] tpg|DAA00872.1| TPA: TPA_exp: PDR4 ABC transporter [Arabidopsis thaliana] gb|AAC32236.1| putative ABC transporter [Arabidopsis thaliana]	1420	4E-35
					>ref|XP_482141.1| putative PDR-like ABC transporter [Oryza sativa (japonicacultivar-group)] dbj|BAD05827.1| putative PDR-like ABC transporter [Oryza sativa (japonica cultivar-group)]	1489	2E-33
					>emb|CAC40990.1| ABC1 protein [Nicotiana plumbaginifolia]	1436	1E-32
					>dbj|BAD07483.1| PDR-type ABC transporter 1 [Nicotiana tabacum]	1434	6E-32
					>dbj|BAB92011.1| pleiotropic drug resistance like protein [Nicotiana tabacum]	1434	6E-32
BM074151	1.01E-02	Mo17<B73=F1	1.43	10	>gb|AAW56866.1| unknown protein [Oryza sativa (japonica cultivar-group)]	254	1E-21
					>ref|NP 973950.1| N-acetyltransferase [Arabidopsis thaliana]gb|AAP22085.1| nuclear shuttle interacting protein [Arabidopsis thaliana]	258	1E-16

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15 % FDR)

<table>
<thead>
<tr><th>GenBank accession no.</th><th>Overall P value</th><th>Significant pattern</th><th>Fold change†</th><th>Sector‡</th><th>BLAST annotation*</th><th>Score</th><th>E value</th></tr>
</thead>
<tbody>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP 564387.1| N-acetyltransferase [Arabidopsis thaliana]gb|AAM64262.1| unknown [Arabidopsis thaliana]</td><td>257</td><td>1E-16</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAG50796.1| unknown protein [Arabidopsis thaliana]</td><td>230</td><td>1E-16</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|YP 476759.1| acetyltransferase, GNAT family [Cyanobacteria bacterium YellowstoneB-Prime]</td><td>174</td><td>2E-13</td></tr>
<tr><td>DV549485</td><td>1.02E-02</td><td>B73=F1<Mo17</td><td>1.64</td><td>4</td><td>>ref|NP_922302.1| kinesin-like protein [Oryza sativa (japonica cultivar-group)]gb|AAG13527.1| kinesin-like protein [Oryza sativa (japonica cultivar-group)] gb|AAP54589.1| kinesin-like protein [Oryza sativa (japonica cultivar-group)]</td><td>859</td><td>2E-10</td></tr>
<tr><td>CA829998</td><td>1.02E-02</td><td>Mo17<B73=F1</td><td>1.33</td><td>11</td><td>>gb|AAC08009.1| DnaJ-related protein ZMDJ1 [Zea mays]</td><td>419</td><td>1E-30</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAX95135.1| DnaJ protein, putative [Oryza sativa (japonica cultivar-group)]</td><td>416</td><td>2E-30</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAU89194.1| DnaJ protein, putative [Oryza sativa (japonica cultivar-group)]gb|AAO72551.1| DNAJ-like protein [Oryza sativa (japonica cultivar-group)]</td><td>417</td><td>2E-30</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA47925.1| cs DnaJ-1 [Cucumis sativus]sp|Q04960|DNJH CUCSA DnaJ protein homolog (DNAJ-1)</td><td>413</td><td>2E-28</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA63965.1| DnaJ protein [Solanum tuberosum]</td><td>419</td><td>4E-28</td></tr>
<tr><td>CD058646</td><td>1.04E-02</td><td>Mo17<B73=F1</td><td>1.23</td><td>10</td><td>>ref|XP 475776.1| putative GTPase [Oryza sativa (japonica cultivar-group)]gb|AAT39219.1| putative GTPase [Oryza sativa (japonica cultivar-group)]</td><td>197</td><td>4E-29</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAD87568.1| putative rab7 protein [Oryza sativa (japonica cultivar-group)]</td><td>207</td><td>7E-24</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP 916633.1| putative RAB7A protein (GTP-binding protein) [Oryza sativa(japonica cultivar-group)]</td><td>198</td><td>7E-24</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA98168.1| RAB7A [Lotus corniculatus var. japonicus]</td><td>205</td><td>3E-23</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>sp|Q41640|RAB7 VIGAC Ras-related protein Rab7gb|AAA34242.1| Rab7p</td><td>206</td><td>2E-22</td></tr>
<tr><td>CD573374</td><td>1.05E-02</td><td>Mo17<B73=F1</td><td>1.25</td><td>10</td><td>>ref|XP_468756.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)] ref|XP_468752.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] gb|AAP20855.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] gb|AAP20842.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] sp|P40978|RS19 ORYSA 40S ribosomal protein S19</td><td>146</td><td>9E-72</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAW34237.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]</td><td>144</td><td>5E-69</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAW34240.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]</td><td>122</td><td>5E-64</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|ABB87116.1| 40S ribosomal protein S19-like [Solanum tuberosum]</td><td>143</td><td>5E-58</td></tr>
<tr><td>DV621401</td><td>1.05E-02</td><td>B73=F1<Mo17</td><td>1.36</td><td>4</td><td>>gb|AAT85043.1| expressed protein [Oryza sativa (japonica cultivar-group)]gb|AAR87334.1| expressed protein [Oryza sativa (japonica cultivar-group)]</td><td>522</td><td>1E-54</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_476441.1| PRLI-interacting factor G-like protein [Oryza sativa (japonicacultivar-group)] dbj|BAC83795.1| PRLI-interacting factor G-like protein [Oryza sativa (japonica cultivar-group)]</td><td>527</td><td>2E-49</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_190647.1| unknown protein [Arabidopsis thaliana]emb|CAB42907.1| putative protein [Arabidopsis thaliana] gb|AAO50646.1| unknown protein [Arabidopsis thaliana] gb|AAO22779.1| unknown protein [Arabidopsis thaliana]</td><td>520</td><td>2E-45</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_473629.1| OSJNBa0011J08.25 [Oryza sativa (japonica cultivar-group)]emb|CAE03270.1| OSJNBa0011J08.25 [Oryza sativa (japonica cultivar-group)] emb|CAD41158.2| OSJNBa0064M23.3 [Oryza sativa (japonica cultivar-group)]</td><td>533</td><td>2E-25</td></tr>
<tr><td>CB351548</td><td>1.05E-02</td><td>Mo17<B73=F1</td><td>1.18</td><td>11</td><td>>gb|ABA93723.1| ribosomal protein S7 [Oryza sativa (japonica cultivar-group)]</td><td>199</td><td>3E-72</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_908322.1| putative 40S ribosomal protein S5 [Oryza sativa (japonicacultivar-group)] dbj|BAB64234.1| putative 40S ribosomal protein S5 [Oryza sativa (japonica cultivar-group)] dbj|BAB62621.1| putative 40S ribosomal protein S5 [Oryza sativa (japonica cultivar-group)]</td><td>200</td><td>1E-70</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_187800.1| ATRPS5A (RIBOSOMAL PROTEIN 5A); structural constituent of ribosome[Arabidopsis thaliana] ref|NP_850564.1| ATRPS5A (RIBOSOMAL PROTEIN 5A); structural constituent of ribosome [Arabidopsis thaliana] gb|AAF23210.1| putative 40S ribosomal protein S5 [Arabidopsis thaliana] gb|AAM14315.1| putative 40S ribosomal protein S5 [Arabidopsis thaliana] gb|AAK76520.1| putative 40S ribosomal protein S5 [Arabidopsis thaliana] gb|AAM64502.1| 40S ribosomal protein S5, putative [Arabidopsis thaliana] dbj|BAB03103.1| 40S ribosomal protein S5-like [Arabidopsis thaliana] sp|P51427|RS5B ARATH 40S ribosomal protein S5-2</td><td>207</td><td>3E-67</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA06491.1| 40S ribosomal protein S5 [Cicer arietinum]sp|O65731|RS5 CICAR 40S ribosomal protein S5</td><td>197</td><td>7E-67</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_181264.1| ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome[Arabidopsis thaliana] ref|NP_001031502.1| ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome [Arabidopsis thaliana] gb|AAC98068.1| 40S ribosomal protein S5 [Arabidopsis thaliana] gb|AAM10231.1| 40S ribosomal protein S5 [Arabidopsis thaliana] gb|AAL24331.1| 40S ribosomal protein S5 [Arabidopsis thaliana] sp|Q9ZUT9|RS5A_ARATH 40S ribosomal protein S5-1</td><td>207</td><td>9E-67</td></tr>
<tr><td>CB334480</td><td>1.06E-02</td><td>Mo17<B73=F1</td><td>1.34</td><td>10</td><td>ns</td><td></td><td></td></tr>
<tr><td>BM073216</td><td>1.06E-02</td><td>F1=Mo17<B73</td><td>2.06</td><td>9</td><td>>ref|XP 468825.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]gb|AAS07307.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]</td><td>235</td><td>2E-13</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAT93896.1| unknown protein [Oryza sativa (japonica cultivar-group)]</td><td>446</td><td>5E-12</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAD88282.1| ribosomal protein-like [Oryza sativa (japonica cultivar-group)]dbj|BAD88086.1| ribosomal protein-like [Oryza sativa (japonica cultivar-group)]</td><td>301</td><td>5E-12</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_550394.1| ribosomal protein -like [Oryza sativa (japonica cultivar-group)]dbj|BAD68081.1| ribosomal protein -like [Oryza sativa (japonica cultivar-group)] dbj|BAD67842.1| ribosomal protein -like [Oryza sativa (japonica cultivar-group)]</td><td>428</td><td>5E-12</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP 450358.1| ribosomal protein-like [Oryza sativa (japonica cultivar-group)]dbj|BAD23759.1| ribosomal protein-like [Oryza sativa (japonica cultivar-group)]</td><td>916</td><td>5E-12</td></tr>
<tr><td>BM335915</td><td>1.06E-02</td><td>B73<F1=Mo17</td><td>1.39</td><td>3</td><td>ns</td><td></td><td></td></tr>
<tr><td>BM347523</td><td>1.06E-02</td><td>F1=Mo17<B73</td><td>1.52</td><td>8</td><td>ns</td><td></td><td></td></tr>
<tr><td>CB329767</td><td>1.06E-02</td><td>Mo17<B73=F1</td><td>1.39</td><td>10</td><td>>ref|XP 481131.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAC99929.1| unknown protein [Oryza sativa (japonica cultivar-group)]</td><td>97</td><td>3E-13</td></tr>
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</table>

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_563992.1| unknown protein [Arabidopsis thaliana]gb|AAL34239.1| unknown protein [Arabidopsis thaliana] gb|AAK44064.1| unknown protein [Arabidopsis thaliana] gb|AAM64726.1| unknown [Arabidopsis thaliana]	92	5E-7
					>gb|AAF18514.1| ESTs gb|T41688, gb|AI992698, gb|AA394805 come from this gene.[Arabidopsis thaliana]	123	5E-7
					>ref|NP_565217.1| unknown protein [Arabidopsis thaliana]gb|AAL31128.1| At1g79660/F20B17_9 [Arabidopsis thaliana] gb|AAK97713.1| At1g79660/F20B17_9 [Arabidopsis thaliana] gb|AAF68107.1| F20B17.9 [Arabidopsis thaliana]	93	2E-6
DV491868	1.06E-02	Mo17<B73	1.65	10	>gb|ABA94623.1| Zinc finger, C3HC4 type, putative [Oryza sativa (japonicacultivar-group)]	325	5E-39
					>ref|NP_179802.2| protein binding / ubiquitin-protein ligase/ zinc ion binding[Arabidopsis thaliana] gb|AAO50515.1| unknown protein [Arabidopsis thaliana] gb|AAO42065.1| unknown protein [Arabidopsis thaliana]	324	4E-32
					>gb|AAD25813.1| hypothetical protein [Arabidopsis thaliana]	252	1E-24
					>gb|AAM65602.1| unknown [Arabidopsis thaliana]	320	2E-13
					>gb|AAB65494.1| hypothetical protein; 51018-49636 [Arabidopsis thaliana]	281	2E-13
DV489540	1.07E-02	B73=F1<Mo17	1.38	5	>ref|XP_475676.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAT44270.1| unknown protein [Oryza sativa (japonica cultivar-group)]	374	2E-50
					>gb|ABA99826.1| DNA binding protein, putative [Oryza sativa (japonicacultivar-group)]	407	2E-18
					>gb|AAU10684.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	400	2E-6
					>ref|XP_472829.1| OSJNBa0089K21.9 [Oryza sativa (japonica cultivar-group)]emb|CAE03055.2| OSJNBa0089K21.9 [Oryza sativa (japonica cultivar-group)]	461	2E-6
					>ref|NP_921846.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]gb|AAM93719.1| hypothetical protein [Oryza sativa (japonica cultivar-group)] gb|AAP54133.1| transposon protein, putative, CACTA, En/Spm sub-class [Oryza sativa (japonica cultivar-group)]	481	6E-6
BM349922	1.07E-02	B73<F1=Mo17	1.46	3	ns		
DV621170	1.08E-02	B73=F1<Mo17	1.41	4	>gb|AAP80862.1| Emr1 [Triticum aestivum]	304	3E-11
					>gb|ABA96655.1| Emr1 [Oryza sativa (japonica cultivar-group)]	609	2E-9
					>gb|ABA96656.1| Emr1 [Oryza sativa (japonica cultivar-group)]	682	6E-8
DV621981	1.08E-02	B73<Mo17	1.24	3	>ref|XP_474268.1| OSJNBa0043A12.5 [Oryza sativa (japonica cultivar-group)]emb|CAE02800.1| OSJNBa0043A12.5 [Oryza sativa (japonica cultivar-group)]	484	2E-46
					>ref|NP_568836.2| ATARP8 (ACTIN-RELATED PROTEIN 8); structural constituent ofcytoskeleton [Arabidopsis thaliana] gb|AAM53248.1| actin-related protein 8B [Arabidopsis thaliana] tpg|DAA00031.1| TPA: actin-related protein 8B; AtARP8B [Arabidopsis thaliana] dbj|BAB09300.1| unnamed protein product [Arabidopsis thaliana]	471	4E-32
					>gb|AAO49331.1| actin [Oxyrrhis marina]	244	6E-8
					>ref|XP_656610.1| actin [Entamoeba histolytica HM-1:IMSS]gb|EAL51224.1| actin [Entamoeba histolytica HM-1:IMSS]	294	1E-7
					>gb|AAA29085.1| actin protein	373	1E-7
CB885939	1.08E-02	B73<Mo17	1.41	3	>emb|CAA69075.1| S-adenosylmethionine decarboxylase [Zea mays]sp|O24575|DCAM_MAIZE S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain]	400	2E-66
					>emb|CAA58762.1| S-adenosylmethionine decarboxylase [Triticum turgidum subsp. durumx Hordeum chilense] sp|Q42829|DCAM_HORCH S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain]	393	3E-40
					>gb|AAD17232.1| S-adenosylmethionine decarboxylase precursor [Triticum aestivum]	392	2E-39
					>ref|XP_473046.1| OSJNBa0067K08.23 [Oryza sativa (japonica cultivar-group)]emb|CAA69074.2| S-adenosylmethionine decarboxylase [Oryza sativa (japonica cultivar-group)] emb|CAD41242.2| OSJNBa0067K08.23 [Oryza sativa (japonica cultivar-group)] sp|O24215|DCAM_ORYSA S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain]	398	7E-39
					>emb|CAD41510.3| OSJNBa0029H02.4 [Oryza sativa (japonica cultivar-group)]	450	7E-39
CD568840	1.09E-02	B73<F1=Mo17	1.45	3	>ref|XP_477068.1| putative DD1A protein [Oryza sativa (japonica cultivar-group)]dbj|BAC83228.1| putative DD1A protein [Oryza sativa (japonica cultivar-group)]	408	4E-29
					>ref|XP_478799.1| putative carboxyl-terminal proteinase [Oryza sativa (japonicacultivar-group)] ref|XP_507376.1| PREDICTED OJ1699_E05.18 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_506420.1| PREDICTED OJ1699_E05.18 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC83152.1| putative carboxyl-terminal proteinase [Oryza sativa (japonica cultivar-group)]	430	8E-28
					>ref|XP_470030.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAP21432.1| unknown protein [Oryza sativa (japonica cultivar-group)]	410	5E-27
					>gb|AAW38991.1| At1g55360 [Arabidopsis thaliana]ref|NP_175933.1| unknown protein [Arabidopsis thaliana] gb|AAN60240.1| unknown [Arabidopsis thaliana] gb|AAG51562.1| unknown protein; 9920-11896 [Arabidopsis thaliana]	422	9E-27
					>gb|AAM65243.1| putative carboxyl-terminal peptidase [Arabidopsis thaliana]	419	5E-26
DV490125	1.09E-02	F1=Mo17<B73	1.54	9	>gb|ABA94173.1| Maf-like protein [Oryza sativa (japonica cultivar-group)]	209	8E-26
					>gb|ABA94182.1| Maf-like protein [Oryza sativa (japonica cultivar-group)]	211	3E-25
					>ref|XP_470606.1| Unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAO06956.1| Unknown protein [Oryza sativa (japonica cultivar-group)] gb|AAO00680.1| Unknown protein [Oryza sativa (japonica cultivar-group)]	359	1E-17
					>gb|AAM91161.1| unknown protein [Arabidopsis thaliana]gb|AAM13078.1| unknown protein [Arabidopsis thaliana]	123	1E-15
					>dbj|BAB10633.1| unnamed protein product [Arabidopsis thaliana]	208	1E-15
DV495000	1.09E-02	Mo17<B73=F1	1.62	11	ns		

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
DV943069	1.10E-02	F1<Mo17	1.67	5	>dbj|BAD28046.1| putative Helicase SKI2W [Oryza sativa (japonica cultivar-group)]	1281	e-107
					>emb|CAB61942.1| putative helicase [Arabidopsis thaliana]	1347	2E-93
					>emb|CAB51169.1| putative helicase, fragment [Arabidopsis thaliana]	705	2E-93
					>ref|NP 190280.2| ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding[Arabidopsis thaliana]	1338	2E-93
					>ref|XP_642686.1| hypothetical protein DDB0169070 [Dictyostelium discoideum]gb|AAO51181.1| similar to putative DEAD/DEAH box helicase [Schizosaccharomyces pombe] [Dictyostelium discoideum] gb|EAL68791.1| hypothetical protein DDB0169070 [Dictyostelium discoideum]	1378	1E-54
CB815632	1.10E-02	Mo17<B73=F1	2.38	10	>gb|AAX92995.1| hypothetical protein LOC_Os11g06760 [Oryza sativa (japonicacultivar-group)] gb|ABA91587.1| hypothetical protein LOC_Os11g06760 [Oryza sativa (japonica cultivar-group)]	302	4E-61
					>ref|XP 472494.1| OSJNBa0042L16.4 [Oryza sativa (japonica cultivar-group)]emb|CAD41015.3| OSJNBa0042L16.6 [Oryza sativa (japonica cultivar-group)]	262	7E-50
					>dbj|BAD46594.1| unknown protein [Oryza sativa (japonica cultivar-group)]	269	1E-48
					>dbj|BAC79194.1| chloroplast nucleoid DNA-binding protein -like protein [Oryzasativa (japonica cultivar-group)]	732	1E-48
					>dbj|BAE71254.1| hypothetical protein [Trifolium pratense]	248	7E-48
DV551377	1.10E-02	Mo17<B73=F1	1.33	10	>ref|NP 912417.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]gb|AAP06860.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	117	4E-16
					>ref|NP_192563.2| unknown protein [Arabidopsis thaliana]gb|AAN15541.1| unknown protein [Arabidopsis thaliana] gb|AAL62398.1| unknown protein [Arabidopsis thaliana]	113	2E-9
CB833624	1.10E-02	Mo17<B73=F1	1.37	10	ns		
CD485180	1.11E-02	B73<F1=Mo17	1.3	3	>gb|AAX95841.1| probable zinc finger protein - alfalfa (fragment) [Oryza sativa(japonica cultivar-group)] gb|AAX92933.1| probable zinc finger protein - alfalfa (fragment) [Oryza sativa (japonica cultivar-group)] gb|ABA92392.1| zinc finger protein, putative [Oryza sativa (japonica cultivar-group)]	264	4E-48
					>gb|AAV25644.1| putative nucleic acid binding protein [Oryza sativa (japonicacultivar-group)]	258	5E-47
					>ref|NP_915084.1| nucleic acid binding protein [Oryza sativa (japonicacultivar-group)] dbj|BAD82135.1| nucleic acid binding protein [Oryza sativa (japonica cultivar-group)] dbj|BAB92630.1| nucleic acid binding protein [Oryza sativa (japonica cultivar-group)] gb|AAC98969.1| nucleic acid binding protein [Oryza sativa]	272	3E-46
					>gb|AAC98962.1| nucleic acid binding protein [Oryza sativa]	271	3E-46
					>ref|XP_466276.1| putative nucleic acid binding protein [Oryza sativa (japonicacultivar-group)] ref|XP_506831.1| PREDICTED OJ1712_E04.22 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD15814.1| putative nucleic acid binding protein [Oryza sativa (japonica cultivar-group)] dbj|BAD15587.1| putative nucleic acid binding protein [Oryza sativa (japonica cultivar-group)]	267	1E-45
CD001840	1.11E-02	F1=Mo17<B73	1.24	8	>ref|XP_483065.1| putative heat-shock protein [Oryza sativa (japonicacultivar-group)] dbj|BAD09415.1| putative heat-shock protein [Oryza sativa (japonica cultivar-group)]	785	e-101
					>emb|CAA82945.1| heat-shock protein [Secale cereale]	781	3E-98
					>gb|AAM19795.1| At2g04030/F3C11.14 [Arabidopsis thaliana]	780	5E-95
					>ref|NP_178487.1| CR88; ATP binding / unfolded protein binding [Arabidopsis thaliana]gb|AAD32922.1| putative heat shock protein [Arabidopsis thaliana] gb|AAL32008.1| At2g04030/F3C11.14 [Arabidopsis thaliana] gb|AAK96633.1| At2g04030/F3C11.14 [Arabidopsis thaliana] gb|AAN72245.1| At2g04030/F3C11.14 [Arabidopsis thaliana]	780	5E-95
					>emb|CAA72515.1| heat shock protein [Arabidopsis thaliana]	768	1E-92
CD651489	1.12E-02	B73<F1=Mo17	1.3	3	>emb|CAA05772.1| Ubiquitin carrier protein [Zea mays]	169	3E-33
					>ref|XP_475366.1| putative ubiquitin-conjugating enzyme E2 [Oryza sativa (japonicacultivar-group)] gb|AAT39166.1| putative ubiquitin-conjugating enzyme E2 [Oryza sativa (japonica cultivar-group)]	169	7E-33
					>gb|AAC12662.1| ubiquitin-conjugating enzyme protein E2 [Zea mays]	169	7E-33
					>ref|NP_915413.1| putative Ubiquitin carrier protein UBC7 [Oryza sativa (japonicacultivar-group)] dbj|BAB93210.1| putative ubiquitin carrier protein UBC7 [Oryza sativa (japonica cultivar-group)] dbj|BAB67890.1| putative ubiquitin carrier protein UBC7 [Oryza sativa (japonica cultivar-group)]	169	1E-32
					>sp|P25868|UBC7 WHEAT Ubiquitin-conjugating enzyme E2 7 (Ubiquitin-protein ligase 7)(Ubiquitin carrier protein 7)	168	1E-30
CB280852	1.12E-02	Mo17<B73	1.35	10	>ref|XP_482897.1| putative zinc-finger protein [Oryza sativa (japonicacultivar-group)] dbj|BAD09868.1| putative zinc-finger protein [Oryza sativa (japonica cultivar group)] dbj|BAD09355.1| putative zinc-finger protein [Oryza sativa (japonica cultivar-group)]	501	3E-97
					>ref|NP 198550.3| protein binding / zinc ion binding [Arabidopsis thaliana]	493	2E-69
					>gb|AAM62849.1| zinc finger protein-like [Arabidopsis thaliana]	493	9E-69
					>gb|AAO42806.1| At5g22480 [Arabidopsis thaliana]	493	9E-69
					>ref|NP 197640.1| protein binding / zinc ion binding [Arabidopsis thaliana]	493	9E-69
CB885428	1.12E-02	Mo17<F1	1.33	11	>ref|XP_475493.1| putative protein translation factor Sui1 [Oryza sativa (japonicacultivar-group)] gb|AAT44286.1| putative protein translation factor Sui1 [Oryza sativa (japonica cultivar-group)]	115	6E-59
					>dbj|BAD53005.1| putative translation initiation factor [Oryza sativa (japonicacultivar-group)]	115	3E-56
					>ref|XP_478516.1| translational initiation factor eIF1 [Oryza sativa (japonicacultivar-group)] emb|CAA36190.1| GOS2 [Oryza sativa (indica cultivar-group)] gb|AAK56324.1| translational initiation factor eIF1 [Porteresia coarctata] dbj|BAC45143.1| translational initiation factor eIF1 [Oryza sativa (japonica cultivar-group)] gb|AAC67556.1| translation initiation factor [Oryza sativa] pir||S21636 GOS2 protein - rice sp|P33278|SUI1_ORYSA PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)	115	1E-54

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>emb|CAB61837.1| putative translation initiation factor eIF-1 [Sporobolusstapfianus] sp|Q9SM41|SUI1 SPOST Protein translation factor SUI1 homolog	115	3E-54
					>sp|P56330|SUI1 MAIZE Protein translation factor SUI1 homolog (GOS2 protein)gb|AAB88615.1| translation initiation factor; GOS2 [Zea mays]	115	5E-54
CB411033	1.12E-02	Mo17<B73=F1	1.29	11	>gb|AAV36518.1| vacuolar ATPase subunit c isoform [Pennisetum glaucum]gb|AAL08022.1| vacuolar H+-ATPase 16 kDa proteolipid subunit c [Pennisetum glaucum]	165	7E-36
					>gb|AAK91135.1| V-ATPase subunit c [Porteresia coarctata]gb|ABA95923.1| V-type ATPase, C subunit [Oryza sativa (japonica cultivar-group)]	165	7E-36
					>gb|AAX93004.1| V-type ATPase, C subunit, putative [Oryza sativa (japonicacultivar-group)] sp|Q40635|VATL_ORYSA Vacuolar ATP synthase 16 kDa proteolipid subunit gb|ABA91617.1| V-type ATPase, C subunit, putative [Oryza sativa (japonica cultivar-group)] gb|AAA68175.1| H+-ATPase	165	7E-36
					>gb|AAU44174.1| putative vacuolar ATP synthase 16 kDa proteolipid subunit [Oryzasativa (japonica cultivar-group)]	166	2E-35
					>ref|XP_466150.1| putative Vacuolar ATP synthase 16 kDa proteolipid subunit [Oryzasativa (japonica cultivar-group)] dbj|BAD33262.1| putative Vacuolar ATP synthase 16 kDa proteolipid subunit [Oryza sativa (japonica cultivar-group)] dbj|BAD16200.1| putative Vacuolar ATP synthase 16 kDa proteolipid subunit [Oryza sativa (japonica cultivar-group)]	167	2E-35
BM073418	1.12E-02	Mo17<B73=F1	1.63	11	>ref|XP_473347.1| OSJNBa0091D06.25 [Oryza sativa (japonica cultivar-group)]emb|CAD41610.1| OSJNBa0091D06.25 [Oryza sativa (japonica cultivar-group)] emb|CAE02779.1| OSJNBa0011L07.3 [Oryza sativa (japonica cultivar-group)]	220	2E-62
					>ref|NP 001031804.1| unknown protein [Arabidopsis thaliana]	217	4E-49
					>emb|CAB80457.1| putative protein [Arabidopsis thaliana]emb|CAB37532.1| putative protein [Arabidopsis thaliana]	673	1E-44
					>ref|ZP 00107433.1| hypothetical protein Npun02006142 [Nostoc punctiforme PCC 73102]	121	1E-23
					>ref|ZP_00517581.1| hypothetical protein CwatDRAFT_2236 [Crocosphaera watsonii WH 8501]gb|EAM49340.1| hypothetical protein CwatDRAFT_2236 [Crocosphaera watsonii WH 8501]	119	3E-23
CB604298	1.12E-02	F1=Mo17<B73	1.19	9	>ref|XP_479167.1| putative 40S ribosomal protein [Oryza sativa (japonicacultivar-group)] ref|XP_507392.1| PREDICTED B1056G08.113 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_507391.1| PREDICTED B1056G08.113 gene product [Oryza sativa (japonica cultivar-group)] ref|XP_506471.1| PREDICTED B1056G08.113 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC79991.1| putative 40S ribosomal protein [Oryza sativa (japonica cultivar-group)]	305	1E-38
					>ref|XP 470555.1| Putative 40S Ribosomal protein [Oryza sativa]gb|AAK92638.1| Putative 40S Ribosomal protein [Oryza sativa]	305	7E-38
					>sp|O22518|RSSA SOYBN 40S ribosomal protein SA (p40)gb|AAB82659.1| ribosome-associated protein p40 [Glycine max]	310	7E-35
					>ref|NP 850515.1| RPSAB; structural constituent of ribosome [Arabidopsis thaliana]	332	6E-32
					>ref|NP_187128.1| RPSAB; structural constituent of ribosome [Arabidopsis thaliana]gb|AAF04903.1| putative 40S ribosomal protein [Arabidopsis thaliana] sp|Q8H173|RSSAB ARATH 40S ribosomal protein SA-2 (p40 protein homolog) gb|AAB67866.1| p40 protein homolog [Arabidopsis thaliana]	280	6E-32
CB334219	1.12E-02	Mo17<B73	1.21	10	>ref|XP_483755.1| putative 60S ribosomal protein L10A (RPL10aC) [Oryza sativa(japonica cultivar-group)] dbj|BAD09090.1| putative 60S ribosomal protein L10A (RPL10aC) [Oryza sativa (japonica cultivar-group)]	216	3E-57
					>dbj|BAD73824.1| putative Csa-19 [Oryza sativa (japonica cultivar-group)]	133	2E-56
					>ref|XP_483761.1| putative 60S ribosomal protein L10A (RPL10aC) [Oryza sativa(japonica cultivar-group)] dbj|BAD13131.1| putative 60S ribosomal protein L10A (RPL10aC) [Oryza sativa (japonica cultivar-group)]	155	2E-56
					>dbj|BAD28853.1| putative ribosomal protein L10a [Oryza sativa (japonicacultivar-group)]	216	9E-55
					>gb|AAW50982.1| ribosomal protein L10A [Triticum aestivum]	216	6E-54
BM348729	1.12E-02	Mo17<B73	3.98	10	ns		
CB380945	1.14E-02	Mo17<B73=F1	1.26	10	>dbj|BAD29382.1| putative Ste24p [Oryza sativa (japonica cultivar-group)]	425	5E-44
					>gb|AAK39514.1| CaaX processing zinc-metallo endoprotease [Arabidopsis thaliana]	424	2E-33
					>ref|NP_567212.1| ATSTE24 [Arabidopsis thaliana]gb|AAL90896.1| AT4g01320/F2N1_21 [Arabidopsis thaliana] gb|AAP21163.1| At4g01320/F2N1_21 [Arabidopsis thaliana]	424	2E-33
					>gb|AAL07084.1| putative CAAX prenyl protease [Arabidopsis thaliana]	424	3E-33
					>emb|CAB80941.1| putative CAAX prenyl protease [Arabidopsis thaliana]	459	5E-28
DV621482	1.15E-02	B73<F1=Mo17	1.21	3	>gb|ABA97248.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]gb|ABB51090.1| mannose-specific jacalin-related lectin [Oryza sativa (japonica cultivar-group)]	306	9E-9
					>gb|AAA87041.1| putative 32.6 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72096.1| 32 kDa protein [Hordeum vulgare]	304	2E-8
					>gb|AAA87042.1| putative 32.7 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72097.1| 32 kDa protein [Hordeum vulgare]	304	3E-8
					>gb|AAR20919.1| jasmonate-induced protein [Triticum aestivum]	304	2E-7
					>ref|NP_909490.1| putative beta-glucosidase-aggregating factor [Oryza sativa]gb|AAK55474.1| putative beta-glucosidase-aggregating factor [Oryza sativa (japonica cultivar-group)]	147	2E-7
DV551153	1.15E-02	B73=F1<Mo17	1.23	4	>ref|XP_469569.1| actin [Oryza sativa (japonica cultivar-group)]gb|AAO38821.1| actin [Oryza sativa (japonica cultivar-group)] dbj|BAC76319.1| actin [Oryza sativa (japonica cultivar-group)] sp|P13362|ACT1 ORYSA Actin-1	377	e-132
					>emb|CAA55923.1| actin [Sorghum bicolor]sp|P53504|ACT1 SORBI Actin-1	377	e-132
					>emb|CAA33874.1| actin [Oryza sativa (indica cultivar-group)]	377	e-132
					>gb|AAF40438.1| actin 1 [Avena nuda]	377	e-130

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>emb|CAA34356.1| unnamed protein product [Oryza sativa (indica cultivar-group)]	377	e-130
CB381628	1.16E-02	Mo17<B73=F1	1.3	10	ns		
DV492987	1.16E-02	B73<F1=Mo17	1.3	3	>gb|AAT93852.1| putative GH1 protein or auxin-regulated protein [Oryza sativa(japonica cultivar-group)] gb|AAS98482.1| putative GH1 protein or auxin regulated protein [Oryza sativa (japonica cultivar-group)]	257	2E-30
					>dbj|BAD81331.1| putative aux/IAA protein [Oryza sativa (japonica cultivar-group)]dbj|BAD81283.1| putative aux/IAA protein [Oryza sativa (japonica cultivar-group)]	263	6E-27
					>ref|NP 913504.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]	281	6E-27
					>gb|AAM12952.1| auxin-regulated protein [Zinnia elegans]	351	2E-22
					>dbj|BAD61890.1| putative auxin-regulated protein [Oryza sativa (japonicacultivar-group)]	266	2E-22
DV622265	1.17E-02	B73=Mo17<F1	1.32	12	group)]	181	5E-81
					>ref|NP_912888.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]dbj|BAA92519.1| putative ADP-ribosylation factor [Oryza sativa (japonica cultivar-group)] dbj|BAA90347.1| putative ADP-ribosylation factor [Oryza sativa (japonica cultivar-group)]	181	5E-81
					>ref|NP_911519.1| ADP-ribosylation factor 1 [Oryza sativa (japonica cultivar-group)]ref|NP_911517.1| ADP-ribosylation factor 1 [Oryza sativa (japonica cultivar-group)] dbj|BAD31195.1| ADP-ribosylation factor 1 [Oryza sativa (japonica cultivar-group)] dbj|BAC45192.1| ADP-ribosylation factor 1 [Oryza sativa (japonica cultivar-group)] dbj|BAC06914.1| ADP-ribosylation factor 1 [Oryza sativa (japonica cultivar-group)] gb|AAB65432.1| ADP-ribosylation factor 1 [Oryza sativa]	181	5E-81
					>gb|AAT08648.1| ADP-ribosylation factor [Hyacinthus orientalis]	199	1E-80
					>ref|NP 172533.2| GTP binding [Arabidopsis thaliana]gb|AAT70455.1| At1g10630 [Arabidopsis thaliana] gb|AAT41759.1| At1g10630 [Arabidopsis thaliana]	181	1E-80
DV622300	1.17E-02	B73<Mo17	1.42	4	>ref|XP_479496.1| putative acyl-CoA dehydrogenase [Oryza sativa (japonicacultivar-group)] dbj|BAD31978.1| putative acyl-CoA dehydrogenase [Oryza sativa (japonica cultivar-group)] dbj|BAC83542.1| putative acyl-CoA dehydrogenase [Oryza sativa (japonica cultivar-group)]	831	3E-83
					>gb|AAF63817.1| acetyl-coA dehydrogenase, putative [Arabidopsis thaliana]	423	3E-73
					>dbj|BAD43785.1| unnamed protein product [Arabidopsis thaliana]	824	3E-73
					>ref|NP_187337.2| ATP binding / acyl-CoA dehydrogenase/ oxidoreductase/ protein kinase[Arabidopsis thaliana] gb|AAN86198.1| unknown protein [Arabidopsis thaliana] gb|AAM14036.1| unknown protein [Arabidopsis thaliana]	824	3E-73
					>dbj|BAC48254.1| blr2989 [Bradyrhizobium japonicum USDA 110]ref|NP 769629.1| putative acyl-CoA dehydrogenase [Bradyrhizobium japonicum USDA 110]	405	2E-53
CD058904	1.17E-02	Mo17<B73=F1	1.24	10	>gb|AAT08725.1| histone H4 [Hyacinthus orientalis]	103	5E-26
					>emb|CAB01913.1| Histone H4 homologue [Sesbania rostrata]	103	5E-26
					>ref|NP_563793.1| DNA binding [Arabidopsis thaliana]ref|NP_850660.1| DNA binding [Arabidopsis thaliana] ref|NP_180441.1| HIS4 [Arabidopsis thaliana] ref|NP_568911.1| DNA binding [Arabidopsis thaliana] ref|NP_568918.1| DNA binding [Arabidopsis thaliana] ref|NP_190941.1| DNA binding [Arabidopsis thaliana] ref|NP_563797.1| DNA binding [Arabidopsis thaliana] ref|NP_850939.1| DNA binding [Arabidopsis thaliana] ref|NP_190179.1| DNA binding [Arabidopsis thaliana] ref|XP_475394.1| histone H4 [Oryza sativa (japonica cultivar-group)] ref|XP_475383.1| putative histone H4 [Oryza sativa (japonica cultivar-group)] ref|NP_912452.1| Unknown protein [Oryza sativa (japonica cultivar-group)] ref|XP_467181.1| histone H4 [Oryza sativa (japonica cultivar-group)] ref|NP_922551.1| histone H4 [Oryza sativa (japonica cultivar-group)] ref|NP_915374.1| putative histone H4 [Oryza sativa (japonica cultivar-group)] ref|NP_910647.1| histone H4 [Oryza sativa (japonica cultivar-group)] ref|XP 473659.1| OSJNBa0088A01.17 [Oryza sativa (japonica cultivar-group)] gb|AAU90170.1| histone H4 [Oryza sativa	103	5E-26
					>sp|P62786|H42 WHEAT Histone H4 variant TH091gb|AAA34292.1| histone H4	103	5E-26
					>prf||1101277A histone H4	102	5E-26
BM074002	1.17E-02	Mo17<B73=F1	1.45	11	>dbj|BAD29288.1| putative beta-alanine synthase [Oryza sativa (japonicacultivar-group)] dbj|BAD28433.1| putative beta-alanine synthase [Oryza sativa (japonica cultivar-group)] dbj|BAB59126.1| putative hydrolase [Oryza sativa (japonica cultivar-group)]	301	3E-19
					>emb|CAB45873.1| beta-alanine synthase [Lycopersicon esculentum]	300	2E-13
					>gb|ABA40443.1| beta-alanine synthase-like protein [Solanum tuberosum]	300	2E-13
					>ref|NP_850101.1| NLP1 (NITRILASE-LIKE PROTEIN 1); hydrolase, acting oncarbon-nitrogen (but not peptide) bonds [Arabidopsis thaliana] gb|AAM67496.1| putative nitrilase [Arabidopsis thaliana] gb|AAL59935.1| putative nitrilase [Arabidopsis thaliana]	326	1E-11
					>ref|NP_565650.1| NLP1 (NITRILASE-LIKE PROTEIN 1); hydrolase, acting oncarbon-nitrogen (but not peptide) bonds [Arabidopsis thaliana] gb|AAD15597.2| putative nitrilase [Arabidopsis thaliana] gb|AAM63266.1| putative nitrilase [Arabidopsis thaliana]	299	1E-11
CD001516	1.18E-02	Mo17<B73=F1	1.6	10	ns		
DV549450	1.19E-02	B73=Mo17<F1	1.31	12	>dbj|BAD53577.1| putative SSR alpha subunit [Oryza sativa (japonica cultivar-group)]	257	9E-75
					>gb|AAM63845.1| putative signal sequence receptor, alpha subunit (SSR-alpha)[Arabidopsis thaliana]	258	4E-51
					>gb|AAW28548.1| At2g21160 [Arabidopsis thaliana]ref|NP_565498.1| ATP binding [Arabidopsis thaliana] gb|AAD29800.2| putative signal sequence receptor, alpha subunit (SSR-alpha) [Arabidopsis thaliana] gb|AAK91368.1| At2g21160/F26H11.8 [Arabidopsis thaliana] sp|P45434|SSRA_ARATH Translocon-associated protein alpha subunit precursor (TRAP-alpha) (Signal sequence receptor alpha subunit) (SSR-alpha)	258	1E-50
					>gb|AAA21820.1| alpha-subunit; putative	253	1E-50
					>ref|NP 179250.2| unknown protein [Arabidopsis thaliana]gb|AAT85767.1| At2g16595 [Arabidopsis thaliana]	251	1E-41
CB815841	1.19E-02	Mo17<B73	1.36	9	>ref|XP_476340.1| unknown protein [Oryza sativa (japonica cultivar-group)]ref|XP_506126.1| PREDICTED B1026C12.9 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD31818.1| unknown protein [Oryza sativa (japonica cultivar-group)]	503	2E-21

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP 181524.1| unknown protein [Arabidopsis thaliana]gb|AAB95280.1| hypothetical protein [Arabidopsis thaliana]	636	1E-15
DV549779	1.19E-02	F1=Mo17<B73	2.17	9	ns		
CA829580	1.19E-02	Mo17<B73=F1	1.31	10	>gb|ABA91392.1| expressed protein [Oryza sativa (japonica cultivar-group)]	298	3E-50
					>gb|ABA96396.1| hypothetical protein LOC Os12g03710 [Oryza sativa (japonicacultivar-group)]	235	5E-38
					>dbj|BAB10406.1| unnamed protein product [Arabidopsis thaliana]	248	1E-28
					>ref|NP 201402.2| RNA binding / nucleic acid binding [Arabidopsis thaliana]	289	1E-28
					>dbj|BAB02497.1| unnamed protein product [Arabidopsis thaliana]	278	2E-24
DV491739	1.19E-02	Mo17<B73	1.39	10	>ref|NP_182304.2| cation transporter/ efflux permease [Arabidopsis thaliana]gb|AAM98140.1| unknown protein [Arabidopsis thaliana] gb|AAP31955.1| At2g47830 [Arabidopsis thaliana] sp|Q8L725|MTPC1 ARATH Metal tolerance protein C1 (AtMTPc1)	471	2E-11
					>ref|NP 850480.1| cation transporter/ efflux permease [Arabidopsis thaliana]	468	2E-9
					>gb|AAC63637.1| unknown protein [Arabidopsis thaliana]	483	3E-9
CB885593	1.20E-02	Mo17<B73=F1	1.27	10	>ref|XP_475493.1| putative protein translation factor Sui1 [Oryza sativa (japonicacultivar-group)] gb|AAT44286.1| putative protein translation factor Sui1 [Oryza sativa (japonica cultivar-group)]	115	6E-59
					>dbj|BAD53005.1| putative translation initiation factor [Oryza sativa (japonicacultivar-group)]	115	3E-56
					>ref|XP_478516.1| translational initiation factor eIF1 [Oryza sativa (japonicacultivar-group)] emb|CAA36190.1| GOS2 [Oryza sativa (indica cultivar-group)] gb|AAK56324.1| translational initiation factor eIF1 [Porteresia coarctata] dbj|BAC45143.1| translational initiation factor eIF1 [Oryza sativa (japonica cultivar-group)] gb|AAC67556.1| translation initiation factor [Oryza sativa] pir||S21636 GOS2 protein - rice sp|P33278|SUI1_ORYSA PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)	115	1E-54
					>emb|CAB61837.1| putative translation initiation factor eIF-1 [Sporobolusstapfianus] sp|Q9SM41|SUI1 SPOST Protein translation factor SUI1 homolog	115	3E-54
					>sp|P56330|SUI1 MAIZE Protein translation factor SUI1 homolog (GOS2 protein)gb|AAB88615.1| translation initiation factor; GOS2 [Zea mays]	115	5E-54
CD001098	1.20E-02	Mo17<B73	1.2	10	>emb|CAA60251.1| 60S acidic ribosomal protein [Zea mays]sp|P46252|RLA2A MAIZE 60S acidic ribosomal protein P2A (P2)	112	2E-28
					>gb|AAC49360.1| acidic ribosomal protein P2	112	2E-28
					>gb|AAD11459.1| acidic ribosomal protein P2a-2 [Zea mays]	112	1E-27
					>gb|AAP80644.1| acidic ribosomal protein P2a-2 [Triticum aestivum]gb|AAP80619.1| acidic ribosomal protein P2 [Triticum aestivum]	112	4E-23
					>ref|NP 914551.1| putative 60S acidic ribosomal protein P2A [Oryza sativa (japonicacultivar-group)]	135	5E-23
CB351628	1.20E-02	B73<F1=Mo17	4.38	3	ns		
DV493287	1.21E-02	F1=Mo17<B73	1.27	9	>ref|XP_483757.1| putative auxin-regulated protein [Oryza sativa (japonicacultivar-group)] dbj|BAD13127.1| putative auxin-regulated protein [Oryza sativa (japonica cultivar-group)] dbj|BAD09092.1| putative auxin-regulated protein [Oryza sativa (japonica cultivar-group)]	341	1E-49
					>ref|NP_568128.1| unknown protein [Arabidopsis thaliana]gb|AAM10048.1| unknown protein [Arabidopsis thaliana] gb|AAK96798.1| Unknown protein [Arabidopsis thaliana]	339	3E-43
					>emb|CAB85508.1| putative protein [Arabidopsis thaliana]dbj|BAB08614.1| unnamed protein product [Arabidopsis thaliana]	331	3E-43
					>gb|AAM65224.1| unknown [Arabidopsis thaliana]	339	1E-42
					>emb|CAB78123.1| putative protein [Arabidopsis thaliana]emb|CAB39624.1| putative protein [Arabidopsis thaliana]	327	3E-15
DV491691	1.21E-02	B73=Mo17<F1	1.36	1	ns		
BM079199	1.21E-02	Mo17<B73=F1	1.38	10	>sp|P49104|RAB2B MAIZE Ras-related protein Rab-2-Bgb|AAA63902.1| GTP binding protein	210	1E-66
					>sp|P49103|RAB2A MAIZE Ras-related protein Rab-2-Agb|AAA63901.1| GTP binding protein	209	5E-66
					>ref|XP_466431.1| putative GTP-binding protein yptm3 [Oryza sativa (japonicacultivar-group)] ref|XP_506841.1| PREDICTED OSJNBb0056I22.32 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD17483.1| putative GTP-binding protein yptm3 [Oryza sativa (japonica cultivar-group)]	210	2E-65
					>gb|AAW52512.1| small GTP-binding protein [Triticum aestivum]	210	1E-64
					>emb|CAD57744.1| RAB-like small G-protein [Hordeum vulgare subsp. vulgare]	215	2E-64
DV942719	1.21E-02	B73<F1=Mo17	1.36	3	>ref|XP 473087.1| OSJNBa0014K14.18 [Oryza sativa (japonica cultivar-group)]emb|CAE05558.1| OSJNBb0116K07.11 [Oryza sativa (japonica cultivar-group)]	659	6E-81
					>emb|CAE02947.3| OSJNBa0014K14.19 [Oryza sativa (japonica cultivar-group)]	657	6E-81
					>gb|AAF66823.1| poly(A)-binding protein [Nicotiana tabacum]	649	1E-72
					>gb|AAF63202.1| poly(A)-binding protein [Cucumis sativus]	649	3E-72
					>ref|XP_450039.1| putative poly(A)-binding protein [Oryza sativa (japonicacultivar-group)] ref|XP_506632.1| PREDICTED OJ1310_F05.15 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD16229.1| putative poly(A)-binding protein [Oryza sativa (japonica cultivar-group)]	662	3E-70
BM349174	1.21E-02	Mo17<B73=F1	1.48	11	>ref|XP_507177.1| PREDICTED OSJNBb0070J06.25 gene product [Oryza sativa (japonicacultivar-group)] ref|XP_480935.1| putative cytochrome P450 reductase [Oryza sativa (japonica cultivar-group)] dbj|BAD05443.1| putative cytochrome P450 reductase [Oryza sativa (japonica cultivar-group)] dbj|BAD05639.1| putative cytochrome P450 reductase [Oryza sativa (japonica cultivar-group)]	568	5E-79
					>emb|CAC83301.1| cytochrome P450 reductase [Triticum aestivum]	703	1E-73
					>emb|CAA81209.1| NADPH-ferrihemoprotein reductase [Helianthus tuberosus]	588	9E-73
					>gb|AAK15261.1| NADPH-cytochrome P450 oxydoreductase isoform 3 [Populus balsamiferasubsp. trichocarpa x Populus deltoides]	712	2E-72

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|AAK15260.1| NADPH-cytochrome P450 oxydoreductase isoform 2 [Populus balsamiferasubsp. trichocarpa x Populus deltoides]	712	2E-72
DV550395	1.21E-02	Mo17<B73=F1	1.27	10	>gb|ABA94507.1| NB-ARC domain, putative [Oryza sativa (japonica cultivar-group)]	911	1E-7
					>gb|ABA94518.1| NB-ARC domain, putative [Oryza sativa (japonica cultivar-group)]	920	2E-6
					>gb|ABA94509.1| NB-ARC domain, putative [Oryza sativa (japonica cultivar-group)]	1812	3E-6
					>gb|ABA94521.1| NB-ARC domain, putative [Oryza sativa (japonica cultivar-group)]	964	5E-6
DV549599	1.21E-02	B73<F1=Mo17	1.22	3	>gb|AAG03094.2| putative ribosomal protein L28 [Oryza sativa (japonicacultivar-group)] gb|AAW56888.1| unknown protein [Oryza sativa (japonica cultivar-group)]	137	2E-39
					>ref|NP_565765.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAM47937.1| putative chloroplast 50S ribosomal protein L28 [Arabidopsis thaliana] gb|AAB80662.2| putative chloroplast 50S ribosomal protein L28 [Arabidopsis thaliana] gb|AAL62365.1| putative chloroplast 50S ribosomal protein L28 [Arabidopsis thaliana] gb|AAM64654.1| putative chloroplast 50S ribosomal protein L28 [Arabidopsis thaliana] sp|O22795|RK28_ARATH 50S ribosomal protein L28, chloroplast precursor	143	8E-37
					>pir||F84745 probable chloroplast 50S ribosomal protein L28 [imported] -Arabidopsis thaliana	140	8E-37
					>ref|XP 493864.1| putative ribosomal protein L28 [Oryza sativa]	88	2E-36
					>emb|CAA48211.1| ribosomal protein CL28 [Nicotiana tabacum]sp|P30956|RK28_TOBAC 50S ribosomal protein L28, chloroplast precursor (CL28) pir||R5NT28 ribosomal protein L28 precursor, chloroplast - tobacco	151	3E-34
CB815778	1.21E-02	Mo17<B73=F1	1.35	11	>emb|CAB57993.1| superoxide dismutase-4A [Zea mays]gb|AAB49913.1| superoxide dismutase 4A	152	4E-40
					>emb|CAB57992.1| superoxide dismutase-4AP [Zea mays]sp|P23345|SODC4 MAIZE Superoxide dismutase [Cu-Zn] 4A	152	4E-40
					>sp|P23346|SODC5 MAIZE Superoxide dismutase [Cu-Zn] 4AP	152	4E-40
					>gb|AAY56345.1| cytoplasmic copper/zinc-superoxide dismutase [Oryza sativa (indicacultivar-group)] sp|P28756|SODC1_ORYSA Superoxide dismutase [Cu-Zn] 1 gb|AAC14464.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00799.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)] prf||2111424A Cu/Zn superoxide dismutase	152	3E-37
					>gb|AAA33917.1| superoxide dismutase	152	3E-37
DV942221	1.22E-02	B73=F1<Mo17	1.37	4	>dbj|BAD82510.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD82157.1| unknown protein [Oryza sativa (japonica cultivar-group)]	408	2E-21
					>ref|NP 916962.1| P0445E10.13 [Oryza sativa (japonica cultivar-group)]	595	8E-21
					>ref|NP 916970.1| P0445E10.21 [Oryza sativa (japonica cultivar-group)]	372	1E-16
CD651155	1.22E-02	Mo17<B73=F1	1.33	10	>ref|XP 463397.1| P0025A05.27 [Oryza sativa (japonica cultivar-group)]	265	2E-56
					>dbj|BAD52984.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD53435.1| unknown protein [Oryza sativa (japonica cultivar-group)]	334	2E-56
					>dbj|BAD52985.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD53434.1| unknown protein [Oryza sativa (japonica cultivar-group)]	524	2E-56
DV489477	1.22E-02	Mo17<B73	2.77	10	ns		
DV550738	1.22E-02	B73=F1<Mo17	1.48	4	>gb|AAQ02664.1| boron transporter [Oryza sativa (japonica cultivar-group)]	711	3E-24
					>gb|ABA98983.1| HCO3- transporter family, putative [Oryza sativa (japonicacultivar-group)]	711	3E-24
					>ref|NP_850469.1| BOR1 (REQUIRES HIGH BORON 1); anion exchanger [Arabidopsisthaliana] gb|AAN31874.1| putative anion exchange protein [Arabidopsis thaliana] gb|AAM20076.1| putative anion exchange protein [Arabidopsis thaliana] gb|AAL49824.1| putative anion exchange protein [Arabidopsis thaliana] dbj|BAC20173.1| BOR1 [Arabidopsis thaliana] sp|Q8VYR7|BOR1 ARATH Boron transporter 1	704	5E-21
					>gb|AAD26598.1| putative anion exchange protein [Arabidopsis thaliana]	542	5E-21
					>ref|NP_191786.1| anion exchanger [Arabidopsis thaliana]emb|CAB71887.1| putative protein [Arabidopsis thaliana] gb|AAM20125.1| unknown protein [Arabidopsis thaliana] gb|AAL67019.1| unknown protein [Arabidopsis thaliana] sp|Q9M1P7|BOR2 ARATH Putative boron transporter 2	703	2E-20
DV494813	1.23E-02	Mo17<B73=F1	1.3	10	>ref|XP_472410.1| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)]emb|CAE02065.2| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)] dbj|BAD29299.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)] dbj|BAD27798.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]	151	2E-63
					>sp|P19951|RS142 MAIZE 40S ribosomal protein S14 (Clone MCH2)	150	1E-62
					>ref|XP_464199.1| putative ribosomal protein S14 [Oryza sativa (japonicacultivar-group)] ref|XP_506724.1| PREDICTED OJ9003_G05.34 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD25218.1| putative ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]	150	6E-61
					>gb|AAO41731.1| cytoplasmic ribosomal protein S14 [Brassica napus]	150	3E-59
					>sp|P19950|RS141 MAIZE 40S ribosomal protein S14 (Clone MCH1)	149	1E-58
DV550821	1.23E-02	Mo17<B73=F1	1.43	11	>gb|ABA81853.1| NADH:ubiquinone oxidoreductase-like [Solanum tuberosum]	229	1E-64
					>emb|CAA59062.1| NADH dehydrogenase; NADH:ubiquinone oxidoreductase (complex I)[Solanum tuberosum] sp|P80269|NUIM_SOLTU NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor (Complex I-23KD) (CI-23KD) (Complex I-28.5KD) (CI-28.5KD)	229	1E-64
					>ref|NP_173114.1| NADH dehydrogenase (ubiquinone)/ electron transporter/ iron ionbinding [Arabidopsis thaliana] gb|AAM10193.1| putative NADH-ubiquinone oxidoreductase [Arabidopsis thaliana] gb|AAL24404.1| Putative NADH-ubiquinone oxidoreductase [Arabidopsis thaliana] gb|AAM62674.1| NADH:ubiquinone oxidoreductase, putative [Arabidopsis thaliana] gb|AAG10813.1| Putative NADH-ubiquinone oxidoreductase [Arabidopsis thaliana]	222	2E-64

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_178022.1| NADH dehydrogenase (ubiquinone)/ electron transporter/ iron ionbinding [Arabidopsis thaliana] emb|CAA59061.1| NADH dehydrogenase; NADH:ubiquinone oxidoreductase (complex I) [Arabidopsis thaliana] gb|AAL62013.1| At1g79010/YUP8H12R_21 [Arabidopsis thaliana] gb|AAK82503.1| At1g79010/YUP8H12R_21 [Arabidopsis thaliana] gb|AAM65847.1| NADH dehydrogenase, putative [Arabidopsis thaliana] gb|AAC17054.1| Match to NADH:ubiquinone oxidoreductase gb|X84318 from A.thaliana. ESTs gb|Z27005, gb|T04711, gb|T45078 and gb|Z28689 come from this gene. [Arabidopsis thaliana] sp|Q42599|NUIM_ARATH NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor (Complex I-23KD) (CI-23KD) (Complex I-28.5KD) (CI-28.5KD)	222	2E-64
					>ref|NP_919060.1| putative NADH dehydrogenase [Oryza sativa (japonicacultivar-group)] gb|AAP68893.1| putative NADH dehydrogenase [Oryza sativa (japonica cultivar-group)]	223	5E-64
BG842494	1.24E-02	Mo17<B73=F1	1.5	10	ns		
DV489746	1.24E-02	B73<F1=Mo17	1.2	2	>ref|XP_473907.1| OSJNBa0093O08.15 [Oryza sativa (japonica cultivar-group)]emb|CAD41896.2| OSJNBa0093O08.15 [Oryza sativa (japonica cultivar-group)] emb|CAD41739.2| OSJNBa0058K23.5 [Oryza sativa (japonica cultivar-group)]	298	9E-67
					>ref|NP_567600.1| GSNAP (GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN); intracellulartransporter [Arabidopsis thaliana] gb|AAF01285.1| gamma-soluble NSF attachment protein; gamma-SNAP [Arabidopsis thaliana] sp|Q9SPE5|SNAG_ARATH Gamma-soluble NSF attachment protein (Gamma-SNAP) (N-ethylmaleimide-sensitive factor attachment protein, gamma)	291	3E-53
					>gb|AAM63730.1| unknown [Arabidopsis thaliana]	291	3E-53
					>emb|CAB79041.1| putative protein [Arabidopsis thaliana]emb|CAB45807.1| putative protein [Arabidopsis thaliana] pir||T10583 hypothetical protein F9F13.60 - Arabidopsis thaliana	319	9E-49
					>gb|ABA40435.1| unknown [Solanum tuberosum]	274	6E-40
CB331033	1.24E-02	B73=Mo17<F1	1.3	12	>ref|NP_910927.2| putative translation elongation factor eEF-1 beta' chain [Oryzasativa (japonica cultivar-group)] ref|XP_506540.1| PREDICTED P0453E03.111 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC22427.2| putative translation elongation factor eEF-1 beta' chain [Oryza sativa (japonica cultivar-group)]	224	2E-30
					>dbj|BAA02253.1| elongation factor 1 beta' [Oryza sativa (japonica cultivar-group)]sp|P29545|EF1B_ORYSA Elongation factor 1-beta (EF-1-beta) (Elongation factor 1B-alpha 2) (eEF-1B alpha) (Elongation factor 1-beta') (EF-1-beta')	223	2E-30
					>dbj|BAA02436.1| elongation factor 1 beta' [Triticum aestivum]sp|P29546|EF1B_WHEAT Elongation factor 1-beta (EF-1-beta) (Elongation factor 1B-alpha 2) (eEF-1B alpha) (Elongation factor 1-beta') (EF-1-beta')	216	6E-29
					>ref|NP_568375.2| translation elongation factor [Arabidopsis thaliana]emb|CAB64730.1| elongation factor 1B alpha-subunit [Arabidopsis thaliana] gb|AAL07240.1| putative elongation factor 1B alpha-subunit [Arabidopsis thaliana] gb|AAK26014.1| putative elongation factor 1B alpha-subunit [Arabidopsis thaliana] sp|Q9SCX3|EF1B2 ARATH Elongation factor 1-beta 2 (EF-1-beta 2) (Elongation factor 1B-alpha 2) (eEF-1B alpha 2) (Elongation factor 1-beta' 2) (EF-1-beta' 2)	224	3E-22
					>gb|ABA40463.1| elongation factor-like protein [Solanum tuberosum]	227	4E-20
DV495467	1.25E-02	Mo17<B73=F1	1.33	10	>ref|NP_920480.1| putative activator-like transposable element [Oryza sativa(japonica cultivar-group)] gb|AAM18172.1| Putative activator-like transposable element [Oryza sativa (japonica cultivar-group)] gb|AAP52767.1| hAT family dimerisation domain, putative [Oryza sativa (japonica cultivar-group)]	737	4E-21
					>prf||2021344A activator-like transposable element	804	3E-20
					>ref|XP 471074.1| OSJNBa0020P07.19 [Oryza sativa (japonica cultivar-group)]emb|CAE01302.2| OSJNBa0020P07.19 [Oryza sativa (japonica cultivar-group)]	741	7E-20
					>emb|CAA25636.1| unnamed protein product [Zea mays]	427	4E-14
					>emb|CAA29005.1| ORFa [Zea mays]gb|ABB59986.1| Ac transposase [Immobile Ac/T-DNA vector pNU400] gb|ABB59981.1| Ac transposase [Immobile Ac/T-DNA vector pKU352NA] sp|P08770|TRA1 MAIZE Putative AC transposase (ORFA)	807	4E-14
DV493472	1.25E-02	Mo17<F1	2.27	11	>ref|XP 472957.1| OJ991113 30.8 [Oryza sativa (japonica cultivar-group)]emb|CAD41325.2| OJ991113 30.8 [Oryza sativa (japonica cultivar-group)]	205	2E-61
					>ref|NP_188871.1| ATRPABC24.3; DNA binding / DNA-directed RNA polymerase [Arabidopsisthaliana] gb|AAL06554.1| AT3g22320/MCB17_5 [Arabidopsis thaliana] gb|AAM63355.1| RNA polymerase I, II and III 24.3 kDa subunit [Arabidopsis thaliana] gb|AAK48978.1| RNA polymerase I, II and III 24.3 kDa subunit [Arabidopsis thaliana] dbj|BAB01769.1| RNA polymerase I, II and III 24.3 kDa subunit [Arabidopsis thaliana] gb|AAN72141.1| RNA polymerase I, II and III 24.3 kDa subunit [Arabidopsis thaliana] gb|AAC28253.1| RNA polymerase I, II and III 24.3 kDa subunit [Arabidopsis thaliana]	205	5E-52
					>dbj|BAD68174.1| putative DNA-directed RNA polymerase II 23K chain [Oryza sativa(japonica cultivar-group)]	210	9E-48
					>ref|XP 396561.1| PREDICTED: similar to ENSANGP00000006082 [Apis mellifera]	210	3E-36
					>gb|AAW26085.1| SJCHGC05306 protein [Schistosoma japonicum]	206	8E-36
CD568437	1.25E-02	B73=F1<Mo17	1.24	4	>ref|XP_472252.1| OSJNBa0072D21.15 [Oryza sativa (japonica cultivar-group)]emb|CAE05283.2| OSJNBa0084N21.1 [Oryza sativa (japonica cultivar-group)] emb|CAD40733.2| OSJNBa0072D21.15 [Oryza sativa (japonica cultivar-group)]	601	2E-61
					>ref|XP 465886.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]dbj|BAD23171.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	403	9E-29
					>ref|NP 911578.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]dbj|BAC21511.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	291	3E-28
					>gb|AAL06537.1| AT3g11590/F24K9 26 [Arabidopsis thaliana]	622	4E-24
					>ref|NP_566392.1| unknown protein [Arabidopsis thaliana]gb|AAG51453.1| unknown protein; 103163-106072 [Arabidopsis thaliana] gb|AAN72254.1| At3g11590/F24K9 26 [Arabidopsis thaliana]	622	4E-24
DV549577	1.25E-02	Mo17<B73	1.53	9	ns		

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
CB281944	1.26E-02	Mo17<B73=F1	1.3	10	>ref|NP_200296.1| unknown protein [Arabidopsis thaliana]gb|AAT41804.1| At5g54850 [Arabidopsis thaliana] gb|AAS99667.1| At5g54850 [Arabidopsis thaliana] dbj|BAB08764.1| unnamed protein product [Arabidopsis thaliana]	202	3E-8
CB815800	1.27E-02	Mo17<B73=F1	1.32	11	>emb|CAB57992.1| superoxide dismutase-4AP [Zea mays]sp|P23345|SODC4 MAIZE Superoxide dismutase [Cu-Zn] 4A	152	2E-61
					>sp|P23346|SODC5 MAIZE Superoxide dismutase [Cu-Zn] 4AP	152	2E-61
					>emb|CAB57993.1| superoxide dismutase-4A [Zea mays]gb|AAB49913.1| superoxide dismutase 4A	152	2E-59
					>gb|AAY56345.1| cytoplasmic copper/zinc-superoxide dismutase [Oryza sativa (indicacultivar-group)] sp|P28756|SODC1_ORYSA Superoxide dismutase [Cu-Zn] 1 gb|AAC14464.1| cytosolic copper/zinc-superoxide dismutase [Oryza sativa] dbj|BAA00799.1| copper/zinc-superoxide dismutase [Oryza sativa (japonica cultivar-group)] prf||2111424A Cu/Zn superoxide dismutase	152	4E-58
					>gb|AAA33917.1| superoxide dismutase	152	1E-57
CD527566	1.27E-02	B73<Mo17	1.35	4	>gb|AAC27715.1| eukaryotic translation initiation factor p28 subunit [Zea mays]sp|O81482|IF4E2_MAIZE Eukaryotic translation initiation factor 4E-2 (eIF4E-2) (eIF-4E-2) (mRNA cap-binding protein) (eIF-(iso)4F 25 kDa subunit) (eIF-(iso)4F p28 subunit)	216	2E-81
					>ref|NP_921914.1| cap-binding protein p28 [Oryza sativa (japonica cultivar-group)]gb|AAK27811.1| cap-binding protein p28 [Oryza sativa (japonica cultivar-group)] gb|AAP54201.1| cap-binding protein p28 [Oryza sativa (japonica cultivar-group)]	206	2E-71
					>sp|P48600|IF4E2_ORYSA Eukaryotic translation initiation factor 4E-2 (eIF4E-2) (eIF-4E-2)(mRNA cap-binding protein) (eIF-(iso)4F 25 kDa subunit) (eIF-(iso)4F p28 subunit) gb|AAB40349.1| p28	206	6E-71
					>gb|AAA34296.1| initiation factor (iso)4F p28 subunit	209	3E-66
					>sp|Q03389|IF4E2_WHEAT Eukaryotic translation initiation factor 4E-2 (eIF4E-2) (eIF-4E-2)(mRNA cap-binding protein) (eIF-(iso)4F 25 kDa subunit) (eIF-(iso)4F p28 subunit) pir||B44452 translation initiation factor eIF-4F isozyme form subunit p28 - wheat gb|AAA34295.1| initiation factor (iso)4F p28 subunit	209	8E-66
CD058883	1.27E-02	Mo17<B73	1.29	10	>gb|ABA94601.1| ribosomal protein S4 [Oryza sativa (japonica cultivar-group)]gb|ABA94599.1| ribosomal protein S4 [Oryza sativa (japonica cultivar-group)]	195	5E-67
					>gb|ABA94602.1| ribosomal protein S4 [Oryza sativa (japonica cultivar-group)]	192	1E-63
					>emb|CAG47084.1| 40S ribosomal protein S9 [Catharanthus roseus]	197	3E-63
					>ref|NP_198801.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAM65655.1| 40S ribosomal protein S9-like [Arabidopsis thaliana] dbj|BAB10209.1| 40S ribosomal protein S9 [Arabidopsis thaliana]	197	4E-63
					>gb|AAU93594.1| putative ribosomal protein [Solanum demissum]	197	3E-62
CB381301	1.28E-02	Mo17<B73	1.46	9	>ref|XP_470037.1| putative 40S ribosomal protein S2 [Oryza sativa (japonicacultivar-group)] gb|AAP21434.1| putative 40S ribosomal protein S2 [Oryza sativa (japonica cultivar-group)]	274	7E-94
					>ref|XP_477083.1| putative 40S ribosomal protein S2 [Oryza sativa (japonicacultivar-group)] dbj|BAC83243.1| putative 40S ribosomal protein S2 [Oryza sativa (japonica cultivar-group)]	276	3E-93
					>ref|NP_191308.1| structural constituent of ribosome [Arabidopsis thaliana]emb|CAB66106.1| 40S ribosomal protein S2 homolog [Arabidopsis thaliana] gb|AAM60846.1| 40S ribosomal protein S2 homolog [Arabidopsis thaliana] gb|AAP12849.1| At3g57490 [Arabidopsis thaliana]	276	1E-88
					>gb|AAM67061.1| ribosomal protein S2, putative [Arabidopsis thaliana]	284	8E-88
					>ref|NP_683443.1| structural constituent of ribosome [Arabidopsis thaliana]ref|NP_564737.1| structural constituent of ribosome [Arabidopsis thaliana] ref|NP_564740.1| structural constituent of ribosome [Arabidopsis thaliana] dbj|BAD94842.1| ribosomal protein S2 [Arabidopsis thaliana] gb|AAM91489.1| At1g59359/T4M14_3 [Arabidopsis thaliana] gb|AAL57668.1| At1g59359/T4M14_3 [Arabidopsis thaliana] gb|AAK62784.1| ribosomal protein S2, putative [Arabidopsis thaliana] gb|AAK62780.1| ribosomal protein S2, putative [Arabidopsis thaliana] dbj|BAB84016.1| ribosomal protein S2 [Arabidopsis thaliana] dbj|BAB84012.1| ribosomal protein S2 [Arabidopsis thaliana] dbj|BAB82426.1| ribosomal protein S2 [Arabidopsis thaliana]	284	8E-88
DV942393	1.28E-02	B73=F1<Mo17	1.26	4	>emb|CAC14890.1| d-TDP-glucose dehydratase [Phragmites australis]	350	3E-60
					>dbj|BAB84334.1| UDP-glucuronic acid decarboxylase [Oryza sativa (japonicacultivar-group)]	350	9E-59
					>gb|AAT80326.1| UDP-D-glucuronate decarboxylase [Hordeum vulgare]	348	2E-57
					>gb|AAB68605.1| thymidine diphospho-glucose 4-6-dehydratase homolog [Prunusarmeniaca]	265	4E-51
					>gb|AAR07600.1| fiber dTDP-glucose 4-6-dehydratase [Gossypium barbadense]	181	7E-49
DV493707	1.29E-02	B73<F1=Mo17	1.32	3	>ref|NP_918865.1| P0458A05.23 [Oryza sativa (japonica cultivar-group)]dbj|BAB64088.1| putative SUMO protease [Oryza sativa (japonica cultivar-group)] dbj|BAB19414.1| putative SUMO protease [Oryza sativa (japonica cultivar-group)]	497	4E-35
					>gb|AAF26995.1| hypothetical protein [Arabidopsis thaliana]	478	3E-24
					>dbj|BAC42191.1| unknown protein [Arabidopsis thaliana]	502	3E-24
					>ref|NP 187347.2| cysteine-type peptidase [Arabidopsis thaliana]	502	3E-24
					>ref|NP_567478.1| ESD4 (EARLY IN SHORT DAYS 4); cysteine-type peptidase [Arabidopsisthaliana] gb|AAM10110.1| unknown protein [Arabidopsis thaliana] gb|AAK62379.1| Unknown protein [Arabidopsis thaliana]	489	3E-21
DV491056	1.29E-02	F1=Mo17<B73	1.31	8	>dbj|BAD27593.1| putative aspartate transaminase [Oryza sativa (japonicacultivar-group)]	432	7E-24
					>dbj|BAA23814.1| aspartate aminotransferase [Oryza sativa (japonica cultivar-group)]	132	1E-23
					>emb|CAA45024.1| aspartate aminotransferase [Panicum miliaceum]dbj|BAA04993.1| aspartate aminotransferase [Panicum miliaceum]	428	2E-23
					>emb|CAA45022.1| aspartate aminotransferase [Panicum miliaceum]	428	4E-23
					>dbj|BAD93907.1| aspartate aminotransferase [Arabidopsis thaliana]	189	8E-23

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

<table>
<thead>
<tr><th>GenBank accession no.</th><th>Overall P value</th><th>Significant pattern</th><th>Fold change[†]</th><th>Sector[‡]</th><th>BLAST annotation*</th><th>Score</th><th>E value</th></tr>
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<tr><td>DV551160</td><td>1.29E-02</td><td>Mo17<B73=F1</td><td>1.62</td><td>10</td><td>ns</td><td></td><td></td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAB69726.1| 3-hydroxy-3-methylglutaryl coenzyme a reductase [Camptothecaacuminata]</td><td>575</td><td>8E-7</td></tr>
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<tr><td>CD661734</td><td>1.29E-02</td><td>Mo17<F1</td><td>1.18</td><td>11</td><td>>gb|AAM95942.1| nucleosome/chromatin assembly factor group D protein [Zea mays]emb|CAA41220.1| high mobility group protein [Zea mays] emb|CAB46752.1| HMGa protein [Zea mays] sp|P27347|MNB1B MAIZE DNA-binding protein MNB1B (HMG1-like protein)</td><td>157</td><td>9E-19</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAB59202.1| serine carboxylase II-2 [Hordeum vulgare subsp. vulgare]gb|AAB31590.1| CP-MII.2=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436 aa] sp|P55748|CBP22_HORVU Serine carboxypeptidase II-2 precursor (CP-MII.2) [Contains: Serine carboxypeptidase II-2 chain A; Serine carboxypeptidase II-2 chain B]</td><td>436</td><td>1E-11</td></tr>
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<tr><td>CB885756</td><td>1.32E-02</td><td>B73=F1<Mo17</td><td>1.43</td><td>4</td><td>>ref|NP_912975.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]dbj|BAA88176.1| putative zwille protein [Oryza sativa (japonica cultivar-group)]</td><td>904</td><td>5E-68</td></tr>
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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_565633.1| AGO4 (ARGONAUTE 4) [Arabidopsis thaliana]gb|AAK93710.1| putative argonaute AGO1 protein [Arabidopsis thaliana] gb|AAK59586.1| putative Argonaute (AGO1) protein [Arabidopsis thaliana] gb|AAC77862.2| Argonaute (AGO1)-like protein [Arabidopsis thaliana]	924	1E-53
					>dbj|BAD81109.1| zwille protein -like [Oryza sativa (japonica cultivar-group)]	879	9E-48
CA829857	1.32E-02	B73<F1	1.21	2	ns		
DV495393	1.32E-02	Mo17<B73	1.32	9	>ref|XP_475553.1| putative isovaleryl-CoA dehydrogenase [Oryza sativa (japonicacultivar-group)] gb|AAT39231.1| putative isovaleryl-CoA dehydrogenase [Oryza sativa (japonica cultivar-group)] gb|AAS90672.2| putative isovaleryl-CoA dehydrogenase [Oryza sativa (japonica cultivar-group)]	409	6E-65
					>emb|CAB55555.1| auxin binding protein (ABP44); isovaleryl-CoA Dehydrogenase [Pisumsativum]	409	2E-60
					>emb|CAB55554.1| Isovaleryl-CoA Dehydrogenase; auxin binding protein (ABP44) [Pisumsativum]	408	2E-60
					>gb|AAM91199.1| isovaleryl-CoA-dehydrogenase precursor IVD [Arabidopsis thaliana]gb|AAL32645.1| isovaleryl-CoA-dehydrogenase precursor (IVD) [Arabidopsis thaliana]	409	3E-60
					>ref|NP_190116.1| IVD (ISOVALERYL-COA-DEHYDROGENASE) [Arabidopsis thaliana]emb|CAA73227.1| Isovaleryl-CoA Dehydrogenase [Arabidopsis thaliana] emb|CAB72479.1| isovaleryl-CoA-dehydrogenase precursor (IVD) [Arabidopsis thaliana]	409	8E-60
CB885626	1.32E-02	B73<F1=Mo17	1.23	3	>gb|ABA95868.1| actin 3, putative [Oryza sativa (japonica cultivar-group)]	260	1E-48
					>gb|AAV83798.1| putative actin 2 [Chorispora bungeana]	363	1E-48
					>gb|AAU44177.1| putative actin [Oryza sativa (japonica cultivar-group)]	377	1E-48
					>gb|AAC49651.1| actin [Striga asiatica]	377	1E-48
					>ref|NP_187818.1| ACT11 (ACTIN-11); structural constituent of cytoskeleton[Arabidopsis thaliana] gb|AAM65277.1| actin 11 (ACT11) [Arabidopsis thaliana] gb|AAG51045.1| actin 11 (ACT11); 24016-22523 [Arabidopsis thaliana] gb|AAO64013.1| putative actin 11 (ACT11) [Arabidopsis thaliana] dbj|BAB01959.1| actin 11 [Arabidopsis thaliana] dbj|BAC42968.1| unknown protein [Arabidopsis thaliana] sp|P53496|ACT11_ARATH Actin-11 gb|AAB39404.1| actin-11	377	1E-48
CB815720	1.33E-02	Mo17<B73	1.25	10	>gb|AAL59231.1| ribosomal protein L35A [Zea mays]	112	4E-59
					>gb|AAK73115.1| ribosomal protein L35A [Zea mays]	112	5E-59
					>ref|XP_468159.1| putative ribosomal protein L35A [Oryza sativa (japonicacultivar-group)] ref|XP_507015.1| PREDICTED OJ1715_H01.42 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD19312.1| putative ribosomal protein L35A [Oryza sativa (japonica cultivar-group)] dbj|BAD19202.1| putative ribosomal protein L35A [Oryza sativa (japonica cultivar-group)]	112	6E-55
					>ref|XP_475896.1| putative ribosomal protein L35A [Oryza sativa (japonicacultivar-group)] ref|XP_475888.1| putative ribosomal protein L35A [Oryza sativa (japonica cultivar-group)] gb|AAT58712.1| putative ribosomal protein L35A [Oryza sativa (japonica cultivar-group)] gb|AAT58704.1| putative ribosomal protein L35A [Oryza sativa (japonica cultivar-group)]	111	4E-51
					>gb|AAK25760.1| ribosomal protein L33 [Castanea sativa]	112	4E-50
BM351629	1.33E-02	F1<B73=Mo17	3.91	7	ns		
CB380586	1.33E-02	Mo17<B73=F1	1.24	11	>ref|XP_464199.1| putative ribosomal protein S14 [Oryza sativa (japonicacultivar-group)] ref|XP_506724.1| PREDICTED OJ9003_G05.34 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD25218.1| putative ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]	150	8E-63
					>ref|XP_472410.1| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)]emb|CAE02065.2| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)] dbj|BAD29299.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)] dbj|BAD27798.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]	151	9E-62
					>sp|P19950|RS141 MAIZE 40S ribosomal protein S14 (Clone MCH1)	149	4E-61
					>gb|AAO41731.1| cytoplasmic ribosomal protein S14 [Brassica napus]	150	4E-60
					>gb|ABC01912.1| ribosomal protein S14-like protein [Solanum tuberosum]gb|ABB87124.1| hypothetical protein [Solanum tuberosum]	150	1E-59
CD527831	1.34E-02	Mo17<B73	1.32	9	>dbj|BAB89354.1| ubiquitin-conjugating enzyme OsUBC5a [Oryza sativa (japonicacultivar-group)]	147	4E-84
					>emb|CAI29540.1| ubiquitin conjugating enzyme E2 [Oryza sativa (indicacultivar-group)]	147	6E-84
					>ref|NP_567791.1| UBC9 (UBIQUITIN CONJUGATING ENZYME 9); ubiquitin conjugatingenzyme/ ubiquitin-like activating enzyme [Arabidopsis thaliana] gb|AAY44849.1| ubiquitinating enzyme [Arabidopsis thaliana]	178	5E-81
					>gb|AAG40371.1| AT4g27960 [Arabidopsis thaliana]	178	5E-81
					>ref|NP_849462.1| UBC9 (UBIQUITIN CONJUGATING ENZYME 9); ubiquitin conjugatingenzyme/ ubiquitin-like activating enzyme [Arabidopsis thaliana] emb|CAA78714.1| ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] emb|CAA51201.1| ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] emb|CAB79598.1| ubiquitin-protein ligase UBC9 [Arabidopsis thaliana] emb|CAB36765.1| ubiquitin-protein ligase UBC9 [Arabidopsis thaliana] gb|AAN13102.1| E2 ubiquitin-conjugating enzyme 9 (UBC9) [Arabidopsis thaliana] sp|P35132|UBC9_ARATH Ubiquitin-conjugating enzyme E2-17 kDa 9 (Ubiquitin-protein ligase 9) (Ubiquitin carrier protein 9) (UBCAT4B) gb|AAA32894.1| ubiquitin conjugating enzyme	148	2E-80
CD484889	1.34E-02	B73<F1=Mo17	1.25	2	>ref|NP_915412.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]dbj|BAB93209.1| putative histone H2B [Oryza sativa (japonica cultivar-group)] dbj|BAB67889.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	139	4E-36
					>ref|XP_483094.1| putative Histone H2B.2 [Oryza sativa (japonica cultivar-group)]dbj|BAD09673.1| putative Histone H2B.2 [Oryza sativa (japonica cultivar-group)]	150	4E-36
					>sp|P05621|H2B2 WHEAT Histone H2B.2	149	4E-36
					>emb|CAA42530.1| histone H2B [Triticum aestivum]sp|P27807|H2B1 WHEAT Histone H2B	152	4E-36

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>emb|CAA49585.1| H2B histone [Zea mays]sp|P49120|H2B4 MAIZE Histone H2B.4	137	4E-36
CB240025	1.35E-02	B73=F1<Mo17	1.47	4	>emb|CAA41024.1| acyl carrier protein [Zea mays]prf||1814481A acyl carrier protein	121	1E-57
					>sp|P15543|ACP3 HORVU Acyl carrier protein 3, chloroplast precursor (Acyl carrier proteinIII) (ACP III) gb|AAA32922.1| acyl carrier protein III	132	4E-48
					>ref|XP_483668.1| putative acyl carrier protein III, chloroplast precursor (ACP III)[Oryza sativa (japonica cultivar-group)] dbj|BAD08953.1| putative acyl carrier protein III, chloroplast precursor (ACP III) [Oryza sativa (japonica cultivar-group)]	138	2E-45
					>sp|P08817|ACP2_HORVU Acyl carrier protein 2, chloroplast precursor (Acyl carrier proteinII) (ACP II) gb|AAA32921.1| acyl carrier protein II prf||1808324A acyl carrier protein II	129	6E-40
					>gb|AAA32924.1| acyl carrier protein III precursor	110	1E-36
DV495273	1.35E-02	B73<F1=Mo17	1.43	3	>ref|XP_467311.1| putative DNA topoisomerase II [Oryza sativa (japonicacultivar-group)] dbj|BAD07880.1| putative DNA topoisomerase II [Oryza sativa (japonica cultivar-group)]	1525	3E-13
CB605294	1.35E-02	Mo17<B73=F1	1.34	11	>gb|AAC08009.1| DnaJ-related protein ZMDJ1 [Zea mays]	419	e-108
					>gb|AAX95135.1| DnaJ protein, putative [Oryza sativa (japonica cultivar-group)]	416	e-107
					>gb|AAU89194.1| DnaJ protein, putative [Oryza sativa (japonica cultivar-group)]gb|AAO72551.1| DNAJ-like protein [Oryza sativa (japonica cultivar-group)]	417	e-107
					>gb|AAT75262.1| putative DnaJ like protein [Oryza sativa (japonicacultivar-group)]	417	6E-98
					>gb|ABB16989.1| DnaJ-like protein [Solanum tuberosum]	419	4E-97
DV621818	1.35E-02	B73<F1=Mo17	1.43	3	>ref|NP_916988.1| guanine nucleotide-binding protein beta subujit-like protein(GPB-LR) (RWD) [Oryza sativa (japonica cultivar-group)] dbj|BAA07404.1| q group of receptor for activated C-kinase [Oryza sativa (japonica cultivar-group)] sp|P49027|GBLP_ORYSA Guanine nucleotide-binding protein beta subunit-like protein (GPB-LR) (RWD)	334	9E-96
					>ref|XP_475866.1| putative guanine nucleotide-binding protein beta subunit [Oryzasativa (japonica cultivar-group)] gb|AAT85192.1| putative guanine nucleotide binding protein beta subunit [Oryza sativa (japonica cultivar-group)] gb|AAT39277.1| putative guanine nucleotide-binding protein beta subunit [Oryza sativa (japonica cultivar-group)]	336	7E-85
					>dbj|BAA76896.1| LeArcA2 protein [Lycopersicon esculentum]	326	1E-77
					>emb|CAA96528.1| G protein beta-subunit-like protein [Nicotiana plumbaginifolia]	328	3E-77
					>sp|P49026|GBLP TOBAC Guanine nucleotide-binding protein beta subunit-like proteindbj|BAA04478.1| G protein beta subunit-like protein [Nicotiana tabacum]	326	1E-76
DV496092	1.35E-02	B73=Mo17<F1	1.48	12	>ref|NP 922194.1| putative peroxidase [Oryza sativa (japonica cultivar-group)]gb|AAM93690.1| putative peroxidase [Oryza sativa (japonica cultivar-group)]	344	2E-14
					>gb|ABB47842.1| peroxidase, putative [Oryza sativa (japonica cultivar-group)]	363	2E-14
BM080260	1.36E-02	Mo17<B73=F1	1.4	11	>ref|XP_506641.1| PREDICTED P0523B07.38-1 gene product [Oryza sativa (japonicacultivar-group)] ref|XP_450347.1| putative polyphosphoinositide binding protein Ssh1 [Oryza sativa (japonica cultivar-group)] dbj|BAD23434.1| putative polyphosphoinositide binding protein Ssh1p [Oryza sativa (japonica cultivar-group)]	335	8E-44
					>gb|AAB94598.1| polyphosphoinositide binding protein Ssh1p [Glycine max]	324	9E-29
					>ref|NP_175980.1| transporter [Arabidopsis thaliana]gb|AAL84992.1| At1g55840/F14J16_2 [Arabidopsis thaliana] gb|AAL31909.1| At1g55840/F14J16_2 [Arabidopsis thaliana]	325	1E-26
					>gb|AAF79312.1| F14J16.8 [Arabidopsis thaliana]	344	1E-26
					>ref|NP 199584.1| binding / transporter [Arabidopsis thaliana]dbj|BAB11320.1| unnamed protein product [Arabidopsis thaliana]	341	1E-25
BM333880	1.36E-02	Mo17<B73=F1	1.49	11	>ref|XP_476878.1| putative auxin-induced protein [Oryza sativa (japonicacultivar-group)] dbj|BAC83117.1| putative auxin-induced protein [Oryza sativa (japonica cultivar-group)]	219	7E-35
					>ref|NP_909949.1| putative auxin-induced protein [Oryza sativa (japonicacultivar-group)] gb|AAP44680.1| putative auxin-induced protein [Oryza sativa (japonica cultivar-group)]	195	1E-32
					>gb|ABA99794.1| AUX/IAA family [Oryza sativa (japonica cultivar-group)]	197	1E-28
					>ref|XP_468971.1| putative auxin-induced protein [Oryza sativa (japonicacultivar-group)] gb|AAS07279.1| putative auxin-induced protein [Oryza sativa (japonica cultivar-group)]	226	5E-28
					>gb|AAD32142.1| Nt-iaa2.3 deduced protein [Nicotiana tabacum]	179	2E-27
CD670180	1.36E-02	Mo17<B73=F1	1.34	10	ns		
CA829343	1.37E-02	Mo17<B73=F1	1.25	10	>ref|XP_476648.1| putative ribosomal protein S12 [Oryza sativa (japonicacultivar-group)] dbj|BAC82908.1| putative ribosomal protein S12 [Oryza sativa (japonica cultivar-group)]	138	6E-12
					>ref|XP_477173.1| putative 40S ribosomal protein S12 [Oryza sativa (japonicacultivar-group)] dbj|BAC20920.1| putative 40S ribosomal protein S12 [Oryza sativa (japonica cultivar-group)]	138	2E-11
					>gb|AAD39838.1| ribosomal protein S12 [Hordeum vulgare]sp|Q9XHS0|RS12 HORVU 40S ribosomal protein S12	143	7E-11
					>ref|XP 757465.1| hypothetical protein UM01318.1 [Ustilago maydis 521]gb|EAK82181.1| hypothetical protein UM01318.1 [Ustilago maydis 521]	145	5E-9
					>gb|AAN52386.1| ribosomal protein S12 [Branchiostoma belcheri]	132	1E-7
CB885605	1.37E-02	B73<F1=Mo17	1.31	3	>ref|NP_912596.1| tubulin beta-4 chain [Oryza sativa (japonica cultivar-group)]dbj|BAB64211.1| putative beta-tubulin 4 [Oryza sativa (japonica cultivar-group)] sp|Q43594|TBB1 ORYSA Tubulin beta-1 chain (Beta-1 tubulin) dbj|BAB39951.1| putative tubulin beta-4 chain [Oryza sativa (japonica cultivar-group)]	447	3E-83

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>emb|CAA52720.1| beta-5 tubulin [Zea mays]sp|Q43697|TBB5 MAIZE Tubulin beta-5 chain (Beta-5 tubulin)	445	3E-83
					>sp|Q9ZRA8|TBB5 WHEAT Tubulin beta-5 chain (Beta-5 tubulin)gb|AAD10492.1| beta-tubulin 5 [Triticum aestivum]	447	3E-83
					>sp|Q9ZPN7|TBB4 ELEIN Tubulin beta-4 chain (Beta-4 tubulin)gb|AAD20181.1| beta-tubulin 4 [Eleusine indica]	446	3E-83
					>sp|Q9ZRB2|TBB1 WHEAT Tubulin beta-1 chain (Beta-1 tubulin)gb|AAD10487.1| beta-tubulin 1 [Triticum aestivum]	445	3E-83
CD650926	1.37E-02	Mo17<B73=F1	1.32	11	>gb|AAR89617.1| 40S ribosomal protein S5 [Capsicum annuum]	212	5E-18
					>ref|NP_908322.1| putative 40S ribosomal protein S5 [Oryza sativa (japonicacultivar-group)] dbj|BAB64234.1| putative 40S ribosomal protein S5 [Oryza sativa (japonica cultivar-group)] dbj|BAB62621.1| putative 40S ribosomal protein S5 [Oryza sativa (japonica cultivar-group)]	200	5E-18
					>emb|CAA70084.1| 40S ribosomal protein S5 [Nicotiana plumbaginifolia]sp|O24111|RS5 NICPL 40S ribosomal protein S5	154	5E-18
					>gb|ABA93723.1| ribosomal protein S7 [Oryza sativa (japonica cultivar-group)]	199	5E-18
					>pir||S56705 ribosomal protein S5 homolog - common tobacco (fragment)	49	5E-18
CB329441	1.37E-02	B73<F1=Mo17	1.37	3	>gb|AAA68209.1| sus1 gene product	816	e-112
					>sp|P49036|SUS2_MAIZE Sucrose synthase 2 (Sucrose-UDP glucosyltransferase 2)gb|AAA33515.1| sucrose synthase 2 gb|AAA33514.1| UDP-glucose:D-fructose 2-glucosyl-transferase	816	e-112
					>prf||2008300A sucrose synthase:ISOTYPE=2	763	e-112
					>gb|AAV64256.2| sucrose synthase [Bambusa oldhamii]	816	e-108
					>gb|AAL50570.1| sucrose synthase [Bambusa oldhamii]	816	e-107
DV493575	1.38E-02	B73=F1<Mo17	1.52	4	>ref|NP_912975.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]dbj|BAA88176.1| putative zwille protein [Oryza sativa (japonica cultivar-group)]	904	6E-55
					>gb|ABC61505.1| AGO4-2 [Nicotiana benthamiana]	905	3E-52
					>gb|ABC61504.1| AGO4-1 [Nicotiana benthamiana]	912	6E-50
					>dbj|BAD94152.1| zwille/pinhead-like protein [Arabidopsis thaliana]	580	3E-49
					>gb|AAO73892.1| PAZ (Piwi Argonaut and Zwille) family [Arabidopsis thaliana]	892	3E-49
BG841775	1.38E-02	Mo17<B73	2.39	9	ns		
CB604549	1.38E-02	Mo17<F1	1.23	12	>emb|CAA46876.1| DNA-binding protein [Zea mays]pir||T03640 high mobility group protein MNB1b - maize (fragment)	168	1E-22
					>gb|AAM95942.1| nucleosome/chromatin assembly factor group D protein [Zea mays]emb|CAA41220.1| high mobility group protein [Zea mays] emb|CAB46752.1| HMGa protein [Zea mays] sp|P27347|MNB1B MAIZE DNA-binding protein MNB1B (HMG1-like protein)	157	4E-22
					>gb|AAP21609.1| HMGB1 [Oryza sativa (indica cultivar-group)]gb|AAN28722.1| HMG1 protein [Oryza sativa (indica cultivar-group)] dbj|BAD61823.1| HMGB1 [Oryza sativa (japonica cultivar-group)] gb|AAC78104.1| high mobility group protein [Oryza sativa]	157	7E-21
					>emb|CAA77641.1| high mobility group protein [Triticum aestivum]sp|P40621|HMGL WHEAT HMG1/2-like protein	161	3E-20
					>emb|CAA90679.1| HMG1/2-like protein [Hordeum vulgare subsp. vulgare]	160	2E-19
CB334507	1.38E-02	Mo17<B73=F1	1.33	10	>ref|XP_480842.1| putative 60S ribosomal protein L7 [Oryza sativa (japonicacultivar-group)] dbj|BAD03800.1| putative 60S ribosomal protein L7 [Oryza sativa (japonica cultivar-group)]	245	1E-81
					>ref|XP_473801.1| OSJNBb0015N08.13 [Oryza sativa (japonica cultivar-group)]emb|CAE03885.2| OSJNBb0015N08.13 [Oryza sativa (japonica cultivar-group)] emb|CAE02124.2| OSJNBa0035M09.3 [Oryza sativa (japonica cultivar-group)]	250	3E-79
					>gb|AAW50989.1| ribosomal protein L7 [Triticum aestivum]	244	3E-74
					>ref|NP_974305.1| structural constituent of ribosome / transcription regulator[Arabidopsis thaliana] ref|NP_974304.1| structural constituent of ribosome / transcription regulator [Arabidopsis thaliana] ref|NP_187967.1| structural constituent of ribosome / transcription regulator [Arabidopsis thaliana] gb|AAL76153.1| AT3g13580/K20M4_2 [Arabidopsis thaliana] gb|AAL06999.1| AT3g13580/K20M4_2 [Arabidopsis thaliana] gb|AAK64004.1| AT3g13580/K20M4_2 [Arabidopsis thaliana] dbj|BAB02600.1| 60S ribosomal protein L7 [Arabidopsis thaliana] sp|Q9LHP1|RL73 ARATH 60S ribosomal protein L7-3	244	1E-69
					>gb|ABB16984.1| thaliana 60S ribosomal protein L7 (At2g44120) [Solanum tuberosum]	242	3E-69
CB334636	1.38E-02	F1=Mo17<B73	1.49	9	>ref|XP_464199.1| putative ribosomal protein S14 [Oryza sativa (japonicacultivar-group)] ref|XP_506724.1| PREDICTED OJ9003_G05.34 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD25218.1| putative ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]	150	8E-63
					>ref|XP_472410.1| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)]emb|CAE02065.2| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)] dbj|BAD29299.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)] dbj|BAD27798.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]	151	9E-62
					>sp|P19950|RS141 MAIZE 40S ribosomal protein S14 (Clone MCH1)	149	4E-61
					>gb|AAO41731.1| cytoplasmic ribosomal protein S14 [Brassica napus]	150	4E-60
					>gb|ABC01912.1| ribosomal protein S14-like protein [Solanum tuberosum]gb|ABB87124.1| hypothetical protein [Solanum tuberosum]	150	1E-59
BM073362	1.38E-02	Mo17<B73	1.35	10	>ref|NP_913796.1| thioredoxin-like [Oryza sativa (japonica cultivar-group)]ref|XP_507213.1| PREDICTED OSJNBb0011E04.120 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD05405.1| thioredoxin-like [Oryza sativa (japonica cultivar-group)] dbj|BAC22569.1| thioredoxin-like [Oryza sativa (japonica cultivar-group)]	189	4E-41
					>gb|AAF75752.1| putative thioredoxin [Lycopersicon esculentum]	175	3E-37
					>gb|AAS80320.1| thioredoxin protein [Nicotiana benthamiana]	181	6E-37

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>gb|AAS80319.1| thioredoxin protein [Nicotiana benthamiana]	181	2E-36
					>gb|AAM61520.1| thioredoxin, putative [Arabidopsis thaliana]	183	5E-36
DV621299	1.38E-02	B73<Mo17	1.39	4	>gb|AAT77062.1| expressed protein [Oryza sativa (japonica cultivar-group)]	241	6E-31
BM074510	1.39E-02	B73<F1	1.44	2	>ref|XP_475366.1| putative ubiquitin-conjugating enzyme E2 [Oryza sativa (japonicacultivar-group)] gb|AAT39166.1| putative ubiquitin-conjugating enzyme E2 [Oryza sativa (japonica cultivar-group)]	169	4E-41
					>emb|CAA05772.1| Ubiquitin carrier protein [Zea mays]	169	7E-41
					>ref|NP_915413.1| putative Ubiquitin carrier protein UBC7 [Oryza sativa (japonicacultivar-group)] dbj|BAB93210.1| putative ubiquitin carrier protein UBC7 [Oryza sativa (japonica cultivar-group)] dbj|BAB67890.1| putative ubiquitin carrier protein UBC7 [Oryza sativa (japonica cultivar-group)]	169	2E-40
					>gb|AAC12662.1| ubiquitin-conjugating enzyme protein E2 [Zea mays]	169	1E-39
					>ref|NP 568902.1| UBC7; ubiquitin conjugating enzyme [Arabidopsis thaliana]	198	2E-39
DV622656	1.39E-02	B73=F1<Mo17	1.45	5	>ref|XP_473275.1| OSJNBa0074L08.23 [Oryza sativa (japonica cultivar-group)]emb|CAE03865.2| OSJNBa0081C01.11 [Oryza sativa (japonica cultivar-group)] emb|CAD41212.2| OSJNBa0074L08.23 [Oryza sativa (japonica cultivar-group)]	770	2E-75
					>ref|NP_196618.1| hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana]emb|CAB89387.1| beta-xylosidase-like protein [Arabidopsis thaliana] gb|AAL09717.1| AT5g10560/F12B17 90 [Arabidopsis thaliana]	792	3E-43
					>dbj|BAC41913.1| putative beta-xylosidase [Arabidopsis thaliana]	732	3E-43
					>dbj|BAD06320.1| putative beta-xylosidase [Triticum aestivum]	573	2E-42
					>gb|AAK38482.1| beta-D-xylosidase [Hordeum vulgare]	777	9E-42
CB604350	1.40E-02	B73=F1<Mo17	1.35	4	>ref|XP 472193.1| OSJNBb0006N15.8 [Oryza sativa (japonica cultivar-group)]emb|CAE04591.2| OSJNBb0006N15.8 [Oryza sativa (japonica cultivar-group)]	123	5E-48
					>ref|XP_507485.1| PREDICTED OJ1126_B06.24 gene product [Oryza sativa (japonicacultivar-group)] ref|XP_465859.1| putative 60S ribosomal protein L35 [Oryza sativa (japonica cultivar-group)] ref|XP_506809.1| PREDICTED OJ1126_B06.24 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD22912.1| putative 60S ribosomal protein L35 [Oryza sativa (japonica cultivar-group)] dbj|BAD23213.1| putative 60S ribosomal protein L35 [Oryza sativa (japonica cultivar-group)]	123	8E-47
					>ref|NP_195881.1| structural constituent of ribosome [Arabidopsis thaliana]emb|CAB85998.1| ribosomal protein L35-like [Arabidopsis thaliana] gb|AAQ22651.1| At5g02610 [Arabidopsis thaliana] sp|Q9LZ41|RL354 ARATH 60S ribosomal protein L35-4 pir||T48282 ribosomal protein L35-like - Arabidopsis thaliana	123	6E-44
					>ref|NP_181471.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAL34210.1| putative 60S ribosomal protein L35 [Arabidopsis thaliana] gb|AAK59609.1| putative 60S ribosomal protein L35 [Arabidopsis thaliana] gb|AAC27830.1| 60S ribosomal protein L35 [Arabidopsis thaliana] gb|AAM61292.1| 60S ribosomal protein L35 [Arabidopsis thaliana] pir||T00549 60S ribosomal protein L35 [imported] - Arabidopsis thaliana sp|O80626|RL352_ARATH 60S ribosomal protein L35-1	123	7E-43
					>ref|NP_187561.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAM64363.1| putative 60S ribosomal protein L35 [Arabidopsis thaliana] gb|AAF23282.1| putative 60S ribosomal protein L35 [Arabidopsis thaliana] gb|AAO50471.1| putative 60S ribosomal protein L35 [Arabidopsis thaliana] gb|AAO42195.1| putative 60S ribosomal protein L35 [Arabidopsis thaliana] sp|Q9SF53|RL351 ARATH 60S ribosomal protein L35-2	123	1E-42
DV492564	1.40E-02	B73=F1<Mo17	1.37	5	>gb|AAR91093.1| hypothetical protein [Zea mays]	140	3E-62
					>gb|AAR91173.1| hypothetical protein [Zea mays]	101	1E-41
DV942454	1.41E-02	F1<Mo17	1.38	6	ns		
BM078533	1.41E-02	Mo17<B73=F1	1.39	11	>gb|ABA99526.1| universal stress protein family [Oryza sativa (japonicacultivar-group)]	169	1E-63
					>gb|ABA99525.1| hypothetical protein LOC Os12g36630 [Oryza sativa (japonicacultivar-group)]	160	1E-54
					>gb|AAR07598.1| fiber protein Fb19 [Gossypium barbadense]	151	3E-50
					>ref|NP_566108.1| unknown protein [Arabidopsis thaliana]gb|AAC63627.1| expressed protein [Arabidopsis thaliana] gb|AAM10097.1| unknown protein [Arabidopsis thaliana] gb|AAK96811.1| Unknown protein [Arabidopsis thaliana]	162	2E-47
					>gb|AAM63890.1| unknown [Arabidopsis thaliana]	162	1E-46
CD528028	1.41E-02	B73<F1=Mo17	1.51	3	>dbj|BAD35901.1| putative Erwinia induced protein 1 [Oryza sativa (japonicacultivar-group)]	409	6E-48
					>gb|AAT99435.1| LysM-domain GPI-anchored protein [Oryza sativa (japonicacultivar-group)]	409	8E-47
					>dbj|BAD38221.1| putative Erwinia induced protein 1 [Oryza sativa (japonicacultivar-group)] dbj|BAD38015.1| putative Erwinia induced protein 1 [Oryza sativa (japonica cultivar-group)]	401	4E-31
					>ref|NP_564153.1| unknown protein [Arabidopsis thaliana]gb|AAU90072.1| At1g21880 [Arabidopsis thaliana] gb|AAL09782.1| At1g21880/T26F17_5 [Arabidopsis thaliana] sp|Q93ZH0|LYM1 ARATH LysM domain GPI-anchored protein 1 precursor	416	2E-30
					>ref|NP_177886.2| unknown protein [Arabidopsis thaliana]gb|AAR24663.1| At1g77630 [Arabidopsis thaliana] dbj|BAD44532.1| predicted GPI-anchored protein [Arabidopsis thaliana]	423	5E-27
DV943329	1.41E-02	Mo17<B73	1.36	10	>dbj|BAD28019.1| unknown protein [Oryza sativa (japonica cultivar-group)]	185	4E-49
					>ref|NP_565561.1| unknown protein [Arabidopsis thaliana]gb|AAC63670.2| expressed protein [Arabidopsis thaliana] gb|AAM10301.1| At2g24020/T29E15.22 [Arabidopsis thaliana] gb|AAK82497.1| At2g24020/T29E15.22 [Arabidopsis thaliana]	182	1E-41
					>gb|AAV84522.1| At4g30620 [Arabidopsis thaliana]ref|NP_194791.1| unknown protein [Arabidopsis thaliana] emb|CAB79780.1| putative protein [Arabidopsis thaliana] gb|AAL75890.1| AT4g30620/F17I23 40 [Arabidopsis thaliana]	180	5E-40

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|AAP89016.1| complex interacting protein 9 [Arabidopsis thaliana]gb|AAM62959.1| unknown [Arabidopsis thaliana]	180	5E-40
					>gb|AAO32624.1| CR084 protein [Chlamydomonas reinhardtii]	157	3E-24
DV943300	1.42E-02	B73<Mo17	1.61	3	>sp|Q43270|PLDA1_MAIZE Phospholipase D alpha 1 (PLD alpha 1) (Choline phosphatase 1)(Phosphatidylcholine-hydrolyzing phospholipase D 1) dbj|BAA11135.1| phospholipase D [Zea mays]	812	3E-17
					>dbj|BAA19467.1| phospholipase D [Oryza sativa (japonica cultivar-group)]sp|Q43007|PLDA1_ORYSA Phospholipase D alpha 1 precursor (PLD alpha 1) (Choline phosphatase 1) (Phosphatidylcholine-hydrolyzing phospholipase D 1) dbj|BAA11136.1| phospholipase D [Oryza sativa (japonica cultivar-group)]	812	1E-14
					>gb|AAB51392.1| phospholipase D [Vigna unguiculata]sp|O04865|PLDA1_VIGUN Phospholipase D alpha 1 (PLD alpha 1) (Choline phosphatase 1) (Phosphatidylcholine-hydrolyzing phospholipase D 1)	809	2E-12
					>ref|NP_175666.1| PLDALPHA2 (PHOSPHLIPASE D ALPHA 2); phospholipase D [Arabidopsisthaliana] gb|AAD55607.1| Similar to gb|AF090445 phospholipase D1 from Brassica oleacea. [Arabidopsis thaliana] sp|Q9SSQ9|PLDA2_ARATH Phospholipase D alpha 2 (AtPLDalpha2) (PLD alpha 2) (Choline phosphatase 2) (Phosphatidylcholine-hydrolyzing phospholipase D 2)	810	1E-11
					>gb|AAG45485.1| phospholipase PLDa1 [Lycopersicon esculentum]	809	3E-11
DV490072	1.42E-02	B73<Mo17	1.35	3	>ref|XP 473247.1| OSJNBa0038O10.19 [Oryza sativa (japonica cultivar-group)]emb|CAE05653.2| OSJNBa0038O10.19 [Oryza sativa (japonica cultivar-group)]	413	6E-39
					>dbj|BAD93817.1| hypothetical protein [Arabidopsis thaliana]	170	9E-29
					>gb|AAY25464.1| At1g17940 [Arabidopsis thaliana]gb|AAF97273.1| F2H15.16 [Arabidopsis thaliana]	405	9E-29
					>ref|NP 173236.1| unknown protein [Arabidopsis thaliana]	394	9E-29
					>gb|AAZ23936.1| At1g17940 [Arabidopsis thaliana]	405	9E-29
DV551015	1.42E-02	Mo17<B73	1.59	10	ns		
CD527746	1.42E-02	Mo17<B73	1.24	10	>gb|AAG36870.1| protein kinase CK2 regulatory subunit CK2B2 [Zea mays]	260	3E-65
					>gb|ABB47995.1| casein kinase II beta subunit, putative [Oryza sativa (japonicacultivar-group)]	233	1E-55
					>gb|ABB47994.1| casein kinase II beta subunit, putative [Oryza sativa (japonicacultivar-group)]	279	1E-55
					>ref|NP_922762.1| putative casein kinase II beta subunit [Oryza sativa (japonicacultivar-group)] gb|AAG60201.1| putative casein kinase II beta subunit [Oryza sativa] gb|AAP55049.1| casein kinase II beta subunit, putative [Oryza sativa (japonica cultivar-group)]	280	3E-54
					>gb|AAG36871.1| protein kinase CK2 regulatory subunit CK2B3 [Zea mays]	273	1E-44
CD001162	1.42E-02	Mo17<B73=F1	1.32	10	>ref|XP_483838.1| glutaredoxin protein family-like [Oryza sativa (japonicacultivar-group)] dbj|BAD10332.1| glutaredoxin protein family-like [Oryza sativa (japonica cultivar-group)] dbj|BAD12949.1| glutaredoxin protein family-like [Oryza sativa (japonica cultivar-group)]	152	4E-23
					>ref|XP_483837.1| glutaredoxin protein family-like [Oryza sativa (japonicacultivar-group)] dbj|BAD10333.1| glutaredoxin protein family-like [Oryza sativa (japonica cultivar-group)] dbj|BAC56010.1| glutaredoxin protein family-like [Oryza sativa (japonica cultivar-group)]	164	4E-23
					>emb|CAB81461.1| putative protein [Arabidopsis thaliana]emb|CAA22979.1| putative protein [Arabidopsis thaliana]	176	4E-15
					>ref|NP_194602.2| electron transporter/ thiol-disulfide exchange intermediate[Arabidopsis thaliana] gb|AAO39931.1| At4g28730 [Arabidopsis thaliana] dbj|BAC43267.1| unknown protein [Arabidopsis thaliana]	174	4E-15
					>ref|NP_179617.1| arsenate reductase (glutaredoxin)/ electron transporter/thiol-disulfide exchange intermediate [Arabidopsis thaliana] gb|AAM67430.1| At2g20270/F11A3.18 [Arabidopsis thaliana] gb|AAM19817.1| At2g20270/F11A3.18 [Arabidopsis thaliana] gb|AAD21761.1| putative glutaredoxin [Arabidopsis thaliana]	179	1E-12
DV491721	1.43E-02	B73<Mo17	1.48	4	>dbj|BAD62124.1| putative oligopeptidase B [Oryza sativa (japonica cultivar-group)]dbj|BAD62483.1| putative oligopeptidase B [Oryza sativa (japonica cultivar-group)]	746	5E-57
					>ref|NP_564567.1| prolyl oligopeptidase/ serine-type endopeptidase/ serine-typepeptidase [Arabidopsis thaliana] gb|AAD50051.1| Similar to oligopeptidases [Arabidopsis thaliana] gb|AAL84967.1| At1g50380/F14I3 27 [Arabidopsis thaliana]	710	2E-53
					>sp|Q59536|PTRB MORLA Protease II (Oligopeptidase B)dbj|BAA07460.1| protease II [Moraxella lacunata]	690	1E-37
					>gb|AAC80459.1| oligopeptidase B [Trypanosoma brucei brucei]	715	2E-34
					>gb|EAN80234.1| oligopeptidase b [Trypanosoma brucei]ref|XP 829346.1| oligopeptidase b [Trypanosoma brucei]	715	2E-34
CB380544	1.43E-02	B73<F1=Mo17	4.69	3	>gb|AAM95942.1| nucleosome/chromatin assembly factor group D protein [Zea mays]emb|CAA41220.1| high mobility group protein [Zea mays] emb|CAB46752.1| HMGa protein [Zea mays] sp|P27347|MNB1B MAIZE DNA-binding protein MNB1B (HMG1-like protein)	157	1E-18
					>emb|CAA46876.1| DNA-binding protein [Zea mays]pir||T03640 high mobility group protein MNB1b - maize (fragment)	168	1E-18
					>gb|AAP21609.1| HMGB1 [Oryza sativa (indica cultivar-group)]gb|AAN28722.1| HMG1 protein [Oryza sativa (indica cultivar-group)] dbj|BAD61823.1| HMGB1 [Oryza sativa (japonica cultivar-group)] gb|AAC78104.1| high mobility group protein [Oryza sativa]	157	1E-15
					>emb|CAA77641.1| high mobility group protein [Triticum aestivum]sp|P40621|HMGL WHEAT HMG1/2-like protein	161	3E-14
					>emb|CAA90679.1| HMG1/2-like protein [Hordeum vulgare subsp. vulgare]	160	1E-12
CB381703	1.43E-02	Mo17<B73=F1	1.38	11	>ref|NP_917627.1| P0410E03.18 [Oryza sativa (japonica cultivar-group)]dbj|BAB21287.1| putative integral membrane Yip1 family protein [Oryza sativa (japonica cultivar-group)]	292	e-103
					>ref|NP 198101.2| unknown protein [Arabidopsis thaliana]	282	5E-86
					>gb|AAF27034.1| unknown protein [Arabidopsis thaliana]	280	2E-85

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15 % FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>ref|NP_187179.2| unknown protein [Arabidopsis thaliana]gb|AAO63894.1| unknown protein [Arabidopsis thaliana] dbj|BAC43538.1| unknown protein [Arabidopsis thaliana]	281	2E-85
					>gb|AAR24768.1| At5g27490 [Arabidopsis thaliana]gb|AAR23733.1| At5g27490 [Arabidopsis thaliana]	282	6E-85
CB833973	1.43E-02	Mo17<B73	1.22	9	ns		
CB411252	1.44E-02	B73<F1=Mo17	1.21	2	>gb|AAR97952.1| rolled leaf1 [Zea mays]	840	5E-91
					>gb|AAR04340.1| homeodomain leucine-zipper protein Hox10 [Oryza sativa (japonicacultivar-group)]	839	1E-81
					>ref|XP_468564.1| Putative homeodomain-leucine zipper protein [Oryza sativa (japonicacultivar-group)] gb|AAN61485.1| Putative homeodomain-leucine zipper protein [Oryza sativa (japonica cultivar-group)]	857	1E-81
					>gb|AAQ98963.1| homeodomain leucine-zipper protein Hox9 [Oryza sativa (japonicacultivar-group)]	840	2E-78
					>ref|NP_922012.1| putative homeodomain leucine zipper protein [Oryza sativa (japonicacultivar-group)] gb|AAK21338.1| putative homeodomain-leucine zipper protein [Oryza sativa (japonica cultivar-group)] gb|ABB47795.1| homeodomain-leucine zipper protein, putative [Oryza sativa (japonica cultivar-group)] gb|AAP54299.1| homeodomain-leucine zipper protein, putative [Oryza sativa (japonica cultivar-group)]	840	2E-78
BM073285	1.44E-02	Mo17<B73=F1	1.35	10	>gb|AAM61373.1| unknown [Arabidopsis thaliana]	274	5E-11
					>ref|NP 568159.1| unknown protein [Arabidopsis thaliana]gb|AAM51559.1| putative guanylate cyclase [Arabidopsis thaliana]	274	5E-11
					>ref|NP 974737.1| unknown protein [Arabidopsis thaliana]	210	5E-11
					>dbj|BAB10798.1| unnamed protein product [Arabidopsis thaliana]	295	1E-9
CB616981	1.44E-02	B73<F1=Mo17	1.37	3	>ref|XP_469569.1| actin [Oryza sativa (japonica cultivar-group)]gb|AAO38821.1| actin [Oryza sativa (japonica cultivar-group)] dbj|BAC76319.1| actin [Oryza sativa (japonica cultivar-group)] sp|P13362|ACT1 ORYSA Actin-1	377	9E-75
					>emb|CAA33874.1| actin [Oryza sativa (indica cultivar-group)]	377	9E-75
					>emb|CAA55923.1| actin [Sorghum bicolor]sp|P53504|ACT1 SORBI Actin-1	377	4E-74
					>emb|CAA34356.1| unnamed protein product [Oryza sativa (indica cultivar-group)]	377	6E-74
					>gb|AAF40438.1| actin 1 [Avena nuda]	377	5E-73
CB816608	1.45E-02	B73<Mo17	1.37	3	>dbj|BAD88098.1| putative replication licensing factor MCM4 [Oryza sativa (japonicacultivar-group)]	911	6E-61
					>ref|NP 918220.1| putative cdc21 protein [Oryza sativa (japonica cultivar-group)]	849	1E-48
					>ref|NP 179236.3| ATP binding / DNA binding / DNA-dependent ATPase/nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	847	3E-41
					>gb|AAD22296.1| putative CDC21 protein [Arabidopsis thaliana]	720	2E-29
					>emb|CAF98465.1| unnamed protein product [Tetraodon nigroviridis]	934	2E-19
CD527296	1.45E-02	B73<F1=Mo17	1.33	2	>gb|AAF67099.1| epsilon-COP [Zea mays]	287	7E-56
					>ref|XP_473864.1| OSJNBa0070C17.12 [Oryza sativa (japonica cultivar-group)]emb|CAE05205.3| OSJNBa0070C17.12 [Oryza sativa (japonica cultivar-group)] dbj|BAA94966.1| epsilon1-COP [Oryza sativa (japonica cultivar-group)]	287	6E-53
					>ref|NP_181030.1| protein transporter [Arabidopsis thaliana]gb|AAM98315.1| At2g34840/F19I3.7 [Arabidopsis thaliana] gb|AAC12824.1| putative coatomer epsilon subunit [Arabidopsis thaliana] gb|AAL91638.1| At2g34840/F19I3.7 [Arabidopsis thaliana] pir||T00466 coatomer complex epsilon chain homolog F19I3.7 - Arabidopsis thaliana sp|O64748|COPE ARATH Probable coatomer epsilon subunit (Epsilon-coat protein) (Epsilon-COP)	293	2E-39
					>gb|AAM65018.1| coatomer-like protein, epsilon subunit [Arabidopsis thaliana]	289	2E-38
					>ref|NP_174351.1| protein transporter [Arabidopsis thaliana]gb|AAK15559.1| putative coatomer protein, epsilon subunit [Arabidopsis thaliana] gb|AAL34287.1| putative coatomer protein, epsilon subunit [Arabidopsis thaliana] gb|AAK44140.1| putative coatomer protein, epsilon subunit [Arabidopsis thaliana] gb|AAD25750.1| Strong similarity to F19I3.7 gi|3033380 putative coatomer epsilon subunit from Arabidopsis thaliana BAC gb|AC004238. ESTs gb|Z17908, gb|AA728673, gb|N96555, gb|H76335, gb|AA712463, gb|W43247, gb|T45611, gb|T21160, gb|T14119 and AI100483 come from this gene	292	2E-38
CB604312	1.46E-02	Mo17<B73=F1	1.19	11	>ref|NP_911223.1| putative secretory carrier membrane protein [Oryza sativa (japonicacultivar-group)] ref|XP_506412.1| PREDICTED OJ1112_E08.118 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC15812.1| putative secretory carrier membrane protein [Oryza sativa (japonica cultivar-group)]	306	1E-45
					>ref|NP 172584.1| carrier [Arabidopsis thaliana]	291	1E-38
					>ref|XP_463469.1| secretory carrier membrane protein [Oryza sativa (japonicacultivar-group)] dbj|BAB63575.1| putative secretory carrier membrane protein [Oryza sativa (japonica cultivar-group)] gb|AAF36688.1| secretory carrier membrane protein [Oryza sativa]	286	1E-37
					>ref|NP_179680.1| carrier [Arabidopsis thaliana]gb|AAT06461.1| At2g20840 [Arabidopsis thaliana] dbj|BAD93720.1| putative secretory carrier-associated membrane protein [Arabidopsis thaliana] gb|AAD20911.1| putative secretory carrier-associated membrane protein [Arabidopsis thaliana]	282	5E-37
					>gb|AAU90239.1| putative secretory carrier membrane protein [Oryza sativa (japonicacultivar-group)] gb|AAU90243.1| putative secretory carrier membrane protein [Oryza sativa (japonica cultivar-group)]	282	7E-36
DV942883	1.46E-02	B73<Mo17	3.93	3	>ref|NP_909810.1| dentin sialophosphoprotein precursor-like protein [Oryza sativa(japonica cultivar-group)] gb|AAM19018.1| hypothetical protein [Oryza sativa (japonica cultivar-group)] gb|AAN65039.1| dentin sialophosphoprotein precursor-like protein [Oryza sativa (japonica cultivar-group)]	494	1E-37
					>ref|NP_001031449.1| unknown protein [Arabidopsis thaliana]ref|NP_180640.2| unknown protein [Arabidopsis thaliana] gb|AAU45205.1| At2g30820 [Arabidopsis thaliana] gb|AAS49046.1| At2g30820 [Arabidopsis thaliana]	421	2E-24
					>gb|AAC20717.1| unknown protein [Arabidopsis thaliana]	419	2E-24
					>gb|AAM13918.1| unknown protein [Arabidopsis thaliana]	337	2E-19

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_172151.2| unknown protein [Arabidopsis thaliana]	481	2E-19
CD001441	1.46E-02	F1=Mo17<B73	1.26	9	>ref|XP_475453.1| putative 60S ribosomal protein L24 [Oryza sativa (japonicacultivar-group)] gb|AAT01333.1| putative 60S ribosomal protein L24 [Oryza sativa (japonica cultivar-group)]	161	1E-47
					>dbj|BAD82702.1| putative 60S ribosomal protein L24 [Oryza sativa (japonicacultivar-group)]	162	7E-46
					>emb|CAA63960.1| L24 ribosomal protein [Hordeum vulgare subsp. vulgare]sp|P50888|RL24 HORVU 60S ribosomal protein L24	162	1E-45
					>ref|NP_911528.1| putative 60S ribosomal protein L24 [Oryza sativa (japonicacultivar-group)] dbj|BAD30738.1| putative 60S ribosomal protein L24 [Oryza sativa (japonica cultivar-group)] dbj|BAC06922.1| putative 60S ribosomal protein L24 [Oryza sativa (japonica cultivar-group)]	160	2E-45
					>gb|AAG13986.1| 60S ribosomal protein L24 [Prunus avium]sp|Q9FUL4|RL24 PRUAV 60S ribosomal protein L24	186	6E-43
DV621069	1.46E-02	B73=F1<Mo17	1.32	4	>gb|AAL76002.1| putative phosphatidylinositol-4-phosphate-5-kinase [Zea mays]	718	2E-16
					>gb|AAM97158.1| putative phosphatidylinositol 4-phosphate 5-kinase [Oryza sativa(japonica cultivar-group)] ref|XP_469458.1| putative phosphatidylinositol 4-phosphate 5-kinase [Oryza sativa (japonica cultivar-group)]	731	4E-15
					>gb|AAF80332.1| putative phosphatidylinositol 4-phosphate 5-kinase [Nicotianarustica]	798	8E-12
					>ref|NP_177897.1| 1-phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]gb|AAG51623.1| putative phosphatidylinositol-4-phosphate-5-kinase; 27989-31218 [Arabidopsis thaliana] sp|Q8L796|PI5K2_ARATH Phosphatidylinositol-4-phosphate 5-kinase 2 (AtPIP5K2) (1-phosphatidylinositol-4-phosphate kinase 2) (PtdIns(4)P-5-kinase 2) (Diphosphoinositide kinase 2)	754	1E-11
					>gb|AAM97057.1| putative phosphatidylinositol-4-phosphate-5-kinase [Arabidopsisthaliana] gb|AAN72123.1| putative phosphatidylinositol-4-phosphate-5-kinase [Arabidopsis thaliana]	318	1E-11
CD001640	1.47E-02	B73=F1<Mo17	1.43	4	ns		
CB617273	1.47E-02	B73<F1=Mo17	1.45	2	ns		
DV622032	1.47E-02	B73=F1<Mo17	1.35	4	>ref|XP_467100.1| putative enoyl-CoA hydratase [Oryza sativa (japonicacultivar-group)] dbj|BAD25316.1| putative enoyl-CoA hydratase [Oryza sativa (japonica cultivar-group)]	300	3E-70
					>emb|CAC39053.1| putative enoyl-CoA hydratase [Oryza sativa]	295	3E-70
					>ref|XP_467099.1| putative enoyl-CoA hydratase [Oryza sativa (japonicacultivar-group)] dbj|BAD25315.1| putative enoyl-CoA hydratase [Oryza sativa (japonica cultivar-group)]	269	2E-63
					>gb|AAM18495.1| enoyl-CoA hydratase [Arabidopsis lyrata subsp. petraea]	229	2E-58
					>emb|CAB88078.1| hypothetical protein [Arabidopsis thaliana]	217	3E-57
BM336587	1.48E-02	Mo17<B73=F1	1.24	10	>ref|XP_475090.1| unknown protein [Oryza sativa (japonica cultivar-group)]	128	3E-40
					>ref|NP_567643.1| unknown protein [Arabidopsis thaliana]emb|CAB79155.1| hypothetical protein [Arabidopsis thaliana] emb|CAA18103.1| hypothetical protein [Arabidopsis thaliana] gb|AAL32600.1| Unknown protein [Arabidopsis thaliana] gb|AAP21339.1| At4g22000 [Arabidopsis thaliana] gb|AAM63302.1| unknown [Arabidopsis thaliana]	130	1E-31
BM080600	1.48E-02	Mo17<B73=F1	1.3	11	>ref|XP_468478.1| putative Vacuolar ATP synthase subunit F [Oryza sativa (japonicacultivar-group)] dbj|BAD22867.1| putative Vacuolar ATP synthase subunit F [Oryza sativa (japonica cultivar-group)]	130	2E-63
					>ref|NP_192171.1| hydrogen-transporting ATP synthase, rotational mechanism /hydrogen-transporting ATPase, rotational mechanism [Arabidopsis thaliana] gb|AAC78269.1| putative vacuolar ATPase [Arabidopsis thaliana] emb|CAB80755.1| putative vacuolar ATPase [Arabidopsis thaliana] gb|AAM51311.1| putative vacuolar ATPase [Arabidopsis thaliana] gb|AAL38753.1| putative vacuolar ATPase [Arabidopsis thaliana] gb|AAM60868.1| putative vacuolar ATPase [Arabidopsis thaliana] pir||T01087 H+-exporting ATPase (EC 3.6.3.6) 14K chain, vacuolar - Arabidopsis thaliana sp|Q9ZQX4|VATF_ARATH Probable vacuolar ATP synthase subunit F (V-ATPase F subunit) (Vacuolar proton pump F subunit) (V-ATPase 14 kDa subunit)	128	1E-57
					>gb|ABC60334.1| putative vacuolar ATP synthase subunit F [Musa acuminata]	117	3E-52
					>emb|CAE57827.1| Hypothetical protein CBG00852 [Caenorhabditis briggsae]	121	5E-32
					>ref|XP_645434.1| hypothetical protein DDB0216933 [Dictyostelium discoideum]gb|EAL71520.1| hypothetical protein DDB0216933 [Dictyostelium discoideum]	120	2E-31
DV489785	1.49E-02	F1<B73=Mo17	1.78	7	>gb|AAO72316.1| multidrug resistance associated protein 1 [Zea mays]gb|AAO72315.1| multidrug resistance associated protein 1 [Zea mays]	1477	6E-19
					>emb|CAD59603.1| MRP-like ABC transporter [Oryza sativa (japonica cultivar-group)]	1202	4E-17
					>gb|AAV59449.1| putative MRP-like ABC transporter [Oryza sativa (japonicacultivar-group)] ref|XP_476085.1| putative MRP-like ABC transporter [Oryza sativa (japonica cultivar-group)]	1474	4E-10
					>gb|AAO49474.1| multidrug resistance-associated protein-like protein [Vitisvinifera]	189	3E-8
					>emb|CAD44995.1| multidrug-resistance related protein [Arabidopsis thaliana]	1294	6E-7
CD651442	1.49E-02	B73<F1=Mo17	1.24	3	ns		
DV492815	1.50E-02	B73<F1=Mo17	1.42	3	>ref|XP_475398.1| putative calcium-dependent protein kinase [Oryza sativa (japonicacultivar-group)] gb|AAT58789.1| putative calcium-dependent protein kinase [Oryza sativa (japonica cultivar-group)] gb|AAT58767.1| putative calcium-dependent protein kinase [Oryza sativa (japonica cultivar-group)]	547	1E-38
					>ref|NP_915342.1| putative calcium-dependent protein kinase [Oryza sativa (japonicacultivar-group)] dbj|BAB92912.1| putative calcium dependent protein kinase [Oryza sativa (japonica cultivar-group)]	551	2E-37
					>dbj|BAD93899.1| calcium-dependent like protein kinase [Arabidopsis thaliana]	111	2E-34
					>gb|AAL32617.1| calcium-dependent protein kinase [Arabidopsis thaliana]gb|AAO29985.1| calcium-dependent protein kinase [Arabidopsis thaliana]	528	2E-34

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|AAA99795.1| calcium-dependent protein kinase	196	2E-34
CB331612	1.50E-02	Mo17<B73	1.25	9	>ref|XP_476919.1| putative ES43 protein [Oryza sativa (japonica cultivar-group)]dbj|BAD30193.1| putative ES43 protein [Oryza sativa (japonica cultivar-group)] dbj|BAC79935.1| putative ES43 protein [Oryza sativa (japonica cultivar-group)]	218	1E-19
					>ref|NP_909931.1| putative DNA-binding protein [Oryza sativa (japonicacultivar-group)] gb|AAO37525.1| putative DNA-binding protein [Oryza sativa (japonica cultivar-group)]	218	2E-11
					>emb|CAA54682.1| ES43 [Hordeum vulgare]	227	4E-11
					>ref|XP_450843.1| putative zinc-finger motif [Oryza sativa (japonica cultivar-group)]ref|XP_506665.1| PREDICTED OSJNBa0048A13.16 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD26108.1| putative zinc-finger motif [Oryza sativa (japonica cultivar-group)]	216	1E-6
DV492134	1.50E-02	B73<F1=Mo17	1.38	3	>emb|CAA55022.1| beta tubulin [Oryza sativa (japonica cultivar-group)]	447	1E-72
					>emb|CAE52516.1| beta tubulin [Setaria viridis]	448	1E-72
					>ref|NP_915874.1| tubulin beta chain [Oryza sativa (japonica cultivar-group)]dbj|BAB92274.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] dbj|BAA06381.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|P45960|TBB4 ORYSA Tubulin beta-4 chain (Beta-4 tubulin)	447	1E-72
					>gb|AAA66495.1| beta-tubulin	447	1E-72
					>sp|Q41783|TBB6 MAIZE Tubulin beta-6 chain (Beta-6 tubulin)gb|AAA20186.1| beta-6 tubulin	446	1E-72
CB331485	1.51E-02	Mo17<B73=F1	1.36	11	ns		
CB381032	1.51E-02	Mo17<B73=F1	1.18	10	>dbj|BAD45217.1| root hair defective 3 GTP-binding protein-like [Oryza sativa(japonica cultivar-group)]	524	3E-42
					>ref|NP 918504.1| putative root hair defective 3 (RHD3) [Oryza sativa (japonicacultivar-group)]	806	3E-42
					>gb|AAS67855.2| root hair defective 3 GTP-binding protein [Triticum aestivum]	804	1E-39
					>ref|NP 177439.1| nucleotide binding [Arabidopsis thaliana]	748	6E-31
					>ref|NP_188003.1| RHD3 (ROOT HAIR DEFECTIVE 3) [Arabidopsis thaliana]gb|AAM91201.1| unknown protein [Arabidopsis thaliana] gb|AAM12987.1| unknown protein [Arabidopsis thaliana] gb|AAB58375.1| root hair defective 3 [Arabidopsis thaliana]	802	2E-29
CB334560	1.52E-02	Mo17<B73=F1	1.21	11	>ref|NP_921134.1| putative hydrolase [Oryza sativa (japonica cultivar-group)]gb|AAM08665.1| Putative hydrolase [Oryza sativa (japonica cultivar-group)] gb|AAM08532.1| Putative hydrolase [Oryza sativa] gb|AAP53421.1| hydrolase, alpha/beta fold family, putative [Oryza sativa (japonica cultivar-group)]	401	2E-75
					>ref|XP 470785.1| putative hydrolase [Oryza sativa (japonica cultivar-group)]gb|AAR06364.1| putative hydrolase [Oryza sativa (japonica cultivar-group)]	333	7E-44
					>ref|XP 479188.1| hydrolase-like protein [Oryza sativa (japonica cultivar-group)]dbj|BAC79905.1| hydrolase-like protein [Oryza sativa (japonica cultivar-group)]	327	5E-41
					>gb|AAY78820.1| hydrolase [Arabidopsis thaliana]	311	3E-36
					>gb|AAM61205.1| putative hydrolase [Arabidopsis thaliana]	328	6E-33
DV621917	1.53E-02	B73=F1<Mo17	1.42	4	ns		
BM080350	1.54E-02	F1=Mo17<B73	1.38	9	>ref|XP_468412.1| putative 3-ketoacyl-CoA thiolase; acetyl-CoA acyltransferase [Oryzasativa (japonica cultivar-group)] ref|XP_507050.1| PREDICTED OJ1136_C12.17 gene product [Oryza sativa (japonica cultivar-group)] gb|AAO72588.1| 3-ketoacyl-CoA thiolase-like protein [Oryza sativa (japonica cultivar-group)] dbj|BAD21525.1| putative 3-ketoacyl-CoA thiolase; acetyl-CoA acyltransferase [Oryza sativa (japonica cultivar-group)]	448	3E-42
					>ref|NP_921813.1| putative thiolase [Oryza sativa (japonica cultivar-group)]gb|AAK54299.1| putative thiolase [Oryza sativa (japonica cultivar-group)] gb|AAP54100.1| thiolase, putative [Oryza sativa (japonica cultivar-group)]	461	3E-41
					>emb|CAA63598.1| glyoxysomal beta-ketoacyl-thiolase [Brassica napus]	462	5E-41
					>gb|ABB45810.1| acetoacetyl-CoA thiolase [Salvia miltiorrhiza]	172	7E-41
					>ref|NP_180873.1| PED1 (PEROXISOME DEFECTIVE 1) [Arabidopsis thaliana]gb|AAK15577.1| putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gb|AAG42910.1| putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gb|AAC04908.1| 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] dbj|BAA25248.1| 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gb|AAL36070.1| At2g33150/F25I18.11 [Arabidopsis thaliana] gb|AAK96606.1| At2g33150/F25I18.11 [Arabidopsis thaliana] gb|AAM65085.1| 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] dbj|BAA25249.1| 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] sp|Q56WD9|THIK2_ARATH 3-ketoacyl-CoA thiolase 2, peroxisomal precursor (Beta-ketothiolase 2) (Acetyl-CoA acyltransferase 2) (Peroxisomal 3-oxoacyl-CoA thiolase 2) (Peroxisome defective protein 1)	462	2E-40
CB411132	1.55E-02	Mo17<B73=F1	1.3	10	>sp|P93554|NDK1_SACOF Nucleoside diphosphate kinase 1 (Nucleoside diphosphate kinase I)(NDK I) (NDP kinase I) (NDPK I) (PP18) gb|AAB40609.1| nucleoside diphosphate kinase	149	8E-68
					>dbj|BAA12982.1| PNDKN1 [Pisum sativum]	149	3E-62
					>emb|CAA50511.1| nucleoside-diphosphate kinase [Pisum sativum]sp|P47922|NDK1_PEA Nucleoside diphosphate kinase 1 (Nucleoside diphosphate kinase I) (NDK I) (NDP kinase I) (NDPK I)	149	7E-62
					>ref|NP_922751.1| putative nucleoside diphosphate kinase [Oryza sativa (japonicacultivar-group)] gb|AAG60181.1| putative nucleoside diphosphate kinase [Oryza sativa] gb|AAP55038.1| nucleoside diphosphate kinase, putative [Oryza sativa (japonica cultivar-group)]	151	2E-61
					>gb|AAA93030.1| nucleoside diphosphate kinase [Glycine max]sp|Q39839|NDK1_SOYBN Nucleoside diphosphate kinase 1 (Nucleoside diphosphate kinase I) (NDK I) (NDP kinase I) (NDPK I)	149	2E-61
DV493491	1.55E-02	Mo17<B73=F1	1.98	11	>ref|XP 473399.1| OSJNBa0079A21.10 [Oryza sativa (japonica cultivar-group)]emb|CAD41468.3| OSJNBa0079A21.12 [Oryza sativa (japonica cultivar-group)]	695	3E-62
					>ref|XP_467102.1| putative protein kinase 5 [Oryza sativa (japonica cultivar-group)]dbj|BAD25318.1| putative protein kinase 5 [Oryza sativa (japonica cultivar-group)]	689	2E-56

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>emb|CAC39054.1| putative protein kinase [Oryza sativa]	609	2E-56
					>gb|AAW38935.1| AvrPto-dependent Pto-interacting protein 3 [Lycopersiconesculentum]	700	3E-56
					>ref|NP 850426.1| kinase [Arabidopsis thaliana]	765	9E-50
CD568962	1.56E-02	Mo17<B73=F1	1.33	10	>ref|XP_472410.1| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)]emb|CAE02065.2| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)] dbj|BAD29299.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)] dbj|BAD27798.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]	151	2E-63
					>sp|P19951|RS142 MAIZE 40S ribosomal protein S14 (Clone MCH2)	150	1E-62
					>ref|XP_464199.1| putative ribosomal protein S14 [Oryza sativa (japonicacultivar-group)] ref|XP_506724.1| PREDICTED OJ9003_G05.34 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD25218.1| putative ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]	150	5E-61
					>gb|AAO41731.1| cytoplasmic ribosomal protein S14 [Brassica napus]	150	2E-59
					>sp|P19950|RS141 MAIZE 40S ribosomal protein S14 (Clone MCH1)	149	1E-58
CB329354	1.56E-02	B73<F1=Mo17	1.31	2	ns		
DV493046	1.56E-02	B73<F1=Mo17	1.38	3	>gb|ABA98935.1| PAPA-1-like conserved region, putative [Oryza sativa (japonicacultivar-group)]	552	4E-28
					>ref|XP 470049.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAP73843.1| unknown protein [Oryza sativa (japonica cultivar-group)]	523	1E-26
					>ref|NP 176041.2| protein binding [Arabidopsis thaliana]dbj|BAC42342.1| unknown protein [Arabidopsis thaliana]	502	2E-25
					>ref|NP 182257.1| protein binding [Arabidopsis thaliana]gb|AAB63835.1| unknown protein [Arabidopsis thaliana]	486	3E-21
					>gb|AAF63832.1| hypothetical protein [Arabidopsis thaliana]	432	2E-17
DV494969	1.56E-02	B73=F1<Mo17	1.27	4	>gb|ABA98280.1| ubiquitin-specific protease 12 [Oryza sativa (japonicacultivar-group)]	1093	e-124
					>gb|AAF23207.1| putative ubiquitin carboxyl-terminal hydrolase [Arabidopsis thaliana]	1124	e-116
					>ref|NP_850783.1| UBP12 (UBIQUITIN-SPECIFIC PROTEASE 12); cysteine-type endopeptidase/double-stranded DNA binding / ubiquitin thiolesterase/ ubiquitin-specific protease [Arabidopsis thaliana] gb|AAN13185.1| putative ubiquitin-specific protease UBP12 [Arabidopsis thaliana] gb|AAK25908.1| putative ubiquitin-specific protease UBP12 [Arabidopsis thaliana]	1115	e-116
					>gb|AAG42754.1| ubiquitin-specific protease 12 [Arabidopsis thaliana]	1116	e-116
					>ref|NP_187797.3| cysteine-type endopeptidase/ double-stranded DNA binding / ubiquitinthiolesterase/ ubiquitin-specific protease [Arabidopsis thaliana] gb|AAO22588.1| putative ubiquitin carboxyl-terminal hydrolase [Arabidopsis thaliana]	1115	e-116
CB605136	1.57E-02	B73<F1	1.4	1	ns		
DV622625	1.57E-02	B73<Mo17	1.33	4	>ref|NP 908448.1| putative receptor serine/threonine kinase [Oryza sativa (japonicacultivar-group)]	674	3E-24
					>ref|XP_549893.1| putative receptor serine/threonine kinase PR5K [Oryza sativa(japonica cultivar-group)] dbj|BAD45146.1| putative receptor serine/threonine kinase PR5K [Oryza sativa (japonica cultivar-group)] dbj|BAD45068.1| putative receptor serine/threonine kinase PR5K [Oryza sativa (japonica cultivar-group)]	601	1E-23
					>ref|XP 471708.1| OSJNBa0079M09.1 [Oryza sativa (japonica cultivar-group)]emb|CAE05332.2| OSJNBa0079M09.1 [Oryza sativa (japonica cultivar-group)]	822	1E-20
					>ref|NP 908445.1| putative receptor serine/threonine kinase [Oryza sativa (japonicacultivar-group)]	649	1E-20
					>ref|XP_549890.1| putative receptor serine/threonine kinase PR5K [Oryza sativa(japonica cultivar-group)] dbj|BAD45143.1| putative receptor serine/threonine kinase PR5K [Oryza sativa (japonica cultivar-group)] dbj|BAD45065.1| putative receptor serine/threonine kinase PR5K [Oryza sativa (japonica cultivar-group)]	652	1E-20
CB603803	1.57E-02	Mo17<B73=F1	1.29	10	ns		
CB604228	1.57E-02	Mo17<B73=F1	1.19	11	>ref|NP_568778.1| oxidoreductase, acting on NADH or NADPH [Arabidopsis thaliana]gb|AAL79599.1| AT5g52840/MXC20_6 [Arabidopsis thaliana] gb|AAL06910.1| AT5g52840/MXC20_6 [Arabidopsis thaliana] dbj|BAB10432.1| unnamed protein product [Arabidopsis thaliana] sp|Q9FLX7|NUFM_ARATH Probable NADH-ubiquinone oxidoreductase 18 kDa subunit, mitochondrial precursor (Complex I-18Kd) (CI-18Kd)	169	7E-51
					>gb|AAL32032.1| NADH-ubiquinone oxidoreductase [Retama raetam]	153	7E-50
					>gb|AAO52022.1| similar to NADH-ubiquinone oxidoreductase 13 KD-B subunit[Caenorhabditis elegans] [Dictyostelium discoideum]	117	8E-12
					>ref|XP 645190.1| hypothetical protein DDB0216983 [Dictyostelium discoideum]gb|EAL71349.1| hypothetical protein DDB0216983 [Dictyostelium discoideum]	117	8E-12
					>ref|XP 504293.1| hypothetical protein [Yarrowia lipolytica]emb|CAG79892.1| unnamed protein product [Yarrowia lipolytica CLIB122]	146	2E-10
BM073392	1.57E-02	Mo17<B73	1.5	9	>gb|ABA96372.1| arabinoxylan arabinofuranohydrolase isoenzyme AXAH-II [Oryza sativa(japonica cultivar-group)] gb|ABA96371.1| arabinoxylan arabinofuranohydrolase isoenzyme AXAH-II [Oryza sativa (japonica cultivar-group)]	660	3E-52
					>gb|AAK21880.1| arabinoxylan arabinofuranohydrolase isoenzyme AXAH-II [Hordeumvulgare]	656	8E-48
					>gb|AAK21879.1| arabinoxylan arabinofuranohydrolase isoenzyme AXAH-I [Hordeumvulgare]	658	1E-45
					>gb|ABA96373.1| arabinoxylan arabinofuranohydrolase isoenzyme AXAH-I, putative[Oryza sativa (japonica cultivar-group)]	508	2E-39
					>gb|ABA96378.1| arabinoxylan arabinofuranohydrolase isoenzyme AXAH-I, putative[Oryza sativa (japonica cultivar-group)]	617	8E-39
DV493742	1.57E-02	F1<B73=Mo17	4.66	7	>gb|AAA33539.1| zein	238	2E-67
					>emb|CAA24723.1| unnamed protein product [Zea mays]sp|P04703|ZEA7 MAIZE Zein-alpha precursor (19 kDa) (Clone A20)	240	2E-67
					>gb|AAR84080.1| mutant 19 kDa S15P alpha-zein [Zea mays]	240	3E-67
					>gb|AAL16987.1| 19kD alpha zein B3 [Zea mays]sp|P06677|ZEA9 MAIZE Zein-alpha precursor (19 kDa) (Clone 19C2) gb|AAA33530.1| 19 kDa zein protein	240	4E-67
					>sp|P06676|ZEA8 MAIZE Zein-alpha precursor (19 kDa) (Clone 19C1)gb|AAA33529.1| 19 kDa zein protein	240	4E-67

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
DV551012	1.58E-02	B73<F1=Mo17	2.37	3	ns		
DV942799	1.58E-02	Mo17<B73	1.65	9	>ref|XP_463137.1| expressed protein [Oryza sativa (japonica cultivar-group)]gb|AAR89874.1| expressed protein [Oryza sativa (japonica cultivar-group)]	608	3E-9
					>gb|AAU10703.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	260	1E-8
					>gb|AAD39599.1| 10A19I.15 [Oryza sativa (japonica cultivar-group)]	275	1E-8
					>gb|AAV44105.1| unknown protein [Oryza sativa (japonica cultivar-group)]	1220	2E-8
					>gb|AAV43825.1| putative polyprotein [Oryza sativa (japonica cultivar-group)]	1067	2E-8
DV492769	1.58E-02	B73<F1=Mo17	4.39	3	>ref|XP_467184.1| putative ZR1 protein [Oryza sativa (japonica cultivar-group)]dbj|BAD27877.1| putative ZR1 protein [Oryza sativa (japonica cultivar-group)] dbj|BAD07566.1| putative ZR1 protein [Oryza sativa (japonica cultivar-group)]	978	4E-17
					>ref|XP_473660.1| OSJNBa0088A01.18 [Oryza sativa (japonica cultivar-group)]emb|CAD41378.2| OSJNBa0088A01.18 [Oryza sativa (japonica cultivar-group)]	1041	1E-11
					>emb|CAC84086.1| ZR1 protein [Medicago sativa]	1035	6E-11
					>dbj|BAD87854.1| putative ZR1 protein [Oryza sativa (japonica cultivar-group)]	1091	2E-9
					>ref|NP_914656.1| P0431G06.4 [Oryza sativa (japonica cultivar-group)]	1086	2E-9
CD568678	1.58E-02	B73<Mo17	1.35	4	>sp|P23225|GLTB_MAIZE Ferredoxin-dependent glutamate synthase, chloroplast precursor(Fd-GOGAT) gb|AAA33463.1| ferredoxin-dependent glutamate synthase	1616	e-107
					>emb|CAA73170.1| Fd-GOGAT protein [Oryza sativa (japonica cultivar-group)]	1169	e-101
					>emb|CAA73169.1| Fd-GOGAT protein [Oryza sativa (japonica cultivar-group)]	746	e-101
					>dbj|BAD31105.1| putative ferredoxin-dependent glutamate synthase, chloroplastprecursor [Oryza sativa (japonica cultivar-group)] dbj|BAD30339.1| putative ferredoxin-dependent glutamate synthase, chloroplast precursor [Oryza sativa (japonica cultivar-group)]	1612	e-101
					>ref|XP_479407.1| putative ferredoxin-dependent glutamate synthase, chloroplastprecursor [Oryza sativa (japonica cultivar-group)]	1640	3E-99
CD568393	1.59E-02	Mo17<B73=F1	1.23	11	>emb|CAB90214.1| putative elongation factor 1 beta [Hordeum vulgare subsp. vulgare]	226	3E-40
					>gb|AAR15081.1| translational elongation factor 1 subunit Bbeta [Pisum sativum]	231	2E-39
					>ref|XP_479153.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)]ref|XP_506463.1| PREDICTED P0616D06.117 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC16499.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)] dbj|BAA04903.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)] sp|Q40680|EF1D_ORYSA Elongation factor 1-delta (EF-1-delta) (Elongation factor 1B-beta) (eEF-1B beta)	229	8E-39
					>gb|AAU89237.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)]dbj|BAA34599.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)] dbj|BAA34598.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)]	226	8E-39
					>gb|ABA81875.1| putative elongation factor 1B alpha-subunit0like [Solanumtuberosum] gb|ABA40427.1| unknown [Solanum tuberosum]	227	2E-38
BM074169	1.59E-02	Mo17<B73	1.41	9	>ref|NP_974857.1| unknown protein [Arabidopsis thaliana]	96	4E-18
					>gb|AAU44468.1| hypothetical protein AT3G01015 [Arabidopsis thaliana]gb|AAY78731.1| hypothetical protein At3g01015 [Arabidopsis thaliana]	488	2E-16
					>ref|NP_186749.1| unknown protein [Arabidopsis thaliana]gb|AAG51320.1| hypothetical protein; 557-2776 [Arabidopsis thaliana]	488	2E-16
					>ref|NP_197055.2| unknown protein [Arabidopsis thaliana]	497	7E-16
					>emb|CAC01750.1| putative protein [Arabidopsis thaliana]	494	5E-14
BM072978	1.60E-02	Mo17<B73	1.28	9	ns		
CB885484	1.60E-02	B73=F1<Mo17	1.44	4	ns		
CD651002	1.60E-02	Mo17<B73=F1	1.24	10	ns		
CD527934	1.61E-02	B73<F1=Mo17	1.21	3	>dbj|BAD35357.1| putative yip1 interacting factor [Oryza sativa (japonicacultivar-group)] dbj|BAD35445.1| putative yip1 interacting factor [Oryza sativa (japonica cultivar-group)]	264	2E-72
					>ref|NP_564367.1| unknown protein [Arabidopsis thaliana]gb|AAM44952.1| unknown protein [Arabidopsis thaliana] gb|AAK64057.1| unknown protein [Arabidopsis thaliana] gb|AAM63447.1| unknown [Arabidopsis thaliana]	269	4E-56
					>ref|XP_474581.1| OSJNBa0019G23.6 [Oryza sativa (japonica cultivar-group)]emb|CAE02114.2| OSJNBa0019G23.6 [Oryza sativa (japonica cultivar-group)]	280	1E-55
					>ref|NP_191509.2| unknown protein [Arabidopsis thaliana]	269	2E-55
					>emb|CAB75447.1| putative protein [Arabidopsis thaliana]	259	3E-55
CA829297	1.61E-02	F1=Mo17<B73	1.62	8	ns		
DV494025	1.61E-02	B73<F1=Mo17	1.26	2	>ref|XP_467656.1| putative caleosin [Oryza sativa (japonica cultivar-group)]dbj|BAD16161.1| putative caleosin [Oryza sativa (japonica cultivar-group)]	217	2E-38
					>ref|XP_467658.1| putative calcium binding protein [Oryza sativa (japonicacultivar-group)] dbj|BAD15887.1| putative calcium binding protein [Oryza sativa (japonica cultivar-group)] dbj|BAD16163.1| putative calcium binding protein [Oryza sativa (japonica cultivar-group)]	373	8E-36
					>dbj|BAD46173.1| putative calcium binding protein [Oryza sativa (japonicacultivar-group)] dbj|BAD45232.1| putative calcium binding protein [Oryza sativa (japonica cultivar-group)]	215	6E-33
					>gb|AAS48644.1| putative ABA-induced protein [Cynodon dactylon]	208	2E-32
					>gb|AAZ23153.1| putative calcium binding protein [Phaseolus vulgaris]	107	2E-30
DV622337	1.61E-02	F1=Mo17<B73	1.25	9	>emb|CAD59410.1| SMC2 protein [Oryza sativa]	1175	7E-50
					>dbj|BAD82795.1| SMC2 protein [Oryza sativa (japonica cultivar-group)]	1175	7E-50

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>ref|NP 201047.1| SMC2 (STRUCTURAL MAINTENANCE OF CHROMOSOMES 2) [Arabidopsis thaliana]	1175	2E-44
					>gb|AAG53093.1| SMC2-1 [Arabidopsis thaliana]	1175	2E-44
					>gb|AAG27593.2| SMC2-like condensin [Arabidopsis thaliana]gb|AAK58634.1| SMC2-like condensin [Arabidopsis thaliana]	1177	2E-44
DV549967	1.61E-02	Mo17<B73=F1	1.28	11	>ref|XP_468478.1| putative Vacuolar ATP synthase subunit F [Oryza sativa (japonicacultivar-group)] dbj|BAD22867.1| putative Vacuolar ATP synthase subunit F [Oryza sativa (japonica cultivar-group)]	130	2E-58
					>ref|NP_192171.1| hydrogen-transporting ATP synthase, rotational mechanism /hydrogen-transporting ATPase, rotational mechanism [Arabidopsis thaliana] gb|AAC78269.1| putative vacuolar ATPase [Arabidopsis thaliana] emb|CAB80755.1| putative vacuolar ATPase [Arabidopsis thaliana] gb|AAM51311.1| putative vacuolar ATPase [Arabidopsis thaliana] gb|AAL38753.1| putative vacuolar ATPase [Arabidopsis thaliana] gb|AAM60868.1| putative vacuolar ATPase [Arabidopsis thaliana] pir||T01087 H+-exporting ATPase (EC 3.6.3.6) 14K chain, vacuolar - Arabidopsis thaliana sp|Q9ZQX4|VATF_ARATH Probable vacuolar ATP synthase subunit F (V-ATPase F subunit) (Vacuolar proton pump F subunit) (V-ATPase 14 kDa subunit)	128	2E-52
					>gb|ABC60334.1| putative vacuolar ATP synthase subunit F [Musa acuminata]	117	2E-47
					>ref|XP 645434.1| hypothetical protein DDB0216933 [Dictyostelium discoideum]gb|EAL71520.1| hypothetical protein DDB0216933 [Dictyostelium discoideum]	120	1E-31
					>emb|CAE57827.1| Hypothetical protein CBG00852 [Caenorhabditis briggsae]	121	2E-31
DV622539	1.61E-02	B73<Mo17	1.26	3	>ref|NP_922506.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAM88632.1| unknown protein [Oryza sativa (japonica cultivar-group)] gb|AAP54793.1| expressed protein [Oryza sativa (japonica cultivar-group)]	246	1E-49
					>ref|NP_194298.1| unknown protein [Arabidopsis thaliana]emb|CAB81378.1| putative protein [Arabidopsis thaliana] emb|CAB43699.1| putative protein [Arabidopsis thaliana] gb|AAM61523.1| unknown [Arabidopsis thaliana] gb|AAO24562.1| At4g25680 [Arabidopsis thaliana]	252	5E-32
					>ref|NP_194296.1| unknown protein [Arabidopsis thaliana]emb|CAB81376.1| putative protein [Arabidopsis thaliana] emb|CAB43697.1| putative protein [Arabidopsis thaliana] gb|AAQ55277.1| At4g25660 [Arabidopsis thaliana] gb|AAN72011.1| putative protein [Arabidopsis thaliana]	255	2E-30
					>ref|XP 550459.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD67713.1| unknown protein [Oryza sativa (japonica cultivar-group)]	187	1E-23
CB605160	1.61E-02	Mo17<B73=F1	1.28	10	>gb|AAI02537.1| Unknown (protein for MGC:127734) [Bos taurus]	157	9E-23
					>gb|AAU12568.1| ribosomal protein S14 [Felis catus]	120	4E-22
					>gb|AAK95196.1| 40S ribosomal protein S14 [Ictalurus punctatus]	151	4E-22
					>dbj|BAC56579.1| similar to ribosomal protein S14 [Bos taurus]	145	4E-22
					>emb|CAA33143.1| unnamed protein product [Rattus norvegicus]ref|NP_073163.1| ribosomal protein S14 [Rattus norvegicus] sp|P13471|RS14_RAT 40S ribosomal protein S14	151	4E-22
CA989073	1.62E-02	F1=Mo17<B73	1.3	9	>ref|XP_463024.1| putative ribosomal protein [Oryza sativa (japonica cultivar-group)]gb|AAR10854.1| putative ribosomal protein [Oryza sativa (japonica cultivar-group)]	228	e-105
					>gb|AAM92710.1| putative 40S ribosomal protein S3 [Triticum aestivum]	227	e-104
					>ref|XP_479106.1| putative 40S ribosomal protein [Oryza sativa (japonicacultivar-group)] dbj|BAD32034.1| putative 40S ribosomal protein [Oryza sativa (japonica cultivar-group)] gb|AAK55780.1| Putative 40S ribosomal protein; contains C-terminal domain [Oryza sativa] dbj|BAC84635.1| putative 40S ribosomal protein [Oryza sativa (japonica cultivar-group)]	233	e-101
					>gb|ABB87113.1| unknown [Solanum tuberosum]	238	4E-99
					>ref|NP_198403.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAM19959.1| AT5g35530/MOK9_14 [Arabidopsis thaliana] gb|AAL24165.1| AT5g35530/MOK9 14 [Arabidopsis thaliana] dbj|BAB08712.1| 40S ribosomal protein S3 [Arabidopsis thaliana]	248	8E-99
CB833692	1.62E-02	Mo17<B73=F1	1.23	10	>ref|XP_464199.1| putative ribosomal protein S14 [Oryza sativa (japonicacultivar-group)] ref|XP_506724.1| PREDICTED OJ9003_G05.34 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD25218.1| putative ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]	150	1E-62
					>sp|P19950|RS141 MAIZE 40S ribosomal protein S14 (Clone MCH1)	149	1E-61
					>ref|XP_472410.1| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)]emb|CAE02065.2| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)] dbj|BAD29299.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)] dbj|BAD27798.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]	151	1E-61
					>gb|AAO41731.1| cytoplasmic ribosomal protein S14 [Brassica napus]	150	4E-60
					>gb|ABC01912.1| ribosomal protein S14-like protein [Solanum tuberosum]gb|ABB87124.1| hypothetical protein [Solanum tuberosum]	150	6E-60
BM340717	1.62E-02	Mo17<B73=F1	1.3	11	>ref|NP_910584.1| EST AU082567(S21715) corresponds to a region of the predictedgene.~Similar to S.tuberosum ubiquinol cytochrome c reductase. (X79275) [Oryza sativa (japonica cultivar-group)] ref|NP_910574.1| EST AU082567(S21715) corresponds to a region of the predicted gene.~Similar to S.tuberosum ubiquinol-cytochrome c reductase. (X79275) [Oryza sativa (japonica cultivar-group)] dbj|BAA95831.1| putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein [Oryza sativa (japonica cultivar-group)] dbj|BAA95821.1| putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein [Oryza sativa (japonica cultivar-group)]	72	6E-34
					>ref|NP_187697.1| ubiquinol-cytochrome-c reductase [Arabidopsis thaliana]gb|AAF19563.1| putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein (QP-C) [Arabidopsis thaliana] gb|AAN17451.1| putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein (QP-C) [Arabidopsis thaliana] gb|AAP21315.1| At3g10860 [Arabidopsis thaliana] gb|AAM64437.1| putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein (QP-C) [Arabidopsis thaliana]	72	8E-28
					>ref|NP_196156.1| ubiquinol-cytochrome-c reductase [Arabidopsis thaliana]gb|AAQ65099.1| At5g05370 [Arabidopsis thaliana] dbj|BAB09980.1| ubiquinol-cytochrome C reductase complex ubiquinone-binding protein [Arabidopsis thaliana]	72	3E-26

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>emb|CAA55862.1| ubiquinol--cytochrome c reductase [Solanum tuberosum]sp|P46269|UCRQ_SOLTU Ubiquinol-cytochrome c reductase complex ubiquinone-binding protein QP-C (Ubiquinol-cytochrome c reductase complex 8.2 kDa protein) prf||2107179A cytochrome c oxidase:SUBUNIT=8.2kD	72	4E-26
					>gb|AAP80673.1| cytochrome reductase [Triticum aestivum]	115	5E-12
CD001357	1.62E-02	B73<F1=Mo17	1.27	3	>sp|P49036|SUS2_MAIZE Sucrose synthase 2 (Sucrose-UDP glucosyltransferase 2)gb|AAA33515.1| sucrose synthase 2 gb|AAA33514.1| UDP-glucose:D-fructose 2-glucosyl-transferase	816	1E-75
					>gb|AAA68209.1| sus1 gene product	816	3E-75
					>gb|AAK52129.1| sucrose-UDP glucosyltransferase 2 [Oryza sativa (japonicacultivar-group)] ref|NP_909830.1| sucrose-UDP glucosyltransferase 2 [Oryza sativa] emb|CAA41774.1| sucrose-UDP glucosyltransferase (isoenzyme 2) [Oryza sativa (japonica cultivar-group)] sp|P31924|SUS2_ORYSA Sucrose synthase 2 (Sucrose-UDP glucosyltransferase 2) prf||2207194A sucrose synthase:ISOTYPE=2	816	3E-72
					>gb|AAV64256.2| sucrose synthase [Bambusa oldhamii]	816	5E-72
					>gb|AAL50570.1| sucrose synthase [Bambusa oldhamii]	816	1E-71
DV491449	1.62E-02	B73<F1=Mo17	1.45	3	>ref|XP_467761.1| putative ATPase [Oryza sativa (japonica cultivar-group)]dbj|BAD16127.1| putative ATPase [Oryza sativa (japonica cultivar-group)] dbj|BAD15543.1| putative ATPase [Oryza sativa (japonica cultivar-group)]	406	2E-34
					>ref|NP_187646.2| ATP binding [Arabidopsis thaliana]	411	4E-32
					>gb|AAF02825.1| putative ATPase [Arabidopsis thaliana]	386	2E-29
					>ref|NP_200881.2| ATP binding [Arabidopsis thaliana]gb|AAV43781.1| At5g60730 [Arabidopsis thaliana] gb|AAU84673.1| At5g60730 [Arabidopsis thaliana]	391	1E-28
					>dbj|BAB09846.1| arsenite translocating ATPase-like protein [Arabidopsis thaliana]	417	1E-28
DV494555	1.63E-02	B73=F1<Mo17	1.48	5	ns		
CB833751	1.63E-02	B73<F1=Mo17	1.22	3	>ref|XP_465873.1| ubiquitin-associated (UBA)/TS-N domain-containing protein-like[Oryza sativa (japonica cultivar-group)] dbj|BAD23227.1| ubiquitin-associated (UBA)/TS-N domain-containing protein-like [Oryza sativa (japonica cultivar-group)]	414	5E-70
					>ref|NP_563718.1| nucleic acid binding / zinc ion binding [Arabidopsis thaliana]gb|AAN15466.1| Unknown protein [Arabidopsis thaliana] gb|AAL32687.1| Unknown protein [Arabidopsis thaliana] gb|AAM65971.1| unknown [Arabidopsis thaliana] gb|AAF40452.1| ESTs gb|N65605, gb|N38087, gb|T20485, gb|T13726, gb|N38339, gb|F15440 and gb|N97201 come from this gene. [Arabidopsis thaliana]	413	7E-54
					>ref|XP_483435.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]dbj|BAD08748.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	417	1E-14
					>gb|AAU44584.1| hypothetical protein AT5G48690 [Arabidopsis thaliana]	193	3E-9
					>ref|NP_199680.2| unknown protein [Arabidopsis thaliana]gb|AAU44583.1| hypothetical protein AT5G48690 [Arabidopsis thaliana] gb|AAX23931.1| hypothetical protein At5g48690 [Arabidopsis thaliana]	323	3E-9
DV549419	1.63E-02	B73=Mo17<F1	1.34	12	>dbj|BAB72003.1| single-strand DNA endonuclease-1 [Oryza sativa (japonicacultivar-group)]	641	4E-6
CD568523	1.63E-02	Mo17<B73=F1	1.62	11	>gb|AAB94293.1| polyphenol oxidase	615	1E-12
CD527510	1.64E-02	B73<Mo17	1.4	4	ns		
BM337218	1.64E-02	Mo17<B73	1.95	10	>ref|XP_472671.1| OSJNBa0086B14.13 [Oryza sativa (japonica cultivar-group)]emb|CAD40841.3| OSJNBa0086B14.13 [Oryza sativa (japonica cultivar-group)]	491	8E-26
					>ref|XP_466409.1| putative glucosyltransferase-10 [Oryza sativa (japonicacultivar-group)] dbj|BAD34262.1| putative glucosyltransferase-10 [Oryza sativa (japonica cultivar-group)]	487	2E-21
					>ref|XP_466413.1| putative UDP-glycosyltransferase 85A8 [Oryza sativa (japonicacultivar-group)] dbj|BAD29561.1| putative UDP-glycosyltransferase 85A8 [Oryza sativa (japonica cultivar-group)] dbj|BAD34266.1| putative UDP-glycosyltransferase 85A8 [Oryza sativa (japonica cultivar-group)]	493	2E-20
					>ref|XP_471822.1| OSJNBb0026L04.6 [Oryza sativa (japonica cultivar-group)]emb|CAE01501.2| OSJNBb0026L04.6 [Oryza sativa (japonica cultivar-group)]	476	3E-20
					>ref|XP_471860.1| OSJNBb0033P05.8 [Oryza sativa (japonica cultivar-group)]emb|CAE05669.3| OSJNBb0033P05.8 [Oryza sativa (japonica cultivar-group)]	492	3E-19
DV491619	1.64E-02	B73=F1<Mo17	1.5	4	>ref|XP_476718.1| putative prolyl-tRNA synthetase [Oryza sativa (japonicacultivar-group)] dbj|BAC79747.1| putative prolyl-tRNA synthetase [Oryza sativa (japonica cultivar-group)]	545	1E-71
					>ref|NP_200065.1| ATP binding / proline-tRNA ligase/ tRNA ligase [Arabidopsisthaliana] gb|AAQ65189.1| At5g52520 [Arabidopsis thaliana] dbj|BAD44184.1| prolyl tRNA synthetase [Arabidopsis thaliana] dbj|BAB10183.1| prolyl tRNA synthetase [Arabidopsis thaliana]	543	1E-60
					>dbj|BAC78195.1| prolyl-tRNA synthetase [Raphanus sativus]	544	2E-58
					>ref|ZP_00768136.1| Prolyl-tRNA synthetase, archael and euk type [Chloroflexusaurantiacus J-10-fl] gb|EAO58777.1| Prolyl-tRNA synthetase, archael and euk type [Chloroflexus aurantiacus J-10-fl]	480	7E-31
					>emb|CAH08215.1| prolyl-tRNA synthetase [Bacteroides fragilis NCTC 9343]dbj|BAD49183.1| prolyl-tRNA synthetase [Bacteroides fragilis YCH46] ref|YP_099717.1| prolyl-tRNA synthetase [Bacteroides fragilis YCH46] ref|YP_212139.1| prolyl-tRNA synthetase [Bacteroides fragilis NCTC 9343]	497	1E-22
CB617023	1.64E-02	B73<F1=Mo17	1.27	2	ns		
CB885490	1.64E-02	B73<F1=Mo17	1.2	3	>ref|XP_464508.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryzasativa (japonica cultivar-group)] dbj|BAD25481.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa (japonica cultivar-group)] dbj|BAD15843.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa (japonica cultivar-group)] dbj|BAB17625.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa (japonica cultivar-group)]	400	8E-85
					>dbj|BAD36121.1| putative 26S proteasome regulatory particle triple-A ATPasesubunit4 [Oryza sativa (japonica cultivar-group)] dbj|BAD35613.1| putative 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa (japonica cultivar-group)]	401	3E-78

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_175120.1| ATP binding / ATPase/ hydrolase/ nucleoside-triphosphatase/nucleotide binding [Arabidopsis thaliana] gb|AAM47992.1| 26S proteasome AAA-ATPase subunit RPT4a-like protein [Arabidopsis thaliana] gb|AAL32787.1| similar to 26S proteasome AAA-ATPase subunit RPT4a [Arabidopsis thaliana] gb|AAF69154.1| F27F5.8 [Arabidopsis thaliana]	399	5E-77
					>ref|NP_199115.1| RPT4A; ATPase [Arabidopsis thaliana]gb|AAL77741.1| AT5g43010/MBD2_21 [Arabidopsis thaliana] gb|AAK50085.1| AT5g43010/MBD2_21 [Arabidopsis thaliana] dbj|BAB09203.1| 26S proteasome AAA-ATPase subunit RPT4a [Arabidopsis thaliana] gb|AAF22524.1| 26S proteasome AAA-ATPase subunit RPT4a [Arabidopsis thaliana]	399	5E-75
					>gb|ABA40428.1| 26S proteasome AAA-ATPase subunit RPT4a-like protein [Solanumtuberosum] dbj|BAC23035.1| 26S proteasome AAA-ATPase subunit RPT4a [Solanum tuberosum]	398	6E-75
DV551276	1.64E-02	B73<Mo17	1.42	4	>dbj|BAD28168.1| putative LepA protein [Oryza sativa (japonica cultivar-group)]dbj|BAD28023.1| putative LepA protein [Oryza sativa (japonica cultivar-group)]	680	8E-38
					>gb|AAM91119.1| GTP-binding protein LepA-like protein [Arabidopsis thaliana]gb|AAM12957.1| GTP-binding protein LepA homolog [Arabidopsis thaliana]	681	4E-36
					>dbj|BAB10014.1| GTP-binding protein LepA homolog [Arabidopsis thaliana]	675	4E-36
					>ref|NP 196482.2| GTP binding / translation elongation factor [Arabidopsis thaliana]	681	4E-36
					>ref|ZP_00518999.1| Small GTP-binding protein domain:GTP-binding protein LepA[Crocosphaera watsonii WH 8501] gb|EAM47913.1| Small GTP-binding protein domain:GTP-binding protein LepA [Crocosphaera watsonii WH 8501]	603	1E-29
DV491119	1.64E-02	B73<F1	1.26	1	>ref|XP_469531.1| putative GTP-binding protein [Oryza sativa (japonicacultivar-group)] gb|AAL58207.1| putative GTP-binding protein [Oryza sativa (japonica cultivar-group)]	611	1E-92
					>ref|NP_172936.1| ADL1C (DYNAMIN-LIKE PROTEIN 5); GTP binding / GTPase [Arabidopsisthaliana] gb|AAN12911.1| putative dynamin protein [Arabidopsis thaliana] gb|AAK64059.1| putative dynamin protein [Arabidopsis thaliana] emb|CAC19656.1| dynamin-like protein DLP1 [Arabidopsis thaliana] sp|Q8LF21|DRP1C ARATH Dynamin-related protein 1C (Dynamin-like protein C) (Dynamin-like protein 5) (Dynamin-like protein DLP1)	614	2E-69
					>gb|AAL92170.1| dynamin-like protein C [Arabidopsis thaliana]	611	2E-69
					>gb|AAF22293.1| dynamin-like protein 5 [Arabidopsis thaliana]	614	2E-69
					>gb|AAM61645.1| dynamin, putative [Arabidopsis thaliana]	614	6E-69
CB381671	1.64E-02	B73<F1=Mo17	1.32	3	>emb|CAA55022.1| beta tubulin [Oryza sativa (japonica cultivar-group)]	447	2E-50
					>emb|CAE52516.1| beta tubulin [Setaria viridis]	448	2E-50
					>ref|NP_915874.1| tubulin beta chain [Oryza sativa (japonica cultivar-group)]dbj|BAB92274.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] dbj|BAA06381.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|P45960|TBB4 ORYSA Tubulin beta-4 chain (Beta-4 tubulin)	447	2E-50
					>gb|AAA66495.1| beta-tubulin	447	2E-50
					>sp|Q41783|TBB6 MAIZE Tubulin beta-6 chain (Beta-6 tubulin)gb|AAA20186.1| beta-6 tubulin	446	2E-50
BM074017	1.64E-02	Mo17<B73=F1	1.26	10	>ref|XP_482582.1| putative ribosomal protein [Oryza sativa (japonica cultivar-group)]dbj|BAD10146.1| putative ribosomal protein [Oryza sativa (japonica cultivar-group)]	118	3E-46
					>ref|XP_480178.1| putative ribosomal protein L34 [Oryza sativa (japonicacultivar-group)] dbj|BAC99505.1| putative ribosomal protein L34 [Oryza sativa (japonica cultivar-group)]	118	3E-46
					>gb|AAW50987.1| ribosomal protein l34 [Triticum aestivum]	119	3E-45
					>gb|AAT38711.1| Ribosomal protein L34e [Solanum demissum]gb|AAT39969.1| 60S ribosomal protein L34 [Solanum demissum]	120	8E-44
					>sp|P41098|RL34 TOBAC 60S ribosomal protein L34gb|AAA57159.1| 60S ribosomal protein L34 gb|AAA57158.1| 60S ribosomal protein L34	120	9E-43
DV621521	1.65E-02	Mo17<B73=F1	1.19	10	>gb|AAV25644.1| putative nucleic acid binding protein [Oryza sativa (japonicacultivar-group)]	258	2E-36
					>ref|NP_172903.1| DNA binding / protein binding / zinc ion binding [Arabidopsisthaliana] gb|AAM65633.1| nucleic acid binding protein (alfin-1), putative [Arabidopsis thaliana] gb|AAP12848.1| At1g14510 [Arabidopsis thaliana]	252	3E-36
					>gb|AAF43952.1| Contains similarity to an Alfalfa nucleic acid binding protein fromMedicago sativa gb|L07291.1 and contains a PHD-finger PF|00628 domain. ESTs gb|AI995787, gb|AA721930, gb|T42258 come from this gene. [Arabidopsis thaliana]	273	3E-36
					>gb|AAY27262.1| putative alfin-like transcription factor [Solanum tuberosum]	248	3E-35
					>gb|AAX95841.1| probable zinc finger protein - alfalfa (fragment) [Oryza sativa(japonica cultivar-group)] gb|AAX92933.1| probable zinc finger protein - alfalfa (fragment) [Oryza sativa (japonica cultivar-group)] gb|ABA92392.1| zinc finger protein, putative [Oryza sativa (japonica cultivar-group)]	264	4E-35
CB885309	1.65E-02	Mo17<B73=F1	1.18	11	>gb|AAL76334.1| putative G-box binding protein [Oryza sativa]dbj|BAD45657.1| G-box binding protein-like [Oryza sativa (japonica cultivar-group)] gb|AAB65433.1| HvB12D homolog [Oryza sativa]	89	4E-40
					>emb|CAA70936.1| B12Dg1 [Hordeum vulgare subsp. vulgare]emb|CAA54065.1| HvB12D [Hordeum vulgare subsp. vulgare]	87	2E-38
					>gb|AAD22104.1| B12D protein [Ipomoea batatas]	90	2E-33
					>ref|NP_190397.1| unknown protein [Arabidopsis thaliana]emb|CAB51061.1| B12D-like protein [Arabidopsis thaliana] gb|AAL91215.1| B12D-like protein [Arabidopsis thaliana] gb|AAN65070.1| B12D-like protein [Arabidopsis thaliana] pir||T13003 hypothetical protein T24C20.20 - Arabidopsis thaliana	88	2E-31
					>ref|XP_477421.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]dbj|BAC84633.1| putative B12D protein [Oryza sativa (japonica cultivar-group)] dbj|BAD31625.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]	98	1E-28
CB331016	1.66E-02	B73=Mo17<F1	1.33	1	>gb|AAU10700.1| putative glucose-1-phosphate adenylyltransferase [Oryza sativa(japonica cultivar-group)]	519	6E-13
					>gb|AAD39597.1| 10A19I.12 [Oryza sativa (japonica cultivar-group)]	529	6E-13

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>dbj|BAA23490.1| ADP glucose pyrophosphorylase large subunit [Oryza sativa (japonicacultivar-group)]	519	6E-13
					>emb|CAD98749.1| ADP-glucose pyrophosphorylase large subunit [Triticum aestivum]	522	1E-12
					>emb|CAA79980.1| ADP-glucose pyrophosphorylase large subunit [Triticum aestivum]sp|P12299|GLGL2_WHEAT Glucose-1-phosphate adenylyltransferase large subunit, chloroplast precursor (ADP-glucose synthase) (ADP-glucose pyrophosphorylase) (AGPASE S) (Alpha-D-glucose-1-phosphate adenyl transferase)	522	1E-12
CB250119	1.66E-02	B73<F1=Mo17	1.31	2	ns		
DV489836	1.66E-02	B73<F1=Mo17	1.64	3	>ref|XP_467554.1| putative proliferating cell nuclear protein P120 [Oryza sativa(japonica cultivar-group)] dbj|BAD13040.1| putative proliferating cell nuclear protein P120 [Oryza sativa (japonica cultivar-group)] dbj|BAD12915.1| putative proliferating cell nuclear protein P120 [Oryza sativa (japonica cultivar-group)]	682	4E-12
					>dbj|BAD33889.1| putative nucleolar protein [Oryza sativa (japonica cultivar-group)]	699	3E-8
DV622298	1.67E-02	B73<F1=Mo17	1.34	3	>ref|XP 483358.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD09694.1| unknown protein [Oryza sativa (japonica cultivar-group)]	447	5E-44
					>ref|NP_188661.2| unknown protein [Arabidopsis thaliana]dbj|BAD94700.1| hypothetical protein [Arabidopsis thaliana] gb|AAM97062.1| unknown protein [Arabidopsis thaliana] gb|AAN72131.1| unknown protein [Arabidopsis thaliana]	437	1E-24
					>ref|NP 177526.2| unknown protein [Arabidopsis thaliana]gb|AAS99684.1| At1g73850 [Arabidopsis thaliana] gb|AAR92284.1| At1g73850 [Arabidopsis thaliana]	559	2E-12
					>ref|NP 909111.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAB03388.1| unknown protein [Oryza sativa (japonica cultivar-group)]	633	5E-12
					>gb|AAG52080.1| unknown protein; 95319-98330 [Arabidopsis thaliana]	651	2E-10
DV942434	1.67E-02	F1=Mo17<B73	1.62	9	>dbj|BAD82523.1| microtubule-associated protein-like [Oryza sativa (japonicacultivar-group)]	689	7E-43
					>gb|AAT85198.1| unknown protein [Oryza sativa (japonica cultivar-group)]	662	2E-38
					>gb|AAT40494.1| putative microtubule-associated protein [Solanum demissum]	730	1E-31
					>ref|NP 199973.1| PLE (PLEIADE) [Arabidopsis thaliana]dbj|BAB08676.1| unnamed protein product [Arabidopsis thaliana]	707	8E-28
					>ref|NP 201031.1| unknown protein [Arabidopsis thaliana]gb|AAY78877.1| microtubule associated protein [Arabidopsis thaliana]	549	1E-23
DV496057	1.67E-02	Mo17<B73=F1	1.34	11	>dbj|BAD73292.1| putative ATP-dependent Clp protease, proteolytic subunit [Oryzasativa (japonica cultivar-group)]	308	5E-92
					>gb|AAM54134.1| ATP-dependent Clp protease [Oryza sativa (indica cultivar-group)]	191	1E-89
					>ref|NP 918617.1| putative ATP-dependent Clp protease [Oryza sativa (japonicacultivar-group)]	317	1E-89
					>ref|NP_564880.1| CLPP3; endopeptidase Clp [Arabidopsis thaliana]gb|AAM64899.1| ATP-dependent Clp protease proteolytic subunit ClpP3 [Arabidopsis thaliana] gb|AAG60075.1| ATP-dependent Clp protease (nClpP3) [Arabidopsis thaliana] gb|AAG51173.1| ATP-dependent Clp protease (nClpP3) [Arabidopsis thaliana] dbj|BAA82067.1| nClpP3 [Arabidopsis thaliana]	309	2E-59
					>gb|AAC35489.1| clp protease [Arabidopsis thaliana]	310	2E-59
DV549666	1.67E-02	B73<F1=Mo17	1.23	2	>ref|XP_477421.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]dbj|BAC84633.1| putative B12D protein [Oryza sativa (japonica cultivar-group)] dbj|BAD31625.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]	98	5E-33
					>gb|AAL76334.1| putative G-box binding protein [Oryza sativa]dbj|BAD45657.1| G-box binding protein-like [Oryza sativa (japonica cultivar-group)] gb|AAB65433.1| HvB12D homolog [Oryza sativa]	89	6E-30
					>gb|AAD22104.1| B12D protein [Ipomoea batatas]	90	8E-30
					>ref|NP_190397.1| unknown protein [Arabidopsis thaliana]emb|CAB51061.1| B12D-like protein [Arabidopsis thaliana] gb|AAL91215.1| B12D-like protein [Arabidopsis thaliana] gb|AAN65070.1| B12D-like protein [Arabidopsis thaliana] pir||T13003 hypothetical protein T24C20.20 - Arabidopsis thaliana	88	7E-29
					>emb|CAA70936.1| B12Dg1 [Hordeum vulgare subsp. vulgare]emb|CAA54065.1| HvB12D [Hordeum vulgare subsp. vulgare]	87	4E-27
CD001711	1.68E-02	B73<F1=Mo17	1.3	3	ns		
CD527826	1.68E-02	B73<F1=Mo17	1.31	3	>emb|CAA66900.2| annexin p33 [Zea mays]	314	1E-97
					>dbj|BAD37678.1| putative annexin [Oryza sativa (japonica cultivar-group)]	317	1E-85
					>ref|XP_467846.1| putative annexin P35 [Oryza sativa (japonica cultivar-group)]dbj|BAD17230.1| putative annexin P35 [Oryza sativa (japonica cultivar-group)] dbj|BAD15571.1| putative annexin P35 [Oryza sativa (japonica cultivar-group)]	314	1E-82
					>emb|CAA66901.1| annexin p35 [Zea mays]	314	1E-78
					>gb|AAC33305.1| fiber annexin [Gossypium hirsutum]	316	1E-68
DV621761	1.68E-02	Mo17<B73=F1	1.27	11	>ref|XP 466633.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD20133.1| unknown protein [Oryza sativa (japonica cultivar-group)]	243	2E-30
CD001707	1.68E-02	Mo17<B73=F1	1.23	10	>gb|ABA93723.1| ribosomal protein S7 [Oryza sativa (japonica cultivar-group)]	199	9E-76
					>ref|NP_908322.1| putative 40S ribosomal protein S5 [Oryza sativa (japonicacultivar-group)] dbj|BAB64234.1| putative 40S ribosomal protein S5 [Oryza sativa (japonica cultivar-group)] dbj|BAB62621.1| putative 40S ribosomal protein S5 [Oryza sativa (japonica cultivar-group)]	200	2E-75
					>gb|AAR89617.1| 40S ribosomal protein S5 [Capsicum annuum]	212	6E-75
					>emb|CAA06491.1| 40S ribosomal protein S5 [Cicer arietinum]sp|O65731|RS5 CICAR 40S ribosomal protein S5	197	2E-74
					>emb|CAA70084.1| 40S ribosomal protein S5 [Nicotiana plumbaginifolia]sp|O24111|RS5 NICPL 40S ribosomal protein S5	154	3E-74
CB380605	1.68E-02	Mo17<B73=F1	1.35	10	ns		
DV489953	1.69E-02	Mo17<B73=F1	1.38	10	>ref|NP_918334.1| B1110C07.25 [Oryza sativa (japonica cultivar-group)]dbj|BAB90624.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAB89067.1| unknown protein [Oryza sativa (japonica cultivar-group)]	242	7E-50
					>emb|CAB96663.1| putative protein [Arabidopsis thaliana]	187	4E-35

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|NP_568247.1| unknown protein [Arabidopsis thaliana]gb|AAM45002.1| unknown protein [Arabidopsis thaliana] gb|AAK76546.1| unknown protein [Arabidopsis thaliana]	209	4E-35
					>gb|AAM13375.1| putative protein [Arabidopsis thaliana]gb|AAL32643.1| putative protein [Arabidopsis thaliana]	209	4E-35
					>gb|AAT69224.1| hypothetical protein At1g80200 [Arabidopsis thaliana]	235	4E-13
CB380918	1.69E-02	F1<Mo17	1.38	6	>gb|AAU44133.1| putative tRNA synthase [Oryza sativa (japonica cultivar-group)]	488	4E-39
					>gb|AAK73131.1| putative tRNA synthase [Oryza sativa]	525	4E-39
					>ref|NP 196950.1| pseudouridylate synthase/ transporter [Arabidopsis thaliana]emb|CAB87785.1| tRNA synthase-like protein [Arabidopsis thaliana]	540	4E-38
					>gb|AAO33771.1| putative tRNA pseudouridine synthase [Oryza sativa (indicacultivar-group)]	458	6E-28
					>ref|ZP_00949860.1| putative tRNA pseudouridine synthase [Croceibacter atlanticusHTCC2559] gb|EAP87999.1| putative tRNA pseudouridine synthase [Croceibacter atlanticus HTCC2559]	238	7E-17
CA829615	1.69E-02	Mo17<B73=F1	1.32	10	>ref|XP_464199.1| putative ribosomal protein S14 [Oryza sativa (japonicacultivar-group)] ref|XP_506724.1| PREDICTED OJ9003_G05.34 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD25218.1| putative ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]	150	7E-63
					>ref|XP_472410.1| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)]emb|CAE02065.2| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)] dbj|BAD29299.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)] dbj|BAD27798.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]	151	8E-62
					>sp|P19950|RS141 MAIZE 40S ribosomal protein S14 (Clone MCH1)	149	4E-61
					>gb|AAO41731.1| cytoplasmic ribosomal protein S14 [Brassica napus]	150	3E-60
					>gb|ABC01912.1| ribosomal protein S14-like protein [Solanum tuberosum]gb|ABB87124.1| hypothetical protein [Solanum tuberosum]	150	1E-59
CB351496	1.69E-02	Mo17<B73	1.28	10	ns		
DV943102	1.70E-02	B73=F1<Mo17	1.44	5	ns		
BM333894	1.70E-02	Mo17<B73=F1	1.74	10	>gb|AAQ06290.1| hypothetical protein [Zea mays]	872	6E-23
					>gb|AAQ06288.1| hypothetical protein [Zea mays]	872	6E-23
					>ref|XP 469012.1| putative yabby protein [Oryza sativa (japonica cultivar-group)]gb|AAC72848.1| unknown [Oryza sativa]	186	2E-21
					>gb|AAX95527.1| Putative YABBY protein [Oryza sativa (japonica cultivar-group)]	154	8E-18
					>gb|ABA99903.1| YABBY protein [Oryza sativa (japonica cultivar-group)]	207	2E-12
DV621943	1.71E-02	B73<F1=Mo17	1.31	3	>gb|AAD20980.1| translation initiation factor 4A2 [Zea mays]	215	1E-60
					>gb|AAB67607.1| translational initiation factor eIF-4A [Zea mays]	414	4E-60
					>emb|CAA55742.1| unnamed protein product [Nicotiana tabacum]sp|Q40467|IF414_TOBAC Eukaryotic initiation factor 4A-14 (ATP-dependent RNA helicase eIF4A-14) (eIF-4A-14)	413	5E-60
					>gb|AAB64289.1| translation initiation factor [Zea mays]	414	7E-60
					>ref|XP_464146.1| putative translational initiation factor eIF-4A [Oryza sativa(japonica cultivar-group)] dbj|BAD13081.1| putative translational initiation factor eIF-4A [Oryza sativa (japonica cultivar-group)]	414	9E-60
DV495564	1.71E-02	B73<F1	1.36	1	>ref|XP_550205.1| putative DNAJ domain-containing; methylation-controlled J protein[Oryza sativa (japonica cultivar-group)] dbj|BAD61437.1| putative DNAJ domain-containing; methylation-controlled J protein [Oryza sativa (japonica cultivar-group)]	112	4E-41
					>ref|NP_566352.1| heat shock protein binding / unfolded protein binding [Arabidopsisthaliana] gb|AAM65828.1| DNAJ protein-like [Arabidopsis thaliana] gb|AAF23300.1| unknown protein [Arabidopsis thaliana] gb|AAO42952.1| At3g09700 [Arabidopsis thaliana] dbj|BAC42440.1| unknown protein [Arabidopsis thaliana]	112	1E-39
					>ref|NP_565824.1| heat shock protein binding / unfolded protein binding [Arabidopsisthaliana] gb|AAM15345.1| expressed protein [Arabidopsis thaliana] gb|AAM15117.1| expressed protein [Arabidopsis thaliana] gb|AAM61135.1| DNAJ protein-like [Arabidopsis thaliana]	112	1E-38
					>ref|NP_195923.1| heat shock protein binding / unfolded protein binding [Arabidopsisthaliana] emb|CAB86070.1| DNAJ protein-like [Arabidopsis thaliana] gb|AAM63105.1| DNAJ protein-like [Arabidopsis thaliana]	112	3E-37
					>ref|NP 909805.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]gb|AAN65026.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	96	1E-31
DV490292	1.72E-02	B73<Mo17	3.03	4	>gb|ABA97510.1| transposon protein, putative, CACTA, En/Spm sub-class [Oryza sativa(japonica cultivar-group)]	754	3E-58
					>ref|NP_919799.1| putative transposase [Oryza sativa (japonica cultivar-group)]gb|AAL25182.1| Putative transposase [Oryza sativa] gb|AAP52086.1| transposon protein, putative, CACTA, En/Spm sub-class [Oryza sativa (japonica cultivar-group)]	435	8E-56
					>ref|NP_919670.1| putative transposase [Oryza sativa (japonica cultivar-group)]gb|AAM08737.1| Putative transposase [Oryza sativa (japonica cultivar-group)] gb|AAP51957.1| transposon protein, putative, CACTA, En/Spm sub-class [Oryza sativa (japonica cultivar-group)]	1003	6E-51
					>ref|XP 472829.1| OSJNBa0089K21.9 [Oryza sativa (japonica cultivar-group)]emb|CAE03055.2| OSJNBa0089K21.9 [Oryza sativa (japonica cultivar-group)]	461	6E-50
					>ref|NP_921846.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]gb|AAM93719.1| hypothetical protein [Oryza sativa (japonica cultivar-group)] gb|AAP54133.1| transposon protein, putative, CACTA, En/Spm sub-class [Oryza sativa (japonica cultivar-group)]	481	1E-49
DV490004	1.72E-02	Mo17<B73=F1	1.42	10	>ref|XP_463300.1| B1003B09.9 [Oryza sativa (japonica cultivar-group)]dbj|BAB91954.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAB89166.1| unknown protein [Oryza sativa (japonica cultivar-group)]	336	6E-12

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
CB604241	1.73E-02	B73<F1	1.38	2	>ref|XP_470658.1| Putative ascorbate peroxidase [Oryza sativa (japonicacultivar-group)] gb|AAP13093.1| ascorbate peroxidase [Oryza sativa (indica cultivar-group)] gb|AAO17000.1| Putative ascorbate peroxidase [Oryza sativa (japonica cultivar-group)] sp|P93404|APX1_ORYSA L-ascorbate peroxidase 1, cytosolic (APXa) dbj|BAA08264.1| ascorbate peroxidase [Oryza sativa]	250	2E-50
					>emb|CAA06996.1| ascorbate peroxidase [Hordeum vulgare subsp. vulgare]	250	1E-49
					>gb|AAA99518.1| ascorbate peroxidasedbj|BAA12890.1| cytosolic ascorbate peroxidase [Spinacia oleracea]	250	2E-49
					>gb|AAL08495.1| ascorbate peroxidase [Hordeum vulgare]	153	4E-49
					>emb|CAA84406.1| cytosolic ascorbate peroxidase [Zea mays]prf||2111423A ascorbate peroxidase	250	1E-48
DV494512	1.73E-02	B73<F1=Mo17	1.45	2	>ref|XP 493734.1| putative early nodulin [Oryza sativa (japonica cultivar-group)]dbj|BAA83567.1| putative early nodulin [Oryza sativa (japonica cultivar-group)]	116	2E-36
					>ref|XP_493732.1| putative early nodulin [Oryza sativa (japonica cultivar-group)]dbj|BAA83565.1| putative early nodulin [Oryza sativa (japonica cultivar-group)] dbj|BAA33814.1| early nodulin [Oryza sativa (japonica cultivar-group)] dbj|BAA33813.1| early nodulin [Oryza sativa (japonica cultivar-group)]	115	2E-36
					>ref|XP 493726.1| putative early nodulin [Oryza sativa (japonica cultivar-group)]dbj|BAA83559.1| putative early nodulin [Oryza sativa (japonica cultivar-group)]	116	4E-36
					>ref|XP 493735.1| putative early nodulin [Oryza sativa (japonica cultivar-group)]dbj|BAA83568.1| putative early nodulin [Oryza sativa (japonica cultivar-group)]	115	7E-36
					>ref|XP 493733.1| putative early nodulin [Oryza sativa (japonica cultivar-group)]dbj|BAA83566.1| putative early nodulin [Oryza sativa (japonica cultivar-group)]	115	9E-36
DV491904	1.73E-02	B73<F1=Mo17	1.25	2	ns		
DV494463	1.74E-02	B73<F1	1.3	1	>ref|NP 913585.1| putative DKFZP564O0463 protein [Oryza sativa (japonicacultivar-group)]	452	e-100
					>gb|AAN28840.1| At4g28450/F20O9_130 [Arabidopsis thaliana]gb|AAK73982.1| At4g28450/F20O9_130 [Arabidopsis thaliana] gb|AAK50083.1| AT4g28450/F20O9 130 [Arabidopsis thaliana]	452	1E-79
					>ref|NP 567810.2| nucleotide binding [Arabidopsis thaliana]	442	1E-79
					>gb|AAL32701.1| SOF1 protein-like protein [Arabidopsis thaliana]	452	4E-79
					>emb|CAB79647.1| SOF1 protein-like protein [Arabidopsis thaliana]emb|CAA16884.1| SOF1 protein-like protein [Arabidopsis thaliana]	283	4E-60
DV621268	1.74E-02	Mo17<B73=F1	1.18	10	>ref|XP_468478.1| putative Vacuolar ATP synthase subunit F [Oryza sativa (japonicacultivar-group)] dbj|BAD22867.1| putative Vacuolar ATP synthase subunit F [Oryza sativa (japonica cultivar-group)]	130	7E-64
					>ref|NP_192171.1| hydrogen-transporting ATP synthase, rotational mechanism /hydrogen-transporting ATPase, rotational mechanism [Arabidopsis thaliana] gb|AAC78269.1| putative vacuolar ATPase [Arabidopsis thaliana] emb|CAB80755.1| putative vacuolar ATPase [Arabidopsis thaliana] gb|AAM51311.1| putative vacuolar ATPase [Arabidopsis thaliana] gb|AAL38753.1| putative vacuolar ATPase [Arabidopsis thaliana] gb|AAM60868.1| putative vacuolar ATPase [Arabidopsis thaliana] pir||T01087 H+-exporting ATPase (EC 3.6.3.6) 14K chain, vacuolar - Arabidopsis thaliana sp|Q9ZQX4|VATF_ARATH Probable vacuolar ATP synthase subunit F (V-ATPase F subunit) (Vacuolar proton pump F subunit) (V-ATPase 14 kDa subunit)	128	1E-57
					>gb|ABC60334.1| putative vacuolar ATP synthase subunit F [Musa acuminata]	117	2E-52
					>ref|XP 645434.1| hypothetical protein DDB0216933 [Dictyostelium discoideum]gb|EAL71520.1| hypothetical protein DDB0216933 [Dictyostelium discoideum]	120	7E-32
					>emb|CAE57827.1| Hypothetical protein CBG00852 [Caenorhabditis briggsae]	121	2E-31
AI629785	1.74E-02	B73<Mo17	1.58	3	>dbj|BAD68693.1| WD-40 repeat family protein-like [Oryza sativa (japonicacultivar-group)]	1377	2E-57
					>ref|NP 917302.1| OSJNBb0006H05.17 [Oryza sativa (japonica cultivar-group)]	1003	2E-57
					>gb|AAZ31064.1| WD-40 repeat family protein [Medicago sativa]	417	4E-48
					>dbj|BAB09653.1| unnamed protein product [Arabidopsis thaliana]	1003	2E-46
					>ref|NP 197859.3| unknown protein [Arabidopsis thaliana]	1407	2E-46
CB885290	1.74E-02	B73=F1<Mo17	1.42	4	group)]	754	1E-7
					>ref|NP_922419.1| putative serine protease [Oryza sativa (japonica cultivar-group)]gb|AAO00703.1| putative serine protease [Oryza sativa (japonica cultivar-group)] gb|AAM12497.1| putative serine protease [Oryza sativa (japonica cultivar-group)] gb|AAP54706.1| serine protease, putative [Oryza sativa (japonica cultivar-	759	2E-6
CB815849	1.74E-02	Mo17<B73=F1	1.27	10	>gb|AAC03423.2| histone acetyltransferase HAT B [Zea mays]gb|AAF06742.1| histone acetyltransferase HAT-B-p50 [Zea mays]	468	2E-63
					>gb|AAM28228.1| histone acetyl transferase [Zea mays]	468	3E-63
					>dbj|BAD28482.1| putative histone acetyltransferase HAT B [Oryza sativa (japonicacultivar-group)] dbj|BAD28560.1| putative histone acetyltransferase HAT B [Oryza sativa (japonica cultivar-group)]	466	7E-50
					>ref|NP 200485.1| histone acetyltransferase [Arabidopsis thaliana]dbj|BAB09892.1| histone acetyltransferase HAT B [Arabidopsis thaliana]	467	2E-17
CB381127	1.75E-02	B73=F1<Mo17	1.38	4	>ref|XP_468744.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAP20836.1| hypothetical protein Os03g31010 [Oryza sativa (japonica cultivar-group)]	548	3E-19
CB250079	1.75E-02	Mo17<B73=F1	1.26	10	>sp|P40280|H2A MAIZE Histone H2Agb|AAB04687.1| histone H2A	159	4E-14
					>ref|NP 918596.1| putative histone H2A [Oryza sativa (japonica cultivar-group)]dbj|BAB44136.1| putative histone H2A [Oryza sativa (japonica cultivar-group)]	159	2E-13
					>ref|XP 475081.1| putative histone H2A [Oryza sativa (japonica cultivar-group)]gb|AAS75248.1| putative histone H2A [Oryza sativa (japonica cultivar-group)]	173	6E-13
					>emb|CAA37828.1| unnamed protein product [Petroselinum crispum]sp|P19177|H2A PETCR Histone H2A	149	2E-12
					>sp|P02276|H2A2 WHEAT Histone H2A.2.1	151	4E-12
CB240014	1.76E-02	Mo17<B73=F1	1.38	11	>gb|AAH67494.1| HIST1H3I protein [Homo sapiens]	137	2E-51
					>sp|P08860|H32 ORYSA Histone H3gb|AAA74190.1| histone H3 gb|AAA33907.1| histone 3	136	4E-51

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

<table>
<tr><th>GenBank accession no.</th><th>Overall P value</th><th>Significant pattern</th><th>Fold change†</th><th>Sector‡</th><th>BLAST annotation*</th><th>Score</th><th>E value</th></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_910496.1| histone H3 [Oryza sativa (japonica cultivar-group)]ref|NP_910502.1| histone H3 [Oryza sativa (japonica cultivar-group)] ref|NP_910501.1| histone H3 [Oryza sativa (japonica cultivar-group)] ref|NP_563838.1| DNA binding [Arabidopsis thaliana] ref|NP_189372.1| DNA binding [Arabidopsis thaliana] ref|NP_568227.1| DNA binding [Arabidopsis thaliana] ref|NP_201339.1| DNA binding [Arabidopsis thaliana] ref|NP_568228.1| DNA binding [Arabidopsis thaliana] ref|XP_475315.1| putative histone H3 [Oryza sativa (japonica cultivar-group)] ref|XP_472456.1| OSJNBb0108J11.17 [Oryza sativa (japonica cultivar-group)] ref|NP_915639.1| putative histone H3 [Oryza sativa (japonica cultivar-group)] gb|AAX92719.1| histone H3 - maize [Oryza sativa (japonica cultivar-group)] gb|AAT07615.1| putative histone H3 [Oryza sativa (japonica cultivar-group)] emb|CAA57811.1| Histone H3 [Asparagus officinalis] emb|CAA31970.1| unnamed protein product [Oryza sativa] emb|CAA31969.1| unnamed protein product [Oryza sativa] emb|CAB89404.1| histone H3-like protein [Arabidopsis thaliana]</td><td>136</td><td>4E-51</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA31965.1| unnamed protein product [Medicago sativa]emb|CAA31964.1| unnamed protein product [Medicago sativa] emb|CAA25451.1| unnamed protein product [Triticum aestivum] sp|P68428|H3_WHEAT Histone H3 gb|AAB81995.1| histone H3 [Onobrychis viciifolia] sp|P68427|H3_PEA Histone H3 sp|P68430|H3 ONOVI Histone H3 sp|P68429|H31 MEDSA Histone H3.1 (Major histone H3) gb|AAB49545.1| histone H3.1</td><td>136</td><td>4E-51</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAA32655.1| histone H3 (H3-1.1)</td><td>136</td><td>4E-51</td></tr>
<tr><td>CD058715</td><td>1.76E-02</td><td>Mo17<B73=F1</td><td>1.17</td><td>11</td><td>>dbj|BAD45357.1| putative Noc3p [Oryza sativa (japonica cultivar-group)]</td><td>846</td><td>6E-82</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP 178036.1| unknown protein [Arabidopsis thaliana]</td><td>495</td><td>4E-60</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAC17047.1| Similar to hypothetical protein YLR002c, gb|Z7314 from S.cerevisiae. [Arabidopsis thaliana]</td><td>884</td><td>2E-54</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAT68044.1| AD24 [Danio rerio]ref|NP_001002863.1| nucleolar complex associated 3 homolog [Danio rerio] sp|Q6DRN3|NOC3L_BRARE Nucleolar complex protein 3 homolog (NOC3 protein homolog) (NOC3-like protein) (Nucleolar complex-associated protein 3-like protein)</td><td>800</td><td>2E-24</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP 421670.1| PREDICTED: similar to chromosome 10 open reading frame 117; AD24protein [Gallus gallus]</td><td>1256</td><td>2E-24</td></tr>
<tr><td>BM349214</td><td>1.76E-02</td><td>Mo17<B73=F1</td><td>2.62</td><td>11</td><td>>dbj|BAD61770.1| putative endo-beta-1,4-mannanase [Oryza sativa (japonicacultivar-group)]</td><td>440</td><td>1E-20</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_916078.1| putative (1-4)-beta-mannan endohydrolase [Oryza sativa (japonicacultivar-group)] dbj|BAC05600.1| putative (1-4)-beta-mannan endohydrolase [Oryza sativa (japonica cultivar-group)] dbj|BAB56016.1| putative (1-4)-beta-mannan endohydrolase [Oryza sativa (japonica cultivar-group)]</td><td>445</td><td>8E-10</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_194561.1| hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana]emb|CAB79634.1| putative (1-4)-beta-mannan endohydrolase [Arabidopsis thaliana]</td><td>431</td><td>8E-8</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAD20927.1| (1-4)-beta-mannan endohydrolase [Arabidopsis thaliana]</td><td>403</td><td>3E-6</td></tr>
<tr><td>CD485021</td><td>1.76E-02</td><td>Mo17<F1</td><td>1.22</td><td>12</td><td>>gb|AAM95942.1| nucleosome/chromatin assembly factor group D protein [Zea mays]emb|CAA41220.1| high mobility group protein [Zea mays] emb|CAB46752.1| HMGa protein [Zea mays] sp|P27347|MNB1B MAIZE DNA-binding protein MNB1B (HMG1-like protein)</td><td>157</td><td>5E-14</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA46876.1| DNA-binding protein [Zea mays]pir||T03640 high mobility group protein MNB1b - maize (fragment)</td><td>168</td><td>5E-14</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAP21609.1| HMGB1 [Oryza sativa (indica cultivar-group)]gb|AAN28722.1| HMG1 protein [Oryza sativa (indica cultivar-group)] dbj|BAD61823.1| HMGB1 [Oryza sativa (japonica cultivar-group)] gb|AAC78104.1| high mobility group protein [Oryza sativa]</td><td>157</td><td>9E-13</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA77641.1| high mobility group protein [Triticum aestivum]sp|P40621|HMGL WHEAT HMG1/2-like protein</td><td>161</td><td>3E-12</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA90679.1| HMG1/2-like protein [Hordeum vulgare subsp. vulgare]</td><td>160</td><td>2E-11</td></tr>
<tr><td>CB605333</td><td>1.76E-02</td><td>Mo17<F1</td><td>1.3</td><td>11</td><td>>gb|AAL76334.1| putative G-box binding protein [Oryza sativa]dbj|BAD45657.1| G-box binding protein-like [Oryza sativa (japonica cultivar-group)] gb|AAB65433.1| HvB12D homolog [Oryza sativa]</td><td>89</td><td>3E-34</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA70936.1| B12Dg1 [Hordeum vulgare subsp. vulgare]emb|CAA54065.1| HvB12D [Hordeum vulgare subsp. vulgare]</td><td>87</td><td>5E-32</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAD22104.1| B12D protein [Ipomoea batatas]</td><td>90</td><td>7E-28</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_190397.1| unknown protein [Arabidopsis thaliana]emb|CAB51061.1| B12D-like protein [Arabidopsis thaliana] gb|AAL91215.1| B12D-like protein [Arabidopsis thaliana] gb|AAN65070.1| B12D-like protein [Arabidopsis thaliana] pir||T13003 hypothetical protein T24C20.20 - Arabidopsis thaliana</td><td>88</td><td>4E-25</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_477421.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]dbj|BAC84633.1| putative B12D protein [Oryza sativa (japonica cultivar-group)] dbj|BAD31625.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]</td><td>98</td><td>8E-24</td></tr>
<tr><td>BM078217</td><td>1.76E-02</td><td>Mo17<B73=F1</td><td>1.24</td><td>11</td><td>>gb|AAL76334.1| putative G-box binding protein [Oryza sativa]dbj|BAD45657.1| G-box binding protein-like [Oryza sativa (japonica cultivar-group)] gb|AAB65433.1| HvB12D homolog [Oryza sativa]</td><td>89</td><td>2E-39</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA70936.1| B12Dg1 [Hordeum vulgare subsp. vulgare]emb|CAA54065.1| HvB12D [Hordeum vulgare subsp. vulgare]</td><td>87</td><td>8E-38</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAD22104.1| B12D protein [Ipomoea batatas]</td><td>90</td><td>8E-33</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_190397.1| unknown protein [Arabidopsis thaliana]emb|CAB51061.1| B12D-like protein [Arabidopsis thaliana] gb|AAL91215.1| B12D-like protein [Arabidopsis thaliana] gb|AAN65070.1| B12D-like protein [Arabidopsis thaliana] pir||T13003 hypothetical protein T24C20.20 - Arabidopsis thaliana</td><td>88</td><td>8E-31</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_477421.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]dbj|BAC84633.1| putative B12D protein [Oryza sativa (japonica cultivar-group)] dbj|BAD31625.1| putative B12D protein [Oryza sativa (japonica cultivar-group)]</td><td>98</td><td>3E-28</td></tr>
<tr><td>DV492984</td><td>1.76E-02</td><td>B73<F1=Mo17</td><td>1.37</td><td>3</td><td>>emb|CAA55022.1| beta tubulin [Oryza sativa (japonica cultivar-group)]</td><td>447</td><td>2E-43</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAE52516.1| beta tubulin [Setaria viridis]</td><td>448</td><td>2E-43</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_915874.1| tubulin beta chain [Oryza sativa (japonica cultivar-group)]dbj|BAB92274.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] dbj|BAA06381.1| beta-tubulin [Oryza sativa (japonica cultivar-group)] sp|P45960|TBB4 ORYSA Tubulin beta-4 chain (Beta-4 tubulin)</td><td>447</td><td>2E-43</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAA66495.1| beta-tubulin</td><td>447</td><td>2E-43</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>sp|Q41783|TBB6 MAIZE Tubulin beta-6 chain (Beta-6 tubulin)gb|AAA20186.1| beta-6 tubulin</td><td>446</td><td>2E-43</td></tr>
</table>

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
DV551119	1.77E-02	B73<F1=Mo17	1.32	2	>dbj|BAD38026.1| chloroplast thylakoidal processing peptidase-like protein [Oryzasativa (japonica cultivar-group)]	411	2E-47
					>ref|XP_469892.1| putative chloroplast thylakoidal processing peptidase [Oryza sativa(japonica cultivar-group)] gb|AAP50954.1| putative chloroplast thylakoidal processing peptidase [Oryza sativa (japonica cultivar-group)]	470	1E-21
					>gb|AAB63091.1| putative signal peptidase I [Arabidopsis thaliana]	250	5E-12
					>ref|NP_180603.2| peptidase/ serine-type peptidase [Arabidopsis thaliana]emb|CAA71502.1| chloroplast thylakoidal processing peptidase [Arabidopsis thaliana] gb|AAM91557.1| putative signal peptidase I [Arabidopsis thaliana] gb|AAW80880.1| At2g30440 [Arabidopsis thaliana]	340	5E-12
					>ref|NP_172171.1| peptidase/ serine-type peptidase [Arabidopsis thaliana]gb|AAF63136.1| putative signal peptidase [Arabidopsis thaliana]	367	2E-11
DV622303	1.77E-02	B73<F1	1.37	2	>dbj|BAD28176.1| putative polysialic acid capsule expression protein [Oryza sativa(japonica cultivar-group)] dbj|BAD28031.1| putative polysialic acid capsule expression protein [Oryza sativa (japonica cultivar-group)]	344	1E-61
					>ref|NP_191029.1| sugar binding [Arabidopsis thaliana]emb|CAB77589.1| sugar-phosphate isomerase-like protein [Arabidopsis thaliana]	350	3E-53
					>emb|CAF24506.1| putative Gut Q protein [Parachlamydia sp. UWE25]ref|YP_008781.1| putative Gut Q protein [Candidatus Protochlamydia amoebophila UWE25]	319	4E-20
					>gb|AAP98476.1| KpsF [Chlamydophila pneumoniae TW-183]gb|AAD18666.1| GutQ/KpsF Family Sugar-P Isomerase [Chlamydophila pneumoniae CWL029] dbj|BAA98732.1| GutQ/KpsF family sugar-P isomerase [Chlamydophila pneumoniae J138] gb|AAF38092.1| carbohydrate isomerase, KpsF/GutQ family [Chlamydophila pneumoniae AR39] ref|NP_876819.1| KpsF [Chlamydophila pneumoniae TW-183] ref|NP_300581.1| GutQ/KpsF family sugar-P isomerase [Chlamydophila pneumoniae J138] ref|NP_224722.1| GutQ/KpsF Family Sugar-P Isomerase [Chlamydophila pneumoniae CWL029] ref|NP_444777.1| carbohydrate isomerase, KpsF/GutQ family [Chlamydophila pneumoniae AR39] sp|Q9Z826|Y526 CHLPN Hypothetical protein CPn0526/CP0226/CPj0526/CpB0547	329	3E-19
					>emb|CAH63672.1| conserved hypothetical protein [Chlamydophila abortus S26/3]ref|YP_219643.1| hypothetical protein CAB215 [Chlamydophila abortus S26/3]	329	1E-18
CD485186	1.77E-02	B73=Mo17<F1	1.22	12	>emb|CAA46876.1| DNA-binding protein [Zea mays]pir||T03640 high mobility group protein MNB1b - maize (fragment)	168	1E-22
					>gb|AAM95942.1| nucleosome/chromatin assembly factor group D protein [Zea mays]emb|CAA41220.1| high mobility group protein [Zea mays] emb|CAB46752.1| HMGa protein [Zea mays] sp|P27347|MNB1B MAIZE DNA-binding protein MNB1B (HMG1-like protein)	157	4E-22
					>gb|AAP21609.1| HMGB1 [Oryza sativa (indica cultivar-group)]gb|AAN28722.1| HMG1 protein [Oryza sativa (indica cultivar-group)] dbj|BAD61823.1| HMGB1 [Oryza sativa (japonica cultivar-group)] gb|AAC78104.1| high mobility group protein [Oryza sativa]	157	7E-21
					>emb|CAA77641.1| high mobility group protein [Triticum aestivum]sp|P40621|HMGL WHEAT HMG1/2-like protein	161	3E-20
					>emb|CAA90679.1| HMG1/2-like protein [Hordeum vulgare subsp. vulgare]	160	2E-19
CB815739	1.77E-02	B73<Mo17	1.37	4	>dbj|BAD81083.1| putative COP9 signalosome complex subunit 2 [Oryza sativa (japonicacultivar-group)]	433	3E-85
					>dbj|BAD94682.1| putative PCI domain protein [Arabidopsis thaliana]	210	6E-67
					>ref|NP_565632.1| FUS12 (FUSCA 12) [Arabidopsis thaliana]gb|AAC77857.2| COP9 complex subunit CSN2, putative [Arabidopsis thaliana] gb|AAL58101.1| CSN complex subunit 2 [Arabidopsis thaliana] gb|AAM65163.1| putative PCI domain protein [Arabidopsis thaliana] sp|Q8W207|CSN2_ARATH COP9 signalosome complex subunit 2 (Signalosome subunit 2) (FUSCA protein 12) (FUSCA12)	439	6E-67
					>gb|AAM91366.1| At2g26990/T20P8.4 [Arabidopsis thaliana]gb|AAK91453.1| At2g26990/T20P8.4 [Arabidopsis thaliana]	439	6E-67
					>ref|XP_780196.1| PREDICTED: similar to COP9 (constitutive photomorphogenic) homolog,subunit 2 isoform 1 [Strongylocentrotus purpuratus]	444	7E-60
DV492318	1.78E-02	B73<F1	1.51	1	>ref|XP_477795.1| 26S proteasome regulatory particle non-ATPase subunit12 [Oryzasativa (japonica cultivar-group)] dbj|BAC84087.1| 26S proteasome regulatory particle non-ATPase subunit12 [Oryza sativa (japonica cultivar-group)] dbj|BAB78490.1| 26S proteasome regulatory particle non-ATPase subunit12 [Oryza sativa (japonica cultivar-group)]	267	2E-72
					>ref|NP_176633.1| peptidase [Arabidopsis thaliana]gb|AAP86673.1| 26S proteasome subunit RPN12 [Arabidopsis thaliana] gb|AAN28827.1| At1g64520/F1N19_10 [Arabidopsis thaliana] gb|AAK95251.1| At1g64520/F1N19_10 [Arabidopsis thaliana] gb|AAK63961.1| At1g64520/F1N19_10 [Arabidopsis thaliana] gb|AAF19671.1| F1N19.9 [Arabidopsis thaliana]	267	5E-65
					>gb|AAP86674.1| 26S proteasome subunit RPN12 [Arabidopsis thaliana]	267	2E-64
					>ref|NP_199019.1| peptidase [Arabidopsis thaliana]gb|AAP83301.1| 26S proteasome subunit RPN12b [Arabidopsis thaliana] dbj|BAB08437.1| unnamed protein product [Arabidopsis thaliana]	159	8E-62
					>ref|XP_625217.1| PREDICTED: similar to ENSANGP00000010608 [Apis mellifera]	266	3E-28
BM334686	1.78E-02	B73<Mo17	1.45	4	>gb|AAC69757.1| endo-1,3-1,4-beta-D-glucanase [Zea mays]sp|Q9ZT66|E134 MAIZE Endo-1,3;1,4-beta-D-glucanase precursor	303	5E-26
					>ref|XP_480885.1| Endo-1,3;1,4-beta-D-glucanase precursor-like protein [Oryza sativa(japonica cultivar-group)] dbj|BAD05244.1| Endo-1,3;1,4-beta-D-glucanase precursor-like protein [Oryza sativa (japonica cultivar-group)]	176	5E-12
					>ref|XP_480878.1| putative Endo-1,3;1,4-beta-D-glucanase precursor [Oryza sativa(japonica cultivar-group)] dbj|BAD05237.1| putative Endo-1,3;1,4-beta-D-glucanase precursor [Oryza sativa (japonica cultivar-group)] dbj|BAD05479.1| putative Endo-1,3;1,4-beta-D-glucanase precursor [Oryza sativa (japonica cultivar-group)]	265	5E-12
					>gb|AAX92844.1| Dienelactone hydrolase family, putative [Oryza sativa (japonicacultivar-group)] gb|ABA92619.1| Dienelactone hydrolase family, putative [Oryza sativa (japonica cultivar-group)]	276	5E-12
					>ref|XP_507574.1| PREDICTED P0682A06.39 gene product [Oryza sativa (japonicacultivar-group)] ref|XP_507174.1| PREDICTED P0682A06.39 gene product [Oryza sativa (japonica cultivar-group)]	272	5E-12

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
CD485020	1.78E-02	Mo17<B73=F1	1.33	11	ns		
BM348600	1.78E-02	F1<B73	3.87	8	ns		
CD001635	1.80E-02	B73<Mo17	1.38	3	ns		
CB380900	1.80E-02	Mo17<B73=F1	1.26	11	>ref|NP_922264.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAM94931.1| unknown protein [Oryza sativa (japonica cultivar-group)] gb|AAP54551.1| expressed protein [Oryza sativa (japonica cultivar-group)]	292	1E-6
DV491332	1.80E-02	F1=Mo17<B73	1.23	8	>ref|NP_849649.1| pyridoxal phosphate binding [Arabidopsis thaliana]gb|AAC17617.1| Similar to hypothetical protein F09E5.8 gb|U37429 from C. elegans. ESTs gb|T42019 and gb|N97000 come from this gene. [Arabidopsis thaliana]	255	3E-70
					>ref|NP_563897.1| pyridoxal phosphate binding [Arabidopsis thaliana]gb|AAM51596.1| At1g11930/F12F1_20 [Arabidopsis thaliana] gb|AAL16123.1| At1g11930/F12F1 20 [Arabidopsis thaliana]	257	8E-69
					>gb|AAK52989.1| AT4g26860/F10M23_200 [Arabidopsis thaliana]gb|AAL47419.1| AT4g26860/F10M23_200 [Arabidopsis thaliana] gb|AAM61322.1| putative proline synthetase associated protein [Arabidopsis thaliana]	244	2E-63
					>ref|NP 567760.1| pyridoxal phosphate binding [Arabidopsis thaliana]	244	2E-63
					>emb|CAD29783.1| putative proline synthetase associated protein [Oryza sativa]	220	3E-63
BM078604	1.80E-02	Mo17<B73	1.32	10	ns		
DV621760	1.80E-02	Mo17<B73	1.24	10	ns		
CB604598	1.81E-02	Mo17<F1	1.34	11	>ref|XP_465219.1| putative fibroblast growth factor 2-interacting factor [Oryzasativa (japonica cultivar-group)] dbj|BAD15974.1| putative fibroblast growth factor 2-interacting factor [Oryza sativa (japonica cultivar-group)]	537	2E-23
					>ref|NP_565777.1| unknown protein [Arabidopsis thaliana]gb|AAQ56832.1| At2g34040 [Arabidopsis thaliana] gb|AAB67622.2| expressed protein [Arabidopsis thaliana] gb|AAM62452.1| unknown [Arabidopsis thaliana] gb|AAN72062.1| expressed protein [Arabidopsis thaliana]	553	3E-12
					>gb|AAF24538.2| F1K23.1 [Arabidopsis thaliana]	347	2E-8
					>ref|NP_174198.2| unknown protein [Arabidopsis thaliana]gb|AAO64012.1| unknown protein [Arabidopsis thaliana] dbj|BAC42863.1| unknown protein [Arabidopsis thaliana]	556	2E-8
CB251915	1.81E-02	B73<Mo17	1.54	4	>ref|NP_915412.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]dbj|BAB93209.1| putative histone H2B [Oryza sativa (japonica cultivar-group)] dbj|BAB67889.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	139	5E-38
					>emb|CAA42530.1| histone H2B [Triticum aestivum]sp|P27807|H2B1 WHEAT Histone H2B	152	5E-38
					>emb|CAA49585.1| H2B histone [Zea mays]sp|P49120|H2B4 MAIZE Histone H2B.4	137	5E-38
					>emb|CAA40564.1| H2B histone [Zea mays]sp|P30755|H2B1 MAIZE Histone H2B.1	151	5E-38
					>ref|XP 475367.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]gb|AAT39167.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	124	7E-38
CB605372	1.82E-02	B73<F1=Mo17	1.22	3	>dbj|BAD98622.1| putative phosphoribosylaminoimidazole carboxylase, chloroplastprecursor [Oryza sativa (japonica cultivar-group)] dbj|BAD73201.1| putative phosphoribosylaminoimidazole carboxylase, chloroplast precursor [Oryza sativa (japonica cultivar-group)]	631	6E-49
					>gb|AAR06291.1| phosphoribosylaminoimidazole carboxylase [Nicotiana tabacum]	621	1E-45
					>gb|AAK14408.1| phosphoribosylaminoimidazole carboxylase [Nicotiana tabacum]	623	1E-45
					>dbj|BAD85025.1| phosphoribosylaminoimidazole carboxylase, catalytic subunit[Thermococcus kodakarensis KOD1] ref|YP_183249.1| phosphoribosylaminoimidazole carboxylase catalytic subunit [Thermococcus kodakarensis KOD1]	174	1E-44
					>gb|AAD35541.1| phosphoribosylaminoimidazole carboxylase, catalytic subunit[Thermotoga maritima MSB8] sp|Q9WYS7|PUR6_THEMA Phosphoribosylaminoimidazole carboxylase catalytic subunit (AIR carboxylase) (AIRC) ref|NP_228256.1| phosphoribosylaminoimidazole carboxylase catalytic subunit [Thermotoga maritima MSB8]	171	2E-44
CA829429	1.82E-02	B73<F1=Mo17	1.36	2	>emb|CAA41024.1| acyl carrier protein [Zea mays]prf||1814481A acyl carrier protein	121	3E-34
					>sp|P15543|ACP3 HORVU Acyl carrier protein 3, chloroplast precursor (Acyl carrier proteinIII) (ACP III) gb|AAA32922.1| acyl carrier protein III	132	1E-27
					>ref|XP_483668.1| putative acyl carrier protein III, chloroplast precursor (ACP III)[Oryza sativa (japonica cultivar-group)] dbj|BAD08953.1| putative acyl carrier protein III, chloroplast precursor (ACP III) [Oryza sativa (japonica cultivar-group)]	138	5E-27
					>gb|AAA32924.1| acyl carrier protein III precursor	110	5E-26
					>sp|P08817|ACP2_HORVU Acyl carrier protein 2, chloroplast precursor (Acyl carrier proteinII) (ACP II) gb|AAA32921.1| acyl carrier protein II prf||1808324A acyl carrier protein II	129	8E-26
DV621426	1.83E-02	B73<F1=Mo17	1.2	3	>emb|CAB40376.1| adenosine kinase [Zea mays]	331	1E-88
					>gb|AAO72629.1| adenosine kinase-like protein [Oryza sativa (japonicacultivar-group)]	370	6E-82
					>ref|XP_506873.1| PREDICTED B1215B07.34 gene product [Oryza sativa (japonicacultivar-group)] ref|XP_466836.1| putative adenosine kinase [Oryza sativa (japonica cultivar-group)] dbj|BAD23787.1| putative adenosine kinase [Oryza sativa (japonica cultivar-group)]	341	6E-82
					>dbj|BAC02723.1| adenosine kinase [Oryza sativa]	296	3E-81
					>ref|XP 473191.1| OSJNBa0073E02.13 [Oryza sativa (japonica cultivar-group)]emb|CAE05453.3| OSJNBa0073E02.13 [Oryza sativa (japonica cultivar-group)]	401	2E-77
CD651652	1.83E-02	Mo17<B73=F1	1.47	10	ns		
CD651168	1.83E-02	Mo17<B73	1.26	10	>ref|XP_466081.1| copper chaperone homolog CCH [Oryza sativa (japonicacultivar-group)] dbj|BAD25440.1| copper chaperone homolog CCH [Oryza sativa (japonica cultivar-group)] gb|AAF15285.1| copper chaperone homolog CCH [Oryza sativa]	132	9E-27

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>dbj|BAD73816.1| putative copper chaperone [Oryza sativa (japonica cultivar-group)]	252	7E-26
					>emb|CAE51321.1| chopper chaperone [Hordeum vulgare subsp. vulgare]	112	5E-25
					>ref|NP_191183.1| CCH [Arabidopsis thaliana]emb|CAB87423.1| copper homeostasis factor [Arabidopsis thaliana] gb|AAK32872.1| AT3g56240/F18O21_200 [Arabidopsis thaliana] gb|AAL47423.1| AT3g56240/F18O21_200 [Arabidopsis thaliana] gb|AAM62878.1| copper homeostasis factor [Arabidopsis thaliana] gb|AAC33510.1| copper homeostasis factor [Arabidopsis thaliana]	121	3E-24
					>gb|AAP06757.1| copper chaperone [Lycopersicon esculentum]	81	5E-23
CD527129	1.84E-02	B73<F1=Mo17	1.29	2	>emb|CAC82203.1| S-adenosylmethionine synthetase [Oryza sativa (indicacultivar-group)]	396	9E-65
					>gb|AAT94053.1| S-adenosylmethionine synthetase [Oryza sativa (japonicacultivar-group)] emb|CAA81481.1| S-adenosyl methionine synthetase [Oryza sativa] sp|P46611|METK ORYSA S-adenosylmethionine synthetase 1 (Methionine adenosyltransferase 1) (AdoMet synthetase 1)	396	9E-65
					>gb|ABB29942.1| S-adenosyl methionine synthase-like [Solanum tuberosum]	393	2E-61
					>emb|CAJ01705.1| putative AdoMet synthase 4 [Hordeum vulgare subsp. vulgare]	396	3E-61
					>ref|NP_908513.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]dbj|BAA96637.1| putative S-adenosyl-L-methionine synthetase [Oryza sativa (japonica cultivar-group)]	396	6E-61
DV490017	1.84E-02	F1=Mo17<B73	1.45	9	>gb|AAU93534.1| unknown protein [Zea mays]	286	1E-25
					>ref|XP_469638.1| unknown protein [Oryza sativa (japonica cultivar-group)]gb|AAR07080.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAC78576.1| hypothetical protein [Oryza sativa (japonica cultivar-group)] gb|AAP03422.1| unknown protein [Oryza sativa (japonica cultivar-group)]	205	5E-22
					>ref|NP_196647.1| unknown protein [Arabidopsis thaliana]emb|CAB96841.1| putative protein [Arabidopsis thaliana] gb|AAK32857.1| AT5g10860/T30N20_130 [Arabidopsis thaliana] gb|AAL47413.1| AT5g10860/T30N20 130 [Arabidopsis thaliana] sp|Q9LEV3|UMP3 ARATH Protein At5g10860, mitochondrial precursor	206	2E-19
					>gb|AAT08729.1| CBS1 [Hyacinthus orientalis]	203	1E-18
					>gb|AAU04402.1| unknown [Citrus limon]	117	3E-15
DV942650	1.84E-02	B73<Mo17	1.35	3	ns		
AI612441	1.84E-02	F1<B73=Mo17	3.78	6	ns		
CB331087	1.85E-02	Mo17<B73=F1	1.33	10	>ref|XP_483837.1| glutaredoxin protein family-like [Oryza sativa (japonicacultivar-group)] dbj|BAD10333.1| glutaredoxin protein family-like [Oryza sativa (japonica cultivar-group)] dbj|BAC56010.1| glutaredoxin protein family-like [Oryza sativa (japonica cultivar-group)]	164	7E-14
					>ref|XP_483838.1| glutaredoxin protein family-like [Oryza sativa (japonicacultivar-group)] dbj|BAD10332.1| glutaredoxin protein family-like [Oryza sativa (japonica cultivar-group)] dbj|BAD12949.1| glutaredoxin protein family-like [Oryza sativa (japonica cultivar-group)]	152	1E-13
					>ref|NP_179617.1| arsenate reductase (glutaredoxin)/ electron transporter/thiol-disulfide exchange intermediate [Arabidopsis thaliana] gb|AAM67430.1| At2g20270/F11A3.18 [Arabidopsis thaliana] gb|AAM19817.1| At2g20270/F11A3.18 [Arabidopsis thaliana] gb|AAD21761.1| putative glutaredoxin [Arabidopsis thaliana]	179	5E-6
					>gb|AAM64584.1| putative glutaredoxin [Arabidopsis thaliana]	179	5E-6
DV491773	1.85E-02	Mo17<B73	1.3	10	>gb|AAA33465.1| glyceraldehyde-3-phosphate dehydrogenase [Zea mays]	234	9E-81
					>sp|Q43247|G3PE MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3gb|AAA87579.1| cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3	337	9E-81
					>gb|AAA87580.1| cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4	337	3E-80
					>gb|AAP83583.1| cytosolic glyceraldehyde-3-phosphate dehydrogenase [Triticumaestivum]	168	1E-74
					>sp|P08477|G3PC_HORVU Glyceraldehyde-3-phosphate dehydrogenase, cytosolicgb|AAA32956.1| glyceraldehyde-3-phosphate dehydrogenase prf||1301218A dehydrogenase,glyceraldehydephosphate	305	2E-74
CB604370	1.86E-02	B73=F1<Mo17	1.43	5	>ref|XP_480155.1| putative snRNP core protein SMX5d [Oryza sativa (japonicacultivar-group)] dbj|BAC99422.1| putative snRNP core protein SMX5d [Oryza sativa (japonica cultivar-group)]	288	9E-45
					>ref|NP 563682.1| unknown protein [Arabidopsis thaliana]	93	2E-42
					>gb|AAC72111.1| Similar to gb|U85207 snRNP core Sm protein homolog Sm-X5 from Musmusculus. EST gb|AA612141 comes from this gene. [Arabidopsis thaliana]	114	7E-42
					>gb|AAM62994.1| snRNP core Sm protein Sm-X5-like protein [Arabidopsis thaliana]	93	1E-41
					>gb|AAL48484.1| GM14851p [Drosophila melanogaster]ref|NP_648570.1| CG10418-PA [Drosophila melanogaster] gb|AAF49929.1| CG10418-PA [Drosophila melanogaster]	95	1E-31
BM335077	1.86E-02	B73<F1=Mo17	4.67	3	ns		
DV491502	1.86E-02	B73=F1<Mo17	1.39	5	>dbj|BAD53258.1| breast carcinoma amplified sequence 3-like protein [Oryza sativa(japonica cultivar-group)]	756	9E-19
					>ref|NP 915725.1| P0415A04.11 [Oryza sativa (japonica cultivar-group)]	953	9E-19
CD670425	1.86E-02	Mo17<B73	1.28	10	>sp|Q08069|RS8 MAIZE 40S ribosomal protein S8gb|AAB06330.1| ribosomal protein S8	221	2E-83
					>emb|CAE05511.1| OSJNBa0038P21.4 [Oryza sativa (japonica cultivar-group)]	221	3E-77
					>ref|XP_465742.1| putative 40S ribosomal protein S8 [Oryza sativa (japonicacultivar-group)] ref|XP_506804.1| PREDICTED P0483C08.42 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD21871.1| putative 40S ribosomal protein S8 [Oryza sativa (japonica cultivar-group)] dbj|BAD21876.1| putative 40S ribosomal protein S8 [Oryza sativa (japonica cultivar-group)]	220	8E-77
					>sp|P49199|RS8 ORYSA 40S ribosomal protein S8dbj|BAA07207.1| ribosomal protein S8 [Oryza sativa (japonica cultivar-group)]	220	1E-73

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>gb|ABA46755.1| unknown [Solanum tuberosum]	224	9E-73
CD572992	1.86E-02	B73<F1=Mo17	1.3	3	>gb|AAW55593.1| minichromosome maintenance protein [Zea mays]	831	e-109
					>gb|AAT93993.1| putative minichromosome maintenance family protein [Oryza sativa(japonica cultivar-group)] gb|AAT73631.1| putative minichromosome maintenance protein [Oryza sativa (japonica cultivar-group)]	830	e-109
					>ref|NP 680393.1| ATP binding / DNA binding / DNA-dependent ATPase [Arabidopsisthaliana]	831	e-103
					>gb|AAN73052.2| mini-chromosome maintenance protein MCM6 [Pisum sativum]	827	e-103
					>gb|AAW41639.1| DNA unwinding-related protein, putative [Cryptococcus neoformans var.neoformans JEC21] gb|EAL22677.1| hypothetical protein CNBB1260 [Cryptococcus neoformans var. neoformans B-3501A] ref|XP 568946.1| DNA unwinding-related protein [Cryptococcus neoformans var. neoformans JEC21]	963	9E-78
CD527783	1.86E-02	B73=F1<Mo17	1.39	4	>emb|CAA44607.1| ocs-binding factor 1 [Zea mays]sp|P24068|OCS1 MAIZE Ocs-element binding factor 1 (OCSBF-1)	151	2E-54
					>emb|CAE92374.1| ocs-element binding factor 1 [Secale cereale]	157	8E-44
					>dbj|BAE16260.1| bZIP protein [Oryza sativa (japonica cultivar-group)]gb|ABA98933.1| ocs-element binding factor 1 [Oryza sativa (japonica cultivar-group)]	145	4E-43
					>gb|AAU10749.1| putative bZIP protein [Oryza sativa (japonica cultivar-group)]emb|CAA40596.1| basic/leucine zipper protein [Oryza sativa (japonica cultivar-group)]	148	8E-20
					>emb|CAC00657.1| common plant regulatory factor 6 [Petroselinum crispum]	147	1E-19
CA829518	1.86E-02	Mo17<B73=F1	1.35	10	>emb|CAB90214.1| putative elongation factor 1 beta [Hordeum vulgare subsp. vulgare]	226	6E-27
					>gb|AAR15081.1| translational elongation factor 1 subunit Bbeta [Pisum sativum]	231	9E-27
					>ref|XP_479153.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)]ref|XP_506463.1| PREDICTED P0616D06.117 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC16499.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)] dbj|BAA04903.1| elongation factor 1 beta [Oryza sativa (japonica cultivar-group)] sp|Q40680|EF1D ORYSA Elongation factor 1-delta (EF-1-delta) (Elongation factor 1B-beta) (eEF-1B beta)	229	5E-26
					>ref|NP_910927.2| putative translation elongation factor eEF-1 beta' chain [Oryzasativa (japonica cultivar-group)] ref|XP_506540.1| PREDICTED P0453E03.111 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC22427.2| putative translation elongation factor eEF-1 beta' chain [Oryza sativa (japonica cultivar-group)]	224	1E-25
					>gb|AAU89237.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)]dbj|BAA34599.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)] dbj|BAA34598.1| elongation factor 1 beta 2 [Oryza sativa (japonica cultivar-group)]	226	1E-25
DV622429	1.87E-02	B73<F1=Mo17	1.2	2	>sp|P00054|CYC SESIN Cytochrome c	111	7E-14
					>sp|P00061|CYC SOLTU Cytochrome c	111	7E-14
					>sp|P00060|CYC LYCES Cytochrome c	111	7E-14
					>pir||CCZM cytochrome c - maize	111	7E-14
					>sp|P00072|CYC FAGES Cytochrome c	111	2E-13
DV621252	1.87E-02	B73<F1=Mo17	1.49	3	>dbj|BAD36064.1| unknown protein [Oryza sativa (japonica cultivar-group)]	546	2E-43
					>gb|AAD28690.1| unknown protein [Arabidopsis thaliana]gb|AAK43902.1| Unknown protein [Arabidopsis thaliana]	302	2E-31
					>ref|NP 178935.2| unknown protein [Arabidopsis thaliana]gb|AAN72054.1| unknown protein [Arabidopsis thaliana]	541	2E-31
					>ref|XP 474087.1| OSJNBa0033G05.10 [Oryza sativa (japonica cultivar-group)]emb|CAD41909.2| OSJNBa0033G05.10 [Oryza sativa (japonica cultivar-group)]	546	1E-28
					>dbj|BAC43452.1| unknown protein [Arabidopsis thaliana]	545	4E-26
CB331032	1.88E-02	Mo17<F1	1.27	12	>gb|AAT81723.1| striated muscle activator-like protein [Oryza sativa (japonicacultivar-group)]	87	1E-33
					>emb|CAB80081.1| putative protein [Arabidopsis thaliana]emb|CAA20577.1| putative protein [Arabidopsis thaliana]	161	8E-31
					>ref|NP 567930.1| unknown protein [Arabidopsis thaliana]gb|AAM64660.1| unknown [Arabidopsis thaliana]	95	1E-30
					>gb|AAH39801.1| 3110003A17Rik protein [Mus musculus]	104	4E-27
					>ref|XP 125510.6| PREDICTED: hypothetical protein LOC73112 [Mus musculus]	187	4E-27
DV494239	1.88E-02	Mo17<B73=F1	1.33	11	>ref|XP_464492.1| putative DNA-damage inducible protein [Oryza sativa (japonicacultivar-group)] dbj|BAD25465.1| putative DNA-damage inducible protein [Oryza sativa (japonica cultivar-group)]	415	7E-26
					>dbj|BAB02792.1| DNA-damage inducible protein DDI1-like [Arabidopsis thaliana]	395	6E-15
					>ref|NP 566451.1| aspartic-type endopeptidase [Arabidopsis thaliana]	414	6E-15
					>gb|AAM61638.1| DNA-damage inducible protein DDI1-like [Arabidopsis thaliana]	414	3E-14
CB885571	1.88E-02	Mo17<F1	1.19	11	>gb|AAM95942.1| nucleosome/chromatin assembly factor group D protein [Zea mays]emb|CAA41220.1| high mobility group protein [Zea mays] emb|CAB46752.1| HMGa protein [Zea mays] sp|P27347|MNB1B MAIZE DNA-binding protein MNB1B (HMG1-like protein)	157	1E-18
					>emb|CAA46876.1| DNA-binding protein [Zea mays]pir||T03640 high mobility group protein MNB1b - maize (fragment)	168	1E-18
					>gb|AAP21609.1| HMGB1 [Oryza sativa (indica cultivar-group)]gb|AAN28722.1| HMG1 protein [Oryza sativa (indica cultivar-group)] dbj|BAD61823.1| HMGB1 [Oryza sativa (japonica cultivar-group)] gb|AAC78104.1| high mobility group protein [Oryza sativa]	157	3E-17
					>emb|CAA77641.1| high mobility group protein [Triticum aestivum]sp|P40621|HMGL WHEAT HMG1/2-like protein	161	1E-16
					>emb|CAA90679.1| HMG1/2-like protein [Hordeum vulgare subsp. vulgare]	160	6E-16

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15 % FDR)

<table>
<tr><th>GenBank accession no.</th><th>Overall P value</th><th>Significant pattern</th><th>Fold change†</th><th>Sector‡</th><th>BLAST annotation*</th><th>Score</th><th>E value</th></tr>
<tr><td>CD670430</td><td>1.88E-02</td><td>Mo17<F1</td><td>1.28</td><td>11</td><td>>ref|NP_910927.2| putative translation elongation factor eEF-1 beta' chain [Oryzasativa (japonica cultivar-group)] ref|XP_506540.1| PREDICTED P0453E03.111 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC22427.2| putative translation elongation factor eEF-1 beta' chain [Oryza sativa (japonica cultivar-group)]</td><td>224</td><td>9E-31</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAA02253.1| elongation factor 1 beta' [Oryza sativa (japonica cultivar-group)]sp|P29545|EF1B_ORYSA Elongation factor 1-beta (EF-1-beta) (Elongation factor 1B-alpha 2) (eEF-1B alpha) (Elongation factor 1-beta') (EF-1-beta')</td><td>223</td><td>9E-31</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAA02436.1| elongation factor 1 beta' [Triticum aestivum]sp|P29546|EF1B_WHEAT Elongation factor 1-beta (EF-1-beta) (Elongation factor 1B-alpha 2) (eEF-1B alpha) (Elongation factor 1-beta') (EF-1-beta')</td><td>216</td><td>1E-29</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_568375.2| translation elongation factor [Arabidopsis thaliana]emb|CAB64730.1| elongation factor 1B alpha-subunit [Arabidopsis thaliana] gb|AAL07240.1| putative elongation factor 1B alpha-subunit [Arabidopsis thaliana] gb|AAK26014.1| putative elongation factor 1B alpha-subunit [Arabidopsis thaliana] sp|Q9SCX3|EF1B2 ARATH Elongation factor 1-beta 2 (EF-1-beta 2) (Elongation factor 1B-alpha 2) (eEF-1B alpha 2) (Elongation factor 1-beta' 2) (EF-1-beta' 2)</td><td>224</td><td>1E-22</td></tr>
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<tr><td>DV490797</td><td>1.88E-02</td><td>Mo17<B73</td><td>1.31</td><td>9</td><td>>gb|AAB64207.1| elongation factor 1-alpha [Zea mays]</td><td>447</td><td>3E-76</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAL79775.1| elongation factor 1 alpha [Saccharum hybrid cultivar CP72-2086]</td><td>441</td><td>7E-76</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAA08249.1| alpha subunit of tlanslation elongation factor 1 [Zea mays]sp|Q41803|EF1A MAIZE Elongation factor 1-alpha (EF-1-alpha)</td><td>447</td><td>1E-75</td></tr>
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<tr><td>CD527474</td><td>1.89E-02</td><td>B73<F1</td><td>1.17</td><td>2</td><td>>ref|XP 549834.1| putative tDET1 protein [Oryza sativa (japonica cultivar-group)]dbj|BAD44839.1| putative tDET1 protein [Oryza sativa (japonica cultivar-group)]</td><td>511</td><td>5E-71</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA11914.1| tDET1 protein [Lycopersicon esculentum]emb|CAA10993.1| tDET1 protein [Lycopersicon esculentum] sp|Q9ZNU6|DET1_LYCES Light-mediated development protein DET1 (Deetiolated1 homolog) (tDET1) (High pigmentation protein 2) (Protein dark green)</td><td>523</td><td>1E-54</td></tr>
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<tr><td>CD651577</td><td>1.90E-02</td><td>B73<F1=Mo17</td><td>1.38</td><td>3</td><td>>emb|CAA69075.1| S-adenosylmethionine decarboxylase [Zea mays]sp|O24575|DCAM_MAIZE S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain]</td><td>400</td><td>1E-19</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA06245.1| elongation factor 1-alpha (EF1-a) [Cicer arietinum]</td><td>326</td><td>5E-47</td></tr>
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<tr><td>BM073883</td><td>1.90E-02</td><td>Mo17<B73=F1</td><td>1.41</td><td>11</td><td>>emb|CAA69256.1| 60S acidic ribosomal protein P0 [Zea mays]sp|O24573|RLA0 MAIZE 60S acidic ribosomal protein P0</td><td>319</td><td>3E-8</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_479932.1| 60S acidic ribosomal protein P0-like [Oryza sativa (japonicacultivar-group)] dbj|BAD09642.1| 60S acidic ribosomal protein P0-like [Oryza sativa (japonica cultivar-group)]</td><td>96</td><td>1E-6</td></tr>
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<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|ABA91328.1| ribosomal protein L10, putative [Oryza sativa (japonicacultivar-group)]</td><td>320</td><td>1E-6</td></tr>
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<tr><td>CD484475</td><td>1.90E-02</td><td>Mo17<B73=F1</td><td>1.28</td><td>10</td><td>>gb|AAM95942.1| nucleosome/chromatin assembly factor group D protein [Zea mays]emb|CAA41220.1| high mobility group protein [Zea mays] emb|CAB46752.1| HMGa protein [Zea mays] sp|P27347|MNB1B MAIZE DNA-binding protein MNB1B (HMG1-like protein)</td><td>157</td><td>2E-17</td></tr>
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Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>emb|CAA46876.1| DNA-binding protein [Zea mays]pir||T03640 high mobility group protein MNB1b - maize (fragment)	168	2E-17
					>gb|AAP21609.1| HMGB1 [Oryza sativa (indica cultivar-group)]gb|AAN28722.1| HMG1 protein [Oryza sativa (indica cultivar-group)] dbj|BAD61823.1| HMGB1 [Oryza sativa (japonica cultivar-group)] gb|AAC78104.1| high mobility group protein [Oryza sativa]	157	3E-16
					>emb|CAA77641.1| high mobility group protein [Triticum aestivum]sp|P40621|HMGL WHEAT HMG1/2-like protein	161	1E-15
					>emb|CAA90679.1| HMG1/2-like protein [Hordeum vulgare subsp. vulgare]	160	8E-15
CB381011	1.90E-02	B73<F1	1.31	2	>ref|NP_922034.1| putative transcription factor [Oryza sativa (japonicacultivar-group)] gb|AAM91875.1| putative transcription factor [Oryza sativa (japonica cultivar-group)] gb|AAP54321.1| transcription factor, putative [Oryza sativa (japonica cultivar-group)] gb|ABB47797.1| transcription factor, putative [Oryza sativa (japonica cultivar-group)]	164	7E-35
					>gb|AAO72645.1| putative transcription factor BTF3 [Oryza sativa (japonicacultivar-group)]	175	1E-33
					>ref|XP_468566.1| Putative transcription factor [Oryza sativa (japonicacultivar-group)] gb|AAN61483.1| Putative transcription factor [Oryza sativa (japonica cultivar-group)]	615	1E-33
					>gb|AAT67244.1| BTF3b-like transcription factor [Musa acuminata]	157	2E-30
					>ref|NP_177466.1| unknown protein [Arabidopsis thaliana]gb|AAL34243.1| putative RNA polymerase B transcription factor 3 [Arabidopsis thaliana] gb|AAK44068.1| putative RNA polymerase B transcription factor BTF3 [Arabidopsis thaliana] gb|AAG52123.1| putative transcription factor BTF3 (RNA polymerase B transcription factor 3); 26343-27201 [Arabidopsis thaliana]	165	2E-30
DV549932	1.92E-02	B73<F1=Mo17	1.57	3	ns		
CB381504	1.92E-02	F1=Mo17<B73	1.42	9	>gb|AAK53813.1| Ran binding protein-1 [Lycopersicon esculentum]	224	1E-51
					>gb|ABB97039.1| unknown [Brassica rapa]	225	7E-46
					>ref|NP_172194.1| SIRANBP; Ran GTPase binding [Arabidopsis thaliana]gb|AAM19880.1| At1g07140/F10K1_27 [Arabidopsis thaliana] gb|AAK95280.1| At1g07140/F10K1_27 [Arabidopsis thaliana] gb|AAK43868.1| Unknown protein [Arabidopsis thaliana] gb|AAF82206.1| Identical to atranbp1a from Arabidopsis thaliana gb|X97377. It contains a RanBP1 domain PF|00638. ESTs gb|H76544, gb|H76880, gb|AA389814, gb|AA712542, gb|T88156, gb|N65434 and gb|AA712288 come from this gene gb|AAN72204.1| Unknown protein [Arabidopsis thaliana] sp|Q9LMK7|RBP1A_ARATH Ran-binding protein 1 homolog a (Ran-binding protein siRanBP)	228	2E-45
					>emb|CAA66045.1| atranbp1a [Arabidopsis thaliana]	234	2E-45
					>ref|NP_200667.2| RANBP1 (RAN BINDING PROTEIN 1) [Arabidopsis thaliana]sp|P92985|RBP1C_ARATH Ran-binding protein 1 homolog c gb|AAB38776.1| Ran binding protein 1 homolog [Arabidopsis thaliana]	219	3E-45
DV493926	1.92E-02	B73<Mo17	1.52	3	>ref|XP_506364.1| PREDICTED P0580A11.104 gene product [Oryza sativa (japonicacultivar-group)] dbj|BAD31171.1| putative DNA repair protein rhp16 [Oryza sativa (japonica cultivar-group)]	569	5E-67
					>ref|XP 478364.1| putative DNA repair protein [Oryza sativa (japonicacultivar-group)]	633	5E-67
					>ref|NP_172004.1| ATP binding / ATP-dependent helicase/ DNA binding / helicase/ nucleicacid binding / ubiquitin-protein ligase/ zinc ion binding [Arabidopsis thaliana]	833	5E-51
					>ref|NP 171767.1| ATP binding / ATP-dependent helicase/ DNA binding / helicase/nucleic acid binding [Arabidopsis thaliana]	678	7E-43
					>ref|XP 625623.1| Swi2/Snf2 ATpase,Rad16 ortholog [Cryptosporidium parvum]gb|EAK87701.1| Swi2/Snf2 ATpase,Rad16 ortholog [Cryptosporidium parvum]	1278	2E-38
DV621825	1.92E-02	B73<F1=Mo17	1.21	3	>ref|XP_475770.1| 'unknown protein, contains IQ calmodulin-binding motif' [Oryzasativa (japonica cultivar-group)] gb|AAT39213.1| 'unknown protein, contains IQ calmodulin-binding motif' [Oryza sativa (japonica cultivar-group)]	574	3E-6
DV490220	1.93E-02	B73<F1	6.93	2	>dbj|BAD29518.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD27882.1| unknown protein [Oryza sativa (japonica cultivar-group)]	283	7E-16
					>dbj|BAD45839.1| unknown protein [Oryza sativa (japonica cultivar-group)]	263	6E-10
CD527264	1.93E-02	B73<Mo17	1.32	4	>emb|CAD23416.1| m31 [Zea mays]	241	2E-39
					>emb|CAD23414.1| m24 [Zea mays]	240	4E-38
					>gb|AAO45879.1| MADS7 [Lolium perenne]	241	8E-37
					>gb|AAS59832.1| MADS-box protein RMADS221 [Oryza sativa (japonica cultivar-group)]	238	1E-36
					>gb|AAS59823.1| MADS-box protein RMADS212 [Oryza sativa (japonica cultivar-group)]	240	1E-36
BG842314	1.93E-02	B73<F1=Mo17	1.47	2	>gb|AAD10528.1| proliferating cell nuclear antigen [Zea mays]	263	2E-51
					>emb|CAA55669.1| proliferative cell nuclear antigen [Zea mays]sp|Q43266|PCNA_MAIZE Proliferating cell nuclear antigen (PCNA) prf||2105195A proliferating cell nuclear antigen	263	7E-51
					>ref|XP_468284.1| SPATULA-like [Oryza sativa (japonica cultivar-group)]emb|CAA37979.1| proliferating cell nuclear antigen [Oryza sativa (japonica cultivar-group)] gb|AAK98707.1| Proliferating cell nuclear antigen (PCNA) [Oryza sativa] dbj|BAD19422.1| SPATULA-like [Oryza sativa (japonica cultivar-group)] sp|P17070|PCNA ORYSA Proliferating cell nuclear antigen (PCNA) (Cyclin)	263	5E-47
					>sp|Q00268|PCNA1 DAUCA Proliferating cell nuclear antigen (PCNA) (Cyclin)	264	3E-43
					>gb|AAC27992.1| proliferating cell nuclear antigen [Nicotiana tabacum]sp|O82797|PCNA_TOBAC Proliferating cell nuclear antigen (PCNA) gb|AAC34126.1| proliferating cell nuclear antigen [Nicotiana tabacum] dbj|BAA76349.1| proliferating cell nuclear antigen [Nicotiana tabacum]	264	4E-43
CA829732	1.93E-02	B73=F1<Mo17	1.85	4	ns		

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
CB605124	1.93E-02	B73<Mo17	1.39	3	>ref|NP_910927.2| putative translation elongation factor eEF-1 beta' chain [Oryzasativa (japonica cultivar-group)] ref|XP_506540.1| PREDICTED P0453E03.111 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAC22427.2| putative translation elongation factor eEF-1 beta' chain [Oryza sativa (japonica cultivar-group)]	224	6E-40
					>gb|ABA81875.1| putative elongation factor 1B alpha-subunit0like [Solanumtuberosum] gb|ABA40427.1| unknown [Solanum tuberosum]	227	4E-39
					>gb|AAT40505.1| putative elongation factor [Solanum demissum]	227	5E-39
					>gb|ABA40463.1| elongation factor-like protein [Solanum tuberosum]	227	1E-38
					>ref|NP_179402.1| translation elongation factor [Arabidopsis thaliana]gb|AAD31355.1| putative elongation factor beta-1 [Arabidopsis thaliana] gb|AAM15146.1| putative elongation factor beta-1 [Arabidopsis thaliana] gb|AAM10130.1| putative elongation factor 1-beta [Arabidopsis thaliana] gb|AAL38335.1| putative elongation factor 1-beta [Arabidopsis thaliana] sp|Q9SI20|EF1D2 ARATH Elongation factor 1-delta 2 (EF-1-delta 2) (Elongation factor 1B-beta 2) (eEF-1B beta 2)	231	5E-38
DV622285	1.93E-02	B73<F1=Mo17	1.25	2	>ref|XP_467100.1| putative enoyl-CoA hydratase [Oryza sativa (japonicacultivar-group)] dbj|BAD25316.1| putative enoyl-CoA hydratase [Oryza sativa (japonica cultivar-group)]	300	8E-64
					>emb|CAC39053.1| putative enoyl-CoA hydratase [Oryza sativa]	295	8E-64
					>ref|XP_467099.1| putative enoyl-CoA hydratase [Oryza sativa (japonicacultivar-group)] dbj|BAD25315.1| putative enoyl-CoA hydratase [Oryza sativa (japonica cultivar-group)]	269	4E-57
					>gb|AAM18495.1| enoyl-CoA hydratase [Arabidopsis lyrata subsp. petraea]	229	1E-52
					>emb|CAB88078.1| hypothetical protein [Arabidopsis thaliana]	217	2E-51
DV491553	1.94E-02	B73<F1=Mo17	1.3	3	>ref|XP_550643.1| RNA-binding protein-like [Oryza sativa (japonica cultivar-group)]dbj|BAD69059.1| RNA-binding protein-like [Oryza sativa (japonica cultivar-group)] dbj|BAD69323.1| RNA-binding protein-like [Oryza sativa (japonica cultivar-group)]	300	1E-50
					>dbj|BAC42069.1| unknown protein [Arabidopsis thaliana]	287	1E-30
					>dbj|BAB01919.1| unnamed protein product [Arabidopsis thaliana]	271	1E-26
					>ref|NP 187983.1| RNA binding / nucleic acid binding [Arabidopsis thaliana]	296	4E-26
					>gb|AAO37215.1| hypothetical protein [Arabidopsis thaliana]	277	6E-15
BM382056	1.94E-02	Mo17<B73	1.29	9	>dbj|BAD11336.1| BRI1-KD interacting protein 108 [Oryza sativa (japonicacultivar-group)]	131	4E-39
					>ref|XP_479487.1| putative 60S ribosomal protein L22 [Oryza sativa (japonicacultivar-group)] dbj|BAC84770.1| putative 60S ribosomal protein L22 [Oryza sativa (japonica cultivar-group)] dbj|BAC83533.1| putative 60S ribosomal protein L22 [Oryza sativa (japonica cultivar-group)]	130	2E-38
					>ref|NP_974229.1| structural constituent of ribosome [Arabidopsis thaliana]ref|NP_187207.1| structural constituent of ribosome [Arabidopsis thaliana] gb|AAF26141.1| putative 60S ribosomal protein L22 [Arabidopsis thaliana] gb|AAM20231.1| putative 60S ribosomal protein L22 [Arabidopsis thaliana] gb|AAL38800.1| putative 60S ribosomal protein L22 [Arabidopsis thaliana] gb|AAP21331.1| At3g05560 [Arabidopsis thaliana] gb|AAM66123.1| 60S ribosomal protein L22-2 [Arabidopsis thaliana] gb|AAO00829.1| putative 60S ribosomal protein L22 [Arabidopsis thaliana] sp|Q9M9W1|RL22B_ARATH 60S ribosomal protein L22-2	124	2E-35
					>ref|NP_198129.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAK00363.1| putative 60S ribosomal protein L22 [Arabidopsis thaliana] gb|AAG41440.1| putative 60S ribosomal protein L22 [Arabidopsis thaliana] gb|AAM63138.1| 60S ribosomal protein L22-like [Arabidopsis thaliana] gb|AAG40072.1| T1G16 [Arabidopsis thaliana] gb|AAO24531.1| At5g27770 [Arabidopsis thaliana] sp|Q9FE58|RL22C ARATH 60S ribosomal protein L22-3	124	1E-34
					>gb|AAK95148.1| ribosomal protein L22 [Ictalurus punctatus]	128	3E-22
CB334259	1.95E-02	Mo17<B73=F1	1.23	11	>ref|NP 915772.1| putative translation initiation factor SUI1 [Oryza sativa (japonicacultivar-group)]	119	7E-30
					>ref|XP_475493.1| putative protein translation factor Sui1 [Oryza sativa (japonicacultivar-group)] gb|AAT44286.1| putative protein translation factor Sui1 [Oryza sativa (japonica cultivar-group)]	115	9E-27
					>dbj|BAD53005.1| putative translation initiation factor [Oryza sativa (japonicacultivar-group)]	115	8E-25
					>sp|P56330|SUI1 MAIZE Protein translation factor SUI1 homolog (GOS2 protein)gb|AAB88615.1| translation initiation factor; GOS2 [Zea mays]	115	2E-24
					>gb|AAM34279.1| translation initiation factor [Triticum aestivum]	115	3E-24
BG840806	1.96E-02	F1=Mo17<B73	1.29	9	>ref|XP_468759.1| putative inosine-uridine preferring nucleoside hydrolase [Oryzasativa (japonica cultivar-group)] gb|AAP20832.1| putative inosine-uridine preferring nucleoside hydrolase [Oryza sativa (japonica cultivar-group)]	322	e-101
					>gb|AAW34239.1| putative inosine-uridine preferring nucleoside hydrolase [Oryzasativa (japonica cultivar-group)] gb|AAS07209.1| putative inosine-uridine preferring nucleoside hydrolase (with alternative splicing) [Oryza sativa (japonica cultivar-group)]	258	e-101
					>gb|AAS07208.1| putative inosine-uridine preferring nucleoside hydrolase,3'-partial (with alternative splicing) [Oryza sativa (japonica cultivar-group)]	313	e-101
					>ref|NP_563745.1| hydrolase [Arabidopsis thaliana]gb|AAP42733.1| At1g05620 [Arabidopsis thaliana] gb|AAM65464.1| unknown [Arabidopsis thaliana] gb|AAN72060.1| expressed protein [Arabidopsis thaliana]	322	3E-86
					>gb|AAD30614.1| Hypothetical protein [Arabidopsis thaliana]	358	3E-83
DV495612	1.96E-02	B73=F1<Mo17	1.73	4	ns		
BM078226	1.96E-02	Mo17<B73	1.27	10	>emb|CAA67225.1| ribosomal protein S21 [Zea mays]sp|Q41852|RS21 MAIZE 40S ribosomal protein S21	81	5E-38
					>emb|CAA70852.1| 40S ribosomal subunit protein S21 [Zea mays]	81	8E-37
					>dbj|BAA02158.1| 40S subunit ribosomal protein [Oryza sativa (japonicacultivar-group)] sp|P35687|RS21 ORYSA 40S ribosomal protein S21	82	2E-34

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

<table>
<tr><th>GenBank accession no.</th><th>Overall P value</th><th>Significant pattern</th><th>Fold change†</th><th>Sector‡</th><th>BLAST annotation*</th><th>Score</th><th>E value</th></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_469197.1| 40S subunit ribosomal protein [Oryza sativa (japonicacultivar-group)] gb|AAP44638.1| 40S subunit ribosomal protein [Oryza sativa (japonica cultivar-group)]</td><td>82</td><td>6E-34</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAU89141.1| 40S ribosomal protein S21, putative [Oryza sativa (japonicacultivar-group)]</td><td>119</td><td>9E-33</td></tr>
<tr><td>CB603887</td><td>1.97E-02</td><td>Mo17<B73=F1</td><td>1.34</td><td>11</td><td>ns</td><td></td><td></td></tr>
<tr><td>DV621296</td><td>1.97E-02</td><td>B73<Mo17</td><td>1.31</td><td>3</td><td>>ref|XP_477630.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAC83661.1| ARP protein-like [Oryza sativa (japonica cultivar-group)] dbj|BAD32097.1| ARP protein-like [Oryza sativa (japonica cultivar-group)]</td><td>647</td><td>2E-6</td></tr>
<tr><td>DV494012</td><td>1.97E-02</td><td>B73<Mo17</td><td>1.41</td><td>4</td><td>>gb|AAC32132.1| ISP42-like protein [Picea mariana]</td><td>94</td><td>3E-36</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAD81111.1| mitochondrial import receptor subunit tom40 -like [Oryza sativa(japonica cultivar-group)]</td><td>345</td><td>7E-34</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_188634.1| TOM40; voltage-gated ion-selective channel [Arabidopsis thaliana]gb|AAM51291.1| putative membrane import protein [Arabidopsis thaliana] gb|AAK93602.1| putative membrane import protein [Arabidopsis thaliana] sp|Q9LHE5|TOM40_ARATH Probable mitochondrial import receptor subunit TOM40 homolog (Translocase of outer membrane 40 kDa subunit homolog)</td><td>309</td><td>3E-31</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAB03165.1| membrane import protein-like [Arabidopsis thaliana]</td><td>290</td><td>3E-31</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_912979.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]</td><td>290</td><td>9E-31</td></tr>
<tr><td>DV942377</td><td>1.97E-02</td><td>B73<Mo17</td><td>2.82</td><td>4</td><td>>gb|AAM74226.1| centromeric histone h3-like protein [Zea mays]</td><td>157</td><td>4E-14</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAT77291.1| histone H3 [Oryza sativa (japonica cultivar-group)]gb|AAR85315.1| centromeric histone 3 [Oryza sativa (japonica cultivar-group)]</td><td>164</td><td>1E-10</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAW40662.1| hypothetical protein CNA00540 [Cryptococcus neoformans var.neoformans JEC21] gb|EAL23402.1| hypothetical protein CNBA0520 [Cryptococcus neoformans var. neoformans B-3501A] ref|XP_566481.1| hypothetical protein CNA00540 [Cryptococcus neoformans var. neoformans JEC21]</td><td>152</td><td>7E-8</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_710644.1| putative centromere-specific histone H3 [Candida albicans SC5314]gb|EAK91396.1| potential centromere-specific histone H3 variant [Candida albicans SC5314]</td><td>211</td><td>9E-8</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_869677.1| PREDICTED: similar to H3 histone, family 3B [Bos taurus]</td><td>122</td><td>2E-7</td></tr>
<tr><td>CB381478</td><td>1.97E-02</td><td>Mo17<B73=F1</td><td>1.42</td><td>11</td><td>>ref|XP_477139.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD31697.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAC83224.1| unknown protein [Oryza sativa (japonica cultivar-group)]</td><td>356</td><td>1E-32</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_197406.1| catalytic [Arabidopsis thaliana]gb|AAN13173.1| unknown protein [Arabidopsis thaliana] gb|AAL66994.1| unknown protein [Arabidopsis thaliana] emb|CAC39243.1| hypothetical protein [Arabidopsis thaliana]</td><td>361</td><td>3E-26</td></tr>
<tr><td>CB815485</td><td>1.98E-02</td><td>B73<Mo17</td><td>1.28</td><td>3</td><td>>gb|AAR15174.1| actin [Ricinus communis]</td><td>377</td><td>2E-89</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAK84080.1| actin [Triticum monococcum]</td><td>190</td><td>2E-89</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAU44177.1| putative actin [Oryza sativa (japonica cultivar-group)]</td><td>377</td><td>2E-89</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAS68183.1| actin [Brassica napus var. napus]</td><td>176</td><td>2E-89</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAN40685.1| actin [Stevia rebaudiana]</td><td>377</td><td>2E-89</td></tr>
<tr><td>BG841920</td><td>1.98E-02</td><td>Mo17<B73=F1</td><td>1.21</td><td>10</td><td>>ref|NP_915931.1| proteasome subunit alpha type 3 [Oryza sativa (japonicacultivar-group)] dbj|BAD68244.1| putative proteasome subunit alpha type 3 [Oryza sativa (japonica cultivar-group)] dbj|BAD68202.1| putative proteasome subunit alpha type 3 [Oryza sativa (japonica cultivar-group)] sp|Q9LSU0|PSA3_ORYSA Proteasome subunit alpha type 3 (20S proteasome alpha subunit G) (20S proteasome subunit alpha-7) dbj|BAA96833.1| alpha 7 subunit of 20S proteasome [Oryza sativa (japonica cultivar-group)]</td><td>249</td><td>2E-85</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|XP_475461.1| putative proteasome subunit alpha type 3 [Oryza sativa (japonicacultivar-group)] gb|AAT69640.1| putative proteasome subunit alpha type 3 [Oryza sativa (japonica cultivar-group)]</td><td>249</td><td>2E-83</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAC43323.1| putative alpha7 proteasome subunit [Nicotiana tabacum]</td><td>249</td><td>2E-80</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>sp|O24362|PSA3_SPIOL Proteasome subunit alpha type 3 (20S proteasome alpha subunit G)(20S proteasome subunit alpha-7) (Proteasome component C8) dbj|BAA21651.1| 26S proteasome alpha subunit [Spinacia oleracea]</td><td>249</td><td>1E-79</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_180270.1| PAG1; endopeptidase/ peptidase/ threonine endopeptidase[Arabidopsis thaliana] gb|AAM70515.1| At2g27020/T20P8.7 [Arabidopsis thaliana] gb|AAC77860.1| 20S proteasome alpha subunit G (PAG1) [Arabidopsis thaliana] gb|AAK53039.1| At2g27020/T20P8.7 [Arabidopsis thaliana] gb|AAM66932.1| 20S proteasome subunit C8 (PAG1/PRC8_ARATH) [Arabidopsis thaliana] sp|O23715|PSA3_ARATH Proteasome subunit alpha type 3 (Proteasome subunit alpha type 7) (20S proteasome alpha subunit G-1) (Proteasome component 8) (DiDi 17A-2a) gb|AAC32064.1| 20S proteasome subunit PAG1 [Arabidopsis thaliana]</td><td>249</td><td>6E-79</td></tr>
<tr><td>CD058624</td><td>1.99E-02</td><td>Mo17<B73</td><td>1.2</td><td>10</td><td>>ref|XP_475453.1| putative 60S ribosomal protein L24 [Oryza sativa (japonicacultivar-group)] gb|AAT01333.1| putative 60S ribosomal protein L24 [Oryza sativa (japonica cultivar-group)]</td><td>161</td><td>2E-20</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAD82702.1| putative 60S ribosomal protein L24 [Oryza sativa (japonicacultivar-group)]</td><td>162</td><td>9E-20</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>ref|NP_911528.1| putative 60S ribosomal protein L24 [Oryza sativa (japonicacultivar-group)] dbj|BAD30738.1| putative 60S ribosomal protein L24 [Oryza sativa (japonica cultivar-group)] dbj|BAC06922.1| putative 60S ribosomal protein L24 [Oryza sativa (japonica cultivar-group)]</td><td>160</td><td>9E-20</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>emb|CAA63960.1| L24 ribosomal protein [Hordeum vulgare subsp. vulgare]sp|P50888|RL24 HORVU 60S ribosomal protein L24</td><td>162</td><td>1E-19</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|ABB72816.1| ribosomal protein L24-like protein [Solanum tuberosum]</td><td>171</td><td>2E-19</td></tr>
<tr><td>CB334533</td><td>1.99E-02</td><td>Mo17<B73=F1</td><td>1.17</td><td>10</td><td>>ref|XP_483755.1| putative 60S ribosomal protein L10A (RPL10aC) [Oryza sativa(japonica cultivar-group)] dbj|BAD09090.1| putative 60S ribosomal protein L10A (RPL10aC) [Oryza sativa (japonica cultivar-group)]</td><td>216</td><td>2E-42</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>gb|AAW50982.1| ribosomal protein L10A [Triticum aestivum]</td><td>216</td><td>1E-41</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td>>dbj|BAD28853.1| putative ribosomal protein L10a [Oryza sativa (japonicacultivar-group)]</td><td>216</td><td>3E-40</td></tr>
</table>

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>dbj|BAD82631.1| putative 60S ribosomal protein L10A [Oryza sativa (japonicacultivar-group)] dbj|BAB91757.1| putative 60S ribosomal protein L10A [Oryza sativa (japonica cultivar-group)]	238	4E-40
					>gb|AAG17879.1| 60S ribosomal protein L10A [Phaseolus coccineus]	88	1E-38
BM380625	1.99E-02	Mo17<B73	1.38	10	>gb|AAV59302.1| unknown protein [Oryza sativa (japonica cultivar-group)]ref|XP_475709.1| unknown protein [Oryza sativa (japonica cultivar-group)] gb|AAU03101.1| putative proline iminopeptidase [Oryza sativa (japonica cultivar-group)]	120	4E-56
					>ref|NP_179037.2| PIP; aminopeptidase/ catalytic/ hydrolase/ prolyl aminopeptidase[Arabidopsis thaliana] gb|AAM48009.1| proline iminopeptidase [Arabidopsis thaliana] gb|AAL24398.1| proline iminopeptidase [Arabidopsis thaliana]	380	5E-51
					>gb|AAL31244.1| At2g14260/T1O16.15 [Arabidopsis thaliana]gb|AAK96488.1| At2g14260/T1O16.15 [Arabidopsis thaliana]	329	5E-51
					>ref|NP_973454.1| PIP; aminopeptidase/ catalytic/ hydrolase/ prolyl aminopeptidase[Arabidopsis thaliana] gb|AAD20113.1| proline iminopeptidase [Arabidopsis thaliana] sp|P93732|PIP ARATH Proline iminopeptidase (PIP) (Prolyl aminopeptidase) (PAP)	329	5E-51
					>gb|AAC49560.1| proline iminopeptidase [Arabidopsis thaliana]	329	2E-49
DV491047	2.00E-02	B73<F1=Mo17	2.24	2	ns		
CD001652	2.00E-02	B73=F1<Mo17	1.35	4	>gb|AAT42243.1| cell death-related protein [Oryza sativa (japonica cultivar-group)]gb|AAW56895.1| cell death-related protein [Oryza sativa (japonica cultivar-group)]	128	2E-41
					>gb|AAP92158.1| apoptosis-related protein [Oryza sativa (indica cultivar-group)]	128	1E-40
					>ref|NP_564336.1| double-stranded DNA binding [Arabidopsis thaliana]gb|AAM20277.1| putative apoptosis-related protein 19 [Arabidopsis thaliana] gb|AAK76518.1| unknown protein [Arabidopsis thaliana] gb|AAL09776.1| At1g29850/F1N18_19 [Arabidopsis thaliana] gb|AAG10611.1| Similar to apoptosis related protein 19 [Arabidopsis thaliana]	129	9E-33
					>ref|NP 849728.1| double-stranded DNA binding [Arabidopsis thaliana]	130	1E-32
					>gb|AAM64794.1| unknown [Arabidopsis thaliana]	129	2E-32
DV622127	2.00E-02	Mo17<B73=F1	1.26	10	>sp|O24415|RLA2B MAIZE 60S acidic ribosomal protein P2Bgb|AAB71080.1| acidic ribosomal protein P2b [Zea mays]	113	5E-20
					>gb|AAU44278.1| putative 60S acidic ribosomal protein [Oryza sativa (japonicacultivar-group)]	113	5E-14
					>gb|AAP80630.1| acidic ribosomal protein [Triticum aestivum]	138	1E-13
					>gb|AAL91663.1| 60s acidic ribosomal protein [Prunus dulcis]	113	4E-13
					>emb|CAA55047.1| 60s acidic ribosomal protein P2 [Parthenium argentatum]sp|P41099|RLA2 PARAR 60S acidic ribosomal protein P2	114	4E-12
DV491007	2.01E-02	B73=F1<Mo17	2.53	4	ns		
CD573554	2.01E-02	B73=F1<Mo17	1.23	4	>dbj|BAD81083.1| putative COP9 signalosome complex subunit 2 [Oryza sativa (japonicacultivar-group)]	433	8E-52
					>ref|NP 913011.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]	652	8E-52
					>ref|NP_565632.1| FUS12 (FUSCA 12) [Arabidopsis thaliana]gb|AAC77857.2| COP9 complex subunit CSN2, putative [Arabidopsis thaliana] gb|AAL58101.1| CSN complex subunit 2 [Arabidopsis thaliana] gb|AAM65163.1| putative PCI domain protein [Arabidopsis thaliana] sp|Q8W207|CSN2_ARATH COP9 signalosome complex subunit 2 (Signalosome subunit 2) (FUSCA protein 12) (FUSCA12)	439	4E-49
					>gb|AAM91366.1| At2g26990/T20P8.4 [Arabidopsis thaliana]gb|AAK91453.1| At2g26990/T20P8.4 [Arabidopsis thaliana]	439	4E-49
					>ref|NP 001015820.1| MGC97656 protein [Xenopus tropicalis]gb|AAH90102.1| MGC97656 protein [Xenopus tropicalis]	443	4E-31
CB604428	2.01E-02	Mo17<B73=F1	1.23	10	ns		
BG841554	2.02E-02	B73=Mo17<F1	2.44	12	>gb|AAK15504.1| unknown [Pennisetum ciliare]	130	6E-41
					>dbj|BAD45806.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	270	2E-28
					>ref|NP_974342.1| TTN9 (TITAN9) [Arabidopsis thaliana]ref|NP_188642.2| TTN9 (TITAN9) [Arabidopsis thaliana] gb|AAM67548.1| unknown protein [Arabidopsis thaliana] gb|AAL36085.1| unknown protein [Arabidopsis thaliana] dbj|BAB01864.1| unnamed protein product [Arabidopsis thaliana]	282	6E-11
CD568450	2.02E-02	Mo17<F1	1.36	11	>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	1E-6
					>gb|ABA96669.1| jakalin homolog [Oryza sativa (japonica cultivar-group)]	258	3E-6
					>gb|ABA96823.1| jasmonate-induced protein homolog, putative [Oryza sativa (japonicacultivar-group)]	154	5E-6
CB886497	2.02E-02	B73<F1=Mo17	1.16	3	>gb|AAT68209.1| putative histone H2B [Cynodon dactylon]	98	2E-20
					>ref|XP_475912.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]gb|AAU44113.1| putative histone H2B [Oryza sativa (japonica cultivar-group)] gb|AAT69583.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	152	2E-20
					>ref|NP_915412.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]dbj|BAB93209.1| putative histone H2B [Oryza sativa (japonica cultivar-group)] dbj|BAB67889.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	139	2E-20
					>ref|NP 909298.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]dbj|BAB44055.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	155	2E-20
					>ref|NP 909263.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]dbj|BAB44008.1| putative histone H2B [Oryza sativa (japonica cultivar-group)]	153	2E-20
DV550845	2.02E-02	B73<Mo17	1.35	3	>ref|XP_465992.1| putative elongation factor 2 [Oryza sativa (japonica cultivar-group)]dbj|BAD26337.1| putative elongation factor 2 [Oryza sativa (japonica cultivar-group)]	843	1E-75
					>ref|XP 471058.1| OSJNBa0020P07.3 [Oryza sativa (japonica cultivar-group)]emb|CAE01286.2| OSJNBa0020P07.3 [Oryza sativa (japonica cultivar-group)]	843	1E-75
					>gb|AAP80650.1| elongation factor [Triticum aestivum]	167	9E-75
					>gb|AAF02837.1| elongation factor EF-2 [Arabidopsis thaliana]	846	3E-72

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|AAN31925.1| putative elongation factor [Arabidopsis thaliana]	665	3E-72
CB329498	2.02E-02	Mo17<B73=F1	1.21	10	>ref|XP_463967.1| putative small nuclear ribonucleoprotein polypeptide E [Oryzasativa (japonica cultivar-group)] dbj|BAD08019.1| putative small nuclear ribonucleoprotein polypeptide E [Oryza sativa (japonica cultivar-group)]	88	2E-40
					>ref|NP_179464.1| unknown protein [Arabidopsis thaliana]gb|AAD08943.1| putative small nuclear ribonucleoprotein E [Arabidopsis thaliana] gb|AAM64436.1| putative small nuclear ribonucleoprotein E [Arabidopsis thaliana] gb|AAO64082.1| putative small nuclear ribonucleoprotein E [Arabidopsis thaliana] dbj|BAC43399.1| putative small nuclear ribonucleoprotein E [Arabidopsis thaliana]	88	4E-39
					>ref|NP_567844.1| unknown protein [Arabidopsis thaliana]gb|AAM65292.1| small nuclear ribonucleoprotein homolog [Arabidopsis thaliana] dbj|BAD44551.1| small nuclear ribonucleoprotein homolog [Arabidopsis thaliana] dbj|BAD43076.1| small nuclear ribonucleoprotein homolog [Arabidopsis thaliana] dbj|BAD42875.1| small nuclear ribonucleoprotein homolog [Arabidopsis thaliana]	88	2E-38
					>emb|CAB81026.1| small nuclear ribonucleoprotein homolog [Arabidopsis thaliana]	86	4E-37
					>gb|EAA07131.2| ENSANGP00000022836 [Anopheles gambiae str. PEST]ref|XP_311506.2| ENSANGP00000022836 [Anopheles gambiae str. PEST]	88	2E-28
CB380403	2.03E-02	Mo17<B73	1.25	10	>ref|XP_472410.1| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)]emb|CAE02065.2| OJ000126_13.9 [Oryza sativa (japonica cultivar-group)] dbj|BAD29299.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)] dbj|BAD27798.1| 40S ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]	151	2E-50
					>ref|XP_464199.1| putative ribosomal protein S14 [Oryza sativa (japonicacultivar-group)] ref|XP_506724.1| PREDICTED OJ9003_G05.34 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD25218.1| putative ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]	150	2E-50
					>sp|P19950|RS141_MAIZE 40S ribosomal protein S14 (Clone MCH1)	149	2E-50
					>sp|P19951|RS142_MAIZE 40S ribosomal protein S14 (Clone MCH2)	150	6E-50
					>ref|NP_187758.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAM66102.1| putative 40S ribosomal protein S14 [Arabidopsis thaliana] gb|AAG51428.1| putative 40S ribosomal protein s14; 67401-66292 [Arabidopsis thaliana] sp|Q9CAX6|RS142_ARATH 40S ribosomal protein S14-2	150	5E-49
CD573095	2.03E-02	F1=Mo17<B73	1.32	8	>ref|XP_468362.1| glutathione reductase [Oryza sativa (japonica cultivar-group)]dbj|BAD22392.1| glutathione reductase [Oryza sativa (japonica cultivar-group)] dbj|BAD21653.1| glutathione reductase [Oryza sativa (japonica cultivar-group)] sp|P48642|GSHRC_ORYSA Glutathione reductase, cytosolic (GR) (GRase) dbj|BAA36283.1| glutathione reductase [Oryza sativa (japonica cultivar-group)] dbj|BAA37092.1| cytosolic glutathione reductase [Oryza sativa (japonica cultivar-group)]	496	8E-98
					>pir||T03766 probable glutathione-disulfide reductase (EC 1.8.1.7) - ricedbj|BAA11214.1| Glutathione Reductase [Oryza sativa (japonica cultivar-group)]	496	2E-95
					>gb|AAQ64632.1| cytosolic glutathione reductase [Triticum monococcum]	496	3E-94
					>sp|Q43154|GSHRP_SPIOL Glutathione reductase, chloroplast precursor (GR) (GRase)dbj|BAA07108.1| Glutathione Reductase precursor [Spinacia oleracea]	489	7E-75
					>emb|CAA66924.1| glutathione reductase [Pisum sativum]sp|Q43621|GSHRC_PEA Glutathione reductase, cytosolic (GR) (GRase) (GOR2)	498	9E-75
CB885254	2.03E-02	Mo17<B73	1.34	9	>dbj|BAB89354.1| ubiquitin-conjugating enzyme OsUBC5a [Oryza sativa (japonicacultivar-group)]	147	5E-83
					>emb|CAI29540.1| ubiquitin conjugating enzyme E2 [Oryza sativa (indicacultivar-group)]	147	8E-83
					>ref|NP_567791.1| UBC9 (UBIQUITIN CONJUGATING ENZYME 9); ubiquitin conjugatingenzyme/ ubiquitin-like activating enzyme [Arabidopsis thaliana] gb|AAY44849.1| ubiquitinating enzyme [Arabidopsis thaliana]	178	6E-80
					>gb|AAG40371.1| AT4g27960 [Arabidopsis thaliana]	178	6E-80
					>ref|NP_849462.1| UBC9 (UBIQUITIN CONJUGATING ENZYME 9); ubiquitin conjugatingenzyme/ ubiquitin-like activating enzyme [Arabidopsis thaliana] emb|CAA78714.1| ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] emb|CAA51201.1| ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] emb|CAB79598.1| ubiquitin-protein ligase UBC9 [Arabidopsis thaliana] emb|CAB36765.1| ubiquitin-protein ligase UBC9 [Arabidopsis thaliana] gb|AAN13102.1| E2 ubiquitin-conjugating enzyme 9 (UBC9) [Arabidopsis thaliana] sp|P35132|UBC9_ARATH Ubiquitin-conjugating enzyme E2-17 kDa 9 (Ubiquitin-protein ligase 9) (Ubiquitin carrier protein 9) (UBCAT4B) gb|AAA32894.1| ubiquitin conjugating enzyme	148	2E-79
CB605152	2.03E-02	Mo17<B73=F1	1.23	11	>emb|CAA98176.1| RAB8E [Lotus corniculatus var. japonicus]	215	2E-17
					>emb|CAA98175.1| RAB8D [Lotus corniculatus var. japonicus]	214	2E-17
					>emb|CAA98174.1| RAB8C [Lotus corniculatus var. japonicus]	212	2E-17
					>emb|CAA98173.1| RAB8B [Lotus corniculatus var. japonicus]	187	2E-17
					>emb|CAA98172.1| RAB8A [Lotus corniculatus var. japonicus]	216	2E-17
CB381574	2.04E-02	B73<Mo17	1.3	3	>gb|AAA20239.1| cyclin IaZm	420	1E-36
					>ref|NP_915872.1| putative cyclin Ia [Oryza sativa (japonica cultivar-group)]dbj|BAB92272.1| putative cyclin [Oryza sativa (japonica cultivar-group)]	449	6E-27
					>ref|XP_475474.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]gb|AAT69653.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	521	2E-21
					>dbj|BAA09368.1| B-type cyclin [Nicotiana tabacum]	473	1E-19
					>gb|AAV41031.1| cyclin B-like protein [Nicotiana tabacum]	473	2E-19
DV622486	2.06E-02	F1<B73=Mo17	1.32	6	>gb|AAO43439.1| branched silkless1 [Zea mays]gb|AAO21119.1| branched silkless1 [Zea mays]	313	2E-9
BM334563	2.06E-02	Mo17<F1	1.42	11	>dbj|BAD44921.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD44911.1| unknown protein [Oryza sativa (japonica cultivar-group)]	90	7E-29
					>ref|NP_849867.1| unknown protein [Arabidopsis thaliana]ref|NP_974115.1| unknown protein [Arabidopsis thaliana] ref|NP_564967.1| unknown protein [Arabidopsis thaliana] gb|AAM91224.1| unknown protein [Arabidopsis thaliana] gb|AAM13228.1| unknown protein [Arabidopsis thaliana] gb|AAM61026.1| unknown [Arabidopsis thaliana] gb|AAG60113.1| unknown protein [Arabidopsis thaliana]	137	1E-13

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GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>gb|AAM64550.1| unknown [Arabidopsis thaliana]	102	5E-13
					>gb|ABA97694.1| expressed protein [Oryza sativa (japonica cultivar-group)]	95	1E-12
					>ref|NP_568985.1| unknown protein [Arabidopsis thaliana]gb|AAM19915.1| AT5g64130/MHJ24_11 [Arabidopsis thaliana] gb|AAL25551.1| AT5g64130/MHJ24_11 [Arabidopsis thaliana] gb|AAM67262.1| unknown [Arabidopsis thaliana]	115	3E-12
BM331929	2.07E-02	B73<F1=Mo17	1.3	2	>dbj|BAD81832.1| transcription initiation factor IID (TFIID) subunit A-like protein[Oryza sativa (japonica cultivar-group)] dbj|BAD82661.1| transcription initiation factor IID (TFIID) subunit A-like protein [Oryza sativa (japonica cultivar-group)]	542	4E-35
					>dbj|BAE46416.1| TATA binding protein associated factor [Solanum tuberosum]	638	3E-10
					>ref|NP_849680.1| transcription initiation factor [Arabidopsis thaliana]ref|NP_564023.1| transcription initiation factor [Arabidopsis thaliana] gb|AAR28016.1| TAF12b [Arabidopsis thaliana] gb|AAM14362.1| unknown protein [Arabidopsis thaliana] gb|AAL07223.1| unknown protein [Arabidopsis thaliana]	683	6E-9
					>dbj|BAD82054.1| transcription initiation factor IID (TFIID) subunit A-like protein[Oryza sativa (japonica cultivar-group)]	295	3E-7
					>gb|AAF97312.1| Unknown protein [Arabidopsis thaliana]	674	1E-6
DV621908	2.07E-02	Mo17<B73=F1	1.2	10	>ref|XP_468756.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)] ref|XP_468752.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] gb|AAP20855.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] gb|AAP20842.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] sp|P40978|RS19_ORYSA 40S ribosomal protein S19	146	9E-72
					>gb|AAW34237.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	144	6E-69
					>gb|AAW34236.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	166	4E-68
					>gb|AAW34240.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	122	6E-64
					>gb|ABB87116.1| 40S ribosomal protein S19-like [Solanum tuberosum]	143	6E-58
DV491930	2.08E-02	B73<Mo17	1.36	4	>ref|XP_550363.1| putative gamma-adaptin 1 [Oryza sativa (japonica cultivar-group)]dbj|BAD67607.1| putative gamma-adaptin 1 [Oryza sativa (japonica cultivar-group)]	870	8E-46
					>gb|AAK98709.1| Putative gamma-adaptin 1 [Oryza sativa]	1354	1E-38
					>gb|AAD28247.1| gamma-adaptin 1 [Arabidopsis thaliana]gb|AAC28338.1| gamma-adaptin 1 [Arabidopsis thaliana]	876	5E-32
					>emb|CAB39730.1| adaptor protein complex AP-1 large subunit; gamma-adaptin 2[Arabidopsis thaliana]	876	3E-31
					>ref|NP_173802.1| GAMMA-ADAPTIN 1 (GAMMA-ADAPTIN 1); clathrin binding [Arabidopsisthaliana] ref|NP_849701.1| GAMMA-ADAPTIN 1 (GAMMA-ADAPTIN 1); clathrin binding [Arabidopsis thaliana] gb|AAO63977.1| putative gamma-adaptin [Arabidopsis thaliana] gb|AAO42305.1| putative gamma-adaptin [Arabidopsis thaliana]	876	3E-31
CD670181	2.08E-02	B73<F1=Mo17	1.31	3	>ref|XP_479646.1| putative HMG type nucleosome/chromatin assembly factor D [Oryzasativa (japonica cultivar-group)] dbj|BAD03552.1| putative HMG type nucleosome/chromatin assembly factor D [Oryza sativa (japonica cultivar-group)]	203	1E-47
					>gb|AAM93218.1| nucleasome/chromatin assembly factor D protein NFD106 [Zea mays]gb|AAL33652.1| HMG type nucleosome/chromatin assembly factor D [Zea mays]	154	5E-42
					>ref|NP_568431.1| HMGB6; transcription factor [Arabidopsis thaliana]gb|AAM63233.1| unknown [Arabidopsis thaliana] dbj|BAC43282.1| unknown protein [Arabidopsis thaliana]	241	1E-30
					>dbj|BAB09558.1| unnamed protein product [Arabidopsis thaliana]	226	2E-16
					>gb|AAM64404.1| putative HMG protein [Arabidopsis thaliana]	138	4E-16
CB885421	2.08E-02	Mo17<B73=F1	1.2	10	>ref|NP_922210.1| putative mitochondrial NAD+-dependent malic enzyme protein [Oryzasativa (japonica cultivar-group)] gb|AAG13628.1| putative mitochondrial NAD+-dependent malic enzyme protein [Oryza sativa (japonica cultivar-group)]	520	2E-63
					>gb|ABB47851.1| mitochondrial NAD+-dependent malic enzyme protein, putative [Oryzasativa (japonica cultivar-group)]	532	2E-63
					>gb|ABB47850.1| mitochondrial NAD+-dependent malic enzyme protein, putative [Oryzasativa (japonica cultivar-group)]	538	2E-63
					>gb|ABB47849.1| mitochondrial NAD+-dependent malic enzyme protein, putative [Oryzasativa (japonica cultivar-group)]	620	2E-63
					>emb|CAA80547.1| precursor of the 59kDa subunit of the mitochondrial NAD+-dependentmalic enzyme [Solanum tuberosum] sp|P37225|MAON_SOLTU NAD-dependent malic enzyme 59 kDa isoform, mitochondrial precursor (NAD-ME)	601	2E-54
DV492328	2.08E-02	B73=F1<Mo17	1.41	4	>ref|ZP_00948066.1| hypothetical protein BbacK_01000360 [Bartonella bacilliformisKC583]	152	6E-38
					>ref|ZP_00679255.1| hypothetical protein PproDRAFT_0591 [Pelobacter propionicus DSM2379] gb|EAO35260.1| hypothetical protein PproDRAFT_0591 [Pelobacter propionicus DSM 2379]	167	1E-34
					>gb|AAU03684.1| conserved hypothetical protein [Rickettsia typhi str. Wilmington]ref|YP_067166.1| hypothetical protein RT0201 [Rickettsia typhi str. Wilmington]	138	2E-33
					>ref|ZP_00733436.1| cell wall-associated hydrolase [Actinobacillus succinogenes 130Z]ref|ZP_00733163.1| cell wall-associated hydrolase [Actinobacillus succinogenes 130Z] ref|ZP_00732815.1| cell wall-associated hydrolase [Actinobacillus succinogenes 130Z] ref|ZP_00732790.1| cell wall-associated hydrolase [Actinobacillus succinogenes 130Z] ref|ZP_00731820.1| cell wall-associated hydrolase [Actinobacillus succinogenes 130Z] gb|EAO51165.1| cell wall-associated hydrolase [Actinobacillus succinogenes 130Z] gb|EAO50163.1| cell wall-associated hydrolase [Actinobacillus succinogenes 130Z] gb|EAO50139.1| cell wall-associated hydrolase [Actinobacillus succinogenes 130Z] gb|EAO49775.1| cell wall-associated hydrolase [Actinobacillus succinogenes 130Z] gb|EAO49498.1| cell wall-associated hydrolase [Actinobacillus succinogenes 130Z]	144	3E-33
					>ref|ZP_00307967.1| hypothetical protein Chut02003441 [Cytophaga hutchinsonii]	152	1E-32
CB886104	2.08E-02	B73=Mo17<F1	1.23	1	>emb|CAA42530.1| histone H2B [Triticum aestivum]sp|P27807|H2B1_WHEAT Histone H2B	152	4E-35

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>sp|P54348|H2B5 MAIZE Histone H2Bgb|AAB04688.1| histone H2B	154	4E-35
					>emb|CAA49584.1| H2B histone [Zea mays]sp|Q43261|H2B3 MAIZE Histone H2B.3	153	1E-33
					>emb|CAA40565.1| H2B histone [Zea mays]sp|P30756|H2B2 MAIZE Histone H2B.2	150	2E-33
					>emb|CAA40564.1| H2B histone [Zea mays]sp|P30755|H2B1 MAIZE Histone H2B.1	151	3E-33
DV942241	2.08E-02	F1=Mo17<B73	1.37	8	ns		
BM073440	2.08E-02	Mo17<B73	1.52	9	>dbj|BAD33948.1| unknown protein [Oryza sativa (japonica cultivar-group)]	244	2E-38
					>ref|XP 482938.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]dbj|BAD09202.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	254	1E-29
					>ref|NP_199082.1| unknown protein [Arabidopsis thaliana]gb|AAU29467.1| At5g42680 [Arabidopsis thaliana] gb|AAT41771.1| At5g42680 [Arabidopsis thaliana] dbj|BAB10624.1| unnamed protein product [Arabidopsis thaliana]	238	1E-16
					>ref|NP_195671.1| unknown protein [Arabidopsis thaliana]emb|CAB80624.1| putative protein [Arabidopsis thaliana] emb|CAB44696.1| putative protein [Arabidopsis thaliana] gb|AAO63334.1| At4g39610 [Arabidopsis thaliana] dbj|BAC43028.1| unknown protein [Arabidopsis thaliana]	264	2E-16
					>gb|AAM67173.1| unknown [Arabidopsis thaliana]	257	7E-16
DV489939	2.09E-02	Mo17<B73	1.54	9	>dbj|BAD61148.1| BY-2 kinesin-like protein 10-like [Oryza sativa (japonicacultivar-group)]	193	4E-19
					>dbj|BAD61147.1| kinesin heavy chain-like [Oryza sativa (japonica cultivar-group)]	258	4E-19
					>ref|NP 917771.1| kinesin-like protein [Oryza sativa (japonica cultivar-group)]	707	4E-19
					>dbj|BAB40710.1| BY-2 kinesin-like protein 10 [Nicotiana tabacum]	703	2E-11
					>dbj|BAB02671.1| unnamed protein product [Arabidopsis thaliana]	706	2E-11
DV550068	2.10E-02	B73<Mo17	3.79	3	>gb|AAP94585.1| putative gag-pol precursor [Zea mays]	1833	9E-80
					>ref|NP 921259.1| putative retroelement [Oryza sativa (japonica cultivar-group)]gb|AAK52121.1| Putative retroelement [Oryza sativa (japonica cultivar-group)]	2079	1E-45
					>ref|XP 474845.1| OSJNBa0035O13.3 [Oryza sativa (japonica cultivar-group)]emb|CAD40114.1| OSJNBa0035O13.3 [Oryza sativa (japonica cultivar-group)]	2008	1E-45
					>gb|ABA98419.1| retrotransposon protein, putative, Ty3-gypsy sub-class [Oryza sativa(japonica cultivar-group)]	1304	4E-45
					>gb|ABA97550.1| retrotransposon protein, putative, Ty3-gypsy sub-class [Oryza sativa(japonica cultivar-group)]	1541	6E-45
CB885984	2.10E-02	B73=F1<Mo17	1.33	4	>dbj|BAD68706.1| putative ketol-acid reductoisomerase precursor [Oryza sativa(japonica cultivar-group)]	548	2E-85
					>ref|NP 917284.1| putative ketol-acid reductoisomerase [Oryza sativa (japonicacultivar-group)]	581	2E-85
					>gb|AAU44107.1| putative ketol-acid reductoisomerase [Oryza sativa (japonicacultivar-group)]	578	2E-84
					>dbj|BAD94384.1| ketol-acid reductoisomerase [Arabidopsis thaliana]	344	6E-81
					>ref|NP_191420.1| ketol-acid reductoisomerase [Arabidopsis thaliana]emb|CAA49506.1| ketol-acid reductoisomerase [Arabidopsis thaliana] emb|CAB68199.1| ketol-acid reductoisomerase [Arabidopsis thaliana] gb|AAN33197.1| At3g58610/F14P22_200 [Arabidopsis thaliana] gb|AAN31816.1| putative ketol-acid reductoisomerase [Arabidopsis thaliana] gb|AAM20206.1| putative ketol-acid reductoisomerase [Arabidopsis thaliana] gb|AAL38839.1| putative ketol-acid reductoisomerase [Arabidopsis thaliana] gb|AAG42917.1| putative ketol-acid reductoisomerase [Arabidopsis thaliana] gb|AAL32973.1| AT3g58610/F14P22_200 [Arabidopsis thaliana] gb|AAG40022.1| AT3g58610 [Arabidopsis thaliana] sp|Q05758|ILV5_ARATH Ketol-acid reductoisomerase, chloroplast precursor (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil reductoisomerase)	591	6E-81
CD059021	2.10E-02	B73=F1<Mo17	1.24	4	>dbj|BAD45854.1| RISBZ5 [Oryza sativa (japonica cultivar-group)]dbj|BAB39175.1| RISBZ5 [Oryza sativa]	295	4E-31
					>ref|XP_464322.1| RISBZ4 [Oryza sativa (japonica cultivar-group)]dbj|BAD27607.1| RISBZ4 [Oryza sativa (japonica cultivar-group)] dbj|BAD26199.1| RISBZ4 [Oryza sativa (japonica cultivar-group)]	277	2E-20
					>dbj|BAD27900.1| putative RISBZ4 [Oryza sativa (japonica cultivar-group)]gb|AAC37418.1| transcriptional activator protein	298	5E-20
					>emb|CAA04639.1| RITA-2 protein [Oryza sativa (japonica cultivar-group)]	199	8E-20
					>dbj|BAB39174.1| RISBZ4 [Oryza sativa]	278	8E-20
CD573390	2.10E-02	Mo17<B73=F1	1.3	11	>gb|AAF13094.1| unknown protein [Arabidopsis thaliana]gb|AAF21186.1| unknown protein [Arabidopsis thaliana]	196	4E-30
					>ref|NP_566319.1| unknown protein [Arabidopsis thaliana]ref|NP_850538.1| unknown protein [Arabidopsis thaliana] gb|AAL47395.1| unknown protein [Arabidopsis thaliana] gb|AAL16180.1| At3g07760/F17A17.10 [Arabidopsis thaliana] gb|AAK96782.1| Unknown protein [Arabidopsis thaliana] gb|AAM66036.1| unknown [Arabidopsis thaliana]	125	4E-30
					>gb|ABA99120.1| AC009176 putative heat-shock protein [Oryza sativa (japonicacultivar-group)]	1210	4E-10
CB604155	2.10E-02	Mo17<B73=F1	1.25	11	>ref|XP_468756.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)] ref|XP_468752.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] gb|AAP20855.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] gb|AAP20842.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] sp|P40978|RS19 ORYSA 40S ribosomal protein S19	146	9E-72
					>gb|AAW34237.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	144	6E-69
					>gb|AAW34236.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	166	4E-68
					>gb|AAW34240.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	122	6E-64
					>gb|ABB87116.1| 40S ribosomal protein S19-like [Solanum tuberosum]	143	6E-58
BM351298	2.11E-02	Mo17<B73	1.33	10	>ref|XP_475883.1| protein phosphatase 2A B'kappa subunit [Oryza sativa (japonicacultivar-group)] gb|AAT58738.1| protein phosphatase 2A B'kappa subunit [Oryza sativa (japonica cultivar-group)] emb|CAC85920.1| protein phosphatase 2A B'kappa subunit [Oryza sativa (japonica cultivar-group)]	510	1E-41

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15 % FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>emb|CAB76153.1| putative B' regulatory subunit of PP2A [Oryza sativa]	143	3E-41
					>ref|NP_197933.1| protein phosphatase type 2A regulator [Arabidopsis thaliana]gb|AAN13126.1| putative AtBgamma protein [Arabidopsis thaliana] gb|AAL24096.1| putative AtBgamma protein [Arabidopsis thaliana] sp|Q93YV6|2A5I_ARATH Serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' iota isoform (PP2A, B' subunit, iota isoform) (AtB' iota)	500	3E-24
					>gb|AAT77357.1| unknown protein [Oryza sativa (japonica cultivar-group)]	491	2E-21
					>ref|NP 188802.1| protein phosphatase type 2A regulator [Arabidopsis thaliana]	546	1E-19
DV489574	2.11E-02	B73<Mo17	1.59	4	>dbj|BAD87534.1| putative beta-N-acetylhexosaminidase [Oryza sativa (japonicacultivar-group)]	526	2E-81
					>ref|NP 915111.1| beta-N-acetylhexosaminidase -like protein [Oryza sativa (japonicacultivar-group)]	496	2E-81
					>gb|AAV32135.1| putative beta-N-acetylhexosaminidase [Oryza sativa (japonicacultivar-group)]	531	5E-68
					>gb|AAT77374.1| putative beta-N-acetylhexosaminidase [Oryza sativa (japonicacultivar-group)]	527	5E-68
					>ref|NP_176737.2| beta-N-acetylhexosaminidase [Arabidopsis thaliana]gb|AAN33206.1| At1g65600/F5I14_13 [Arabidopsis thaliana] gb|AAM91092.1| At1g65600/F5I14 13 [Arabidopsis thaliana]	535	4E-63
CB617035	2.11E-02	Mo17<F1	1.27	11	>gb|AAT73618.1| calmodulin cam-205 [Daucus carota]	149	2E-61
					>emb|CAA06307.1| CaM-2 [Nicotiana plumbaginifolia]emb|CAA06306.1| CaM-1 [Nicotiana plumbaginifolia]	122	2E-61
					>gb|AAQ63462.1| calmodulin 8 [Daucus carota]gb|AAQ63461.1| calmodulin 4 [Daucus carota]	150	2E-61
					>emb|CAA74307.1| calmodulin [Zea mays]emb|CAA46150.1| calmodulin [Oryza sativa] gb|AAD10246.1| calmodulin [Phaseolus vulgaris]	149	2E-61
					>emb|CAA36644.1| unnamed protein product [Medicago sativa]gb|AAM81203.1| calmodulin 2 [Medicago truncatula] gb|AAA34238.1| calmodulin [Vigna radiata] gb|AAD10244.1| calmodulin [Phaseolus vulgaris] sp|P17928|CALM_MEDSA Calmodulin (CaM) gb|AAA34014.1| calmodulin gb|AAA34013.1| calmodulin prf||2121384C calmodulin prf||2121384A calmodulin	149	2E-61
CB381685	2.11E-02	Mo17<B73=F1	1.27	10	>gb|AAL59231.1| ribosomal protein L35A [Zea mays]	112	4E-59
					>gb|AAK73115.1| ribosomal protein L35A [Zea mays]	112	6E-59
					>ref|XP_468159.1| putative ribosomal protein L35A [Oryza sativa (japonicacultivar-group)] ref|XP_507015.1| PREDICTED OJ1715_H01.42 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD19312.1| putative ribosomal protein L35A [Oryza sativa (japonica cultivar-group)] dbj|BAD19202.1| putative ribosomal protein L35A [Oryza sativa (japonica cultivar-group)]	112	6E-55
					>ref|XP_475896.1| putative ribosomal protein L35A [Oryza sativa (japonicacultivar-group)] ref|XP_475888.1| putative ribosomal protein L35A [Oryza sativa (japonica cultivar-group)] gb|AAT58712.1| putative ribosomal protein L35A [Oryza sativa (japonica cultivar-group)] gb|AAT58704.1| putative ribosomal protein L35A [Oryza sativa (japonica cultivar-group)]	111	4E-51
					>gb|AAK25760.1| ribosomal protein L33 [Castanea sativa]	112	5E-50
DV550679	2.12E-02	B73=Mo17<F1	1.44	1	ns		
DV550393	2.12E-02	B73=Mo17<F1	1.35	12	>ref|XP_478106.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAC84361.1| unknown protein [Oryza sativa (japonica cultivar-group)] dbj|BAD31502.1| unknown protein [Oryza sativa (japonica cultivar-group)]	145	2E-11
DV621294	2.12E-02	B73=F1<Mo17	1.26	4	ns		
CD651750	2.12E-02	B73=Mo17<F1	1.29	12	>gb|AAF71261.2| beta-glucosidase aggregating factor precursor [Zea mays]	306	4E-22
					>gb|AAA87041.1| putative 32.6 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72096.1| 32 kDa protein [Hordeum vulgare]	304	1E-21
					>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	2E-21
					>gb|AAA87042.1| putative 32.7 kDa jasmonate-induced protein [Hordeum vulgare]gb|AAB72097.1| 32 kDa protein [Hordeum vulgare]	304	7E-21
					>gb|AAR20919.1| jasmonate-induced protein [Triticum aestivum]	304	2E-20
DV495219	2.12E-02	B73<F1=Mo17	1.35	2	>ref|XP 468505.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD23057.1| unknown protein [Oryza sativa (japonica cultivar-group)]	819	1E-25
					>dbj|BAD94762.1| hypothetical protein [Arabidopsis thaliana]	438	5E-17
					>ref|NP_173224.2| unknown protein [Arabidopsis thaliana]gb|AAQ56797.1| At1g17820 [Arabidopsis thaliana] gb|AAM91570.1| unknown protein [Arabidopsis thaliana]	803	5E-17
					>gb|AAF97262.1| Strong similarity to a hypothetical protein T18K17.13 gi|6598861from Arabidopsis thaliana BAC T18K17 gb|AC010556 and contains a PH PF|00169 domain	797	5E-17
					>ref|NP 177463.1| unknown protein [Arabidopsis thaliana]gb|AAG52130.1| hypothetical protein; 41134-44253 [Arabidopsis thaliana]	779	2E-13
BM075951	2.12E-02	Mo17<B73=F1	1.86	10	ns		
DV621517	2.13E-02	B73<F1	1.63	1	>ref|NP_908924.1| P0463A02.21 [Oryza sativa (japonica cultivar-group)]dbj|BAB89617.1| beta-glucosidase aggregating factor precursor-like protein [Oryza sativa (japonica cultivar-group)]	150	6E-21
					>dbj|BAD53304.1| putative beta-glucosidase aggregating factor [Oryza sativa(japonica cultivar-group)]	169	1E-19
					>ref|NP_920772.1| putative disease resistance protein [Oryza sativa (japonicacultivar-group)] gb|AAM74358.1| Putative disease resistance response protein [Oryza sativa (japonica cultivar-group)] gb|AAP53059.1| hypothetical protein LOC Os10g18760 [Oryza sativa (japonica cultivar-group)]	175	8E-18
					>gb|AAV50047.1| dirigent-like protein [Saccharum hybrid cultivar]	187	1E-17
					>gb|ABA96667.1| jacalin homolog [Oryza sativa (japonica cultivar-group)]	307	2E-17
CB815586	2.13E-02	Mo17<F1	1.29	11	>ref|XP 467233.1| unknown protein [Oryza sativa (japonica cultivar-group)]dbj|BAD07680.1| unknown protein [Oryza sativa (japonica cultivar-group)]	84	1E-15

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15% FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
					>ref|XP_473709.1| OSJNBa0086O06.9 [Oryza sativa (japonica cultivar-group)]emb|CAE04861.2| OSJNBa0086O06.9 [Oryza sativa (japonica cultivar-group)]	83	1E-14
BM079979	2.13E-02	B73=F1<Mo17	1.42	4	ns		
CD568430	2.13E-02	B73<Mo17	1.26	3	>ref|XP_493706.1| arginine decarboxylase [Oryza sativa (japonica cultivar-group)]gb|AAT37534.1| arginine decarboxylase [Oryza sativa] dbj|BAA84799.1| arginine decarboxylase [Oryza sativa (japonica cultivar-group)] sp|Q9SNN0|SPE1 ORYSA Arginine decarboxylase (ARGDC) (ADC)	702	4E-47
					>emb|CAA65585.1| arginine decarboxylase [Vitis vinifera]	630	1E-29
					>dbj|BAE71301.1| putative arginine decarboxylase [Trifolium pratense]	729	2E-29
					>dbj|BAE71251.1| putative arginine decarboxylase [Trifolium pratense]	729	2E-29
					>dbj|BAE71214.1| putative arginine decarboxylase [Trifolium pratense]	280	2E-29
DV622013	2.13E-02	B73<Mo17	1.48	4	>gb|AAP80862.1| Emr1 [Triticum aestivum]	304	5E-20
					>gb|ABA96655.1| Emr1 [Oryza sativa (japonica cultivar-group)]	609	2E-17
					>gb|ABA96656.1| Emr1 [Oryza sativa (japonica cultivar-group)]	682	2E-12
CB334161	2.14E-02	Mo17<B73=F1	1.28	10	>dbj|BAD31463.1| putative zinc finger (C3HC4-type RING finger) protein [Oryza sativa(japonica cultivar-group)]	570	3E-11
CB605131	2.14E-02	Mo17<F1	1.25	11	>ref|XP_468756.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)] ref|XP_468752.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] gb|AAP20855.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] gb|AAP20842.1| putative ribosomal protein S19 [Oryza sativa (japonica cultivar-group)] sp|P40978|RS19 ORYSA 40S ribosomal protein S19	146	7E-74
					>gb|AAW34237.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	144	4E-71
					>gb|AAW34236.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	166	3E-70
					>gb|AAW34240.1| putative ribosomal protein S19 [Oryza sativa (japonicacultivar-group)]	122	2E-63
					>gb|ABB87116.1| 40S ribosomal protein S19-like [Solanum tuberosum]	143	5E-61
CB605478	2.15E-02	Mo17<B73	1.3	10	>ref|XP_472755.1| OSJNBa0072F16.12 [Oryza sativa (japonica cultivar-group)]emb|CAD40987.2| OSJNBa0072F16.12 [Oryza sativa (japonica cultivar-group)]	183	3E-43
					>emb|CAA10984.1| hypothetical protein [Hordeum vulgare subsp. vulgare]sp|O48609|RRP3_HORVU Plastid-specific 30S ribosomal protein 3, chloroplast precursor (PSRP-3)	181	5E-39
					>gb|AAF64163.1| plastid-specific ribosomal protein 3 precursor [Spinacia oleracea]sp|P82412|RRP3_SPIOL Plastid-specific 30S ribosomal protein 3, chloroplast precursor (PSRP-3)	179	2E-28
					>ref|NP_564934.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAO50623.1| unknown protein [Arabidopsis thaliana] gb|AAO42029.1| unknown protein [Arabidopsis thaliana] gb|AAD49984.1| ESTs gb|H37416, gb|T21163, gb|T76138 and gb|AA651329 come from this gene. [Arabidopsis thaliana] sp|Q9SX22|RRP31 ARATH Plastid-specific 30S ribosomal protein 3-1, chloroplast precursor (PSRP-3 1)	166	1E-25
					>gb|AAM63350.1| plastid-specific ribosomal protein 3 precursor [Arabidopsisthaliana]	166	1E-25
DV491655	2.16E-02	F1<Mo17	2.99	5	ns		
DV490951	2.16E-02	F1=Mo17<B73	1.31	9	>dbj|BAD31081.1| unknown protein [Oryza sativa (japonica cultivar-group)]	288	7E-53
					>ref|NP_172707.1| unknown protein [Arabidopsis thaliana]gb|AAQ62869.1| At1g12450 [Arabidopsis thaliana] dbj|BAD93843.1| hypothetical protein [Arabidopsis thaliana]	303	1E-27
					>emb|CAB79240.1| predicted protein [Arabidopsis thaliana]emb|CAA19800.1| putative protein [Arabidopsis thaliana] emb|CAA16570.1| predicted protein [Arabidopsis thaliana]	217	1E-26
					>ref|NP_194016.2| unknown protein [Arabidopsis thaliana]gb|AAO50499.1| unknown protein [Arabidopsis thaliana] gb|AAO42138.1| unknown protein [Arabidopsis thaliana]	296	1E-26
					>ref|NP_565283.1| unknown protein [Arabidopsis thaliana]gb|AAN28822.1| At2g02370/T16F16.16 [Arabidopsis thaliana] gb|AAL15376.1| At2g02370/T16F16.16 [Arabidopsis thaliana] gb|AAC78519.2| expressed protein [Arabidopsis thaliana] gb|AAK32779.1| At2g02370/T16F16.16 [Arabidopsis thaliana]	320	3E-24
BM333812	2.16E-02	Mo17<B73=F1	1.51	10	>ref|NP_917674.1| putative acetyl transferase [Oryza sativa (japonicacultivar-group)] dbj|BAB17110.1| taxadienol acetyl transferase-like [Oryza sativa (japonica cultivar-group)]	424	1E-45
					>ref|NP_917673.1| putative acetyl transferase [Oryza sativa (japonicacultivar-group)] dbj|BAB17109.1| 10-deacetylbaccatin III-10-O-acetyl transferase-like [Oryza sativa (japonica cultivar-group)]	446	1E-33
					>gb|AAL73122.1| putative 0-deacetylbaccatin III-10-O-acetyl transferase-likeprotein [Musa acuminata]	272	1E-11
					>dbj|BAD86875.1| 3'-N-debenzoyltaxol N-benzoyltransferase -like [Oryza sativa(japonica cultivar-group)]	439	2E-10
					>ref|NP_908495.1| unnamed protein product [Oryza sativa (japonica cultivar-group)]	153	2E-10
DV942810	2.16E-02	B73=F1<Mo17	1.37	5	>ref|XP_473409.1| OSJNBa0079A21.20 [Oryza sativa (japonica cultivar-group)]	207	1E-15
					>emb|CAE02020.1| OSJNBa0079A21.22 [Oryza sativa (japonica cultivar-group)]	192	1E-15
					>ref|NP_199542.1| unknown protein [Arabidopsis thaliana]gb|AAO64931.1| At5g47310 [Arabidopsis thaliana] dbj|BAA97165.1| unnamed protein product [Arabidopsis thaliana]	245	2E-12
					>emb|CAI64488.1| OSJNBa0065H10.7 [Oryza sativa (japonica cultivar-group)]	158	6E-11
					>ref|XP_467112.1| EREBP-4 like protein [Oryza sativa (japonica cultivar-group)]dbj|BAD25328.1| EREBP-4 like protein [Oryza sativa (japonica cultivar-group)] dbj|BAD25669.1| EREBP-4 like protein [Oryza sativa (japonica cultivar-group)]	204	6E-11

Table 4. Microarray analysis results, mode of gene action classification, and BLAST annotation for the 1,367 ESTs identified as differentially expressed among genotypes (15 % FDR)

GenBank accession no.	Overall P value	Significant pattern	Fold change†	Sector‡	BLAST annotation*	Score	E value
DV622487	2.16E-02	Mo17<B73	1.29	10	>dbj|BAD68235.1| putative CGI-94 protein [Oryza sativa (japonica cultivar-group)]dbj|BAD68234.1| putative CGI-94 protein [Oryza sativa (japonica cultivar-group)] sp|Q8S1Z1|UTP11_ORYSA Probable U3 small nucleolar RNA-associated protein 11 (U3 snoRNA-associated protein 11)	229	3E-62
					>ref|NP_915921.1| P0468B07.17 [Oryza sativa (japonica cultivar-group)]	214	7E-50
					>ref|NP_191595.1| unknown protein [Arabidopsis thaliana]emb|CAB81822.1| putative protein [Arabidopsis thaliana] gb|AAN31867.1| unknown protein [Arabidopsis thaliana] gb|AAM26635.1| AT3g60360/T8B10_20 [Arabidopsis thaliana] gb|AAK63980.1| AT3g60360/T8B10_20 [Arabidopsis thaliana] gb|AAM61709.1| unknown [Arabidopsis thaliana] pir||T47847 hypothetical protein T8B10.20 - Arabidopsis thaliana sp|Q9M223|UT11_ARATH Probable U3 small nucleolar RNA-associated protein 11 (U3 snoRNA-associated protein 11)	228	2E-34
					>ref|XP_788181.1| PREDICTED: similar to UTP11-like, U3 small nucleolarribonucleoprotein, [Strongylocentrotus purpuratus]	250	2E-11
					>gb|AAH49053.1| UTP11-like, U3 small nucleolar ribonucleoprotein [Danio rerio]ref|NP_956292.1| UTP11-like, U3 small nucleolar ribonucleoprotein [Danio rerio]	250	6E-11
CB885743	2.18E-02	B73=F1<Mo17	1.64	4	ns		
CD527560	2.18E-02	B73<Mo17	1.47	3	>pir||JS0657 ubiquitin / ribosomal protein S27a - maizegb|AAA70105.1| ubiquitin fusion protein gb|AAA33519.1| ubiquitin fusion protein prf||2211240B ubiquitin fusion protein	155	3E-69
					>ref|XP_475630.1| putative ubiquitin / ribosomal protein S27a [Oryza sativa (japonicacultivar-group)] gb|AAV43924.1| putative ubiquitin fusion protein [Oryza sativa (japonica cultivar-group)] gb|AAT93912.1| putative ubiquitin extension protein [Oryza sativa (japonica cultivar-group)]	155	7E-68
					>gb|AAA62698.1| ubiquitin	155	7E-68
					>ref|NP_908721.1| ubiquitin / ribosomal protein S27a [Oryza sativa (japonicacultivar-group)] dbj|BAB39294.1| ubiquitin / ribosomal protein S27a.1 [Oryza sativa (japonica cultivar-group)]	155	9E-68
					>gb|AAA62699.1| ubiquitin	155	1E-67
CD527180	2.18E-02	Mo17<B73=F1	1.21	11	>ref|XP_469336.1| unknown protein [Oryza sativa]dbj|BAC78563.1| hypothetical protein [Oryza sativa (japonica cultivar-group)] gb|AAK14411.1| unknown protein [Oryza sativa]	138	1E-29
					>ref|NP_201245.1| unknown protein [Arabidopsis thaliana]gb|AAL34219.1| unknown protein [Arabidopsis thaliana] gb|AAK59405.1| unknown protein [Arabidopsis thaliana] dbj|BAB09871.1| unnamed protein product [Arabidopsis thaliana]	144	4E-26
					>ref|NP_196519.1| unknown protein [Arabidopsis thaliana]gb|AAO39889.1| At5g09570 [Arabidopsis thaliana] dbj|BAC43288.1| unknown protein [Arabidopsis thaliana] emb|CAB89373.1| putative protein [Arabidopsis thaliana]	139	8E-21
					>gb|AAS21010.1| unknown [Hyacinthus orientalis]	150	5E-19
					>ref|NP_001032137.1| unknown protein [Arabidopsis thaliana]	162	2E-12
DV489806	2.18E-02	B73<Mo17	1.79	3	>ref|NP_912581.1| Putative abscisic acid-induced protein - rice [Oryza sativa(japonica cultivar-group)] gb|AAN05334.1| Putative abscisic acid-induced protein - rice [Oryza sativa (japonica cultivar-group)]	271	8E-59
					>gb|AAQ74238.1| caleosin 1 [Hordeum vulgare]gb|AAQ74237.1| caleosin 1 [Hordeum vulgare]	301	5E-33
					>gb|AAF13743.1| caleosin [Sesamum indicum]	245	5E-33
					>ref|XP_473143.1| OSJNBa0004N05.7 [Oryza sativa (japonica cultivar-group)]emb|CAE03383.1| OSJNBa0004N05.7 [Oryza sativa (japonica cultivar-group)] emb|CAA61981.1| EFA27 for EF hand, abscisic acid, 27kD [Oryza sativa]	244	1E-32
					>gb|AAB71227.1| Ca+2-binding EF hand protein [Glycine max]	239	1E-32
DV491909	2.18E-02	B73<F1=Mo17	1.32	3	>sp|P49036|SUS2_MAIZE Sucrose synthase 2 (Sucrose-UDP glucosyltransferase 2)gb|AAA33515.1| sucrose synthase 2 gb|AAA33514.1| UDP-glucose:D-fructose 2-glucosyl-transferase	816	1E-21
					>gb|AAV64256.2| sucrose synthase [Bambusa oldhamii]	816	2E-21
					>gb|AAA68209.1| sus1 gene product	816	2E-21
					>gb|AAK52129.1| sucrose-UDP glucosyltransferase 2 [Oryza sativa (japonicacultivar-group)] ref|NP_909830.1| sucrose-UDP glucosyltransferase 2 [Oryza sativa] emb|CAA41774.1| sucrose-UDP glucosyltransferase (isoenzyme 2) [Oryza sativa (japonica cultivar-group)] sp|P31924|SUS2_ORYSA Sucrose synthase 2 (Sucrose-UDP glucosyltransferase 2) prf||2207194A sucrose synthase:ISOTYPE=2	816	2E-21
					>gb|AAL50570.1| sucrose synthase [Bambusa oldhamii]	816	1E-20
DV621209	2.18E-02	B73<F1=Mo17	1.3	3	ns		
DV494735	2.19E-02	F1=Mo17<B73	1.37	9	>gb|ABA94601.1| ribosomal protein S4 [Oryza sativa (japonica cultivar-group)]gb|ABA94599.1| ribosomal protein S4 [Oryza sativa (japonica cultivar-group)]	195	7E-80
					>ref|NP_198801.1| structural constituent of ribosome [Arabidopsis thaliana]gb|AAM65655.1| 40S ribosomal protein S9-like [Arabidopsis thaliana] dbj|BAB10209.1| 40S ribosomal protein S9 [Arabidopsis thaliana]	197	2E-78
					>emb|CAG47084.1| 40S ribosomal protein S9 [Catharanthus roseus]	197	3E-78
					>gb|AAU93594.1| putative ribosomal protein [Solanum demissum]	197	5E-78
					>gb|ABA46767.1| unknown [Solanum tuberosum]	197	5E-78
DV620995	2.19E-02	B73<F1=Mo17	1.23	3	>ref|NP_922172.1| putative microtubule-associated protein [Oryza sativa (japonicacultivar-group)] gb|AAM93680.1| putative microtubule-associated protein [Oryza sativa (japonica cultivar-group)] gb|AAP54459.1| microtubule-associated protein, putative [Oryza sativa (japonica cultivar-group)]	332	9E-67
					>ref|NP_201528.1| ATEB1C (MICROTUBULE END BINDING PROTEIN 1); microtubule binding[Arabidopsis thaliana] gb|AAM65311.1| microtubule-associated protein EB1-like protein [Arabidopsis thaliana] dbj|BAD43258.1| unknown protein [Arabidopsis thaliana] dbj|BAB09646.1| unnamed protein product [Arabidopsis thaliana]	329	4E-31

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>ref|NP_201056.1| ATEB1B; microtubule binding [Arabidopsis thaliana]gb|AAM61163.1| microtubule-associated protein EB1-like protein [Arabidopsis thaliana] dbj|BAB11500.1| microtubule-associated protein EB1-like protein [Arabidopsis thaliana]	293	8E-14
					>ref|XP_474072.1| OSJNBb0079B02.14 [Oryza sativa (japonica cultivar-group)]emb|CAE05968.2| OSJNBa0063C18.9 [Oryza sativa (japonica cultivar-group)] emb|CAD41855.2| OSJNBb0079B02.14 [Oryza sativa (japonica cultivar-group)]	269	4E-13
					>ref|NP 190353.3| ATEB1A; microtubule binding [Arabidopsis thaliana]gb|AAP88341.1| At3g47690 [Arabidopsis thaliana]	276	5E-13
DV490948	2.20E-02	Mo17<B73	5.58	9	ns		
BM381413	2.20E-02	Mo17<B73=F1	1.31	10	>gb|ABA96024.1| photosystem i reaction centre subunit n, chloroplast precursor[Oryza sativa (japonica cultivar-group)]	149	2E-45
					>gb|AAC26197.1| photosystem I complex PsaN subunit precursor [Zea mays]sp|O65107|PSAN_MAIZE Photosystem I reaction centre subunit N, chloroplast precursor (PSI-N)	112	4E-45
					>emb|CAA47056.1| photosystem I subunit N [Hordeum vulgare subsp. vulgare]sp|P31093|PSAN_HORVU Photosystem I reaction centre subunit N, chloroplast precursor (PSI-N)	145	6E-44
					>gb|AAO49652.1| photosystem I-N subunit [Phaseolus vulgaris]	170	5E-41
					>ref|NP_201209.1| PSI-N; calmodulin binding [Arabidopsis thaliana]gb|AAM10156.1| photosystem I reaction center subunit psaN precursor [Arabidopsis thaliana] gb|AAL32913.1| photosystem I reaction centre subunit psaN precursor [Arabidopsis thaliana] dbj|BAB10272.1| photosystem I reaction centre subunit psaN precursor [Arabidopsis thaliana] gb|AAA93075.1| PSI-N sp|P49107|PSAN ARATH Photosystem I reaction centre subunit N, chloroplast precursor (PSI-N)	171	2E-39
CD001387	2.21E-02	B73<Mo17	1.18	3	>gb|AAB33304.1| GF14-6 [Zea mays]sp|P49106|14331 MAIZE 14-3-3-like protein GF14-6	261	e-103
					>gb|AAB33305.1| GF14-12=GRF2 product/14-3-3 protein homolog [Zea mays, XL80,Peptide, 261 aa] sp|Q01526|14332 MAIZE 14-3-3-like protein GF14-12	261	e-102
					>ref|XP_472763.1| OSJNBa0072F16.20 [Oryza sativa (japonica cultivar-group)]emb|CAE76003.1| B1358B12.12 [Oryza sativa (japonica cultivar-group)] emb|CAE01538.2| OSJNBa0072F16.20 [Oryza sativa (japonica cultivar-group)] gb|AAB07456.1| GF14-b protein	262	e-100
					>emb|CAA74592.1| 14-3-3 protein [Hordeum vulgare]	263	1E-98
					>emb|CAB77673.1| 14-3-3-like protein [Oryza sativa]dbj|BAD29578.1| putative GF14-b protein [Oryza sativa (japonica cultivar-group)] dbj|BAD27625.1| putative GF14-b protein [Oryza sativa (japonica cultivar-group)]	262	8E-98
BM268021	2.21E-02	F1<Mo17	1.75	5	>ref|XP 469591.1| expressed protein [Oryza sativa (japonica cultivar-group)]gb|AAR01643.1| expressed protein [Oryza sativa (japonica cultivar-group)]	95	1E-36
					>ref|XP 480594.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]dbj|BAD05323.1| hypothetical protein [Oryza sativa (japonica cultivar-group)]	128	7E-36
					>gb|AAM62578.1| unknown [Arabidopsis thaliana]	86	9E-28
					>ref|NP 568055.1| unknown protein [Arabidopsis thaliana]	86	3E-27
					>ref|NP_187208.1| unknown protein [Arabidopsis thaliana]gb|AAR92313.1| At3g05570 [Arabidopsis thaliana] gb|AAF26140.1| unknown protein [Arabidopsis thaliana] gb|AAR24155.1| At3g05570 [Arabidopsis thaliana]	90	3E-25
CD001528	2.22E-02	Mo17<B73	1.36	10	ns		
DV550252	2.22E-02	B73<F1=Mo17	1.38	3	>gb|AAT12488.1| copper chaperone [Populus alba x Populus tremula var. glandulosa]	85	1E-31
					>ref|NP_564870.1| metal ion binding [Arabidopsis thaliana]gb|AAL76156.1| At1g66240/T6J19_6 [Arabidopsis thaliana] gb|AAK64002.1| At1g66240/T6J19_6 [Arabidopsis thaliana]	106	2E-30
					>ref|XP_480605.1| putative copper chaperone [Oryza sativa (japonica cultivar-group)]dbj|BAD11546.1| putative copper chaperone [Oryza sativa (japonica cultivar-group)] dbj|BAD05334.1| putative copper chaperone [Oryza sativa (japonica cultivar-group)]	81	2E-30
					>gb|AAP06757.1| copper chaperone [Lycopersicon esculentum]	81	2E-28
					>ref|NP_191183.1| CCH [Arabidopsis thaliana]emb|CAB87423.1| copper homeostasis factor [Arabidopsis thaliana] gb|AAK32872.1| AT3g56240/F18O21_200 [Arabidopsis thaliana] gb|AAL47423.1| AT3g56240/F18O21_200 [Arabidopsis thaliana] gb|AAM62878.1| copper homeostasis factor [Arabidopsis thaliana] gb|AAC33510.1| copper homeostasis factor [Arabidopsis thaliana]	121	4E-28
CB886447	2.22E-02	Mo17<B73=F1	1.23	10	>ref|NP 567948.1| EMB2758 [Arabidopsis thaliana]	823	2E-8
					>ref|NP 189042.1| unknown protein [Arabidopsis thaliana]dbj|BAB03018.1| unnamed protein product [Arabidopsis thaliana]	633	3E-8
					>ref|NP 176062.1| unknown protein [Arabidopsis thaliana]gb|AAG09095.1| Hypothetical protein [Arabidopsis thaliana]	704	4E-8
					>emb|CAJ26357.1| Selenium binding protein [Brachypodium sylvaticum]	624	6E-8
					>ref|NP 172412.1| unknown protein [Arabidopsis thaliana]gb|AAC33201.1| Hypothetical protein [Arabidopsis thaliana]	705	8E-8
BM338596	2.24E-02	Mo17<B73=F1	2.5	11	>dbj|BAD73827.1| unknown protein [Oryza sativa (japonica cultivar-group)]	152	1E-15
					>dbj|BAD29318.1| unknown protein [Oryza sativa (japonica cultivar-group)]	236	1E-15
CB886181	2.24E-02	Mo17<B73	1.29	9	>dbj|BAA28170.1| phosphoenolpyruvate carboxylase [Zea mays]	960	4E-59
					>emb|CAA46267.1| phosphoenolpyruvate carboxylase [Sorghum bicolor]emb|CAA39197.1| phosphoenolpyruvate carboxylase [Sorghum bicolor] sp|P29195|CAPP1 SORBI Phosphoenolpyruvate carboxylase 1 (PEPCase 1) (PEPC 1) (CP21)	960	3E-58
					>gb|AAR84575.1| C3 phosphoenolpyruvate carboxylase [Setaria italica]	961	5E-57
					>gb|AAP06951.1| phosphoenolpyruvate carboxylase [Echinochloa crus-galli]	961	3E-56
					>dbj|BAD27732.1| putative phosphoenolpyruvate carboxylase [Oryza sativa (japonicacultivar-group)]	968	1E-54
CD568937	2.25E-02	Mo17<F1	1.24	12	>gb|AAM95942.1| nucleosome/chromatin assembly factor group D protein [Zea mays]emb|CAA41220.1| high mobility group protein [Zea mays] emb|CAB46752.1| HMGa protein [Zea mays] sp|P27347|MNB1B MAIZE DNA-binding protein MNB1B (HMG1-like protein)	157	3E-22

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GenBank accession no.	Overall P value	Significant pattern	Fold change[†]	Sector[‡]	BLAST annotation*	Score	E value
					>emb|CAA46876.1| DNA-binding protein [Zea mays]pir||T03640 high mobility group protein MNB1b - maize (fragment)	168	3E-22
					>gb|AAP21609.1| HMGB1 [Oryza sativa (indica cultivar-group)]gb|AAN28722.1| HMG1 protein [Oryza sativa (indica cultivar-group)] dbj|BAD61823.1| HMGB1 [Oryza sativa (japonica cultivar-group)] gb|AAC78104.1| high mobility group protein [Oryza sativa]	157	7E-21
					>emb|CAA77641.1| high mobility group protein [Triticum aestivum]sp|P40621|HMGL WHEAT HMG1/2-like protein	161	3E-20
					>emb|CAA90679.1| HMG1/2-like protein [Hordeum vulgare subsp. vulgare]	160	2E-19
CB381532	2.25E-02	Mo17<B73=F1	1.31	11	>ref|XP_468159.1| putative ribosomal protein L35A [Oryza sativa (japonicacultivar-group)] ref|XP_507015.1| PREDICTED OJ1715_H01.42 gene product [Oryza sativa (japonica cultivar-group)] dbj|BAD19312.1| putative ribosomal protein L35A [Oryza sativa (japonica cultivar-group)] dbj|BAD19202.1| putative ribosomal protein L35A [Oryza sativa (japonica cultivar-group)]	112	2E-18
					>gb|AAL59231.1| ribosomal protein L35A [Zea mays]	112	8E-18
					>gb|AAK73115.1| ribosomal protein L35A [Zea mays]	112	1E-17
					>gb|AAK25760.1| ribosomal protein L33 [Castanea sativa]	112	2E-16
					>ref|XP_475896.1| putative ribosomal protein L35A [Oryza sativa (japonicacultivar-group)] ref|XP_475888.1| putative ribosomal protein L35A [Oryza sativa (japonica cultivar-group)] gb|AAT58712.1| putative ribosomal protein L35A [Oryza sativa (japonica cultivar-group)] gb|AAT58704.1| putative ribosomal protein L35A [Oryza sativa (japonica cultivar-group)]	111	3E-16

[*] Individual ESTs or the corresponding EST contigs (if available) were screened against a copy of the NCBI nr database downloaded February 2006 by using BLASTX. ns indicates no significant BLAST hits by using an *E*-value cutoff of e-5.

[†] Fold changes were calculated between highest- and lowest-expressing genotypes.

[‡] Sector location in Fig. 2.