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

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

How to Interpret This Image:

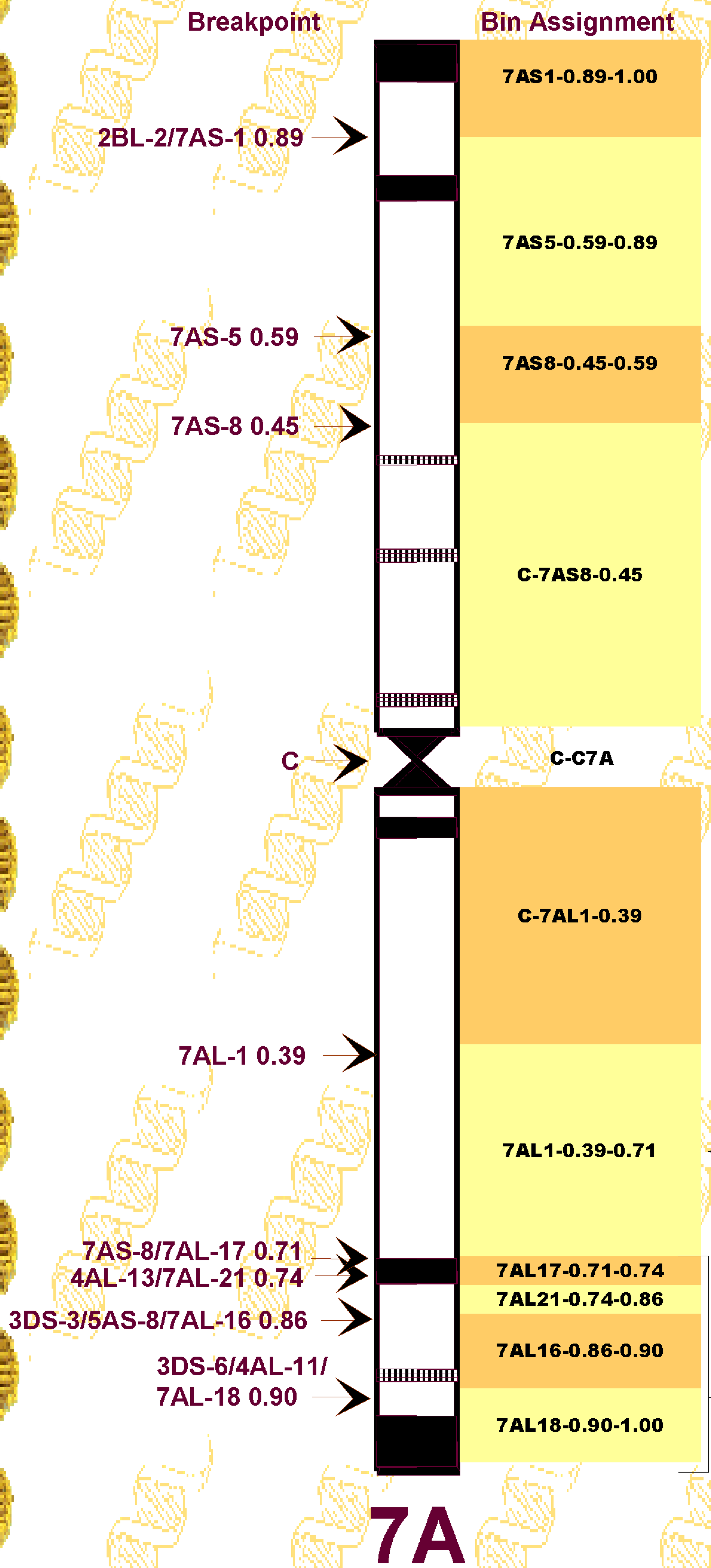
Bin Identity

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

*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.



7AS1-0.89-1.00

Locus ID	e-value	Best nucleic acid match	e-value	Best peptide match
CSU046BE444280-4	6.0e-40	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04:	1.0e-58	(AP002818) putative C-8,7 sterol isomerase [Oryza sativa]
KSU001BE442648-7	2.0e-18	Oryza sativa genomic DNA, chromosome 1, PAC clone:P06	7.0e-45	(AP003047) hypothetical protein [Oryza sativa]
KSU001BE443794-2	0.064	Human DNA sequence from clone RP3-393K13 on chromos	5.9	(AE003500) CG8184 gene product [Drosophila melanogaste
KSU001BE444421-5	0.09	Homo sapiens chromosome 5 clone RP11-138C1, complete sequence		
KSU001BE444470-5,6	2.0e-89	Hordeum vulgare genomic DNA fragment\; clone MWG0866	8.0e-87	(AB016885) protein kinase-like protein [Arabidopsis thaliar
KSU012BE406897-1	4.0e-34	Arabidopsis thaliana AT4g22310 (AT4g22310\/T10I14_140) m	5.0e-47	hypothetical protein T10I14.140 - Arabidopsis thaliana
KSU012BE489999-4	5.0e-93	Rice mRNA for T complex polypeptide, partial sequence	7.0e-89	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CC
KSU012BE490728-7	0	Hordeum vulgare methyljasmonate-inducible lipoxygenas	3.0e-94	lipoxygenase (EC 1.13.11.12) 2 - barley
KSU012BE490790-4	0.015	Genomic Sequence For Arabidopsis thaliana Clone T1G16	2.0e-18	(AF160912) BcDNA.LD06837 [Drosophila melanogaster]
KSU019BE422466-4	5.0e-30	Rice (YK426) mRNA, complete cds	2.0e-11	probable ribosomal protein L9 - rice (fragment)
KSU019BE443559-10	7.0e-06	Arabidopsis thaliana unknown protein (F6F3.4) mRNA, com	2.0e-19	(AC023628) Unknown protein [Arabidopsis thaliana]
KSU024BE498428-3	e-141	Zea mays sucrose synthase (Sus1) mRNA, complete cds	2.0e-85	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFER
KSU024BE499049-1	0	Zea mays strain W64A x A182E putative cytosolic 6-phosph	e-116	phosphogluconate dehydrogenase (decarboxylating) (EC 1
KSU030BE490186-6	5.0e-24	Oryza sativa subsp. japonica clone C2421_1A putative gluta	3.0e-37	(AF309379) putative glutathione S-transferase OsGSTU3 [O
KSU030BE606678-1	0	Wheat mRNA coding for chloroform\/methanol-soluble (CM	1.0e-75	ALPHA-AMYLASE\/TRYPSIN INHIBITOR CM2 PRECURSOR (CHI
KSU035BE497624-3	0.5	Bovine herpesvirus type 1.1, complete genome	6.0e-06	(AP001168) ESTs C26000(C11448),AU082130(C11448) corres
KSU038BE443120-3,4	3.0e-10	Oryza sativa geneomic DNA, chromosome 6, PAC clone:P0	4.0e-07	(AP001552) EST AU082058(C12976) corresponds to a region
NDS043BG274687-5	1.0e-06	Vibrio cholerae chromosome II, section 62 of 93 of the cor	7.0e-59	PROBABLE UDP-GLUCOSE 4-EPIMERASE AT4G23920 (GALAC
TTU025BE489999-4	5.0e-93	Rice mRNA for T complex polypeptide, partial sequence	7.0e-89	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CC
TTU025BE490728-4	0	Hordeum vulgare methyljasmonate-inducible lipoxygenas	3.0e-94	lipoxygenase (EC 1.13.11.12) 2 - barley
TTU025BE490790-1	0.015	Genomic Sequence For Arabidopsis thaliana Clone T1G16	2.0e-18	(AF160912) BcDNA.LD06837 [Drosophila melanogaster]
UCD028BE426203-3	0.36	Nicotiana tabacum cultivar Xanthi arginine decarboxylase 1	1.0e-33	(AC007727) ESTs gb|N96028, gb|F14286, gb|T20680, gb|F1444
UCD037BE443129-12	1.0e-53	Oryza sativa geneomic DNA, chromosome 6, PAC clone:P0	6.0e-54	(AP001552) ESTs AU032452(S10068),C23571(S10068) corresp
UCD037BE443535-2	5.0e-93	Zea mays dihydrolipoamide S-acetyltransferase mRNA, co	e-110	(AP001129) ESTs AU033004(S0924),C74754(E50863) correspo
UCW020BG262472-4	0.005	Dictyostelium discoideum gene for AmiB, complete cds	4.0e-15	AVENIN-3 PRECURSOR (PROLAMIN)
UMC040BE590484-5	4.0e-04	A.sativa avenin mRNA, complete cds	9.0e-16	avenin-3 - oat Narymsky 943, Peptide, 201 aa]
UMC040BE590763-9	e-126	Hordeum vulgare peroxidase BP 1 (Prx5) mRNA, complete	6.0e-45	peroxidase (EC 1.11.1.7) BP1 precursor - barley
UMN013BE443549-2	5.0e-16	Rpg1=stem rust resistance gene [barley, Genomic Mutant	5.0e-16	(AF207842) Pi-ta protein [Oryza sativa]
UNL001BE444421-4	0.09	Homo sapiens chromosome 5 clone RP11-138C1, complete sequence		
UNL001BE444470-3	2.0e-89	Hordeum vulgare genomic DNA fragment\; clone MWG0866	8.0e-87	(AB016885) protein kinase-like protein [Arabidopsis thaliar
UNL036BG262302-4	0.023	Helobdella robusta homeodomain protein LOX5 (Lox5) mR	3.0e-16	avenin N9 - oat

7AS5-0.59-0.89

Locus ID	e-value	Best nucleic acid match	e-value	Best peptide match
CNL001BE426715-2	0.1	Homo sapiens BAC clone RP11-493I5 from 2, complete seq	2.2	transcription initiation factor IID-associated protein, 80K - f
CNL014BE444113-5	0.029	Caenorhabditis elegans cosmid C52A11, complete sequer	6.5	probable lipR protein - Mycobacterium tuberculosis (strair
CNL014BE446622-1	5.0e-25	Oryza sativa mRNA for zinc finger protein, complete cds, c	5.0e-70	zinc-finger protein R2931 [imported] - rice
KSU002BE403518-7,8	1.0e-65	Oryza sativa Ca2+ sensitive 3'(2'),5-diphosphonucleoside 3	2.0e-70	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHC
KSU002BE426715-8	0.1	Homo sapiens BAC clone RP11-493I5 from 2, complete seq	2.2	transcription initiation factor IID-associated protein, 80K - f
KSU012BE404724-1,6	1.0e-10	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	1.0e-34	(AB013395) poly(A)-binding protein II-like [Arabidopsis thal
KSU012BE442812-3	8.0e-30	Oryza sativa putative zinc finger protein mRNA, complete	1.0e-61	(AP000399) ESTs AU077984(C62969),D41648(S4289), AU06358
KSU012BE443401-6	4.0e-63	Hordeum vulgare mRNA for hypothetical protein, clone RG	3.0e-84	(AC003672) putative heme A: farnesyltransferase [Arabido
KSU012BE490643-1	1.0e-49	Hordeum vulgare mRNA for vacuolar membrane proton-tr	8.0e-12	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTC
KSU019BE606973-3	2.0e-71	Oryza sativa genomic DNA, chromosome 6, BAC clone:OSJ	e-106	(AP000399) EST AU056133(S20320) corresponds to a region
KSU024BE499049-3	0	Zea mays strain W64A x A182E putative cytosolic 6-phosph	e-116	phosphogluconate dehydrogenase (decarboxylating) (EC 1
KSU027BE590752-2	6.0e-06	Oryza sativa osr8 mRNA for hydrophobic polypeptide, com	9.0e-07	(AC005170) unknown protein [Arabidopsis thaliana]
KSU038BE443542-3	0.028	Homo sapiens, chromosome 11 open reading frame2, clo	9.0e-09	thioredoxin (clone GIF2) - Arabidopsis thaliana
KSU038BE489090-1	0.02	Sequence of BAC F16N3 from Arabidopsis thaliana chromc	6.0e-07	(AP002543) selenium-binding protein-like [Arabidopsis tha
KSU038BE489882-1	0.24	Human DNA sequence from PAC 57A13 between markers	2.0e-16	(AB013389) contains similarity to ATP binding protein asso
NDS034BE403826-6	e-170	L.temulentum mRNA for histone H3	2.0e-71	HISTONE H3.2, MINOR predicted gene.\; Similar to histone H:
NDS034BE405850-2	0.055	Heliocoverpa armigera nucleopolyhedrovirus G4, complet	2.0e-24	glucuronosyl transferase homolog, ripening-related - tom
TTU025BE490643-1	1.0e-49	Hordeum vulgare mRNA for vacuolar membrane proton-tr	8.0e-12	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTC
UCD037BE443044-3	2.0e-29	Oryza sativa genomic DNA, chromosome 6, clone:P0535G0	4.0e-42	(AP000399) ESTs AU077984(C62969),D41648(S4289), AU06358
UCD037BE499248-4	e-129	Zea mays mRNA for Caffeoyl CoA O-methyltransferase (cc	2.0e-61	(AB023482) ESTs AU058067(E20733), AAU058070(E20873) cor
UCW016BE517844-10	e-157	Oryza sativa H3 histone gene H3R-11	2.0e-61	HISTONE H3
UCW039BE494425-3	0.35	Homo sapiens 12 BAC RP11-685B13 (Roswell Park Cancer I	6.0e-06	(AE003587) CG4896 gene product [alt 1] [Drosophila melanc
UMC015BE606357-6	1.0e-15	Sorghum bicolor BAC clone 25.M18, complete sequence	3.0e-52	(AF114171) hypothetical protein [Sorghum bicolor]
UMN013BE442812-2	8.0e-30	Oryza sativa putative zinc finger protein mRNA, complete	1.0e-61	(AP000399) ESTs AU077984(C62969),D41648(S4289), AU06358
UNL001BE444470-2	2.0e-89	Hordeum vulgare genomic DNA fragment\; clone MWG0866	8.0e-87	(AB016885) protein kinase-like protein [Arabidopsis thaliar
UNL002BE515566-1	0	H.vulgare mRNA for glutamyl-tRNA reductase (1st isoform)	2.0e-90	GLUTAMYL-TRNA REDUCTASE 2 (GLUTR)
UNL053BF474584-6	0.11	Rattus norvegicus acyl-CoA thioesterase 1, cytosolic (Cte	2.0e-74	(AF302671) ubiquitin-specific protease 23 [Arabidopsis tha

7AS8-0.45-0.59

Locus ID	e-value	Best nucleic acid match	e-value	Best peptide match
CSU001BE426715-3	0.1	Homo sapiens BAC clone RP11-493I5 from 2, complete seq	2.2	transcription initiation factor IID-associated protein, 80K - f
KSU001BE399989-3	0.2	Homo sapiens genomic DNA, chromosome 4q22-q24, clon	3.9	(U67190) origin recognition complex protein 1 [Xenopus la
KSU002BE405224-1	0.44	Human chromosome 14 DNA sequence BAC R-757K12 of lit	2.0e-16	(AC009465) unknown protein\; 32997-32284 [Arabidopsis th
KSU024BE498038-6	0	Triticum aestivum p34cdc2 (cdc2TaA) mRNA, complete cds	e-125	(U23409) p34cdc2 [Triticum aestivum]
KSU024BE499652-3	6.0e-80	Citrus X paradisi pyrophosphate-dependent phosphofruct	6.0e-85	(AF095520) pyrophosphate-dependent phosphofructokina
KSU027BE352570-1	e-101	Oryza sativa mRNA for aldehyde dehydrogenase ALDH2b,	1.0e-60	(AB044537) aldehyde dehydrogenase ALDH2b [Oryza sativa
KSU030BE590566-4,7	1.0e-09	Thuja plicata clone 1 pinoresinol-lariciresinol reductase m	8.0e-62	ISOFLAVONE REDUCTASE HOMOLOG lupine
KSU038BE443596-2	0	Hordeum vulgare (cv. Bomi) B12D mRNA	9.0e-45	B12D protein - barley
NDS034BE590566-6	1.0e-09	Thuja plicata clone 1 pinoresinol-lariciresinol reductase m	8.0e-62	ISOFLAVONE REDUCTASE HOMOLOG lupine
NDS043BG274662-1	e-100	Rice mRNA for major intrinsic protein, complete cds	3.0e-45	major intrinsic protein - rice
TTU047BE445220-3,5	0.38	Arabidopsis thaliana chromosome II section 126 of 255 of t	5.0e-89	(AC007168) unknown protein [Arabidopsis thaliana]
TTU047BE495005-3,5	e-160	Oryza sativa chromosome 10 BAC OSJNBa0076F20 genomi	1.0e-80	(AC025296) putative gamma-lyase [Oryza sativa]
UCD001BE442939-3	1.1	Homo sapiens clone H41 unknown mRNA	5.1	anti-mullerian hormone homolog precursor - chicken
UCD037BE498662-1	6.0e-09	Populus x canescens POPARB mRNA, partial cds	2.0e-46	(AC002329) unknown protein [Arabidopsis thaliana]
UCW026BE497999-1	0	Hordeum sp. x Triticum sp. glycine decarboxylase P subur	e-118	glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) [imp
UNL002BE492286-1	0.078	Drosophila melanogaster genomic scaffold 1420000133860	8	(X00269) open reading frame [Zea mays]
UNL053BF292870-2	2.0e-09	Oryza sativa osRAD23 mRNA, complete cds	4.0e-47	(AB005248) DNA repair protein RAD23 homolog [Arabidopsi

C-7AS8-0.45

Locus ID	e-value	Best nucleic acid match	e-value	Best peptide match
CSU059BE606458-3	1.0e-46	Hordeum vulgare genomic DNA fragment\; clone MWG0626	1.0e-57	(AB025969) NAD-dependent sorbitol dehydrogenase [Prunu
KSU012BE443396-3,7	0	Zea mays glucose-6-phosphate\/phosphate-translocator p	e-100	glucose-6-phosphate\/phosphate-translocator precursor,
KSU019BE426692-3	8.0e-21	Oryza sativa manganese superoxide dismutase (rmsod1)	2.0e-80	(AF039000) putative serine-glyoxylate aminotransferase [F
KSU024BE499303-1	2.0e-11	Arabidopsis thaliana putative methionine aminopeptidase	6.0e-13	(AF300880) putative methionine aminopeptidase 2 [Arabido
KSU030BE404899-3	2.0e-36	Arabidopsis thaliana AT5g11200\/F2I11_90 mRNA, complete	1.0e-85	(AF378868) AT5g11200\/F2I11_90 [Arabidopsis thaliana]
KSU035BE404540-4	3.0e-29	S.tuberosum (Desiree) cyc1 II mRNA. for cytochrome c1	2.0e-49	(AP000381) ubiquinol-cytochrome c1 reductase cytochrom
KSU035BE404728-2	0.25	Human cosmid Xq28_IA649, complete sequence [Homo sa	4.0e-33	(Y15367) MtN19 [Medicago truncatula]
KSU035BE406976-1	2.0e-55	Oryza sativa mRNA for spermidine synthase 1 (spdSyn1 gi	1.0e-76	SPERMIDINE SYNTHASE 1 (PUTRESCINE AMINOPROPYLTRANS
KSU038BE442797-1,3	4.0e-04	Arabidopsis thaliana chromosome 1 BAC F24D7 genomic s	5.0e-50	(AC009999) Contains similarity to Ariadne-2 protein from D
NDS021BE493897-3	1.0e-44	Oryza sativa putative dihydroflavonol reductase mRNA, co	6.0e-62	(AF134807) putative dihydroflavonol reductase [Oryza sativ
NDS021BE494078-3	1.2	Oryza sativa chromosome 10 BAC OSJNBa0001O14 genomi	2.1	claudin 18 [Homo sapiens]
NDS043BF293124-3	4.0e-04	Volvox carteri f. nagariensis clone G32 unknown mRNA	7.0e-35	(AC006220) unknown protein [Arabidopsis thaliana]
NDS043BG605575-1	0	T.aestivum L mRNA for histone H2B	4.0e-43	HISTONE H2B
UCD037BE489419-2	0.33	Homo sapiens BAC clone RP11-221H10 from 8, complete se	2.0e-27	GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYF
UNL036BE590582-2,3	0	Triticum aestivum small subunit ADP glucose pyrophosph	e-120	(AF244997) small subunit ADP glucose pyrophosphorylase
UNL044BG263859-3	0.12	Leishmania major chromosome 35 clone L1905 strain Frie	3.0e-14	hypothetical protein - Arabidopsis thaliana

C-7AL1-0.39

Locus ID	e-value	Best nucleic acid match	e-value	Best peptide match
KSU012BE403622-1	2.0e-09	Sequence of BAC F7H2 from Arabidopsis thaliana chromos	7.0e-95	(AC018849) unknown protein\; 52184-57536 [Arabidopsis th
KSU012BE442619-1	5.0e-09	Arabidopsis thaliana chromosome 1 BAC T6J19 genomic s	8.0e-28	copper homeostasis factor [imported] - Arabidopsis thalia
KSU024BE498418-2	3.0e-11	Arabidopsis thaliana chromosome II section 192 of 255 of t	2.0e-58	(AC007060) Strong similarity to F19I3.8 gi UDP-galactose-4-e
KSU024BE498849-3	1.0e-34	Arabidopsis thaliana RNA recognition motif-type RNA-bindi	7.0e-60	(AC017118) F6N18.17 [Arabidopsis thaliana]
KSU030BF483454-3,6	0.42	Genomic Sequence for Oryza sativa, Nipponbare strain, clc	4.0e-13	(AF030386) NOI protein [Arabidopsis thaliana]
KSU038BE446029-1	5.0e-06	Oryza sativa copper chaperone homolog CCH mRNA, comp	8.0e-28	copper homeostasis factor [imported] - Arabidopsis thalia
NDS018BE404240-3	7.0e-34	T.aestivumn (subclone pAWJL175) AWJL175 gene	1.0e-04	(AF133839) papain-like cysteine protease [Sandersonia au
UNL002BF473119-4	0	Triticum aestivum Cu\/Zn superoxide dismutase (SOD1.2)	6.0e-62	superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 2, chloroplast -

7AL1-0.39-0.71

Locus ID	e-value	Best nucleic acid match	e-value	Best peptide match
CNL031BE403624-13	0	Hordeum vulgare germin F (GerF) gene, complete cds	e-118	(AF250935) germin F [Hordeum vulgare]
CSU057BE490023-3	1.0e-19	Arabidopsis thaliana genomic DNA, chromosome 3, BAC cl	1.0e-98	(AP001298) contains similarity to the auxin-independent gr
KSU001BE444301-1	1.5	Arabidopsis thaliana chromosome I BAC F25I16 genomic s	0.24	(AE003581) Chd1 gene product [Drosophila melanogaster]
KSU012BE443436-1	e-151	Oryza sativa genomic DNA, chromosome 2, clone:P0437H0:	3.0e-95	(AP000366) Similar to maize transposon MuDR mudrA-like
KSU019BE445239-3	e-125	Oryza sativa mRNA for 26S proteasome ATPase subunit Rp	1.0e-67	(AB033537) 26S proteasome regulatory particle triple-A AT
KSU019BE498785-6	1.0e-06	Mycobacterium smegmatis adhC gene for alcohol dehydr	3.0e-32	PROBABLE MANNITOL DEHYDROGENASE (NAD-DEPENDENT M
KSU019BE606698-7	e-179	Oryza sativa GTP-binding protein mRNA, complete cds	3.0e-72	(AF327517) GTP-binding protein [Oryza sativa]
KSU019BE637878-9	7.0e-14	Oryza sativa chromosome 3 BAC OSJNBa0013M12 genomic	1.0e-08	(AP002070) Similar to Arabidopsis thaliana low temperatur
KSU024BE495644-1	0	Oryza sativa blast and wounding induced mitogen-activate	e-128	(AF194415) MAP kinase homolog [Oryza sativa]
KSU024BF484707-3	0.37	Homo sapiens chromosome 3, olfactory receptor pseudo	6.0e-08	(AB023042) gene_id:MUL3.13~pir||T04254~similar to unknov
KSU027BE490007-2,3	e-150	Oryza sativa mRNA for glyoxalase I, complete cds	6.0e-90	(AB017042) glyoxalase I [Oryza sativa]
KSU035BE403471-6	5.0e-15	Oryza sativa microsatellite MRG2437 containing (CT)X18, g	6.0e-57	(AF370443) Ran binding protein-1 [Lycopersicon esculentu
KSU035BE403740-2	8.0e-09	Arabidopsis thaliana AT4g13360\/T9E8_100 mRNA, complete	2.0e-75	3-hydroxyisobutyryl-coenzyme A hydrolase homolog T9E8
KSU035BE406937-3	1.2	S.pombe chromosome II cosmid c3B8	3.0e-22	(AF096247) ethylene-responsive elongation factor EF-Ts pr
KSU035BE406943-9	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
NDS021BE406148-1	8.0e-14	Arabidopsis thaliana cyclophilin (ROC7) mRNA, complete c	4.0e-44	cyclophilin CYP5 [imported] - Arabidopsis thaliana
NDS021BF201644-1	0.9	Oryza sativa chromosome 4 BAC q3037-207F1 complete ge	1.7	BALBIANI RING PROTEIN 3 PRECURSOR
NDS043BF293596-1	e-119	Oryza sativa chromsome 9 clone PAC0645D04, complete s	2.0e-85	zinc finger protein F15B8.140 - Arabidopsis thaliana
UCD017BE488496-1	0	Hordeum vulgare Mg-chelatase subunit (Xantha-h) mRNA,	1.0e-47	protoporphyrin IX magnesium chelatase (EC 4.99.1.-) Xanth
UCD017BE488670-2	1.0e-53	Oryza sativa partial mRNA for putative aminopropyltransfe	6.0e-51	(AJ251302) putative aminopropyltransferase [Oryza sativa]
UCD037BE443010-5	3.0e-82	Oryza sativa mRNA for adenylate kinase-a, complete cds	1.0e-53	ADENYLATE KINASE A (ATP-AMP TRANSPHOSPHORYLASE)
UCW001BE398631-2	3.3	Oryza sativa chromsome 9 clone PAC0663H05, complete s	1.9	BETA-2 ADRENERGIC RECEPTOR
UCW016BE497215-3	e-119	Zea mays thiamine biosynthetic enzyme (thi1-1) mRNA, co	6.0e-60	THIAZOLE BIOSYNTHETIC ENZYME 1-2, CHLOROPLAST PRECI
UCW039BE405131-5	3.0e-57	Musa acuminata mRNA for unknown ripening-related prot	1.0e-75	(AB023034) ATP citrate lyase [Arabidopsis thaliana]
UMN013BE443312-1	2.0e-08	Sequence of BAC T2D23 from Arabidopsis thaliana chromc	1.0e-62	(AF253474) acyl-CoA oxidase [Arabidopsis thaliana]
UNL001BE442845-4	1.1	Drosophila melanogaster, chromosome 2R, region 45E1-4I	1.0e-51	pitrilysin (EC 3.4.24.55) - garden pea
UNL036BE497239-2	0	H.vulgare mRNA for aminolevulinate dehydratase	2.0e-68	DELTA-AMINOLEVULINIC ACID DEHYDRATASE PRECURSOR (F
UNL044BG274514-10	e-147	Rice mRNA for ubiquitin protein fused to a ribosomal prot	2.0e-60	ubiquitin \/ ribosomal protein CEP52 - rice
UNL048BE446586-1	0.38	Drosophila melanogaster genomic scaffold 1420000133860	1.0e-24	(AC079041) unknown protein [Arabidopsis thaliana]
UNL048BE494049-4	4.0e-25	Sorghum bicolor N-hydroxylating, multifunctional cytochro	4.0e-74	CYTOCHROME P450 79A1 (CYTOCHROME P450TYR) sorghun
UNL048BE591273-1,4,5	0.087	Homo sapiens chromosome 3 clone RP11-127I14 map 3p, c	2.0e-24	hypothetical protein T10K17.100 - Arabidopsis thaliana

7AL17-0.71-0.74

Locus ID	e-value	Best nucleic acid match	e-value	Best peptide match
UCD028BF291608-3	2.0e-64	Lupinus luteus ribosomal protein S14 (rps14) mRNA, comp	1.0e-66	40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
UNL048BF428786-3	0.019	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, c	2.0e-46	(AC007060) T5I8.13 [Arabidopsis thaliana]

7AL21-0.74-0.86

Locus ID	e-value	Best nucleic acid match	e-value	Best peptide match
CNL023BF483150-16	9.0e-97	Wheat mRNA for ubiquitin	1.0e-26	(AF093504) tetra-ubiquitin [Saccharum hybrid cultivar H32-8
KSU001BE442572-5,6	5.0e-19	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	8.0e-87	(AB024036) contains similarity to EH domain containing pro
KSU002BE425207-6	8.0e-08	Nicotiana tabacum (clone: L24-2) chloroplast ribosomal pro	3.0e-36	(AB016879) 50S ribosomal protein L24, chloroplast precurs
KSU024BE499664-9	0	Maize gene for beta 1 tubulin	1.0e-96	TUBULIN BETA-1 CHAIN
KSU035BE404434-3	e-114	Lycopersicon esculentum elongation factor 2 mRNA, parti	2.0e-96	ELONGATION FACTOR 2 (EF-2)
UCD001BE442572-4,5	5.0e-19	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	8.0e-87	(AB024036) contains similarity to EH domain containing pro
UNL036BE517670-3	2.0e-70	Oryza sativa chromosome 10 BAC OSJNBa0027P10 genomi	8.0e-28	(AC084763) putative ribosomal protein L27 [Oryza sativa]

7AL16-0.86-0.90

Locus ID	e-value	Best nucleic acid match	e-value	Best peptide match
CSU059BG604419-1	7.0e-14	Arabidopsis thaliana ISA1 gene	3.0e-52	(Y14404) putative arabinose kinase [Arabidopsis thaliana]
KSU002BE426715-7	0.1	Homo sapiens BAC clone RP11-493I5 from 2, complete seq	2.2	transcription initiation factor IID-associated protein, 80K - f
KSU024BG274853-3	9.0e-57	Arabidopsis thaliana zinc dependent protease (VAR2) mRI	6.0e-57	(AJ012165) chloroplast protease [Capsicum annuum]
KSU030BE518357-3,5	3.0e-60	Oryza sativa subsp. japonica clone S4892 putative glutathic	5.0e-55	(AF309381) putative glutathione S-transferase OsGSTZ1 [O
NDS018BE426274-6,7	3.0e-75	Hordeum vulgare mRNA for hypothetical protein, partial, cl	1.0e-50	(AB007627) homeobox gene [Oryza sativa]
NDS018BE426802-4	7.0e-06	O.sativa mRNA for cyclin 2	2.0e-39	cyclin III - maize
UCD001BE406505-3	0.95	Mus musculus Strain C57BL6\/J Chromosome 8 RP23-21B7	1.0e-16	(AB005245) contains similarity to ubiquitin conjugating enz
UMC015BE426274-5	3.0e-75	Hordeum vulgare mRNA for hypothetical protein, partial, cl	1.0e-50	(AB007627) homeobox gene [Oryza sativa]
UMC040BG262287-2	e-159	Hordeum vulgare HVA\/68 mRNA for vacuolar proton-ATPa	1.0e-62	(AB032840) vacuolar proton-ATPase [Hordeum vulgare]
UNL053BF293421-1,6	2.0e-16	Chlamydomonas reinhardtii histone H1 (ch1), histone H2A	6.0e-21	(AJ006768) histone H2A [Cicer arietinum]

7AL17-0.71-1.00

Locus ID	e-value	Best nucleic acid match	e-value	Best peptide match
CSU001BE425207-2	8.0e-08	Nicotiana tabacum (clone: L24-2) chloroplast ribosomal pro	3.0e-36	(AB016879) 50S ribosomal protein L24, chloroplast precurs

7AL18-0.90-1.00

Locus ID	e-value	Best nucleic acid match	e-value	Best peptide match
CNL031BE403423-5	4.0e-06	Arabidopsis thaliana timing of CAB expression 1 protein (TOC1) mRNA, complete cds		
KSU001BE405507-6	3.0e-08	Aegilops ventricosa partial rae7 gene for resistance gene	3.0e-50	(AJ249948) resistance gene alike [Aegilops ventricosa]
KSU012BE403180-4	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
KSU019BE404737-2	6.0e-06	Arabidopsis thaliana chromosome III BAC F13E7 genomic s	2.0e-77	(AB005242) S-adenosylmethionine:2-demethylmenaquinon
KSU038BE445506-3	1.0e-07	Oryza sativa genomic DNA, chromosome 6, clone:P0535G0	1.0e-46	(AC007127) putative protein kinase [Arabidopsis thaliana]
KSU038BE446244-1,4	0.091	Human DNA sequence from clone RP13-153N15 on chromo	2.0e-33	(AC037197) Putative hypersensitivity-related protein [Oryz
TTU047BE405648-4,6	e-114	Zea mays mus1 gene, exons 1-13	e-102	DNA MISMATCH REPAIR PROTEIN MSH2 (MUS1)
TTU047BE494712-1	1.0e-06	Arabidopsis thaliana chromosome II section 126 of 255 of t	1.0e-39	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase-li
UCD029BE591469-1,5,6	0	Hordeum vulgare catalase 1 (CAT1) gene, partial cds	e-129	(AF021938) catalase 1 [Hordeum vulgare]
UMC015BE426274-6	3.0e-75	Hordeum vulgare mRNA for hypothetical protein, partial, cl	1.0e-50	(AB007627) homeobox gene [Oryza sativa]
UMC015BE426680-8	0	Avena fatua ras-like small monomeric GTP-binding protei	7.0e-79	(AF084005) ras-like small monomeric GTP-binding protein
UMC015BE426802-4	7.0e-06	O.sativa mRNA for cyclin 2	2.0e-39	cyclin III - maize
UNL036BE637476-1,4,5	0	Hordeum vulgare catalase (Cat1) mRNA, complete cds	1.0e-91	CATALASE ISOZYME 1

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