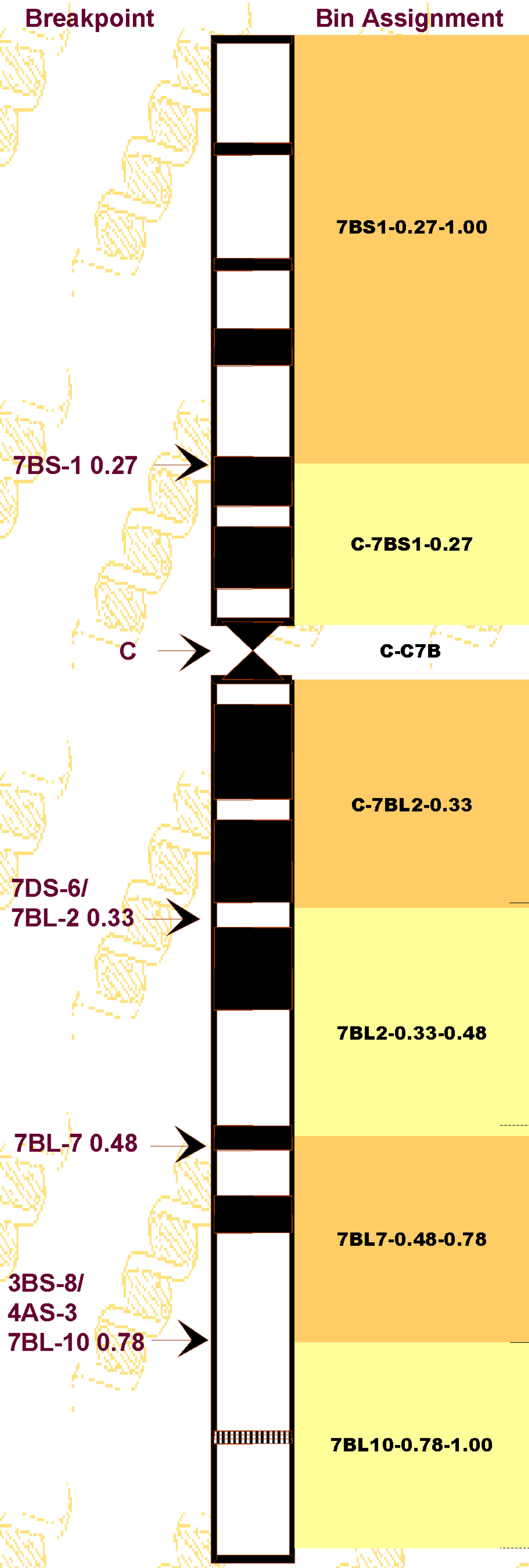
The Structure and Function of the Expressed Portion of the Wheat Genomes

Deletion Map of *Triticum aestivum* cv. Chinese Spring (Chromosome 7B)*

*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 : 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

7BS1-0.27-1.00

CNL014BE424554-6	5.0e-65	Oryza sativa OsENOD93b mRNA for early nodulin, complete	3.0e-33	(AB018377) early nodulin [Oryza sativa]
CNL014BE446622-3	5.0e-25	Oryza sativa mRNA for zinc finger protein, complete cds, c	5.0e-70	zinc-finger protein R2931 [imported] - rice
CNL014BE490643-2	1.0e-49	Hordeum vulgare mRNA for vacuolar membrane proton-tr	8.0e-12	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTC
CSU102BE403192-3	1.2	Homo sapiens chromosome 3 clone RP11-245A6 map 3p, c	2.0e-47	(AC008263) F25A4.24 [Arabidopsis thaliana]
CSU102BE406499-4	6.0e-04	Saccharomyces cerevisiae chromosome XV, complete chromosome sequence		
KSU001BE399989-1,6	0.2	Homo sapiens genomic DNA, chromosome 4q22-q24, clon	3.9	(U67190) origin recognition complex protein 1 [Xenopus lae
KSU001BE442924-3	0.007	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K6M13		
KSU012BE404724-2,5	1.0e-10	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	1.0e-34	(AB013395) poly(A)-binding protein II-like [Arabidopsis thal
KSU012BE490643-2	1.0e-49	Hordeum vulgare mRNA for vacuolar membrane proton-tr	8.0e-12	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTC
KSU019BE443559-6	7.0e-06	Arabidopsis thaliana unknown protein (F6F3.4) mRNA, com	2.0e-19	(AC023628) Unknown protein [Arabidopsis thaliana]
KSU024BE405060-4	3.0e-85	Oryza sativa protein kinase mRNA, complete cds	1.0e-58	protein kinase homolog - rice
KSU024BE405399-5	1.3	Human chromosome 14 DNA sequence BAC C-2014B16 of I	0.62	(AE003590) spen gene product [alt 1] [Drosophila melanoga
KSU024BE498038-7	0	Triticum aestivum p34cdc2 (cdc2TaA) mRNA, complete cds	e-125	(U23409) p34cdc2 [Triticum aestivum]
KSU024BE499652-6	6.0e-80	Citrus X paradisi pyrophosphate-dependent phosphofruct	6.0e-85	(AF095520) pyrophosphate-dependent phosphofructokina
KSU027BE352570-2	e-101	Oryza sativa mRNA for aldehyde dehydrogenase ALDH2b,	1.0e-60	(AB044537) aldehyde dehydrogenase ALDH2b [Oryza sativa
KSU027BE590752-3	6.0e-06	Oryza sativa osr8 mRNA for hydrophobic polypeptide, com	9.0e-07	(AC005170) unknown protein [Arabidopsis thaliana]
KSU030BE590566-2,3	1.0e-09	Thuja plicata clone 1 pinoresinol-lariciresinol reductase m	8.0e-62	ISOFLAVONE REDUCTASE HOMOLOG lupine
KSU030BE606874-1	0	Triticum aestivum granule-bound starch synthase I (Wx-DI	1.0e-58	(AB019624) starch synthase (GBSSI) [Triticum aestivum] ta
KSU038BE443542-4,5	0.028	Homo sapiens, chromosome 11 open reading frame2, clo	9.0e-09	thioredoxin (clone GIF2) - Arabidopsis thaliana
KSU038BE443596-3	0	Hordeum vulgare (cv. Bomi) B12D mRNA	9.0e-45	B12D protein - barley
KSU038BE489090-3,5	0.02	Sequence of BAC F16N3 from Arabidopsis thaliana chromo	6.0e-07	(AP002543) selenium-binding protein-like [Arabidopsis tha
KSU038BE489882-7	0.24	Human DNA sequence from PAC 57A13 between markers	2.0e-16	(AB013389) contains similarity to ATP binding protein asso
NDS001BE444294-2	0.36	Caenorhabditis elegans cosmid C08G9	5.0e-45	(AB024035) gb|AAD55473.1~gene_id:MHM17.18~similar to ui
NDS021BE493897-2	1.0e-44	Oryza sativa putative dihydroflavonol reductase mRNA, co	6.0e-62	(AF134807) putative dihydroflavonol reductase [Oryza sativ
NDS021BE494078-1	1.2	Oryza sativa chromosome 10 BAC OSJNBa0001O14 genomi	2.1	claudin 18 [Homo sapiens]
NDS034BE405850-4	0.055	Heliocoverpa armigera nucleopolyhedrovirus G4, complet	2.0e-24	glucuronosyl transferase homolog, ripening-related - tom
NDS034BE590566-2,3	1.0e-09	Thuja plicata clone 1 pinoresinol-lariciresinol reductase m	8.0e-62	ISOFLAVONE REDUCTASE HOMOLOG lupine
NDS043BF291338-1	3.0e-04	Arabidopsis thaliana chromosome II section 235 of 255 of	7.0e-28	BIOTIN SYNTHASE (BIOTIN SYNTHETASE)
NDS043BG274662-2	e-100	Rice mRNA for major intrinsic protein, complete cds	3.0e-45	major intrinsic protein - rice
TTU025BE490643-2	1.0e-49	Hordeum vulgare mRNA for vacuolar membrane proton-tr	8.0e-12	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTC
TTU047BE445220-1	0.38	Arabidopsis thaliana chromosome II section 126 of 255 of	5.0e-89	(AC007168) unknown protein [Arabidopsis thaliana]
TTU047BE495005-1	e-160	Oryza sativa chromosome 10 BAC OSJNBa0076F20 genomi	1.0e-80	(AC025296) putative gamma-lyase [Oryza sativa]
UCD001BE405200-6	1.5	Homo sapiens chromosome 5 clone CTB-70H11, complete	8.1	testis expressed sequence 14 [Homo sapiens]
UCD029BF484868-1	2.0e-52	A.majus mRNA for DAG protein	5.0e-72	DAG PROTEIN, CHLOROPLAST PRECURSOR
UCD037BE443282-3	0.016	Genomic sequence for Arabidopsis thaliana BAC F28K19 fr	3.0e-36	(AC073942) Contains similarity to a phosphoglyceromutase
UCD037BE498662-2,4	6.0e-09	Populus x canescens POPARB mRNA, partial cds	2.0e-46	(AC002329) unknown protein [Arabidopsis thaliana]
UCD037BE499248-1	e-129	Zea mays mRNA for Caffeoyl CoA O-methyltransferase (cc	2.0e-61	(AB023482) ESTs AU058067(E20733), AAU058070(E20873) cor
UCW016BE496839-1,4	3.0e-87	Triticum aestivum WESR2 mRNA, partial sequence	4.0e-36	hypothetical protein F8F16.160 - Arabidopsis thaliana
UCW020BF200891-2,4	8.0e-75	Z.mays mRNA for annexin p33	3.0e-41	(X98244) annexin p33 [Zea mays]
UCW026BE497999-2	0	Hordeum sp. x Triticum sp. glycine decarboxylase P subu	e-118	glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) [impo
UCW039BE494425-1	0.35	Homo sapiens 12 BAC RP11-685B13 (Roswell Park Cancer I	6.0e-06	(AE003587) CG4896 gene product [alt 1] [Drosophila melanc
UMC015BE590976-3	0	Hordeum vulgare mRNA for formate dehydrogenase, com	3.0e-98	(D88272) formate dehydrogenase [Hordeum vulgare]
UMC040BF474284-12	0	T.aestivum VDAC2 mRNA for voltage dependent anion cha	3.0e-61	porin VDAC2 - wheat (fragment)
UMN013BE443746-4	5.0e-18	Oryza sativa genomic DNA, chromosome 6, clone P0680A0	1.0e-19	(AB023482) ESTs C22458(C62866),C22459(C62866) correspo
UNL002BE492286-3	0.078	Drosophila melanogaster genomic scaffold 1420000133860	8	(X00269) open reading frame [Zea mays]
UNL002BE591190-5	1.2	Homo sapiens clone RP11-736E3, complete sequence	1.0e-25	(AJ302292) MLA6 protein [Hordeum vulgare]
UNL053BF292870-1	2.0e-09	Oryza sativa osRAD23 mRNA, complete cds	4.0e-47	(AB005248) DNA repair protein RAD23 homolog [Arabidopsi
UNL053BF474584-7	0.11	Rattus norvegicus acyl-CoA thioesterase 1, cytosolic (Cte	2.0e-74	(AF302671) ubiquitin-specific protease 23 [Arabidopsis tha

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CNL001BE405234-14	2.0e-67	Oryza sativa COX6b2 mRNA for cytochrome c oxidase subu	2.0e-35	(AB047923) cytochrome c oxidase subunit 6b [Oryza sativa]
CNL023BE405613-3	0	T.aestivum beta glucanase mRNA, complete CDS	e-106	(Z22873) beta glucanase [Triticum aestivum]
CNL031BE500122-5	4.0e-04	Arabidopsis thaliana peroxisome biogenesis protein PEX1	3.0e-57	(AF275382) peroxisome biogenesis protein PEX1 [Arabidop
CNL031BE500502-8	0	Barley acyl carrier protein III (ACP III) mRNA, complete cds	5.0e-66	ACYL CARRIER PROTEIN III PRECURSOR (ACP III)
CSU059BE606458-2	1.0e-46	Hordeum vulgare genomic DNA fragment\; clone MWG0626	1.0e-57	(AB025969) NAD-dependent sorbitol dehydrogenase [Prunu
KSU001BE442648-11	2.0e-18	Oryza sativa genomic DNA, chromosome 1, PAC clone:P06	7.0e-45	(AP003047) hypothetical protein [Oryza sativa]
KSU001BE443755-8,16	0.007	Dictyostelium discoideum nucleoside diphosphate kinase	6	(AF202730) Niemann-Pick type C1 disease protein [Oryctola
KSU012BE443396-1,2,6	0	Zea mays glucose-6-phosphate\/phosphate-translocator p	e-100	glucose-6-phosphate\/phosphate-translocator precursor,
KSU019BE426692-2	8.0e-21	Oryza sativa manganese superoxide dismutase (rmsod1)	2.0e-80	(AF039000) putative serine-glyoxylate aminotransferase [F
KSU024BE499303-2	2.0e-11	Arabidopsis thaliana putative methionine aminopeptidase	6.0e-13	(AF300880) putative methionine aminopeptidase 2 [Arabido
KSU030BE404899-1	2.0e-36	Arabidopsis thaliana AT5g11200\/F2I11_90 mRNA, complete	1.0e-85	(AF378868) AT5g11200\/F2I11_90 [Arabidopsis thaliana]
KSU035BE404540-3	3.0e-29	S.tuberosum (Desiree) cyc1 II mRNA. for cytochrome c1	2.0e-49	(AP000381) ubiquinol-cytochrome c1 reductase cytochrom
KSU035BE404728-3,4,5	0.25	Human cosmid Xq28_IA649, complete sequence [Homo sa	4.0e-33	(Y15367) MtN19 [Medicago truncatula]
KSU035BE406976-3,5	2.0e-55	Oryza sativa mRNA for spermidine synthase 1 (spdSyn1 ge	1.0e-76	SPERMIDINE SYNTHASE 1 (PUTRESCINE AMINOPROPYLTRANS
KSU038BE442797-5	4.0e-04	Arabidopsis thaliana chromosome 1 BAC F24D7 genomic s	5.0e-50	(AC009999) Contains similarity to Ariadne-2 protein from D
NDS034BE471126-1	1.0e-06	Zea mays pyruvate dehydrogenase E1 beta subunit isofor	0.018	(AF069910) pyruvate dehydrogenase E1 beta subunit isofor
NDS043BF293124-2	4.0e-04	Volvox carteri f. nagariensis clone G32 unknown mRNA	7.0e-35	(AC006220) unknown protein [Arabidopsis thaliana]
NDS043BG605575-3	0	T.aestivum L mRNA for histone H2B	4.0e-43	HISTONE H2B
UCD001BE442939-2	1.1	Homo sapiens clone H41 unknown mRNA	5.1	anti-mullerian hormone homolog precursor - chicken
UCD029BE497604-2,4	4.0e-13	Pisum sativum poly(A) polymerase mRNA, nuclear gene e	6.0e-58	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST F
UCD029BF483478-2	2.0e-24	Arabidopsis thaliana putative methionine aminopeptidase	1.0e-62	(AF300880) putative methionine aminopeptidase 2 [Arabido
UCD037BE489419-3	0.33	Homo sapiens BAC clone RP11-221H10 from 8, complete se	2.0e-27	GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYR
UMC040BE590847-7	0	Triticum aestivum (wali7) mRNA, 3' end, partial cds	6.0e-59	hypothetical protein wali7 - wheat (fragment)
UMC040BE637511-8	2.0e-15	Z.mays ABP1 mRNA for actin-depolymerizing factor	6.0e-46	actin-depolymerizing factor 3 - maize
UMN013BE444179-2,3	e-136	Oryza sativa GDP dissociation inhibitor protein OsGDI2 (Os	6.0e-64	GDP dissociation inhibitor protein - rice
UNL036BE590582-4,5	0	Triticum aestivum small subunit ADP glucose pyrophosph	e-120	(AF244997) small subunit ADP glucose pyrophosphorylase
UNL044BF485408-2	0.022	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA conti	9.0e-42	hypothetical protein - Arabidopsis thaliana

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CNL031BF200525-4	8.0e-33	Zantedeschia aethiopica ascorbate peroxidase (cmApx) m	5.0e-71	L-ascorbate peroxidase (EC 1.11.1.11), glyoxysomal - uplan
KSU001BE443755-13	0.007	Dictyostelium discoideum nucleoside diphosphate kinase	6	(AF202730) Niemann-Pick type C1 disease protein [Oryctola
KSU012BE403622-3	2.0e-09	Sequence of BAC F7H2 from Arabidopsis thaliana chromos	7.0e-95	(AC018849) unknown protein\; 52184-57536 [Arabidopsis th
KSU024BE498418-3	3.0e-11	Arabidopsis thaliana chromosome II section 192 of 255 of	2.0e-58	(AC007060) Strong similarity to F19I3.8 gi UDP-galactose-4-e
KSU024BE498849-1	1.0e-34	Arabidopsis thaliana RNA recognition motif-type RNA-bindi	7.0e-60	(AC017118) F6N18.17 [Arabidopsis thaliana]
KSU030BE500513-5	e-100	Hordeum vulgare ECA1 protein mRNA, complete cds	7.0e-41	(AF109193) ECA1 protein [Hordeum vulgare]
KSU030BF483454-1	0.42	Genomic Sequence for Oryza sativa, Nipponbare strain, clo	4.0e-13	(AF030386) NOI protein [Arabidopsis thaliana]
KSU030BG313350-2	3.0e-17	A.thaliana mRNA for CaLB protein	9.0e-91	CaLB protein - Arabidopsis thaliana
NDS018BE404240-2	7.0e-34	T.aestivumn (subclone pAWJL175) AWJL175 gene	1.0e-04	(AF133839) papain-like cysteine protease [Sandersonia aur
NDS021BF201644-2	0.9	Oryza sativa chromosome 4 BAC q3037-207F1 complete ge	1.7	BALBIANI RING PROTEIN 3 PRECURSOR
NDS034BE403826-1	e-170	L.temulentum mRNA for histone H3	2.0e-71	HISTONE H3.2, MINOR predicted gene.\; Similar to histone H3
UCD001BE406324-9	3.0e-15	Zea mays seven transmembrane protein Mlo7 mRNA, com	1.0e-06	MLO PROTEIN HOMOLOG 1 (ATMLO-H1)
UCD001BE443755-16	0.007	Dictyostelium discoideum nucleoside diphosphate kinase	6	(AF202730) Niemann-Pick type C1 disease protein [Oryctola
UCW016BE497215-1	e-119	Zea mays thiamine biosynthetic enzyme (thi1-1) mRNA, co	6.0e-60	THIAZOLE BIOSYNTHETIC ENZYME 1-2, CHLOROPLAST PRECI
UNL036BE517871-1	4.0e-04	N.tabacum mRNA for tyrosyl-tRNA synthetase	1.0e-53	probable tyrosine--tRNA ligase (EC 6.1.1.1) - common tobac

7BL2-0.33-0.48

KSU001BE399288-2,5	0.078	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIG10		
KSU001BE442845-1	1.1	Drosophila melanogaster, chromosome 2R, region 45E1-4	1.0e-51	pitrilysin (EC 3.4.24.55) - garden pea
KSU001BE444301-3	1.5	Arabidopsis thaliana chromosome I BAC F25I16 genomic s	0.24	(AE003581) Chd1 gene product [Drosophila melanogaster]
KSU012BE404507-4,5	0	A.sativa (Pewi) ASTCP-K36 mRNA for t complex polypeptid	1.0e-79	T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON) (
KSU012BE442619-3	5.0e-09	Arabidopsis thaliana chromosome 1 BAC T6J19 genomic s	8.0e-28	copper homeostasis factor [imported] - Arabidopsis thalia
KSU012BE443436-3	e-151	Oryza sativa genomic DNA, chromosome 2, clone:P0437H0	3.0e-95	(AP000366) Similar to maize transposon MuDR mudrA-like
KSU019BE445239-2	e-125	Oryza sativa mRNA for 26S proteasome ATPase subunit Rp	1.0e-67	(AB033537) 26S proteasome regulatory particle triple-A AT
KSU019BE498785-10,11	1.0e-06	Mycobacterium smegmatis adhC gene for alcohol dehydr	3.0e-32	PROBABLE MANNITOL DEHYDROGENASE (NAD-DEPENDENT M.
KSU019BE606698-5	e-179	Oryza sativa GTP-binding protein mRNA, complete cds	3.0e-72	(AF327517) GTP-binding protein [Oryza sativa]
KSU027BE490007-1	e-150	Oryza sativa mRNA for glyoxalase I, complete cds	6.0e-90	(AB017042) glyoxalase I [Oryza sativa]
KSU027BF482769-4	0	Lolium perenne caffeic acid O-methyltransferase (OMT3) r	2.0e-87	(AF033538) caffeic acid O-methyltransferase\; LPOMT1 [Lol
KSU035BE403740-1	8.0e-09	Arabidopsis thaliana AT4g13360\/T9E8_100 mRNA, complete	2.0e-75	3-hydroxyisobutyryl-coenzyme A hydrolase homolog T9E8
KSU035BE406937-1	1.2	S.pombe chromosome II cosmid c3B8	3.0e-22	(AF096247) ethylene-responsive elongation factor EF-Ts pr
KSU035BE406943-8	5.0e-45	Oryza sativa mRNA for elongation factor 1B gamma, compl	8.0e-35	ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA) (EEF-1B GAI
KSU038BE446029-3,4	5.0e-06	Oryza sativa copper chaperone homolog CCH mRNA, comp	8.0e-28	copper homeostasis factor [imported] - Arabidopsis thalia
UCD017BE488670-3	1.0e-53	Oryza sativa partial mRNA for putative aminopropyltransfe	6.0e-51	(AJ251302) putative aminopropyltransferase [Oryza sativa]
UCD029BF485273-5	8.0e-14	Arabidopsis thaliana IAA9 (F6H11.210) mRNA, complete cds	1.0e-34	phytochrome-associated protein PAP2 - Arabidopsis thalia
UCD037BE443010-1	3.0e-82	Oryza sativa mRNA for adenylate kinase-a, complete cds	1.0e-53	ADENYLATE KINASE A (ATP-AMP TRANSPHOSPHORYLASE)
UCD037BE638123-2,4	e-142	Oryza sativa mRNA for succinate dehydrogenase iron-prot	6.0e-74	(AJ012374) iron sulfur subunit of succinate dehydrogenase
UCW039BE446052-1	0.78	Rattus norvegicus antioxidant enzyme B166 mRNA, comple	6.0e-08	(AJ291817) expansin [Cicer arietinum]
UMN013BE442619-3,4	5.0e-09	Arabidopsis thaliana chromosome 1 BAC T6J19 genomic s	8.0e-28	copper homeostasis factor [imported] - Arabidopsis thalia
UNL001BE442845-1	1.1	Drosophila melanogaster, chromosome 2R, region 45E1-4	1.0e-51	pitrilysin (EC 3.4.24.55) - garden pea
UNL002BE518338-1	3.0e-07	E.gunnii mRNA for cinnamyl alcohol dehydrogenase	2.0e-46	(AC002332) putative cinnamoyl-CoA reductase [Arabidopsi
UNL036BE497375-4,5	1.0e-07	Lycopersicon esculentum auxin-regulated IAA6 (IAA6) mR	1.0e-10	auxin-induced protein IAA9 - Arabidopsis thaliana
UNL036BE517670-2	2.0e-70	Oryza sativa chromosome 10 BAC OSJNBa0027P10 genomi	8.0e-28	(AC084763) putative ribosomal protein L27 [Oryza sativa]

7BL2-0.33-0.78

UMN013BE443312-2	2.0e-08	Sequence of BAC T2D23 from Arabidopsis thaliana chromo	1.0e-62	(AF253474) acyl-CoA oxidase [Arabidopsis thaliana]

7BL7-0.48-0.78

CSU057BE490023-1,2	1.0e-19	Arabidopsis thaliana genomic DNA, chromosome 3, BAC cl	1.0e-98	(AP001298) contains similarity to the auxin-independent gr
KSU001BE403860-8	3.0e-10	Oryza sativa microsatellite MRG5838 containing (TCT)X14,	7.0e-30	(AF198054) NAC1 [Arabidopsis thaliana]
KSU002BE425207-4	8.0e-08	Nicotiana tabacum (clone: L24-2) chloroplast ribosomal pr	3.0e-36	(AB016879) 50S ribosomal protein L24, chloroplast precurs
NDS001BE443753-5	1.3	Tauraco erythrolophus cytochrome b gene, partial cds\; mitochondrial gene for mitochondrial product		
NDS018BE426274-9	3.0e-75	Hordeum vulgare mRNA for hypothetical protein, partial, cl	1.0e-50	(AB007627) homeobox gene [Oryza sativa]
NDS018BE426802-5,6	7.0e-06	O.sativa mRNA for cyclin 2	2.0e-39	cyclin III - maize
NDS021BE406148-3	8.0e-14	Arabidopsis thaliana cyclophilin (ROC7) mRNA, complete c	4.0e-44	cyclophilin CYP5 [imported] - Arabidopsis thaliana
NDS021BE496817-1,2	0.31	Mustela vison tyrosine aminotransferase gene, complete cds		
NDS034BE497604-2	4.0e-13	Pisum sativum poly(A) polymerase mRNA, nuclear gene e	6.0e-58	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST F
UMC015BE606573-10	6.0e-22	Aerides japonica 3-hydroxy-3-methylglutaryl-CoA-synthas	9.0e-92	(AF148847) HMG-CoA synthase [Brassica juncea]
UNL002BE426789-5	0.007	Cricetulus griseus mRNA for RNA polymerase II largest su	4.0e-41	(AF158634) Vrga1 [Aegilops ventricosa]
UNL002BE426790-5	0.39	Bos taurus blue cone pigment protein mRNA, complete cd	1.0e-09	(AF114171) disease resistance protein RPM1 homolog [So
UNL044BG274514-9	e-147	Rice mRNA for ubiquitin protein fused to a ribosomal prot	2.0e-60	ubiquitin \/ ribosomal protein CEP52 - rice
UNL048BE591273-2	0.087	Homo sapiens chromosome 3 clone RP11-127I14 map 3p, c	2.0e-24	hypothetical protein T10K17.100 - Arabidopsis thaliana
UNL048BF428786-2	0.019	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, c	2.0e-46	(AC007060) T5I8.13 [Arabidopsis thaliana]

7BL7-0.48-1.00

CSU001BE425207-1	8.0e-08	Nicotiana tabacum (clone: L24-2) chloroplast ribosomal pr	3.0e-36	(AB016879) 50S ribosomal protein L24, chloroplast precurs

7BL10-0.78-1.00

CSU059BG604419-2	7.0e-14	Arabidopsis thaliana ISA1 gene	3.0e-52	(Y14404) putative arabinose kinase [Arabidopsis thaliana]
KSU001BE442572-1,4	5.0e-19	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	8.0e-87	(AB024036) contains similarity to EH domain containing pro
KSU001BE443753-5	1.3	Tauraco erythrolophus cytochrome b gene, partial cds\; mitochondrial gene for mitochondrial product		
KSU012BE403180-5	e-163	Oryza sativa OsPBC1 mRNA for beta 3 subunit of 20S prote	2.0e-87	(AB026565) beta 3 subunit of 20S proteasome [Oryza sativa
KSU012BE443423-9	1.0e-19	Oryza sativa chromosome 3 BAC OSJNBa0091J19 genomic	4.2	(AL117195) Y57A10A.1 [Caenorhabditis elegans]
KSU012BE490643-4	1.0e-49	Hordeum vulgare mRNA for vacuolar membrane proton-tr	8.0e-12	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTC
KSU019BE404737-1	6.0e-06	Arabidopsis thaliana chromosome III BAC F13E7 genomic s	2.0e-77	(AB005242) S-adenosylmethionine:2-demethylmenaquinon
KSU024BF484707-2	0.37	Homo sapiens chromosome 3, olfactory receptor pseudo	6.0e-08	(AB023042) gene_id:MUL3.13~pir||T04254~similar to unknov
KSU024BG274853-2	9.0e-57	Arabidopsis thaliana zinc dependent protease (VAR2) mRI	6.0e-57	(AJ012165) chloroplast protease [Capsicum annuum]
KSU027BE517627-4	2.0e-95	Oryza sativa mRNA for translation initiation factor eIF-5A	4.0e-78	(AF094773) translation initiation factor 5A [Oryza sativa]
KSU030BE518357-1	3.0e-60	Oryza sativa subsp. japonica clone S4892 putative glutathic	5.0e-55	(AF309381) putative glutathione S-transferase OsGSTZ1 [Oi
KSU038BE445506-1	1.0e-07	Oryza sativa genomic DNA, chromosome 6, clone:P0535G0	1.0e-46	(AC007127) putative protein kinase [Arabidopsis thaliana]
KSU038BE446244-2,3	0.091	Human DNA sequence from clone RP13-153N15 on chromo	2.0e-33	(AC037197) Putative hypersensitivity-related protein [Oryza
UCD001BE406505-1	0.95	Mus musculus Strain C57BL6\/J Chromosome 8 RP23-21B7	1.0e-16	(AB005245) contains similarity to ubiquitin conjugating enz
UCD001BE442572-1,3	5.0e-19	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	8.0e-87	(AB024036) contains similarity to EH domain containing pro
UCD001BE443753-5	1.3	Tauraco erythrolophus cytochrome b gene, partial cds\; mitochondrial gene for mitochondrial product		
UCD017BE488496-2	0	Hordeum vulgare Mg-chelatase subunit (Xantha-h) mRNA,	1.0e-47	protoporphyrin IX magnesium chelatase (EC 4.99.1.-) Xanth
UCD028BF291608-4	2.0e-64	Lupinus luteus ribosomal protein S14 (rps14) mRNA, com	1.0e-66	40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
UCD029BE497373-1,2,3	6.0e-12	Sorghum bicolor chalcone synthase 1 (CHS1) gene, compl	3.0e-17	CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE
UCD029BE591469-4,7	0	Hordeum vulgare catalase 1 (CAT1) gene, partial cds	e-129	(AF021938) catalase 1 [Hordeum vulgare]
UCD037BE488895-2,4,5,8,9	0.38	Carex divisa internal transcribed spacer 1, partial sequen	8.0e-10	(U63012) lectin precursor [Sophora japonica]
UCD037BE489651-1,3	2.0e-16	Hordeum vulgare mRNA for putative thiol protease, clone I	0.027	probable cysteine proteinase (EC 3.4.22.-) - barley (fragme
UMC015BE426274-8	3.0e-75	Hordeum vulgare mRNA for hypothetical protein, partial, cl	1.0e-50	(AB007627) homeobox gene [Oryza sativa]
UMC015BE426802-5	7.0e-06	O.sativa mRNA for cyclin 2	2.0e-39	cyclin III - maize
UMC015BE606573-5	6.0e-22	Aerides japonica 3-hydroxy-3-methylglutaryl-CoA-synthas	9.0e-92	(AF148847) HMG-CoA synthase [Brassica juncea]
UMN013BE443038-8	2.0e-94	Hordeum vulgare thaumatin-like protein TLP8 mRNA, com	1.0e-18	(AF355458) thaumatin-like protein TLP8 [Hordeum vulgare]
UNL002BF199604-3	0.37	Caenorhabditis elegans cosmid C09G4, complete sequen	2.0e-08	hypothetical protein T29F13.4 - Arabidopsis thaliana
UNL036BE637476-3,6	0	Hordeum vulgare catalase (Cat1) mRNA, complete cds	1.0e-91	CATALASE ISOZYME 1
UNL053BF293421-9	2.0e-16	Chlamydomonas reinhardtii histone H1 (ch1), histone H2A	6.0e-21	(AJ006768) histone H2A [Cicer arietinum]

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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