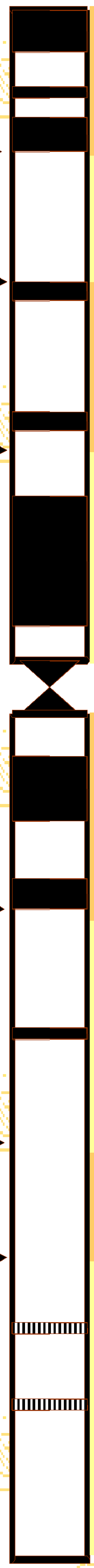
The Structure and Function of the Expressed Portion of the Wheat Genomes

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

*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.

Breakpoint	Bin Assignment
	3BS8-0.78-1.00
3BS-8 0.78	
	3BS9-0.57-0.78
3BS-9 0.57	
	3BS1-0.33-0.57
3BS-1 0.33	
	C-3BS1-0.33
C	C-C3B
	C-3BL2-0.22
3BL-2 0.22	
	3BL2-0.22-0.50
3BL-10 0.50	
	3BL10-0.50-0.63
3BL-7 0.63	
	3BL7-0.63-1.00



3BS8-0.78-1.00

KSU001BE444576-2	0.056	Arabidopsis thaliana chromosome 1 BAC F5I6 genomic se	3.0e-24	(AB007650) 3-isopropylmalate dehydrogenase [Arabidopsi
KSU002BE425222-7,9	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
KSU019BE422466-5	5.0e-30	Rice (YK426) mRNA, complete cds	2.0e-11	probable ribosomal protein L9 - rice (fragment)
KSU035BE517903-1,2,3,4,5	e-139	H.vulgare ltp4.3 gene	3.0e-38	lipid transfer protein [Hordeum vulgare]
KSU038BE446244-6,8	0.091	Human DNA sequence from clone RP13-153N15 on chromo	2.0e-33	(AC037197) Putative hypersensitivity-related protein [Oryz
NDS018BE426676-3	5.0e-16	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	5.0e-26	(AP002882) putative acetoacyl-CoA-thiolase [Oryza sativa]
UCD001BE406567-1	1.0e-14	Arabidopsis thaliana ubiquitin carrier protein (UBC1) mRNA	2.0e-23	(AF262934) ubiquitin conjugating protein [Avicennia marina
UCD001BE443404-1,6	0.021	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	6.0e-24	(AP002913) contains ESTs AU032141(R3625),AU162501(R3625
UCD001BE444576-2	0.056	Arabidopsis thaliana chromosome 1 BAC F5I6 genomic se	3.0e-24	(AB007650) 3-isopropylmalate dehydrogenase [Arabidopsi
UCD017BE488609-2	4.0e-19	Porteresia coarctata metallothionein mRNA, complete cds	9.0e-17	metallothionein-like protein - rice
UCD028BE498551-10	2.0e-36	Oryza sativa poly(A)-binding protein gene, partial cds	5.0e-35	(AF153689) poly(A)-binding protein [Oryza sativa]
UCD037BE442882-1	1.0e-10	G.max gene encoding epoxide hydrolase	4.0e-55	(D16628) ATsEH [Arabidopsis thaliana] thaliana] thaliana]
UCW001BE425222-2,5,7,8,10	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
UCW020BF293537-2	1.0e-09	Arabidopsis thaliana signal peptidase mRNA, complete cd	2.0e-49	(AP002526) Similar to Arabidopsis thaliana signal peptidase
UMC001BE444576-1	0.056	Arabidopsis thaliana chromosome 1 BAC F5I6 genomic se	3.0e-24	(AB007650) 3-isopropylmalate dehydrogenase [Arabidopsi
UMN013BE442933-8	3.0e-17	Orobanche ramosa NADPH-dependent mannose 6-phosph	4.0e-68	(AC006841) putative NADPH dependent mannose 6-phosph
UNL002BE517312-1,7	8.0e-08	Arabidopsis thaliana YLS7 mRNA for leaf-senescence-rela	8.0e-49	(AB018109) gene_id:K17N15.19~pir||T10216~strong similarity
UNL002BF200008-4	1.6	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt	2.0e-14	(AP001073) Similar to Oryza sativa gene for Pib. (AB013448)
UNL002BF483203-3	3.0e-04	Oryza sativa chromosome 10 clone OSJNBa0056A20, comp	6.0e-20	(AC079128) Putative MLA6 protein [Oryza sativa]
UNL036BE496983-1,2,3	0	Triticum aestivum lipid transfer protein precursor (LTP2)	1.0e-45	(AF334185) lipid transfer protein precursor [Triticum aesti
UNL036BF473786-3,4,5,6,7,8	8.0e-74	Hordeum vulgare lipid transfer protein (blt4.9) gene, comp	4.0e-11	lipid transfer protein [Hordeum vulgare]
UNL048BE605229-2	1.0e-61	Rice mRNA for low molecular weight heat shock protein, c	5.0e-15	17.4 KD CLASS I HEAT SHOCK PROTEIN

3BS9-0.57-0.78

CNL001BE406567-1	1.0e-14	Arabidopsis thaliana ubiquitin carrier protein (UBC1) mRNA	2.0e-23	(AF262934) ubiquitin conjugating protein [Avicennia marina
CNL014BE591226-12	3.0e-20	Hordeum vulgare mRNA for expressed sequence tag	1.0e-46	(AF321858) putative cytochrome P450 [Lolium rigidum]
CNL023BG274134-4	2.0e-04	Nicotiana tabacum sucrose-6-phosphate synthase (SPS) m	7.0e-25	SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE
CNL031BE403624-12	0	Hordeum vulgare germin F (GerF) gene, complete cds	e-118	(AF250935) germin F [Hordeum vulgare]
CNL031BF203138-8	6.0e-13	Musa acuminata metallothionein-like protein (MWMT2B) m	3.0e-05	METALLOTHIONEIN-LIKE PROTEIN 2 (MT-2)
CSU001BE406607-3	2.0e-48	Oryza sativa mRNA for gigantea homologue, partial	1.0e-48	(AP003047) gigantea-like protein [Oryza sativa]
KSU001BE406607-3	2.0e-48	Oryza sativa mRNA for gigantea homologue, partial	1.0e-48	(AP003047) gigantea-like protein [Oryza sativa]
KSU001BE442648-9	2.0e-18	Oryza sativa genomic DNA, chromosome 1, PAC clone:P06	7.0e-45	(AP003047) hypothetical protein [Oryza sativa]
KSU002BE406567-1	1.0e-14	Arabidopsis thaliana ubiquitin carrier protein (UBC1) mRNA	2.0e-23	(AF262934) ubiquitin conjugating protein [Avicennia marina
KSU012BE407082-2,3,6	0.005	Arabidopsis thaliana chromosome II section 243 of 255 of	7.0e-41	(AP000391) ESTs AU056036(S20239),C72753(E2173), AU05603
KSU035BE403373-5	0	Triticum aestivum oxalate oxidase mRNA, partial cds	1.0e-72	(AF005084) oxalate oxidase [Triticum aestivum]
KSU035BE403471-5	5.0e-15	Oryza sativa microsatellite MRG2437 containing (CT)X18, g	6.0e-57	(AF370443) Ran binding protein-1 [Lycopersicon esculentu
NDS001BE443995-1	1.6	Homo sapiens 12 BAC RP11-547C5 (Roswell Park Cancer In	4.0e-71	(AC079281) unknown protein [Arabidopsis thaliana]
NDS001BE444576-2	0.056	Arabidopsis thaliana chromosome 1 BAC F5I6 genomic se	3.0e-24	(AB007650) 3-isopropylmalate dehydrogenase [Arabidopsi
NDS021BF473016-1	0	Oryza sativa mRNA for aspartate aminotransferase, compl	e-123	ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAI
UCD017BE495304-1	0	S.cereale tpi gene for triosephosphate isomerase	7.0e-42	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
UCD029BE471274-1	0	Triticum turgidum subsp. durum 1-Cys peroxiredoxin (PEI	5.0e-87	(AF327046) 1-Cys peroxiredoxin [Triticum turgidum subsp.
UCW001BE399103-2,3	3.8	Arabidopsis thaliana F23M19.13\F23M19.13 gene, complete	5.6	tachykinin 2 [Rattus norvegicus]
UMC055BF484678-2,9	2.0e-58	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-84	(AC069471) sphingosine-1-phosphate lyase, putative [Arab
UNL044BG263366-4	5.0e-08	Hordeum vulgare glucan endo-1,3-beta-glucosidase isoen	4.0e-17	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, ACIDIC ISOFORM PR
UNL048BE591013-3	2.0e-36	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	e-103	(AP002540) putative CER3 [Oryza sativa]

3BS1-0.33-0.57

CNL001BE405234-16	2.0e-67	Oryza sativa COX6b2 mRNA for cytochrome c oxidase subu	2.0e-35	(AB047923) cytochrome c oxidase subunit 6b [Oryza sativa
CNL014BE490440-2	5.0e-61	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-58	(AP001800) EST AU082314(E2976) corresponds to a region c
CSU001BE444474-4	2.0e-30	Oryza sativa genomic DNA, chromosome 1, BAC clone:OSJ	1.0e-61	(AC002387) putative O-sialoglycoprotein endopeptidase [A
KSU001BE398929-3	1.1	Acronicta sp.1 dopa decarboxylase (DDC) gene, partial cds	4.0e-05	(AC024128) putative protein kinase, 3' partial [Arabidopsis
KSU001BE443960-2	1.0e-07	Oryza sativa genomic DNA, chromosome 1, BAC clone:OSJ	1.0e-50	(AP003210) contains ESTs AU030536(E51208),AU030535(E512
KSU002BE405234-10	2.0e-67	Oryza sativa COX6b2 mRNA for cytochrome c oxidase subu	2.0e-35	(AB047923) cytochrome c oxidase subunit 6b [Oryza sativa
KSU002BE426356-1	2.0e-36	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	6.0e-78	(AP002092) EST AU090587(C30149) corresponds to a region
KSU012BE490440-2	5.0e-61	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-58	(AP001800) EST AU082314(E2976) corresponds to a region c
KSU019BE443559-12	7.0e-06	Arabidopsis thaliana unknown protein (F6F3.4) mRNA, com	2.0e-19	(AC023628) Unknown protein [Arabidopsis thaliana]
KSU019BE500394-5	2.0e-21	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	3.0e-51	(AP002744) putative late embryogenesis abundant protein
KSU027BE495182-3	4.0e-13	Arabidopsis thaliana AT3g58680 (AT3g58680\T20N10_30) m	5.0e-60	(AC006931) unknown protein [Arabidopsis thaliana]
KSU027BF292892-2	0	Oryza sativa DNA for phospholipase D, complete cds	e-120	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATA
KSU035BE497469-1,4	2.0e-97	Oryza sativa mRNA for NLS receptor, complete cds	3.0e-53	(AB004660) NLS receptor [Oryza sativa] region of the predi
KSU038BE442681-4	0.026	Arabidopsis thaliana chromosome II section 127 of 255 of	5.0e-54	(AJ011892) cyclin D2.1 protein [Nicotiana tabacum]
NDS018BE404868-1,7	4.0e-71	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	9.0e-55	(AP002524) putative 0-deacetylbaccatin III-10-O-acetyl trans
NDS043BF291720-2	e-118	Oryza sativa mRNA, similar to yeast SRP1, complete cds	1.0e-77	SRP1 protein homolog - rice
TTU025BE490440-2	5.0e-61	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-58	(AP001800) EST AU082314(E2976) corresponds to a region c
UCD017BE488921-1	0	Triticum aestivum triose phosphate translocator (tpt1) mR	e-101	(AF314187) triose phosphate translocator [Triticum aestivu
UMC015BE426222-1	1.0e-38	Oryza sativa genomic DNA, chromosome 1, clone:P0705D0	1.0e-79	(AP000492) EST AU078118(E3904) corresponds to a region c
UNL036BE590609-1	0	Triticum durum mRNA for lipid transfer protein (ltp7.1 gen	4.0e-34	(AJ297768) lipid transfer protein [Triticum turgidum subsp
UNL048BE591804-2	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
UNL053BG275060-2	8.0e-05	Arabidopsis thaliana AIM1 protein (AIM1) gene, complete	2.0e-51	AIM1 protein - Arabidopsis thaliana

C-3BS1-0.33

CSU046BE444280-2,5	6.0e-40	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-58	(AP002818) putative C-8,7 sterol isomerase [Oryza sativa]
KSU019BE637878-3	7.0e-14	Oryza sativa chromosome 3 BAC OSJNBa0013M12 genomic	1.0e-08	(AP002070) Similar to Arabidopsis thaliana low temperatur
KSU035BE404580-2	5.0e-16	Arabidopsis thaliana ubiquitin-specific protease 7 (UBP7) g	6.0e-73	(AF302661) ubiquitin-specific protease 7 [Arabidopsis thali
KSU035BE406903-2	0.73	Homo sapiens BAC clone RP11-459K11 from 2, complete se	9.0e-27	(AF302660) ubiquitin-specific protease 6 [Arabidopsis thali
UCD037BE443276-3	0	ric1=ras-related GTP binding protein possessing GTPase	9.0e-87	RAS-RELATED PROTEIN RIC1 activity=ric1 [Oryza sativa=rice,
UCW020BE494850-2	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
UCW039BE405131-6	3.0e-57	Musa acuminata mRNA for unknown ripening-related prot	1.0e-75	(AB023034) ATP citrate lyase [Arabidopsis thaliana]

C-3BL2-0.22

CNL023BE405374-3	1.0e-19	Solanum tuberosum GDP-mannose pyrophosphorylase (G	2.0e-90	(AF022716) GDP-mannose pyrophosphorylase [Solanum tu
CNL031BE500460-2	e-125	Oryza sativa mRNA for fructose-1,6-bisphosphatase (cytos	7.0e-53	(AF218845) fructose-1,6-bisphosphatase [Porteresia coarc
KSU001BE442571-1	1.5	Mesorhizobium loti, complete genome	2.0e-11	(AB017063) gb|AAD29063.1~gene_id:K3K7.3~similar to unkn
KSU001BE442924-1	0.007	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K6M13		
KSU001BE443755-2,7	0.007	Dictyostelium discoideum nucleoside diphosphate kinase	6	(AF202730) Niemann-Pick type C1 disease protein [Oryctol
KSU001BE444171-2	3.0e-72	Oryza sativa genomic DNA, chromosome 1, clone:P0708G0	6.0e-73	(AP001539) Similar to Arabidopsis thaliana chromosome 4
KSU019BE404709-3,4	4.0e-06	Arabidopsis thaliana chromosome II section 112 of 255 of	4.0e-36	hypothetical protein F27F23.18 - Arabidopsis thaliana
KSU019BE606250-1	e-105	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	e-102	(AP002844) contains ESTs AU069322(C60381),AU070001(E31
KSU035BE403637-4	9.0e-76	Beta vulgaris cDNA for elongation factor 2	5.0e-97	ELONGATION FACTOR 2 (EF-2)
KSU035BE404434-4	e-114	Lycopersicon esculentum elongation factor 2 mRNA, parti	2.0e-96	ELONGATION FACTOR 2 (EF-2)
KSU035BE517931-2	0.4	Halobacterium sp. NRC-1 section 106 of 170 of the complet	3.0e-23	(AF084201) similar to chloroplast 50S ribosomal protein L3
KSU038BE445496-1	0.39	Homo sapiens KIAA1072 protein (KIAA1072), mRNA	1.0e-75	(AC010926) protein phosphatase 2C (AtP2C-HA); 19519-176
KSU038BE446731-2,4	4.0e-50	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	5.0e-75	(AP002844) putative H+-transporting ATPase [Oryza sativa]
NDS034BE403201-2	0	H.vulgare (Gerbel) mRNA for adenosine triphosphatase	3.0e-58	(U84268) YLP [Hordeum vulgare]
TTU047BE445539-3	6.0e-06	Arabidopsis thaliana chromosome 1 BAC F22G10 genomic	8.0e-69	(U74610) glyoxalase II [Arabidopsis thaliana]
UCD001BE443753-1	1.3	Tauraco erythrolophus cytochrome b gene, partial cds\; mitochondrial gene for mitochondrial product		
UCD001BE443755-2	0.007	Dictyostelium discoideum nucleoside diphosphate kinase	6	(AF202730) Niemann-Pick type C1 disease protein [Oryctol
UCD029BE494776-3	0	Oryza sativa NADP-specific isocitrate dehydrogenase mRN	e-109	(AF155333) NADP-specific isocitrate dehydrogenase [Oryza
UCD029BE500510-1	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
UCD037BE442595-4	4.0e-23	Oryza sativa genomic DNA, chromosome 1, PAC clone:P07	2.0e-15	PROTEIN KINASE AFC2
UMC040BE606632-7	1.0e-98	Hordeum vulgare cv. Haisa mRNA for MCB1 protein	3.0e-31	(AJ303354) MCB1 protein [Hordeum vulgare]
UNL002BE500083-1	0.089	Homo sapiens, CD63 antigen (melanoma 1 antigen), clone	3.0e-68	(AC079829) hypothetical protein [Arabidopsis thaliana]
UNL002BE607045-1	e-130	O.sativa mRNA for dihydroflavonol reductase	6.0e-88	DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEI
UNL036BF200700-5	e-121	Rice mRNA for succinyl-CoA synthetase (475 gene), partial s	7.0e-46	SUCCINYL-COA LIGASE [GDP-FORMING] ALPHA-CHAIN, MITC

3BL2-0.22-0.50

CSU046BE445343-4	5.0e-71	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	7.0e-27	(AC007071) unknown protein [Arabidopsis thaliana]
KSU001BE444252-2	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
KSU012BE404385-5	e-170	Zea mays golgi associated protein se-wap41 mRNA, comp	e-108	(AF294725) reversibly glycosylated polypeptide [Oryza sati
KSU012BE406587-2	4.0e-06	Arabidopsis thaliana chromosome V map near 60.5 cM, co	5.0e-46	(AF049930) PGPD14 [Petunia x hybrida]
KSU012BE490613-1	9.0e-05	Homo sapiens PAC clone RP3-430N8 from 22q12.1-qter, co	2.0e-09	(AC022354) unknown protein [Arabidopsis thaliana]
KSU012BE490651-2	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
KSU024BE499348-2,4	3.0e-17	Oryza meyeriana serine\threonine protein kinase (R1) ger	1.0e-37	(AP000410) receptor protein kinase-like protein [Arabidop
KSU027BE406676-2	3.0e-96	Triticum aestivum germin protein precursor, mRNA, comp	2.0e-40	GERMIN GF-2.8 PRECURSOR
KSU027BE495226-2,6	0.2	Homo sapiens ALPP, ALPPL2, ALPI, XCE, CHRND, and CHRNG genes, complete sequence		
KSU027BF485179-1	0	Triticum aestivum WC1 mRNA for cysteine proteinase inhi	2.0e-64	(AB038392) cysteine proteinase inhibitor [Triticum aestivu
KSU030BE404799-1	6.0e-09	Arabidopsis thaliana RNA polymerase I, II and III 24.3 kDa su	3.0e-33	(AF019248) RNA polymerase I, II and III 24.3 kDa subunit [Ar
KSU035BE403268-2	e-152	Triticum aestivum metallothionein-like protein (wali1) mR	4.0e-12	METALLOTHIONEIN-LIKE PROTEIN 1
KSU035BE403348-2	0.058	Streptomyces coelicolor cosmid 9C5	2.0e-08	nucleoid DNA-binding protein cnd41-like protein - Arabidop
KSU035BE403438-2	0.069	Human DNA sequence from clone RP1-101A2 on chromosc	5.0e-07	(AB007648) contains similarity to ABA-responsive protein~
KSU035BE403439-2	1.0e-74	Panicum miliaceum mRNA for 2-oxoglutarate\malate trans	1.0e-61	2-oxoglutarate\malate translocator (clone OMT103), mitocl
KSU035BE403619-3	0.82	Homo sapiens 12q BAC RP11-798P24 (Roswell Park Cancer	4.0e-06	(AF098458) latex-abundant protein [Hevea brasiliensis]
KSU035BE497366-2	2.0e-27	Oryza sativa subsp. japonica clone S14511 putative glutathi	6.0e-09	(AF309376) putative glutathione S-transferase OsGSTU6 [Or
KSU038BE442699-4	4.0e-53	Rice mRNA for q group of receptor for activated C-kinase,	2.0e-42	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
KSU038BE443568-1,4	4.0e-04	Arabidopsis thaliana chromosome 1 BAC F1O17 genomic s	2.0e-84	glycerophosphodiester phosphodiesterase-like protein -
KSU038BE445803-2	6.0e-40	Oryza sativa mRNA for NADH dependent Glutamate Synthas	2.0e-28	(AB008845) NADH dependent Glutamate Synthase [Oryza sa
KSU038BE489323-6	0.086	Arabidopsis thaliana DNA chromosome 3, BAC clone F1P2	9.0e-15	(AF247646) transposase [Zea mays]
NDS001BE443755-1	0.007	Dictyostelium discoideum nucleoside diphosphate kinase	6	(AF202730) Niemann-Pick type C1 disease protein [Oryctola
TTU025BE490613-1	9.0e-05	Homo sapiens PAC clone RP3-430N8 from 22q12.1-qter, co	2.0e-09	(AC022354) unknown protein [Arabidopsis thaliana]
TTU025BE490651-2	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
TTU025BE490658-2	e-104	Eleusine indica alpha-tubulin 2 (TUA2) mRNA, complete cds	1.0e-65	TUBULIN ALPHA-2 CHAIN (ALPHA-2 TUBULIN)
TTU047BE494345-1	0.27	Streptomyces coelicolor cosmid 1B5	1.0e-25	(AB022210) gene_id:K16E1.4~unknown protein [Arabidopsi
UCD037BE499348-2,4	3.0e-17	Oryza meyeriana serine\threonine protein kinase (R1) ger	1.0e-37	(AP000410) receptor protein kinase-like protein [Arabidop
UCD037BE500112-3,4,6	0	T.aestivum (Chinese spring) chi gene for endochitinase	3.0e-52	chitinase (EC 3.2.1.14) - wheat
UMC015BE406587-2,6	4.0e-06	Arabidopsis thaliana chromosome V map near 60.5 cM, co	5.0e-46	(AF049930) PGPD14 [Petunia x hybrida]
UMC015BE444252-2	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
UMC015BE606723-3,4,8,11	e-127	Secale cereale RKIN1 mRNA, complete CDS	8.0e-60	(D82035) OSK4 [Oryza sativa]
UMC032BE425919-3	2.0e-42	Oryza sativa chromosome 10 clone nbeb0039C14, complet	4.0e-62	(AL392174) rev interacting protein mis3-like [Arabidopsis t
UMC040BE606881-2	1.0e-46	Zea mays nuclear-encoded mitochondrial F1F0 ATP syntha	2.0e-28	ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL mitochonc
UMC055BF483799-2	3.0e-74	Oryza sativa genomic DNA, chromosome 1, PAC clone:P06	1.0e-29	(AP002972) contains EST D15166(C0193)~unknown protein |
UMC055BF483930-3,4	1.0e-28	Hordeum vulgare cysteine proteinase precursor, mRNA, c	2.0e-48	(U34747) cysteine proteinase [Phalaenopsis sp. SM9108]
UMN013BE442694-1	0	Triticum aestivum calmodulin TaCaM1-2 mRNA, complete	2.0e-62	(AJ005039) CaM-1 [Nicotiana plumbaginifolia]
UNL036BF200697-2	0.31	Caenorhabditis elegans cosmid F49E12, complete sequen	8.0e-13	(AC005311) hypothetical protein [Arabidopsis thaliana]

3BL10-0.50-0.63

CNL014BE444736-5,7,14,15	2.0e-08	Arabidopsis thaliana chromosome 1 BAC T1F15 sequence	4.0e-54	hypothetical protein T1F15.13 - Arabidopsis thaliana (fragn
CNL014BE444961-3	4.0e-07	Arabidopsis thaliana chromosome II section 115 of 255 of	9.0e-45	(AC006081) 50S ribosomal protein L4 [Arabidopsis thaliana
CSU001BE443747-3,4	1.5	Sorghum bicolor ADP-glucose pyrophosphorylase subuni	5.0e-25	(AB025632) dihydroflavonol 4-reductase-like [Arabidopsis
CSU046BE442943-3	0.42	Drosophila melanogaster, chromosome 2R, region 49E-49I	2.0e-54	(AC016661) unknown protein [Arabidopsis thaliana]
KSU019BE445011-2	0.005	Zea mays indeterminate spikelet 1 (ids1) mRNA, complete	2.0e-26	indeterminate spikelet 1 - maize
KSU035BE496857-1	1.0e-80	Z.mays mRNA for CAAT-box DNA binding protein subunit B	2.0e-56	(X59714) CAAT-box DNA binding protein subunit B (NF-YB)
KSU035BE497323-3	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
KSU038BE443191-1,3	e-115	Triticum aestivum 70 kDa heat shock protein (TaHSP70d) n	2.0e-62	dnaK-type molecular chaperone hsp70 - rice (fragment)
KSU038BE443770-2	5.0e-56	Sorghum bicolor cinnamic acid 4-hydroxylase (C4H) mRNA	2.0e-34	(U29243) trans-cinnamic acid hydroxylase [Pisum sativum]
NDS001BE444252-2	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
UCD001BE405214-2,5,8	3.0e-11	Arabidopsis thaliana respiratory burst oxidase protein D (	4.0e-56	(AB015475) respiratory burst oxidase protein [Arabidopsis
UCD017BE488783-4	8.0e-12	Arabidopsis thaliana DNA chromosome 3, BAC clone T14E1	9.0e-51	ABC transporter-like protein - Arabidopsis thaliana
UCD017BE489603-1	1.0e-24	Oryza sativa genomic DNA, chromosome 1, PAC clone:P06	3.0e-31	PROBABLE CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOI
UCW016BE517914-2	2.0e-52	P.sativum mRNA for small G protein	2.0e-41	(AB015475) Rab-type small GTP-binding protein-like [Arabi
UMN013BE442875-2,6	6.0e-12	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	7.0e-66	(AB019227) gb|AAF01562.1~gene_id:MBM17.7~strong simila
UMN013BE443349-2	1.0e-25	L.japonicus mRNA for small GTP-binding protein, RAB11C	1.0e-57	RAS-RELATED PROTEIN RAB11C
UNL036BF200549-1	6.0e-61	Oryza sativa Os SBP mRNA for putative selenium binding p	2.0e-37	(AB059401) putative selenium binding protein [Oryza sativa

3BL7-0.63-1.00

CNL014BE444864-1	4.0e-07	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	7.0e-73	(AB023042) phosphatidylserine decarboxylase [Arabidopsi
CNL014BE445136-3	3.0e-07	Barley pHVA1 mRNA for an ABA-inducible protein	0.79	(AJ275365) immunoglobulin heavy chain variable region [H
CNL014BE490613-1	9.0e-05	Homo sapiens PAC clone RP3-430N8 from 22q12.1-qter, co	2.0e-09	(AC022354) unknown protein [Arabidopsis thaliana]
KSU001BE444473-7,8	0.016	Drosophila melanogaster genomic scaffold 142000013386	2.0e-23	(AC084763) hypothetical protein [Oryza sativa]
KSU012BE442674-1	0	Oryza sativa Os SBP mRNA for putative selenium binding p	e-103	(AB059401) putative selenium binding protein [Oryza sativa
KSU012BE442875-1,5	6.0e-12	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	7.0e-66	(AB019227) gb|AAF01562.1~gene_id:MBM17.7~strong simila
KSU012BE443397-1,4	3.0e-05	Mesembryanthemum crystallinum cinnamyl-alcohol dehy	2.0e-77	(AC010926) putative cinnamyl-alcohol dehydrogenase\; 496
KSU012BE443423-8	1.0e-19	Oryza sativa chromosome 3 BAC OSJNBa0091J19 genomic	4.2	(AL117195) Y57A10A.1 [Caenorhabditis elegans]
KSU019BE442624-4	1.3	Caenorhabditis elegans cosmid F54D7, complete sequenc	5.0e-40	(AB036735) allyl alcohol dehydrogenase [Nicotiana tabacum
KSU019BE494330-2	3.0e-75	O.sativa mRNA for SMT3 protein	1.0e-34	UBIQUITIN-LIKE PROTEIN SMT3
KSU019BE494450-7	7.0e-40	Avena maroccana clone Ma7 ribulose-1,5-bisphosphate ca	3.0e-15	(AB042068) ribulose-1,5-bisphosphate carboxylase\oxyger
KSU024BE405348-2,4	1.0e-93	Oryza sativa clone C23033 truncated UMP synthase (UMPS	1.0e-60	(AB031395) UMP synthase 1 [Oryza sativa]
KSU024BE499186-1,4	e-136	Oryza sativa mRNA for asparaginyl endopeptidase, comple	4.0e-70	(AJ251454) putative legumain [Zea mays]
KSU024BE499303-4	2.0e-11	Arabidopsis thaliana putative methionine aminopeptidase	6.0e-13	(AF300880) putative methionine aminopeptidase 2 [Arabido
KSU030BE495145-1	0.001	Arabidopsis thaliana mRNA for putative beta-galactosidase	4.0e-55	(AC010704) putative beta-galactosidase, 3' partial\; 3669-1 [
KSU030BE497740-1	1.0e-16	Arabidopsis thaliana mRNA for Dr1	1.0e-47	DR1-like protein - Arabidopsis thaliana
KSU030BE499696-1	5.0e-65	Glycine max beta-ketoacyl-ACP synthetase I-2 mRNA, com	3.0e-76	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURS
KSU030BE499968-2	0	Triticum aestivum alpha 1,4-glucan phosphorylase mRNA,	6.0e-82	(AF326977) alpha 1,4-glucan phosphorylase H isozyme [Ory
KSU030BF485004-3	1.0e-18	Lycopersicon esculentum transaldolase (TAL) mRNA, com	4.0e-34	transaldolase-like protein - Arabidopsis thaliana
KSU035BE403395-4	5.0e-96	N.tabacum mRNA for elongation factor 2	e-103	ELONGATION FACTOR 2 (EF-2)
KSU035BE403428-1,7	1.4	Oryctolagus cuniculus heat shock protein 47 mRNA, partia	1.0e-35	(AC069300) putative dioxygenase [Oryza sativa]
KSU035BE403647-3	3.0e-23	Solanum tuberosum partial mRNA for serine palmitoyltran	3.0e-85	(AB025633) serine palmitoyltransferase [Arabidopsis thali
KSU038BE442681-8	0.026	Arabidopsis thaliana chromosome II section 127 of 255 of	5.0e-54	(AJ011892) cyclin D2.1 protein [Nicotiana tabacum]
KSU038BE445556-7	0.002	Oryza sativa genomic DNA, chromosome 1, PAC clone:P07	5.0e-54	probable peptidylprolyl isomerase (EC 5.2.1.8) FKBP15-1 - A
NDS018BE405221-1	5.0e-65	Oryza sativa chromosome 1 clone OSJNBa0048I01, complet	1.0e-69	(AF000657) unknown protein [Arabidopsis thaliana]
NDS034BE499968-3,7	0	Triticum aestivum alpha 1,4-glucan phosphorylase mRNA,	6.0e-82	(AF326977) alpha 1,4-glucan phosphorylase H isozyme [Ory
NDS043BF292596-4	1.3	Mesorhizobium loti, complete genome	7.0e-12	comes from this gene. [Arabidopsis thaliana]
TTU047BE495913-7	0.011	Mus musculus 1 BAC RP23-337F12 (Roswell Park Cancer In	1.0e-11	hypothetical protein - garden asparagus
UCD001BE406551-2,6	0.85	Rhizobium sp. NGR234 plasmid pNGR234a, section 8 of 46 o	2.0e-34	(AB019232) gb|AAC28507.1~gene_id:MIL23.25~strong simila
UCD001BE443755-11	0.007	Dictyostelium discoideum nucleoside diphosphate kinase	6	(AF202730) Niemann-Pick type C1 disease protein [Oryctola
UCD001BE443798-3	0.39	Escherichia coli O157:H7 EDL933 genome, contig 2 of 3, section 31 of 55		
UCD017BE488620-1	2.0e-11	Vigna unguiculata VuP5CR mRNA, complete cds	1.0e-50	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDU
UCD028BF484536-3,5,12	1.1	Methylococcus capsulatus putative nonaheme c-cytochro	0.43	(AF277399) cat eye syndrome critical region 6 [Mus muscu
UCD029BF483478-4,5	2.0e-24	Arabidopsis thaliana putative methionine aminopeptidase	1.0e-62	(AF300880) putative methionine aminopeptidase 2 [Arabido
UCD037BE489274-2	0.023	Homo sapiens, clone hRPK.2_A_1, complete sequence	6.0e-59	fructokinase-like protein - Arabidopsis thaliana
UCD037BE497664-1	e-130	Oryza sativa ALDH1a mRNA for cytosolic aldehyde dehydro	1.0e-94	(AB037421) cytosolic aldehyde dehydrogenase [Oryza sativ
UCD037BE497800-5	5.0e-15	Arabidopsis thaliana AT5g50430\MXI22_15 mRNA, complet	2.0e-54	(AB012248) ubiquitin conjugating enzyme-like protein [Aral
UCW001BE398631-1	3.3	Oryza sativa chromsome 9 clone PAC0663H05, complete s	1.9	BETA-2 ADRENERGIC RECEPTOR
UCW001BE443798-3	0.39	Escherichia coli O157:H7 EDL933 genome, contig 2 of 3, section 31 of 55		
UCW016BE637789-4	2.0e-70	O.sativa mRNA for cytochrome b5	1.0e-65	CYTOCHROME B5
UCW020BE494854-1	2.0e-15	Oryza sativa subsp. indica putative dnaJ-like protein, putat	1.0e-49	(AF111710) hypothetical protein [Oryza sativa subsp. indica
UCW020BE499900-3	4.0e-44	Arabidopsis thaliana AT3g52990\F8J2_160 mRNA, complete	1.0e-85	pyruvate kinase-like protein - Arabidopsis thaliana
UCW020BF478499-2	4.0e-41	Oryza sativa thioredoxin F isoform mRNA, complete cds	3.0e-30	THIOREDOXIN F-TYPE 2, CHLOROPLAST PRECURSOR (TRX-F2
UCW026BG263365-2	3.0e-50	Saccharum officinarum mRNA for Sucrose-Phosphate Syn	1.0e-61	sucrose-phosphate synthase (EC 2.4.1.14) 1 - rice
UCW039BE404125-2	0.002	Oryza sativa microsatellite MRG2602 containing (GA)X13, cl	6.0e-64	(AB016877) beta-glucosidase [Arabidopsis thaliana]
UMC015BE489841-5	8.0e-30	Arabidopsis thaliana At2g27860\F15K20.4 gene, complete	8.0e-95	(AC011438) T23G18.6 [Arabidopsis thaliana]
UMC040BG262287-5	e-159	Hordeum vulgare HVA\68 mRNA for vacuolar proton-ATPa	1.0e-62	(AB032840) vacuolar proton-ATPase [Hordeum vulgare]
UMN013BE443288-1	1.0e-07	Arabidopsis thaliana ADL2 mRNA, complete cds	4.0e-85	(AF012833) similar to dynamin-like protein encoded by Ger
UMN013BE443397-1,3	3.0e-05	Mesembryanthemum crystallinum cinnamyl-alcohol dehy	2.0e-77	(AC010926) putative cinnamyl-alcohol dehydrogenase\; 496
UNL002BE499910-3,5	1.4	Homo sapiens, clone MGC:13105, mRNA, complete cds	1.0e-13	(AF209484) disease resistance-like protein [Brassica napu
UNL002BE517312-4	8.0e-08	Arabidopsis thaliana YLS7 mRNA for leaf-senescence-rela	8.0e-49	(AB018109) gene_id:K17N15.19~pir||T10216~strong similarity
UNL036BE517923-2	2.0e-30	Arabidopsis thaliana putative 60S ribosomal protein L10A	3.0e-65	(AF360146) putative 60S ribosomal protein L10A [Arabidop
UNL036BE590549-2	7.0e-12	A.sativa avenin mRNA, complete cds	2.0e-24	gliadin - wheat
UNL036BF474092-1	0.059	R.norvegicus mRNA for microtubule associated protein IB	5.0e-13	THYLAKOID LUMENAL 17.4 KDA PROTEIN, CHLOROPLAST PR
UNL048BE445579-5	1.2	Streptomyces antibioticus putative 3-ketoreductase (oleW	1.0e-53	(AF002109) unknown protein [Arabidopsis thaliana]

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 : Nora Lapitan, Colorado State University, Fort Collins
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

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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