The Structure and Function of the Expressed Portion of the Wheat Genomes

Deletion Map of *Triticum aestivum* cv. Chinese Spring (Chromosome 3D)*

*Contained here are Candidate Loci assigned to deletion bins based on hybridization data from the mapping laboratories as of January 2, 2002; assignments require verification from curators for each chromosome.

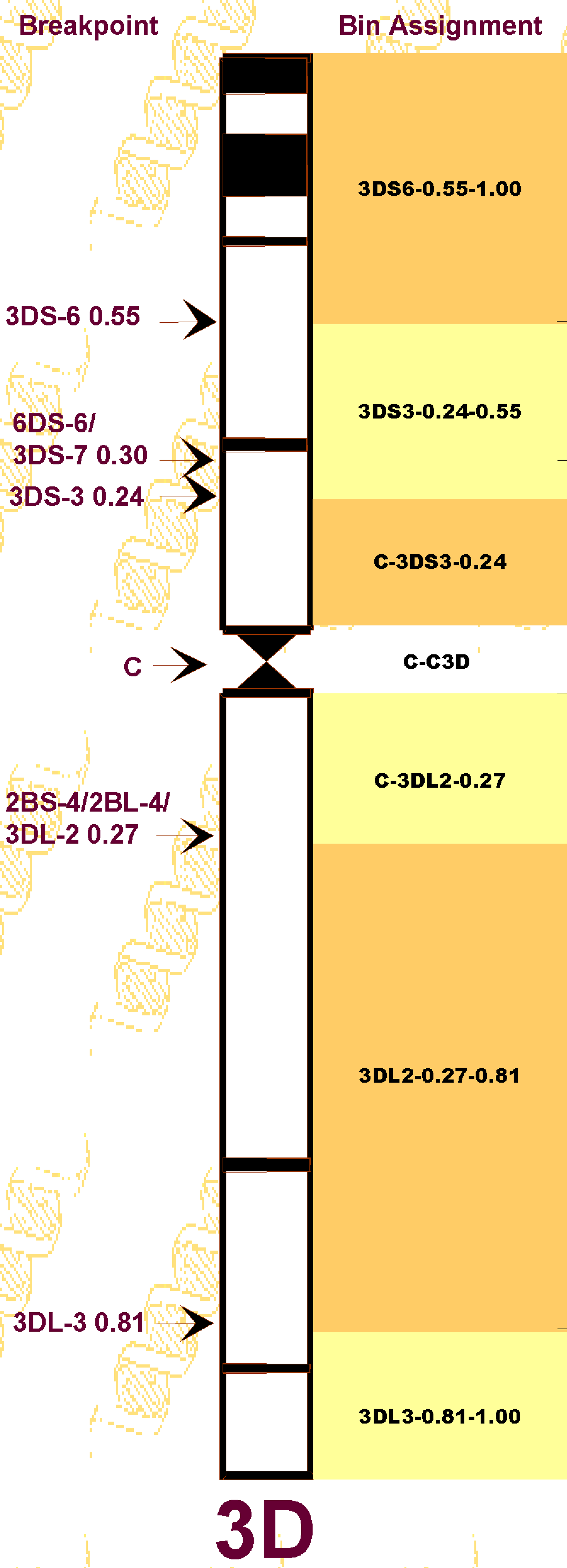
How to Interpret This Image:

Bin Identity

Locus ID	*e-value*	Best nucleic acid match (NCBI non-redundant database)	*e-value*	Best peptide match (NCBI non-redundant database)

Sample Locus ID : KSU012BE406450-4,6
KSU : Mapping Laboratory Prefix
012 : Mapping Laboratory Plate Identity
BE406450 : NCBI Genbank Accession Number
-4,6 : Number designation of hybridizing band(s)

Mapping Laboratory Prefix for Locus ID :
CNL : Mark E. Sorrells, Cornell University, Ithaca, NY
CSU : [illegible]
KSU : Bikram S. Gill, Kansas State University, Manhattan
NDS : Shahryar F. Kianian, North Dakota State University, Fargo
TTU : Henry T. Nguyen, Texas Tech University, Lubbock
UCD : Jan Dvorak, University of California, Davis
UCW : Jorge Dubcovsky, University of California, Davis
UMC : J. Perry Gustafson, University of Missouri, Columbia
UMN : James A. Anderson, University of Minnesota, Twin Cities
UNL : Kulvinder S. Gill, University of Nebraska, Lincoln



3DS6-0.55-1.00

CNL001BE406607-1	2.0e-48	Oryza sativa mRNA for gigantea homologue, partial	1.0e-48	(AP003047) gigantea-like protein [Oryza sativa]
CNL014BE446610-7,9	5.0e-62	Glycine max small GTP-binding protein (sra2) mRNA, comp	5.0e-71	(Z73932) RAB1C [Lotus japonicus]
CNL014BE591226-3,5,7	3.0e-20	Hordeum vulgare mRNA for expressed sequence tag	1.0e-46	(AF321858) putative cytochrome P450 [Lolium rigidum]
CNL023BE405260-4,5	0	Hordeum vulgare glutamine-dependent asparagine synth	e-121	(AF307145) glutamine-dependent asparagine synthetase 1
CNL031BF203138-3	6.0e-13	Musa acuminata metallothionein-like protein (MWMT2B) m	3.0e-05	METALLOTHIONEIN-LIKE PROTEIN 2 (MT-2)
CSU046BE444280-1	6.0e-40	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-58	(AP002818) putative C-8,7 sterol isomerase [Oryza sativa]
KSU001BE406607-1	2.0e-48	Oryza sativa mRNA for gigantea homologue, partial	1.0e-48	(AP003047) gigantea-like protein [Oryza sativa]
KSU001BE442648-10	2.0e-18	Oryza sativa genomic DNA, chromosome 1, PAC clone:P06	7.0e-45	(AP003047) hypothetical protein [Oryza sativa]
KSU001BE444576-1	0.056	Arabidopsis thaliana chromosome 1 BAC F5I6 genomic se	3.0e-24	(AB007650) 3-isopropylmalate dehydrogenase [Arabidopsi
KSU002BE406567-2	1.0e-14	Arabidopsis thaliana ubiquitin carrier protein (UBC1) mRN	2.0e-23	(AF262934) ubiquitin conjugating protein [Avicennia marina
KSU002BE425222-3,8	1.0e-04	Oryza sativa rbbi3-1 gene for putative Bowman Birk trypsi	4.0e-63	Chain A, Human Muscle L-Lactate Dehydrogenase M Chain
KSU012BE407082-5,7	0.005	Arabidopsis thaliana chromosome II section 243 of 255 of	7.0e-41	(AP000391) ESTs AU056036(S20239),C72753(E2173), AU05603
KSU019BE422466-2	5.0e-30	Rice (YK426) mRNA, complete cds	2.0e-11	probable ribosomal protein L9 - rice (fragment)
KSU027BF292892-1	0	Oryza sativa DNA for phospholipase D, complete cds	e-120	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATA
KSU035BE406998-6,8	2.0e-35	ric1=ras-related GTP binding protein possessing GTPase	3.0e-43	(AP002524) putative GTP-binding protein [Oryza sativa]
KSU035BE517736-3	3.0e-07	Tobacco mRNA for RNA helicase like protein DB10	2.0e-15	DRH1 DEAD box protein-like - Arabidopsis thaliana
UCD001BE406567-2	1.0e-14	Arabidopsis thaliana ubiquitin carrier protein (UBC1) mRN	2.0e-23	(AF262934) ubiquitin conjugating protein [Avicennia marina
UCD001BE443404-5	0.021	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	6.0e-24	(AP002913) contains ESTs AU032141(R3625),AU162501(R362
UCD001BE444576-1	0.056	Arabidopsis thaliana chromosome 1 BAC F5I6 genomic se	3.0e-24	(AB007650) 3-isopropylmalate dehydrogenase [Arabidopsi
UCD017BE488609-3	4.0e-19	Porteresia coarctata metallothionein mRNA, complete cds	9.0e-17	metallothionein-like protein - rice
UCD017BE495304-2	0	S.cereale tpi gene for triosephosphate isomerase	7.0e-42	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
UCD037BE489586-2	0	Triticum aestivum gamma-type tonoplast intrinsic protein	7.0e-28	tonoplast intrinsic protein gamma - barley
UCW001BE425222-4,9	1.0e-04	Oryza sativa rbbi3-1 gene for putative Bowman Birk trypsi	4.0e-63	Chain A, Human Muscle L-Lactate Dehydrogenase M Chain
UCW020BF293537-1	1.0e-09	Arabidopsis thaliana signal peptidase mRNA, complete cd	2.0e-49	(AP002526) Similar to Arabidopsis thaliana signal peptidas
UMC055BF484678-7	2.0e-58	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-84	(AC069471) sphingosine-1-phosphate lyase, putative [Arab
UMN013BE442933-6	3.0e-17	Orobanche ramosa NADPH-dependent mannose 6-phosph	4.0e-68	(AC006841) putative NADPH dependent mannose 6-phosph
UNL001BE442648-5	2.0e-18	Oryza sativa genomic DNA, chromosome 1, PAC clone:P06	7.0e-45	(AP003047) hypothetical protein [Oryza sativa]
UNL002BE499177-1	0.095	Homo sapiens clone BAC 9H13 chromosome 8 map 8q21,	1.0e-16	(AF202179) disease resistance protein BS2 [Capsicum cha
UNL036BE496983-4	0	Triticum aestivum lipid transfer protein precursor (LTP2)	1.0e-45	(AF334185) lipid transfer protein precursor [Triticum aesti
UNL044BG263366-5	5.0e-08	Hordeum vulgare glucan endo-1,3-beta-glucosidase isoen	4.0e-17	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, ACIDIC ISOFORM PR
UNL048BE591013-1	2.0e-36	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	e-103	(AP002540) putative CER3 [Oryza sativa]
UNL048BE605229-9	1.0e-61	Rice mRNA for low molecular weight heat shock protein, c	5.0e-15	17.4 KD CLASS I HEAT SHOCK PROTEIN

3DS7-0.30-0.55

UCD001BE405197-10,14	1.0e-31	Zea mays ZmHP2 mRNA for histidine-containing phosphot	3.0e-27	(AB024292) histidine-containing phosphotransfer protein [
UCD001BE405234-10,14	2.0e-67	Oryza sativa COX6b2 mRNA for cytochrome c oxidase subu	2.0e-35	(AB047923) cytochrome c oxidase subunit 6b [Oryza sativa]

3DS3-0.24-0.55

CNL001BE405234-11,17	2.0e-67	Oryza sativa COX6b2 mRNA for cytochrome c oxidase subu	2.0e-35	(AB047923) cytochrome c oxidase subunit 6b [Oryza sativa]
CNL014BE490440-3	5.0e-61	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-58	(AP001800) EST AU082314(E2976) corresponds to a region c
CSU001BE426356-1	2.0e-36	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	6.0e-78	(AP002092) EST AU090587(C30149) corresponds to a region
CSU001BE444474-2,3	2.0e-30	Oryza sativa genomic DNA, chromosome 1, BAC clone:OSJ	1.0e-61	(AC002387) putative O-sialoglycoprotein endopeptidase [A
KSU001BE398929-2	1.1	Acronicta sp.1 dopa decarboxylase (DDC) gene, partial cds	4.0e-05	(AC024128) putative protein kinase, 3' partial [Arabidopsis
KSU001BE443960-1	1.0e-07	Oryza sativa genomic DNA, chromosome 1, BAC clone:OSJ	1.0e-50	(AP003210) contains ESTs AU030536(E51208),AU030535(E512
KSU001BE444359-4	2.0e-06	Arabidopsis thaliana chromosome III BAC F3E22 genomic	3.0e-37	(AC023912) unknown protein [Arabidopsis thaliana]
KSU002BE405234-8,11	2.0e-67	Oryza sativa COX6b2 mRNA for cytochrome c oxidase subu	2.0e-35	(AB047923) cytochrome c oxidase subunit 6b [Oryza sativa]
KSU002BE426356-3	2.0e-36	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	6.0e-78	(AP002092) EST AU090587(C30149) corresponds to a region
KSU012BE442694-1	0	Triticum aestivum calmodulin TaCaM1-2 mRNA, complete	2.0e-62	(AJ005039) CaM-1 [Nicotiana plumbaginifolia]
KSU012BE490440-3	5.0e-61	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-58	(AP001800) EST AU082314(E2976) corresponds to a region c
KSU024BE498137-2	2.0e-42	Poa secunda metallothionein-like protein type 2 mRNA, co	0.009	(AF246982) metallothionein-like protein type 2 [Poa secunc
KSU027BE495182-4	4.0e-13	Arabidopsis thaliana AT3g58680 (AT3g58680\T20N10_30) m	5.0e-60	(AC006931) unknown protein [Arabidopsis thaliana]
KSU035BE497469-5,6	2.0e-97	Oryza sativa mRNA for NLS receptor, complete cds	3.0e-53	(AB004660) NLS receptor [Oryza sativa] region of the predi
KSU038BE442782-1	0	Hordeum vulgare L. (Alexis) mRNA for serine carboxypept	e-106	SERINE CARBOXYPEPTIDASE II-1 PRECURSOR (CP-MII.1) Alexi
KSU038BE489323-3	0.086	Arabidopsis thaliana DNA chromosome 3, BAC clone F1P2	9.0e-15	(AF247646) transposase [Zea mays]
NDS001BE444576-1	0.056	Arabidopsis thaliana chromosome 1 BAC F5I6 genomic se	3.0e-24	(AB007650) 3-isopropylmalate dehydrogenase [Arabidopsi
NDS018BE404868-6	4.0e-71	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	9.0e-55	(AP002524) putative 0-deacetylbaccatin III-10-O-acetyl trans
NDS021BF473016-2	0	Oryza sativa mRNA for aspartate aminotransferase, compl	e-123	ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAI
NDS043BF291720-1	e-118	Oryza sativa mRNA, similar to yeast SRP1, complete cds	1.0e-77	SRP1 protein homolog - rice
TTU025BE490440-3	5.0e-61	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-58	(AP001800) EST AU082314(E2976) corresponds to a region c
UCD017BE488921-3	0	Triticum aestivum triose phosphate translocator (tpt1) mF	e-101	(AF314182) triose phosphate translocator [Triticum aestivu
UCD037BE489538-4	e-109	Triticum aestivum clone CYP73-TA cytochrome P450 mRNA	6.0e-29	(AF123608) cytochrome P450 [Triticum aestivum]
UMC015BE426222-2	1.0e-38	Oryza sativa genomic DNA, chromosome 1, clone:P0705D0	1.0e-79	(AP000492) EST AU078118(E3904) corresponds to a region c
UNL036BE590609-3	0	Triticum durum mRNA for lipid transfer protein (ltp7.1 gen	4.0e-34	(AJ297768) lipid transfer protein [Triticum turgidum subsp
UNL048BE591804-1	8.0e-44	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	8.0e-19	(AB020746) gene_id:MOB24.15~ref|NP_013352.1~similar to u

C-3DS3-0.24

CNL014BE490613-3	9.0e-05	Homo sapiens PAC clone RP3-430N8 from 22q12.1-qter, co	2.0e-09	(AC022354) unknown protein [Arabidopsis thaliana]
KSU035BE404580-4,5	5.0e-16	Arabidopsis thaliana ubiquitin-specific protease 7 (UBP7) g	6.0e-73	(AF302661) ubiquitin-specific protease 7 [Arabidopsis thali
UCD037BE443276-2	0	ric1=ras-related GTP binding protein possessing GTPase	9.0e-87	RAS-RELATED PROTEIN RIC1 activity=ric1 [Oryza sativa=rice,
UCW020BE494850-3	e-162	Oryza sativa OsPBB1 mRNA for beta 2 subunit of 20S prote	7.0e-91	(AB026564) beta 2 subunit of 20S proteasome [Oryza sativa
UCW039BE405131-3	3.0e-57	Musa acuminata mRNA for unknown ripening-related prot	1.0e-75	(AB023034) ATP citrate lyase [Arabidopsis thaliana]
UMN013BE443955-4	1.0e-13	Arabidopsis thaliana DNA chromosome 4, contig fragment	4.0e-72	hypothetical protein T22F8.20 - Arabidopsis thaliana thalian

C-3DL2-0.27

CNL001BE406545-10	1.0e-44	Setaria italica actin mRNA, complete cds	1.0e-27	ACTIN 2
CNL014BE444380-1	1.0e-13	Arabidopsis thaliana AT3g28710 (AT3g28710\MZN14_20) m	8.0e-72	PROBABLE VACUOLAR ATP SYNTHASE SUBUNIT D 2 (V-ATPA
CNL014BE445348-2	7.0e-06	Homo sapiens, Similar to polymerase (RNA) II (DNA directe	4.0e-47	(AF019248) RNA polymerase I, II and III 24.3 kDa subunit [Ar
CSU046BE445343-1,2	5.0e-71	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	7.0e-27	(AC007071) unknown protein [Arabidopsis thaliana]
KSU019BE404709-2	4.0e-06	Arabidopsis thaliana chromosome II section 112 of 255 of	4.0e-36	hypothetical protein F27F23.18 - Arabidopsis thaliana
KSU019BE500394-6	2.0e-21	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	3.0e-51	(AP002744) putative late embryogenesis abundant protein
KSU019BE606250-3,4	e-105	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	e-102	(AP002844) contains ESTs AU069322(C60381),AU070001(E31
KSU019BE637878-11	7.0e-14	Oryza sativa chromosome 3 BAC OSJNBa0013M12 genomic	1.0e-08	(AP002070) Similar to Arabidopsis thaliana low temperatur
KSU035BE406903-3	0.73	Homo sapiens BAC clone RP11-459K11 from 2, complete s	9.0e-27	(AF302660) ubiquitin-specific protease 6 [Arabidopsis thali
KSU035BE517931-1	0.4	Halobacterium sp. NRC-1 section 106 of 170 of the complet	3.0e-23	(AF084201) similar to chloroplast 50S ribosomal protein L3
KSU038BE444512-4	6.0e-15	Arabidopsis thaliana putative protein translocation comple	4.0e-16	PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT
KSU038BE445496-3	0.39	Homo sapiens KIAA1072 protein (KIAA1072), mRNA	1.0e-75	(AC010926) protein phosphatase 2C (AtP2C-HA)\; 19519-176
KSU038BE446731-5,6	4.0e-50	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	5.0e-75	(AP002844) putative H+-transporting ATPase [Oryza sativa]
NDS034BE403201-3	0	H.vulgare (Gerbel) mRNA for adenosine triphosphatase	3.0e-58	(U84268) YLP [Hordeum vulgare]
TTU047BE445539-2	6.0e-06	Arabidopsis thaliana chromosome 1 BAC F22G10 genomic	8.0e-69	(U74610) glyoxalase II [Arabidopsis thaliana]
TTU047BE494345-3	0.27	Streptomyces coelicolor cosmid 1B5	1.0e-25	(AB022210) gene_id:K16E1.4~unknown protein [Arabidopsi
UCD001BE443753-3	1.3	Tauraco erythrolophus cytochrome b gene, partial cds\; mitochondrial gene for mitochondrial product		
UCD029BE494776-2	0	Oryza sativa NADP-specific isocitrate dehydrogenase mRN	e-109	(AF155333) NADP-specific isocitrate dehydrogenase [Oryza
UCD029BE500510-3	2.0e-36	Arabidopsis thaliana Col-0 casein kinase I-like protein mR	7.0e-72	probable kasein kinase (EC 2.7.1.-) - Arabidopsis thaliana t
UCD037BE442595-5	4.0e-23	Oryza sativa genomic DNA, chromosome 1, PAC clone:P07	2.0e-15	PROTEIN KINASE AFC2
UMN013BE443143-3	0	H.vulgare mRNA for peptidase of D1 protein	8.0e-84	probable carboxy-terminal proteinase (EC 3.4.21.-) D1 - bar
UNL002BE500083-3	0.089	Homo sapiens, CD63 antigen (melanoma 1 antigen), clone	3.0e-68	(AC079829) hypothetical protein [Arabidopsis thaliana]
UNL002BE607045-3	e-130	O.sativa mRNA for dihydroflavonol reductase	6.0e-88	DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFE
UNL036BE590775-1	9.0e-33	Arabidopsis thaliana AT3g28710 (AT3g28710\MZN14_20) m	7.0e-96	PROBABLE VACUOLAR ATP SYNTHASE SUBUNIT D 1 (V-ATPA
UNL036BF200700-3	e-121	Rice mRNA for succinyl-CoA synthetase (475 gene), partial	7.0e-46	SUCCINYL-COA LIGASE [GDP-FORMING] ALPHA-CHAIN, MITC

C-3DL3-0.81

CSU001BE443747-2	1.5	Sorghum bicolor ADP-glucose pyrophosphorylase subuni	5.0e-25	(AB025632) dihydroflavonol 4-reductase-like [Arabidopsis t

3DL2-0.27-0.81

CNL014BE444736-11,12,13	2.0e-08	Arabidopsis thaliana chromosome 1 BAC T1F15 sequence	4.0e-54	hypothetical protein T1F15.13 - Arabidopsis thaliana (fragn
CNL014BE444961-1	4.0e-07	Arabidopsis thaliana chromosome II section 115 of 255 of	9.0e-45	(AC006081) 50S ribosomal protein L4 [Arabidopsis thaliana
CNL031BE500460-7	e-125	Oryza sativa mRNA for fructose-1,6-bisphosphatase (cytos	7.0e-53	(AF218845) fructose-1,6-bisphosphatase [Porteresia coarc
CSU046BE442943-2	0.42	Drosophila melanogaster, chromosome 2R, region 49E-49	2.0e-54	(AC016661) unknown protein [Arabidopsis thaliana]
CSU057BE490678-1	0	Triticum aestivum mRNA for wpk4 protein kinase, comple	3.0e-98	(AB011670) wpk4 protein kinase [Triticum aestivum]
CSU101BE490744-2	0.001	Arabidopsis thaliana ATCDPMEK mRNA for 4-(cytidine 5'-ph	1.0e-29	(AF258339) 4-diphosphocytidyl-2C-methyl-D-erythritol kina
KSU001BE406602-5	2.0e-16	Zea mays 40S ribosomal protein S24 mRNA, complete cds	3.0e-19	(AF298769) 40S ribosomal protein S24 [Zea mays]
KSU001BE442571-3	1.5	Mesorhizobium loti, complete genome	2.0e-11	(AB017063) gb|AAD29063.1~gene_id:K3K7.3~similar to unkn
KSU001BE444171-3,4	3.0e-72	Oryza sativa genomic DNA, chromosome 1, clone:P0708G	6.0e-73	(AP001539) Similar to Arabidopsis thaliana chromosome 4
KSU001BE444252-1	4.0e-28	Pisum sativum mRNA for F1 ATPase, complete cds	1.0e-10	H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mito
KSU012BE404385-3	e-170	Zea mays golgi associated protein se-wap41 mRNA, comp	e-108	(AF294725) reversibly glycosylated polypeptide [Oryza sati
KSU012BE406587-3	4.0e-06	Arabidopsis thaliana chromosome V map near 60.5 cM, co	5.0e-46	(AF049930) PGPD14 [Petunia x hybrida]
KSU012BE406602-5	2.0e-16	Zea mays 40S ribosomal protein S24 mRNA, complete cds	3.0e-19	(AF298769) 40S ribosomal protein S24 [Zea mays]
KSU012BE442674-2	0	Oryza sativa Os SBP mRNA for putative selenium binding p	e-103	(AB059401) putative selenium binding protein [Oryza sativa
KSU012BE490613-3	9.0e-05	Homo sapiens PAC clone RP3-430N8 from 22q12.1-qter, co	2.0e-09	(AC022354) unknown protein [Arabidopsis thaliana]
KSU012BE490651-3	3.0e-04	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	2.0e-30	(AB026651) dbj|BAA91806.1~gene_id:MQD19.4~similar to un
KSU019BE442624-1,5,6,8	1.3	Caenorhabditis elegans cosmid F54D7, complete sequenc	5.0e-40	(AB036735) allyl alcohol dehydrogenase [Nicotiana tabacum
KSU019BE445011-1	0.005	Zea mays indeterminate spikelet 1 (ids1) mRNA, complete	2.0e-26	indeterminate spikelet 1 - maize
KSU019BE494330-1	3.0e-75	O.sativa mRNA for SMT3 protein	1.0e-34	UBIQUITIN-LIKE PROTEIN SMT3
KSU019BE494450-5	7.0e-40	Avena maroccana clone Ma7 ribulose-1,5-bisphosphate ca	3.0e-15	(AB042068) ribulose-1,5-bisphosphate carboxylase\oxyger
KSU019BE636993-2	3.0e-41	Catharanthus roseus ubiquitin-conjugating enzyme E2 (UB	1.0e-75	(AC051629) Putative ubiquitin-conjugating enzyme E2 [Arab
KSU024BE499348-1,5	3.0e-17	Oryza meyeriana serine\threonine protein kinase (R1) ge	1.0e-37	(AP000410) receptor protein kinase-like protein [Arabidop
KSU027BE495028-5	e-147	Oryza sativa calmodulin (CaM2) mRNA, complete cds	5.0e-72	(X65016) calmodulin [Oryza sativa]
KSU027BE495226-5	0.2	Homo sapiens ALPP, ALPPL2, ALPI, XCE, CHRND, and CHRNG genes, complete sequence		
KSU027BF485179-3	0	Triticum aestivum WC1 mRNA for cysteine proteinase inhi	2.0e-64	(AB038392) cysteine proteinase inhibitor [Triticum aestivu
KSU030BE404799-2	6.0e-09	Arabidopsis thaliana RNA polymerase I, II and III 24.3 kDa s	3.0e-33	(AF019248) RNA polymerase I, II and III 24.3 kDa subunit [Ar
KSU030BE495145-2,5,6,7	0.001	Arabidopsis thaliana mRNA for putative beta-galactosidase	4.0e-55	(AC010704) putative beta-galactosidase, 3' partial\; 3669-1 [
KSU030BE499968-1	0	Triticum aestivum alpha 1,4-glucan phosphorylase mRNA,	6.0e-82	(AF326977) alpha 1,4-glucan phosphorylase H isozyme [Ory
KSU035BE403619-1	0.82	Homo sapiens 12q BAC RP11-798P24 (Roswell Park Cancer	4.0e-06	(AF098458) latex-abundant protein [Hevea brasiliensis]
KSU035BE403647-1	3.0e-23	Solanum tuberosum partial mRNA for serine palmitoyltran	3.0e-85	(AB025633) serine palmitoyltransferase [Arabidopsis thali
KSU035BE403721-6,8	4.0e-53	Oryza sativa beta-glucosidase mRNA, nuclear gene encodi	2.0e-77	beta-glucosidase BGQ60 precursor - barley
KSU035BE497323-2	1.0e-05	Mus musculus 13 days embryo liver cDNA, RIKEN full-lengt	1.0e-05	DNA-DIRECTED RNA POLYMERASE II 8.2 KDA POLYPEPTIDE (R
KSU038BE443191-2,8	e-115	Triticum aestivum 70 kDa heat shock protein (TaHSP70d) n	2.0e-62	dnaK-type molecular chaperone hsp70 - rice (fragment)
KSU038BE443568-2,6	4.0e-04	Arabidopsis thaliana chromosome 1 BAC F1O17 genomic s	2.0e-84	glycerophosphodiester phosphodiesterase-like protein -
KSU038BE443770-4	5.0e-56	Sorghum bicolor cinnamic acid 4-hydroxylase (C4H) mRNA	2.0e-34	(U29243) trans-cinnamic acid hydroxylase [Pisum sativum]
NDS001BE403519-1	7.0e-09	Arabidopsis thaliana chromosome II section 144 of 255 of	1.0e-70	(AC006053) hypothetical protein [Arabidopsis thaliana]
NDS001BE444252-1	4.0e-28	Pisum sativum mRNA for F1 ATPase, complete cds	1.0e-10	H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mito
NDS018BE426304-8	e-148	Z.mays mRNA for calmodulin	5.0e-72	(X65016) calmodulin [Oryza sativa]
NDS034BE499968-2	0	Triticum aestivum alpha 1,4-glucan phosphorylase mRNA,	6.0e-82	(AF326977) alpha 1,4-glucan phosphorylase H isozyme [Ory
NDS043BF292596-2	1.3	Mesorhizobium loti, complete genome	7.0e-12	comes from this gene. [Arabidopsis thaliana]
TTU025BE490613-3	9.0e-05	Homo sapiens PAC clone RP3-430N8 from 22q12.1-qter, co	2.0e-09	(AC022354) unknown protein [Arabidopsis thaliana]
TTU025BE490651-3	3.0e-04	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	2.0e-30	(AB026651) dbj|BAA91806.1~gene_id:MQD19.4~similar to un
TTU025BE490658-3	e-104	Eleusine indica alpha-tubulin 2 (TUA2) mRNA, complete cds	1.0e-65	TUBULIN ALPHA-2 CHAIN (ALPHA-2 TUBULIN)
UCD001BE405214-1,6,7	3.0e-11	Arabidopsis thaliana respiratory burst oxidase protein D (	4.0e-56	(AB015475) respiratory burst oxidase protein [Arabidopsis
UCD001BE444252-1	4.0e-28	Pisum sativum mRNA for F1 ATPase, complete cds	1.0e-10	H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mito
UCD017BE488783-7	8.0e-12	Arabidopsis thaliana DNA chromosome 3, BAC clone T14E1	9.0e-51	ABC transporter-like protein - Arabidopsis thaliana
UCD017BE489603-3,4	1.0e-24	Oryza sativa genomic DNA, chromosome 1, PAC clone:P06	3.0e-31	PROBABLE CYSTEINE SYNTHASE, CHLOROPLAST PRECURSO
UCD028BE490596-1	0	T.aestivum atp-2 mRNA for ATP synthase beta subunit	2.0e-96	H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mito
UCD037BE489274-4,5,6	0.023	Homo sapiens, clone hRPK.2_A_1, complete sequence	6.0e-59	fructokinase-like protein - Arabidopsis thaliana
UCD037BE497664-3	e-130	Oryza sativa ALDH1a mRNA for cytosolic aldehyde dehydro	1.0e-94	(AB037421) cytosolic aldehyde dehydrogenase [Oryza sativ
UCD037BE500112-2,7	0	T.aestivum (Chinese spring) chi gene for endochitinase	3.0e-52	chitinase (EC 3.2.1.14) - wheat
UCW020BF478499-3	4.0e-41	Oryza sativa thioredoxin F isoform mRNA, complete cds	3.0e-30	THIOREDOXIN F-TYPE 2, CHLOROPLAST PRECURSOR (TRX-F2
UCW026BG263365-1	3.0e-50	Saccharum officinarum mRNA for Sucrose-Phosphate Syn	1.0e-61	sucrose-phosphate synthase (EC 2.4.1.14) 1 - rice
UMC015BE406587-4	4.0e-06	Arabidopsis thaliana chromosome V map near 60.5 cM, co	5.0e-46	(AF049930) PGPD14 [Petunia x hybrida]
UMC032BE425919-1	2.0e-42	Oryza sativa chromosome 10 clone nbeb0039C14, complet	4.0e-62	(AL392174) rev interacting protein mis3-like [Arabidopsis t
UMC032BE471312-1	e-157	S.cereale L12-2 mRNA for ribosomal protein L12	2.0e-35	50S RIBOSOMAL PROTEIN L12-1, CHLOROPLAST PRECURSO
UMC040BE606881-3	1.0e-46	Zea mays nuclear-encoded mitochondrial F1F0 ATP syntha	2.0e-28	ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL mitochon
UMN013BE443049-3	7.0e-06	Arabidopsis thaliana chromosome II section 191 of 255 of	3.0e-48	hypothetical protein T29F13.10 - Arabidopsis thaliana
UMN013BE443288-4	1.0e-07	Arabidopsis thaliana ADL2 mRNA, complete cds	4.0e-85	(AF012833) similar to dynamin-like protein encoded by Ger
UMN013BE443349-1	1.0e-25	L.japonicus mRNA for small GTP-binding protein, RAB11C	1.0e-57	RAS-RELATED PROTEIN RAB11C
UNL002BE499834-3	3.0e-65	Triticum aestivum single-stranded nucleic acid binding protein (whGRP-1) gene, complete cds		
UNL036BE518446-4	5.0e-16	Capsicum annuum GTP-binding protein mRNA, complete c	1.0e-88	(AF108896) GTP-binding protein [Capsicum annuum]
UNL036BF200549-2	6.0e-61	Oryza sativa Os SBP mRNA for putative selenium binding p	2.0e-37	(AB059401) putative selenium binding protein [Oryza sativa
UNL036BF200697-3	0.31	Caenorhabditis elegans cosmid F49E12, complete sequen	8.0e-13	(AC005311) hypothetical protein [Arabidopsis thaliana]

3DL3-0.81-1.00

CNL001BE406551-7	0.85	Rhizobium sp. NGR234 plasmid pNGR234a, section 8 of 46 c	2.0e-34	(AB019232) gb|AAC28507.1~gene_id:MIL23.25~strong simila
CNL014BE444864-2	4.0e-07	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	7.0e-73	(AB023042) phosphatidylserine decarboxylase [Arabidopsi
CNL014BE445136-1,4	3.0e-07	Barley pHVA1 mRNA for an ABA-inducible protein	0.79	(AJ275365) immunoglobulin heavy chain variable region [H
CSU057BE407052-1,3	7.0e-24	Zea mays ZmRCP1 mRNA for root cap protein 1, complete	4.0e-52	(AB021175) root cap protein 1 [Zea mays]
KSU001BE444473-10	0.016	Drosophila melanogaster genomic scaffold 1420000133860	2.0e-23	(AC084763) hypothetical protein [Oryza sativa]
KSU012BE442818-2	4.0e-10	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	4.0e-71	(AP000604) contains similarity to unknown protein~gb|AAF
KSU012BE442875-3,4	6.0e-12	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	7.0e-66	(AB019227) gb|AAF01562.1~gene_id:MBM17.7~strong simila
KSU012BE443397-3,5,7	3.0e-05	Mesembryanthemum crystallinum cinnamyl-alcohol dehy	2.0e-77	(AC010926) putative cinnamyl-alcohol dehydrogenase\; 496
KSU024BE405348-1,3	1.0e-93	Oryza sativa clone C23033 truncated UMP synthase (UMPS	1.0e-60	(AB031395) UMP synthase 1 [Oryza sativa]
KSU024BE499049-4	0	Zea mays strain W64A x A182E putative cytosolic 6-phosph	e-116	phosphogluconate dehydrogenase (decarboxylating) (EC 1
KSU024BE499186-2,5,6,7,9	e-136	Oryza sativa mRNA for asparaginyl endopeptidase, comple	4.0e-70	(AJ251454) putative legumain [Zea mays]
KSU027BF482769-5	0	Lolium perenne caffeic acid O-methyltransferase (OMT3)	2.0e-87	(AF033538) caffeic acid O-methyltransferase\; LPOMT1 [Lol
KSU030BE497740-4	1.0e-16	Arabidopsis thaliana mRNA for Dr1	1.0e-47	DR1-like protein - Arabidopsis thaliana
KSU030BE499696-4	5.0e-65	Glycine max beta-ketoacyl-ACP synthetase I-2 mRNA, com	3.0e-76	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURS
KSU030BF485004-2	1.0e-18	Lycopersicon esculentum transaldolase (TAL) mRNA, com	4.0e-34	transaldolase-like protein - Arabidopsis thaliana
KSU035BE403428-6	1.4	Oryctolagus cuniculus heat shock protein 47 mRNA, partia	1.0e-35	(AC069300) putative dioxygenase [Oryza sativa]
KSU035BE404540-6	3.0e-29	S.tuberosum (Desiree) cyc1 II mRNA. for cytochrome c1	2.0e-49	(AP000381) ubiquinol-cytochrome c1 reductase cytochrom
UCD001BE406551-4,8,9	0.85	Rhizobium sp. NGR234 plasmid pNGR234a, section 8 of 46 c	2.0e-34	(AB019232) gb|AAC28507.1~gene_id:MIL23.25~strong simila
UCD001BE443798-1	0.39	Escherichia coli O157:H7 EDL933 genome, contig 2 of 3, section 31 of 55		
UCD017BE488620-2	2.0e-11	Vigna unguiculata VuP5CR mRNA, complete cds	1.0e-50	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDU
UCD028BF484536-1,4,6,9,11	1.1	Methylococcus capsulatus putative nonaheme c-cytochro	0.43	(AF277399) cat eye syndrome critical region 6 [Mus muscu
UCD037BE442882-4	1.0e-10	G.max gene encoding epoxide hydrolase	4.0e-55	(D16628) ATsEH [Arabidopsis thaliana] thaliana] thaliana]
UCW001BE443798-1	0.39	Escherichia coli O157:H7 EDL933 genome, contig 2 of 3, section 31 of 55		
UCW016BE637789-2,3	2.0e-70	O.sativa mRNA for cytochrome b5	1.0e-65	CYTOCHROME B5
UCW020BE494854-3	2.0e-15	Oryza sativa subsp. indica putative dnaJ-like protein, putat	1.0e-49	(AF111710) hypothetical protein [Oryza sativa subsp. indica
UCW039BE404125-1	0.002	Oryza sativa microsatellite MRG2602 containing (GA)X13, c	6.0e-64	(AB016877) beta-glucosidase [Arabidopsis thaliana]
UMC015BE489841-3	8.0e-30	Arabidopsis thaliana At2g27860\F15K20.4 gene, complete	8.0e-95	(AC011438) T23G18.6 [Arabidopsis thaliana]
UMC015BE606723-6,7,9,10	e-127	Secale cereale RKIN1 mRNA, complete CDS	8.0e-60	(D82035) OSK4 [Oryza sativa]
UMN013BE442818-2	4.0e-10	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	4.0e-71	(AP000604) contains similarity to unknown protein~gb|AAF
UMN013BE442875-5	6.0e-12	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	7.0e-66	(AB019227) gb|AAF01562.1~gene_id:MBM17.7~strong simila
UMN013BE443397-4	3.0e-05	Mesembryanthemum crystallinum cinnamyl-alcohol dehy	2.0e-77	(AC010926) putative cinnamyl-alcohol dehydrogenase\; 496
UNL001BE444473-7	0.016	Drosophila melanogaster genomic scaffold 1420000133860	2.0e-23	(AC084763) hypothetical protein [Oryza sativa]
UNL036BE590549-3	7.0e-12	A.sativa avenin mRNA, complete cds	2.0e-24	gliadin - wheat

These mapping data are being made public in a preliminary, unverified state because of their potential value to the research community. These data are in the process of validation and are therefore subject to change. Users may not publish or redistribute the data or derivatives thereof without the written consent of the Project's mapping coordinator, Bikram Gill (bsg@ksu.edu). NSF Project #DBI-9975989

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