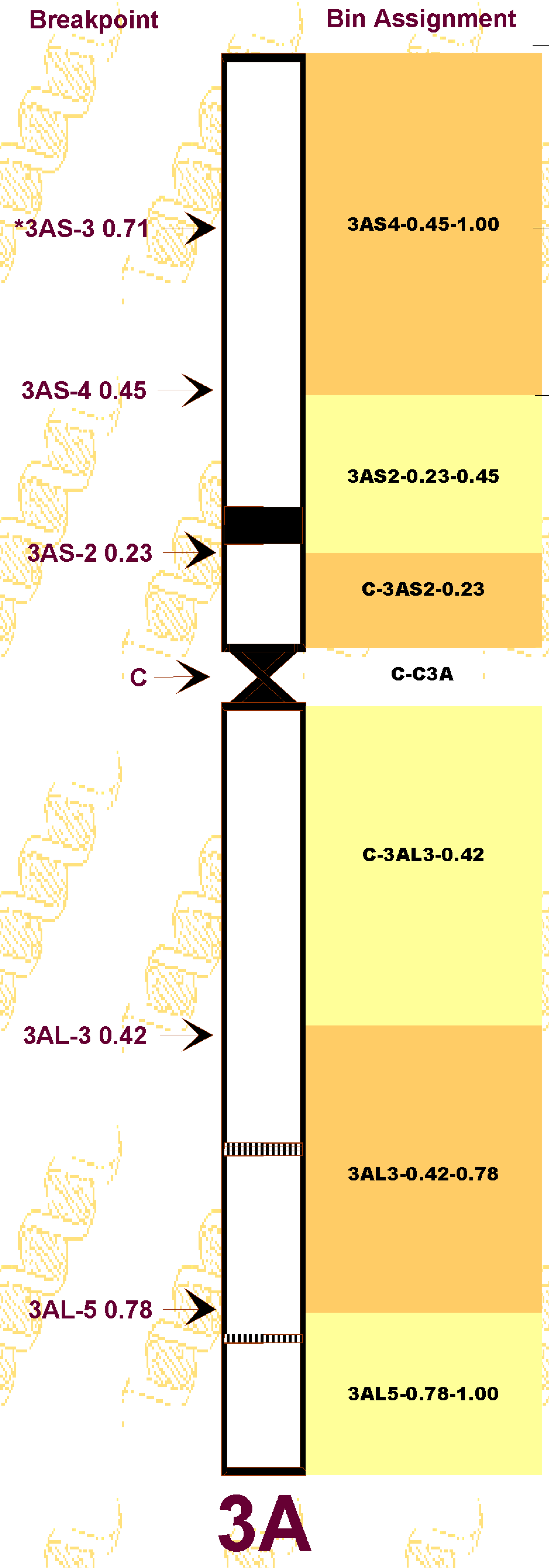
The Structure and Function of the Expressed Portion of the Wheat Genomes

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

*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.



* 3AS-3 is not confirmed

3AS3*-0.71-1.00

CSU001BE426356-4	2.0e-36	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	6.0e-78	(AP002092) EST AU090587(C30149) corresponds to a region
UCD001BE405200-7	1.5	Homo sapiens chromosome 5 clone CTB-70H11, complete	8.1	testis expressed sequence 14 [Homo sapiens]
UCD001BE406567-3	1.0e-14	Arabidopsis thaliana ubiquitin carrier protein (UBC1) mRNA	2.0e-23	(AF262934) ubiquitin conjugating protein [Avicennia marina
UCD001BE443404-3,4	0.021	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	6.0e-24	(AP002913) contains ESTs AU032141(R3625),AU162501(R3625
UCD001BE444576-3	0.056	Arabidopsis thaliana chromosome 1 BAC F5I6 genomic se	3.0e-24	(AB007650) 3-isopropylmalate dehydrogenase [Arabidopsi
UMN013BE443955-3	1.0e-13	Arabidopsis thaliana DNA chromosome 4, contig fragment	4.0e-72	hypothetical protein T22F8.20 - Arabidopsis thaliana thalian
UNL002BE499177-2	0.095	Homo sapiens clone BAC 9H13 chromosome 8 map 8q21, c	1.0e-16	(AF202179) disease resistance protein BS2 [Capsicum cha

3AS4-0.45-1.00

CNL001BE406567-3	1.0e-14	Arabidopsis thaliana ubiquitin carrier protein (UBC1) mRNA	2.0e-23	(AF262934) ubiquitin conjugating protein [Avicennia marina
CNL001BE426356-4,5	2.0e-36	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	6.0e-78	(AP002092) EST AU090587(C30149) corresponds to a region
CNL014BE446610-4,6,8	5.0e-62	Glycine max small GTP-binding protein (sra2) mRNA, comp	5.0e-71	(Z73932) RAB1C [Lotus japonicus]
CNL014BE490440-1	5.0e-61	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-58	(AP001800) EST AU082314(E2976) corresponds to a region c
CNL014BE591226-1,2,4	3.0e-20	Hordeum vulgare mRNA for expressed sequence tag	1.0e-46	(AF321858) putative cytochrome P450 [Lolium rigidum]
CNL023BE405260-3	0	Hordeum vulgare glutamine-dependent asparagine synthe	e-121	(AF307145) glutamine-dependent asparagine synthetase 1
CNL023BG274134-2,3	2.0e-04	Nicotiana tabacum sucrose-6-phosphate synthase (SPS) m	7.0e-25	SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE
CNL031BF203138-5	6.0e-13	Musa acuminata metallothionein-like protein (MWMT2B) m	3.0e-05	METALLOTHIONEIN-LIKE PROTEIN 2 (MT-2)
CSU001BE406607-2	2.0e-48	Oryza sativa mRNA for gigantea homologue, partial	1.0e-48	(AP003047) gigantea-like protein [Oryza sativa]
CSU046BE444280-3	6.0e-40	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-58	(AP002818) putative C-8,7 sterol isomerase [Oryza sativa]
KSU001BE398929-1	1.1	Acronicta sp.1 dopa decarboxylase (DDC) gene, partial cds	4.0e-05	(AC024128) putative protein kinase, 3' partial [Arabidopsis
KSU001BE406607-2	2.0e-48	Oryza sativa mRNA for gigantea homologue, partial	1.0e-48	(AP003047) gigantea-like protein [Oryza sativa]
KSU001BE442648-8	2.0e-18	Oryza sativa genomic DNA, chromosome 1, PAC clone:P06	7.0e-45	(AP003047) hypothetical protein [Oryza sativa]
KSU001BE444576-3	0.056	Arabidopsis thaliana chromosome 1 BAC F5I6 genomic se	3.0e-24	(AB007650) 3-isopropylmalate dehydrogenase [Arabidopsi
KSU002BE405200-5	1.5	Homo sapiens chromosome 5 clone CTB-70H11, complete	8.1	testis expressed sequence 14 [Homo sapiens]
KSU002BE406567-4	1.0e-14	Arabidopsis thaliana ubiquitin carrier protein (UBC1) mRNA	2.0e-23	(AF262934) ubiquitin conjugating protein [Avicennia marina
KSU002BE425222-1,4,6	1.0e-04	Oryza sativa rbbi3-1 gene for putative Bowman Birk trypsin	4.0e-63	Chain A, Human Muscle L-Lactate Dehydrogenase M Chain
KSU002BE426356-5	2.0e-36	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	6.0e-78	(AP002092) EST AU090587(C30149) corresponds to a region
KSU012BE407082-8	0.005	Arabidopsis thaliana chromosome II section 243 of 255 of	7.0e-41	(AP000391) ESTs AU056036(S20239),C72753(E2173), AU05603
KSU012BE490440-1	5.0e-61	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-58	(AP001800) EST AU082314(E2976) corresponds to a region c
KSU024BE498137-3	2.0e-42	Poa secunda metallothionein-like protein type 2 mRNA, co	0.009	(AF246982) metallothionein-like protein type 2 [Poa secund
KSU027BE495182-1	4.0e-13	Arabidopsis thaliana AT3g58680 (AT3g58680\T20N10_30) m	5.0e-60	(AC006931) unknown protein [Arabidopsis thaliana]
KSU027BF292892-3	0	Oryza sativa DNA for phospholipase D, complete cds	e-120	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATA
KSU035BE406998-1,3,4,7	2.0e-35	ric1=ras-related GTP binding protein possessing GTPase	3.0e-43	(AP002524) putative GTP-binding protein [Oryza sativa]
KSU035BE517736-1	3.0e-07	Tobacco mRNA for RNA helicase like protein DB10	2.0e-15	DRH1 DEAD box protein-like - Arabidopsis thaliana
NDS001BE443995-3,4	1.6	Homo sapiens 12 BAC RP11-547C5 (Roswell Park Cancer In	4.0e-71	(AC079281) unknown protein [Arabidopsis thaliana]
NDS018BE404868-4	4.0e-71	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	9.0e-55	(AP002524) putative 0-deacetylbaccatin III-10-O-acetyl trans
TTU025BE490440-1	5.0e-61	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-58	(AP001800) EST AU082314(E2976) corresponds to a region c
UCD017BE488609-1	4.0e-19	Porteresia coarctata metallothionein mRNA, complete cds	9.0e-17	metallothionein-like protein - rice
UCD037BE443276-1	0	ric1=ras-related GTP binding protein possessing GTPase	9.0e-87	RAS-RELATED PROTEIN RIC1 activity=ric1 [Oryza sativa=rice,
UCW001BE425222-6	1.0e-04	Oryza sativa rbbi3-1 gene for putative Bowman Birk trypsin	4.0e-63	Chain A, Human Muscle L-Lactate Dehydrogenase M Chain
UCW020BF293537-3	1.0e-09	Arabidopsis thaliana signal peptidase mRNA, complete cds	2.0e-49	(AP002526) Similar to Arabidopsis thaliana signal peptidase
UMN013BE442933-7	3.0e-17	Orobanche ramosa NADPH-dependent mannose 6-phosph	4.0e-68	(AC006841) putative NADPH dependent mannose 6-phosph
UNL002BE444148-2	0.1	Human DNA sequence from clone RP5-1027O11 on chromo	1.0e-20	(AC079128) Putative bacterial blight resistance protein Xa1
UNL002BE492524-2	2.0e-41	Zea mays eukaryotic translation initiation factor 3 large su	2.0e-49	(AP002487) putative eukaryotic translation initiation factor
UNL036BE517719-1,2	0.07	Homo sapiens mRNA\; cDNA DKFZp434G1812 (from clone DI	1.0e-09	(AC022455) hydrophilic protein, putative\; 29542-30030 [Aral
UNL036BE590609-2	0	Triticum durum mRNA for lipid transfer protein (ltp7.1 gen	4.0e-34	(AJ297768) lipid transfer protein [Triticum turgidum subsp
UNL036BF474158-3	0.11	Homo sapiens chromosome 16 clone RP11-112G1, complete	1.0e-13	c-myc binding protein [Homo sapiens]
UNL044BF484475-2	7.0e-23	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-26	(AC073405) rice EST BE041002 corresponds to a region of t
UNL044BG263366-1,2	5.0e-08	Hordeum vulgare glucan endo-1,3-beta-glucosidase isoen	4.0e-17	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, ACIDIC ISOFORM PR
UNL048BE591013-2	2.0e-36	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	e-103	(AP002540) putative CER3 [Oryza sativa]
UNL048BE591804-3	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
UNL048BF428780-3	9.0e-27	Z.mays mRNA for alpha-tubulin 3	1.0e-10	TUBULIN ALPHA CHAIN
UNL053BG275060-3	8.0e-05	Arabidopsis thaliana AIM1 protein (AIM1) gene, complete	2.0e-51	AIM1 protein - Arabidopsis thaliana

3AS2-0.23-0.45

KSU012BE442694-3	0	Triticum aestivum calmodulin TaCaM1-2 mRNA, complete	2.0e-62	(AJ005039) CaM-1 [Nicotiana plumbaginifolia]
KSU035BE497469-2,7	2.0e-97	Oryza sativa mRNA for NLS receptor, complete cds	3.0e-53	(AB004660) NLS receptor [Oryza sativa] region of the predi
UCW039BE405131-2	3.0e-57	Musa acuminata mRNA for unknown ripening-related prot	1.0e-75	(AB023034) ATP citrate lyase [Arabidopsis thaliana]

C-3AS4-0.45

KSU001BE443960-3	1.0e-07	Oryza sativa genomic DNA, chromosome 1, BAC clone:OSJ	1.0e-50	(AP003210) contains ESTs AU030536(E51208),AU030535(E512

C-3AS2-0.23

CSU001BE426356-6	2.0e-36	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	6.0e-78	(AP002092) EST AU090587(C30149) corresponds to a region
KSU035BE404580-1	5.0e-16	Arabidopsis thaliana ubiquitin-specific protease 7 (UBP7)	6.0e-73	(AF302661) ubiquitin-specific protease 7 [Arabidopsis thali
UCD029BE494776-1	0	Oryza sativa NADP-specific isocitrate dehydrogenase mRN	e-109	(AF155333) NADP-specific isocitrate dehydrogenase [Oryza

C-3AL3-0.42

CNL031BE500460-5	e-125	Oryza sativa mRNA for fructose-1,6-bisphosphatase (cytos	7.0e-53	(AF218845) fructose-1,6-bisphosphatase [Porteresia coarc
KSU001BE442571-2	1.5	Mesorhizobium loti, complete genome	2.0e-11	(AB017063) gb|AAD29063.1~gene_id:K3K7.3~similar to unkn
KSU019BE404709-1	4.0e-06	Arabidopsis thaliana chromosome II section 112 of 255 of	4.0e-36	hypothetical protein F27F23.18 - Arabidopsis thaliana
KSU019BE606250-2,5	e-105	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	e-102	(AP002844) contains ESTs AU069322(C60381),AU070001(E31
KSU035BE403721-7	4.0e-53	Oryza sativa beta-glucosidase mRNA, nuclear gene encodi	2.0e-77	beta-glucosidase BGQ60 precursor - barley
KSU035BE517931-3	0.4	Halobacterium sp. NRC-1 section 106 of 170 of the complet	3.0e-23	(AF084201) similar to chloroplast 50S ribosomal protein L3
KSU038BE444681-2	2.0e-61	Oryza sativa GTP-binding protein mRNA, complete cds	1.0e-56	RAS-RELATED PROTEIN RAB2BV
KSU038BE445496-2,4	0.39	Homo sapiens KIAA1072 protein (KIAA1072), mRNA	1.0e-75	(AC010926) protein phosphatase 2C (AtP2C-HA)\; 19519-176
KSU038BE446731-1,3	4.0e-50	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	5.0e-75	(AP002844) putative H+-transporting ATPase [Oryza sativa]
NDS001BE444252-3	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
NDS034BE403201-1	0	H.vulgare (Gerbel) mRNA for adenosine triphosphatase	3.0e-58	(U84268) YLP [Hordeum vulgare]
UCD029BE500510-2	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
UCD037BE442595-3,6	4.0e-23	Oryza sativa genomic DNA, chromosome 1, PAC clone:P07	2.0e-15	PROTEIN KINASE AFC2
UNL002BE500083-2,4	0.089	Homo sapiens, CD63 antigen (melanoma 1 antigen), clone	3.0e-68	(AC079829) hypothetical protein [Arabidopsis thaliana]
UNL036BE590775-2	9.0e-33	Arabidopsis thaliana AT3g28710 (AT3g28710\MZN14_20) m	7.0e-96	PROBABLE VACUOLAR ATP SYNTHASE SUBUNIT D 1 (V-ATPA
UNL036BF200700-4	e-121	Rice mRNA for succinyl-CoA sythetase (475 gene), partial	7.0e-46	SUCCINYL-COA LIGASE [GDP-FORMING] ALPHA-CHAIN, MITC

3AL3-0.42-0.78

CNL014BE423756-4	2.0e-77	Oryza sativa subsp. japonica BAC nbxb0015J03, chromoso	2.0e-21	(AJ001161) rpS28 [Hordeum vulgare]
CSU001BE443747-1	1.5	Sorghum bicolor ADP-glucose pyrophosphorylase subuni	5.0e-25	(AB025632) dihydroflavonol 4-reductase-like [Arabidopsis
CSU046BE442943-1	0.42	Drosophila melanogaster, chromosome 2R, region 49E-49I	2.0e-54	(AC016661) unknown protein [Arabidopsis thaliana]
CSU046BE445343-3	5.0e-71	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	7.0e-27	(AC007071) unknown protein [Arabidopsis thaliana]
CSU057BE490678-2,4	0	Triticum aestivum mRNA for wpk4 protein kinase, comple	3.0e-98	(AB011670) wpk4 protein kinase [Triticum aestivum]
CSU101BE490744-1	0.001	Arabidopsis thaliana ATCDPMEK mRNA for 4-(cytidine 5'-ph	1.0e-29	(AF258339) 4-diphosphocytidyl-2C-methyl-D-erythritol kina
KSU001BE406602-3	2.0e-16	Zea mays 40S ribosomal protein S24 mRNA, complete cds	3.0e-19	(AF298769) 40S ribosomal protein S24 [Zea mays]
KSU001BE443995-2	1.6	Homo sapiens 12 BAC RP11-547C5 (Roswell Park Cancer In	4.0e-71	(AC079281) unknown protein [Arabidopsis thaliana]
KSU001BE444252-3	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
KSU012BE404385-2,10	e-170	Zea mays golgi associated protein se-wap41 mRNA, comp	e-108	(AF294725) reversibly glycosylated polypeptide [Oryza sati
KSU012BE406587-1	4.0e-06	Arabidopsis thaliana chromosome V map near 60.5 cM, co	5.0e-46	(AF049930) PGPD14 [Petunia x hybrida]
KSU012BE442674-3	0	Oryza sativa Os SBP mRNA for putative selenium binding p	e-103	(AB059401) putative selenium binding protein [Oryza sativa
KSU012BE490613-2	9.0e-05	Homo sapiens PAC clone RP3-430N8 from 22q12.1-qter, co	2.0e-09	(AC022354) unknown protein [Arabidopsis thaliana]
KSU012BE490651-1	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
KSU019BE445011-3	0.005	Zea mays indeterminate spikelet 1 (ids1) mRNA, complete	2.0e-26	indeterminate spikelet 1 - maize
KSU019BE636993-1	3.0e-41	Catharanthus roseus ubiquitin-conjugating enzyme E2 (UB	1.0e-75	(AC051629) Putative ubiquitin-conjugating enzyme E2 [Arab
KSU024BE499348-3	3.0e-17	Oryza meyeriana serine\threonine protein kinase (R1) ge	1.0e-37	(AP000410) receptor protein kinase-like protein [Arabidop
KSU027BE495226-1	0.2	Homo sapiens ALPP, ALPPL2, ALPI, XCE, CHRND, and CHRNG genes, complete sequence		
KSU027BF485179-2	0	Triticum aestivum WC1 mRNA for cysteine proteinase inhi	2.0e-64	(AB038392) cysteine proteinase inhibitor [Triticum aestivu
KSU030BE404799-3	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
KSU030BE499968-4	0	Triticum aestivum alpha 1,4-glucan phosphorylase mRNA,	6.0e-82	(AF326977) alpha 1,4-glucan phosphorylase H isozyme [Ory
KSU035BE496857-2	1.0e-80	Z.mays mRNA for CAAT-box DNA binding protein subunit E	2.0e-56	(X59714) CAAT-box DNA binding protein subunit B (NF-YB)
KSU035BE497323-1	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
KSU038BE443191-10	e-115	Triticum aestivum 70 kDa heat shock protein (TaHSP70d) n	2.0e-62	dnaK-type molecular chaperone hsp70 - rice (fragment)
KSU038BE443568-3,5	4.0e-04	Arabidopsis thaliana chromosome 1 BAC F1O17 genomic s	2.0e-84	glycerophosphodiester phosphodiesterase-like protein -
KSU038BE443770-3	5.0e-56	Sorghum bicolor cinnamic acid 4-hydroxylase (C4H) mRNA	2.0e-34	(U29243) trans-cinnamic acid hydroxylase [Pisum sativum]
KSU038BE445803-4	6.0e-40	Oryza sativa mRNA for NADH dependent Glutamate Synthas	2.0e-28	(AB008845) NADH dependent Glutamate Synthase [Oryza sa
NDS021BF473016-4	0	Oryza sativa mRNA for aspartate aminotransferase, compl	e-123	ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSA
NDS034BE499968-1,5	0	Triticum aestivum alpha 1,4-glucan phosphorylase mRNA,	6.0e-82	(AF326977) alpha 1,4-glucan phosphorylase H isozyme [Ory
TTU025BE490613-2	9.0e-05	Homo sapiens PAC clone RP3-430N8 from 22q12.1-qter, co	2.0e-09	(AC022354) unknown protein [Arabidopsis thaliana]
TTU025BE490651-1	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
TTU025BE490658-1	e-104	Eleusine indica alpha-tubulin 2 (TUA2) mRNA, complete cds	1.0e-65	TUBULIN ALPHA-2 CHAIN (ALPHA-2 TUBULIN)
TTU047BE445539-1	6.0e-06	Arabidopsis thaliana chromosome 1 BAC F22G10 genomic	8.0e-69	(U74610) glyoxalase II [Arabidopsis thaliana]
UCD001BE405214-3	3.0e-11	Arabidopsis thaliana respiratory burst oxidase protein D (	4.0e-56	(AB015475) respiratory burst oxidase protein [Arabidopsis
UCD001BE444252-3	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
UCD037BE489274-1,3	0.023	Homo sapiens, clone hRPK.2_A_1, complete sequence	6.0e-59	fructokinase-like protein - Arabidopsis thaliana
UCD037BE499348-3	3.0e-17	Oryza meyeriana serine\threonine protein kinase (R1) ge	1.0e-37	(AP000410) receptor protein kinase-like protein [Arabidop
UCD037BE500112-5	0	T.aestivum (Chinese spring) chi gene for endochitinase	3.0e-52	chitinase (EC 3.2.1.14) - wheat
UMC001BE406380-2	0.23	Homo sapiens 12 BAC RP11-173C20 (Roswell Park Cancer I	2.9	nidogen 2\; nidogen 2 (osteonidogen) [Homo sapiens]
UMC001BE443995-2	1.6	Homo sapiens 12 BAC RP11-547C5 (Roswell Park Cancer In	4.0e-71	(AC079281) unknown protein [Arabidopsis thaliana]
UMC015BE406587-1	4.0e-06	Arabidopsis thaliana chromosome V map near 60.5 cM, co	5.0e-46	(AF049930) PGPD14 [Petunia x hybrida]
UMC015BE444252-3	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
UMC040BE606881-1	1.0e-46	Zea mays nuclear-encoded mitochondrial F1F0 ATP syntha	2.0e-28	ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL mitochon
UMC040BF474333-3	0.072	Chlamydomonas reinhardtii flagellar autotomy protein Fa1	5.0e-13	(AF240462) plastid-specific ribosomal protein 2 precursor
UMC055BF483799-4	3.0e-74	Oryza sativa genomic DNA, chromosome 1, PAC clone:P06	1.0e-29	(AP002972) contains EST D15166(C0193)~unknown protein [
UMN013BE443288-3	1.0e-07	Arabidopsis thaliana ADL2 mRNA, complete cds	4.0e-85	(AF012833) similar to dynamin-like protein encoded by Ger
UNL002BE607045-2	e-130	O.sativa mRNA for dihydroflavonol reductase	6.0e-88	DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFE
UNL036BF200697-1	0.31	Caenorhabditis elegans cosmid F49E12, complete sequen	8.0e-13	(AC005311) hypothetical protein [Arabidopsis thaliana]

3AL5-0.78-1.00

CNL001BE406551-3	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
CNL014BE444864-3,4	4.0e-07	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	7.0e-73	(AB023042) phosphatidylserine decarboxylase [Arabidopsi
KSU001BE444473-6	0.016	Drosophila melanogaster genomic scaffold 1420000133860	2.0e-23	(AC084763) hypothetical protein [Oryza sativa]
KSU002BE405234-6	2.0e-67	Oryza sativa COX6b2 mRNA for cytochrome c oxidase subu	2.0e-35	(AB047923) cytochrome c oxidase subunit 6b [Oryza sativa
KSU012BE442818-1,6	4.0e-10	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	4.0e-71	(AP000604) contains similarity to unknown protein~gb|AAF
KSU012BE442875-2	6.0e-12	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	7.0e-66	(AB019227) gb|AAF01562.1~gene_id:MBM17.7~strong simila
KSU012BE443397-2,6	3.0e-05	Mesembryanthemum crystallinum cinnamyl-alcohol dehy	2.0e-77	(AC010926) putative cinnamyl-alcohol dehydrogenase\; 496
KSU019BE442624-2,7	1.3	Caenorhabditis elegans cosmid F54D7, complete sequenc	5.0e-40	(AB036735) allyl alcohol dehydrogenase [Nicotiana tabacum
KSU019BE494330-3	3.0e-75	O.sativa mRNA for SMT3 protein	1.0e-34	UBIQUITIN-LIKE PROTEIN SMT3
KSU019BE494450-6	7.0e-40	Avena maroccana clone Ma7 ribulose-1,5-bisphosphate ca	3.0e-15	(AB042068) ribulose-1,5-bisphosphate carboxylase\oxyger
KSU019BE606698-8	e-179	Oryza sativa GTP-binding protein mRNA, complete cds	3.0e-72	(AF327517) GTP-binding protein [Oryza sativa]
KSU024BE499049-6	0	Zea mays strain W64A x A182E putative cytosolic 6-phosph	e-116	phosphogluconate dehydrogenase (decarboxylating) (EC 1
KSU024BE499186-8	e-136	Oryza sativa mRNA for asparaginyl endopeptidase, comple	4.0e-70	(AJ251454) putative legumain [Zea mays]
KSU027BF482769-3	0	Lolium perenne caffeic acid O-methyltransferase (OMT3)	2.0e-87	(AF033538) caffeic acid O-methyltransferase\; LPOMT1 [Lol
KSU030BE495145-3	0.001	Arabidopsis thaliana mRNA for putative beta-galactosidase	4.0e-55	(AC010704) putative beta-galactosidase, 3' partial\; 3669-1 [
KSU030BE497740-2,3	1.0e-16	Arabidopsis thaliana mRNA for Dr1	1.0e-47	DR1-like protein - Arabidopsis thaliana
KSU030BE499696-2,3	5.0e-65	Glycine max beta-ketoacyl-ACP synthetase I-2 mRNA, com	3.0e-76	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURS
KSU030BF485004-1	1.0e-18	Lycopersicon esculentum transaldolase (TAL) mRNA, com	4.0e-34	transaldolase-like protein - Arabidopsis thaliana
KSU035BE403428-5	1.4	Oryctolagus cuniculus heat shock protein 47 mRNA, partia	1.0e-35	(AC069300) putative dioxygenase [Oryza sativa]
KSU035BE404540-5	3.0e-29	S.tuberosum (Desiree) cyc1 II mRNA. for cytochrome c1	2.0e-49	(AP000381) ubiquinol-cytochrome c1 reductase cytochrom
KSU038BE444681-6	2.0e-61	Oryza sativa GTP-binding protein mRNA, complete cds	1.0e-56	RAS-RELATED PROTEIN RAB2BV
KSU038BE445556-4,6	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
NDS018BE405221-2	5.0e-65	Oryza sativa chromosome 1 clone OSJNBa0048I01, complet	1.0e-69	(AF000657) unknown protein [Arabidopsis thaliana]
NDS043BF292596-3	1.3	Mesorhizobium loti, complete genome	7.0e-12	comes from this gene. [Arabidopsis thaliana]
UCD001BE406551-1,5	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
UCD001BE443798-2	0.39	Escherichia coli O157:H7 EDL933 genome, contig 2 of 3, section 31 of 55		
UCD028BE490596-4	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
UCD028BF484536-2,10	1.1	Methylococcus capsulatus putative nonaheme c-cytochro	0.43	(AF277399) cat eye syndrome critical region 6 [Mus muscu
UCD037BE497664-2	e-130	Oryza sativa ALDH1a mRNA for cytosolic aldehyde dehydro	1.0e-94	(AB037421) cytosolic aldehyde dehydrogenase [Oryza sativ
UCD037BE499131-13	6.0e-73	O.sativa RAc2 gene for actin	2.0e-55	ACTIN 1
UCW001BE398631-3	3.3	Oryza sativa chromsome 9 clone PAC0663H05, complete s	1.9	BETA-2 ADRENERGIC RECEPTOR
UCW001BE443798-2	0.39	Escherichia coli O157:H7 EDL933 genome, contig 2 of 3, section 31 of 55		
UCW016BE637789-1	2.0e-70	O.sativa mRNA for cytochrome b5	1.0e-65	CYTOCHROME B5
UCW020BE494854-2	2.0e-15	Oryza sativa subsp. indica putative dnaJ-like protein, putat	1.0e-49	(AF111710) hypothetical protein [Oryza sativa subsp. indica
UCW020BF478499-1	4.0e-41	Oryza sativa thioredoxin F isoform mRNA, complete cds	3.0e-30	THIOREDOXIN F-TYPE 2, CHLOROPLAST PRECURSOR (TRX-F2
UCW026BG263365-3	3.0e-50	Saccharum officinarum mRNA for Sucrose-Phosphate Sym	1.0e-61	sucrose-phosphate synthase (EC 2.4.1.14) 1 - rice
UMC015BE426274-4	3.0e-75	Hordeum vulgare mRNA for hypothetical protein, partial, cl	1.0e-50	(AB007627) homeobox gene [Oryza sativa]
UMC040BE590763-6,7	e-126	Hordeum vulgare peroxidase BP 1 (Prx5) mRNA, complete	6.0e-45	peroxidase (EC 1.11.1.7) BP1 precursor - barley
UMN013BE442818-1	4.0e-10	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	4.0e-71	(AP000604) contains similarity to unknown protein~gb|AAF
UMN013BE442875-3	6.0e-12	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	7.0e-66	(AB019227) gb|AAF01562.1~gene_id:MBM17.7~strong simila
UNL002BE499910-2	1.4	Homo sapiens, clone MGC:13105, mRNA, complete cds	1.0e-13	(AF209484) disease resistance-like protein [Brassica napu
UNL002BE517312-2,3	8.0e-08	Arabidopsis thaliana YLS7 mRNA for leaf-senescence-rela	8.0e-49	(AB018109) gene_id:K17N15.19~pir||T10216~strong similarity
UNL002BE591154-3	0.002	Oryza sativa mRNA for RPR1h, complete cds	3.0e-54	(AB019240) RPR1h [Oryza sativa]
UNL036BE518446-3	5.0e-16	Capsicum annuum GTP-binding protein mRNA, complete c	1.0e-88	(AF108896) GTP-binding protein [Capsicum annuum]
UNL036BE590549-1	7.0e-12	A.sativa avenin mRNA, complete cds	2.0e-24	gliadin - wheat
UNL048BE445579-4	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**

http://wheat.pw.usda.gov/wEST