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

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

*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:

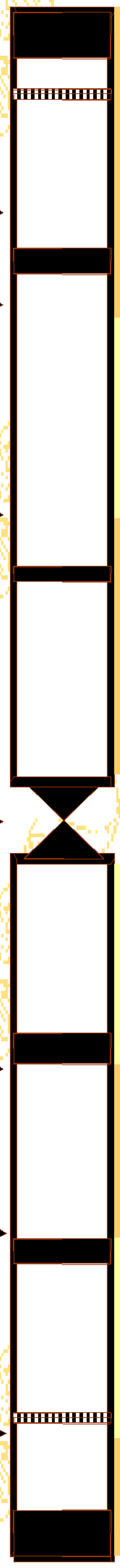
Bin Identity

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

Breakpoint | **Bin Assignment**



*7DS-6 0.73
7DS-4 0.61
7DS-5 0.36
C
7DL-5 0.30
7DL-2 0.61
7DL-3 0.82

7DS4-0.61-1.00
7DS5-0.36-0.61
C-7DS5-0.36
C-C7D
C-7DL5-0.30
7DL5-0.30-0.61
7DL2-0.61-0.82
7DL3-0.82-1.00

*7DS6 is normal

7D

7DS4-0.61-1.00

CNL001BE403518-10	1.0e-65	Oryza sativa Ca2+ sensitive 3'(2'),5-diphosphonucleoside 3	2.0e-70	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHO
CNL014BE424554-7,8,9	5.0e-65	Oryza sativa OsENOD93b mRNA for early nodulin, complete	3.0e-33	(AB018377) early nodulin [Oryza sativa]
CNL014BE424647-6,9	1.0e-79	Wheat signal recognition particle (SRP) 7S RNA variant 1	1.2	(AE003787) CG10395 gene product [Drosophila melanogast
CNL014BE446622-2	5.0e-25	Oryza sativa mRNA for zinc finger protein, complete cds, c	5.0e-70	zinc-finger protein R2931 [imported] - rice
CNL014BE489999-7	5.0e-93	Rice mRNA for T complex polypeptide, partial sequence	7.0e-89	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CC
CNL014BE490643-3	1.0e-49	Hordeum vulgare mRNA for vacuolar membrane proton-tr	8.0e-12	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTO
CNL014BE490790-6	0.015	Genomic Sequence For Arabidopsis thaliana Clone T1G16	2.0e-18	(AF160912) BcDNA.LD06837 [Drosophila melanogaster]
CNL031BE500122-2	4.0e-04	Arabidopsis thaliana peroxisome biogenesis protein PEX1	3.0e-57	(AF275382) peroxisome biogenesis protein PEX1 [Arabidop
CSU001BE403512-3	2.0e-48	Oryza sativa chromosome 7 clone OSJNBb0024A20, compl	2.0e-36	(AC079038) Putative nucleic acid binding protein [Oryza sat
CSU057BE425880-3,4	1.0e-37	Zea mays mRNA for peroxidase (pox1 gene)	2.0e-51	(AJ401274) peroxidase [Zea mays]
KSU001BE442648-1	2.0e-18	Oryza sativa genomic DNA, chromosome 1, PAC clone:P06	7.0e-45	(AP003047) hypothetical protein [Oryza sativa]
KSU001BE443412-2,3	4.4	Homo sapiens BAC clone RP11-319A7 from 2, complete se	1.4	(AF207842) Pi-ta protein [Oryza sativa]
KSU002BE403518-9	1.0e-65	Oryza sativa Ca2+ sensitive 3'(2'),5-diphosphonucleoside 3	2.0e-70	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHO
KSU002BE406387-2	9.0e-26	Oryza sativa aldehyde dehydrogenase (Aldh) mRNA, comp	6.0e-13	(AB044537) aldehyde dehydrogenase ALDH2b [Oryza sativa
KSU002BE426715-4	0.1	Homo sapiens BAC clone RP11-493I5 from 2, complete seq	2.2	transcription initiation factor IID-associated protein, 80K - f
KSU012BE406897-2	4.0e-34	Arabidopsis thaliana AT4g22310 (AT4g22310\/T10I14_140) m	5.0e-47	hypothetical protein T10I14.140 - Arabidopsis thaliana
KSU012BE406987-2	7.0e-05	Oryza sativa genomic DNA, chromosome 6, BAC clone:OSJNBa0015I14, complete sequence		
KSU012BE442576-4	2.0e-12	Mucor racemosus p-glycoprotein gene, complete cds	1.0e-55	(AP002051) multidrug resistance p-glycoprotein [Arabidop
KSU012BE442812-2	8.0e-30	Oryza sativa putative zinc finger protein mRNA, complete c	1.0e-61	(AP000399) ESTs AU077984(C62969),D41648(S4289), AU06358
KSU012BE443401-8	4.0e-63	Hordeum vulgare mRNA for hypothetical protein, clone RG	3.0e-84	(AC003672) putative heme A: farnesyltransferase [Arabido
KSU012BE489999-7	5.0e-93	Rice mRNA for T complex polypeptide, partial sequence	7.0e-89	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CC
KSU012BE490643-3	1.0e-49	Hordeum vulgare mRNA for vacuolar membrane proton-tr	8.0e-12	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTO
KSU012BE490728-8	0	Hordeum vulgare methyljasmonate-inducible lipoxygenas	3.0e-94	lipoxygenase (EC 1.13.11.12) 2 - barley
KSU012BE490790-8	0.015	Genomic Sequence For Arabidopsis thaliana Clone T1G16	2.0e-18	(AF160912) BcDNA.LD06837 [Drosophila melanogaster]
KSU019BE606973-4	2.0e-71	Oryza sativa genomic DNA, chromosome 6, BAC clone:OSJ	e-106	(AP000399) EST AU056133(S20320) corresponds to a region
KSU024BE498428-2	e-141	Zea mays sucrose synthase (Sus1) mRNA, complete cds	2.0e-85	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFER.
KSU024BE499049-5	0	Zea mays strain W64A x A182E putative cytosolic 6-phosph	e-116	phosphogluconate dehydrogenase (decarboxylating) (EC 1
KSU027BE495226-4	0.2	Homo sapiens ALPP, ALPPL2, ALPI, XCE, CHRND, and CHRNG genes, complete sequence		
KSU027BE590752-1	6.0e-06	Oryza sativa osr8 mRNA for hydrophobic polypeptide, com	9.0e-07	(AC005170) unknown protein [Arabidopsis thaliana]
KSU030BE490186-1,7	5.0e-24	Oryza sativa subsp. japonica clone C2421_1A putative gluta	3.0e-37	(AF309379) putative glutathione S-transferase OsGSTU3 [Or
KSU030BE606678-3	0	Wheat mRNA coding for chloroform\/methanol-soluble (CM	1.0e-75	ALPHA-AMYLASE\/TRYPSIN INHIBITOR CM2 PRECURSOR (CHI
KSU030BE606874-2	0	Triticum aestivum granule-bound starch synthase I (Wx-Dl	1.0e-58	(AB019624) starch synthase (GBSSI) [Triticum aestivum] ta
KSU035BE406923-2	2.0e-11	Amaranthus hypochondriacus C4 photosynthetic NAD-dep	2.0e-57	NAD-DEPENDENT MALIC ENZYME 65 KDA ISOFORM, MITOCHO
KSU035BE497624-4	0.5	Bovine herpesvirus type 1.1, complete genome	6.0e-06	(AP001168) ESTs C26000(C11448),AU082130(C11448) corresp
KSU038BE443120-5	3.0e-10	Oryza sativa geneomic DNA, chromosome 6, PAC clone:P0	4.0e-07	(AP001552) EST AU082058(C12976) corresponds to a region
KSU038BE443542-1,2	0.028	Homo sapiens, chromosome 11 open reading frame2, clo	9.0e-09	thioredoxin (clone GIF2) - Arabidopsis thaliana
KSU038BE489090-2,4	0.02	Sequence of BAC F16N3 from Arabidopsis thaliana chromo	6.0e-07	(AP002543) selenium-binding protein-like [Arabidopsis tha
KSU038BE489882-4,6	0.24	Human DNA sequence from PAC 57A13 between markers	2.0e-16	(AB013389) contains similarity to ATP binding protein asso
NDS034BE403826-3	e-170	L.temulentum mRNA for histone H3	2.0e-71	HISTONE H3.2, MINOR predicted gene.\; Similar to histone H
NDS034BE405850-3	0.055	Heliocoverpa armigera nucleopolyhedrovirus G4, complet	2.0e-24	glucuronosyl transferase homolog, ripening-related - tom
TTU025BE489999-5	5.0e-93	Rice mRNA for T complex polypeptide, partial sequence	7.0e-89	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CC
TTU025BE490643-3	1.0e-49	Hordeum vulgare mRNA for vacuolar membrane proton-tr	8.0e-12	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTO
TTU025BE490728-5	0	Hordeum vulgare methyljasmonate-inducible lipoxygenas	3.0e-94	lipoxygenase (EC 1.13.11.12) 2 - barley
TTU025BE490790-7	0.015	Genomic Sequence For Arabidopsis thaliana Clone T1G16	2.0e-18	(AF160912) BcDNA.LD06837 [Drosophila melanogaster]
UCD028BE426203-4	0.36	Nicotiana tabacum cultivar Xanthi arginine decarboxylase 1	1.0e-33	(AC007727) ESTs gb|N96028, gb|F14286, gb|T20680, gb|F1444
UCD037BE443044-2	2.0e-29	Oryza sativa genomic DNA, chromosome 6, clone:P0535G0	4.0e-42	(AP000399) ESTs AU077984(C62969),D41648(S4289), AU06358
UCD037BE443129-3	1.0e-53	Oryza sativa geneomic DNA, chromosome 6, PAC clone:P0	6.0e-54	(AP001552) ESTs AU032452(S10068),C23571(S10068) corresp
UCD037BE443535-3	5.0e-93	Zea mays dihydrolipoamide S-acetyltransferase mRNA, co	e-110	(AP001129) ESTs AU033004(S0924),C74754(E50863) correspo
UCD037BE499248-3	e-129	Zea mays mRNA for Caffeoyl CoA O-methyltransferase (cc	2.0e-61	(AB023482) ESTs AU058067(E20733), AAU058070(E20873) cor
UCW020BG262472-1,2	0.005	Dictyostelium discoideum gene for AmiB, complete cds	4.0e-15	AVENIN-3 PRECURSOR (PROLAMIN)
UCW039BE446195-1	0.39	Pyricularia grisea chromosome 7 clone BAC 6J18, genomi	3.0e-39	(X99923) male sterility 2-like protein [Arabidopsis thaliana]
UCW039BE494425-2	0.35	Homo sapiens 12 BAC RP11-685B13 (Roswell Park Cancer I	6.0e-06	(AE003587) CG4896 gene product [alt 1] [Drosophila melanc
UMN013BE443436-3	e-151	Oryza sativa genomic DNA, chromosome 2, clone:P0437H0	3.0e-95	(AP000366) Similar to maize transposon MuDR mudrA-like
UMN013BE443746-1	5.0e-18	Oryza sativa genomic DNA, chromosome 6, clone P0680A0	1.0e-19	(AB023482) ESTs C22458(C62866),C22459(C62866) correspo
UNL002BE591190-2	1.2	Homo sapiens clone RP11-736E3, complete sequence	1.0e-25	(AJ302292) MLA6 protein [Hordeum vulgare]
UNL053BF474584-8	0.11	Rattus norvegicus acyl-CoA thioesterase 1, cytosolic (Cte	2.0e-74	(AF302671) ubiquitin-specific protease 23 [Arabidopsis tha
UNL053BG274908-1	e-101	Lolium rigidum 5-enolpyruvylshikimate 3-phosphate synt	8.0e-46	(AB016765) 3-phosphoshikimate 1-carboxyvinyltransferase

7DS4-0.61-0.73

UCD001BE405852-6	1.4	Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome	2.0e-13	(AB035183) N-hydroxycinnamoyl\/benzoyltransferase [Ipom

7DS5-0.36-0.61

CNL023BE405227-1	0.36	Heliothis virescens ryanodine receptor (ryr) mRNA, partial	0.13	(AB040407) elicitor inducible protein [Nicotiana tabacum]
KSU012BE404724-3,4	1.0e-10	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	1.0e-34	(AB013395) poly(A)-binding protein II-like [Arabidopsis thal
KSU024BE499652-1	6.0e-80	Citrus X paradisi pyrophosphate-dependent phosphofruct	6.0e-85	(AF095520) pyrophosphate-dependent phosphofructokina
KSU027BE352570-3	e-101	Oryza sativa mRNA for aldehyde dehydrogenase ALDH2b,	1.0e-60	(AB044537) aldehyde dehydrogenase ALDH2b [Oryza sativa
KSU030BE590566-6	1.0e-09	Thuja plicata clone 1 pinoresinol-lariciresinol reductase m	8.0e-62	ISOFLAVONE REDUCTASE HOMOLOG lupine
KSU038BE442681-7	0.026	Arabidopsis thaliana chromosome II section 127 of 255 of t	5.0e-54	(AJ011892) cyclin D2.1 protein [Nicotiana tabacum]
KSU038BE443596-1	0	Hordeum vulgare (cv. Bomi) B12D mRNA	9.0e-45	B12D protein - barley
NDS021BE493897-1	1.0e-44	Oryza sativa putative dihydroflavonol reductase mRNA, co	6.0e-62	(AF134807) putative dihydroflavonol reductase [Oryza sativ
NDS034BE497604-1	4.0e-13	Pisum sativum poly(A) polymerase mRNA, nuclear gene e	6.0e-58	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST F
NDS034BE590566-5,7	1.0e-09	Thuja plicata clone 1 pinoresinol-lariciresinol reductase m	8.0e-62	ISOFLAVONE REDUCTASE HOMOLOG lupine
NDS043BF291338-3	3.0e-04	Arabidopsis thaliana chromosome II section 235 of 255 of t	7.0e-28	BIOTIN SYNTHASE (BIOTIN SYNTHETASE)
TTU047BE445220-2	0.38	Arabidopsis thaliana chromosome II section 126 of 255 of t	5.0e-89	(AC007168) unknown protein [Arabidopsis thaliana]
TTU047BE495005-2	e-160	Oryza sativa chromosome 10 BAC OSJNBa0076F20 genomi	1.0e-80	(AC025296) putative gamma-lyase [Oryza sativa]
UCD029BF483478-3	2.0e-24	Arabidopsis thaliana putative methionine aminopeptidase	1.0e-62	(AF300880) putative methionine aminopeptidase 2 [Arabido
UCD029BF484868-2	2.0e-52	A.majus mRNA for DAG protein	5.0e-72	DAG PROTEIN, CHLOROPLAST PRECURSOR
UCD037BE443282-2	0.016	Genomic sequence for Arabidopsis thaliana BAC F28K19 fr	3.0e-36	(AC073942) Contains similarity to a phosphoglyceromutas
UCD037BE489419-1	0.33	Homo sapiens BAC clone RP11-221H10 from 8, complete se	2.0e-27	GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYF
UCD037BE498662-3	6.0e-09	Populus x canescens POPARB mRNA, partial cds	2.0e-46	(AC002329) unknown protein [Arabidopsis thaliana]
UCW020BE406932-3	0.32	Salmo salar heat shock protein hsp90 beta (hsp90 beta) m	6.0e-34	hypothetical protein - maize
UCW026BE497999-3	0	Hordeum sp. x Triticum sp. glycine decarboxylase P subu	e-118	glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) [imp
UMC040BE590847-9	0	Triticum aestivum (wali7) mRNA, 3' end, partial cds	6.0e-59	hypothetical protein wali7 - wheat (fragment)
UMC040BF474284-9	0	T.aestivum VDAC2 mRNA for voltage dependent anion cha	3.0e-61	porin VDAC2 - wheat (fragment)
UNL002BE492286-2	0.078	Drosophila melanogaster genomic scaffold 1420000133860	8	(X00269) open reading frame [Zea mays]
UNL053BF292870-3	2.0e-09	Oryza sativa osRAD23 mRNA, complete cds	4.0e-47	(AB005248) DNA repair protein RAD23 homolog [Arabidopsi

C-7DS5-0.36

CSU059BE606458-1	1.0e-46	Hordeum vulgare genomic DNA fragment\; clone MWG0626	1.0e-57	(AB025969) NAD-dependent sorbitol dehydrogenase [Prun
KSU001BE443755-12	0.007	Dictyostelium discoideum nucleoside diphosphate kinase	6	(AF202730) Niemann-Pick type C1 disease protein [Oryctola
KSU012BE443396-4,5	0	Zea mays glucose-6-phosphate\/phosphate-translocator p	e-100	glucose-6-phosphate\/phosphate-translocator precursor,
KSU019BE426692-1	8.0e-21	Oryza sativa manganese superoxide dismutase (rmsod1)	2.0e-80	(AF039000) putative serine-glyoxylate aminotransferase [F
KSU024BE499303-3	2.0e-11	Arabidopsis thaliana putative methionine aminopeptidase	6.0e-13	(AF300880) putative methionine aminopeptidase 2 [Arabido
KSU024BE500081-8,9	1.0e-07	Arabidopsis thaliana genomic DNA, chromosome 5, BAC cl	2.0e-71	(AP002029) N-glyceraldehyde-2-phosphotransferase-like [
KSU027BF478434-1	2.0e-05	Gibberella zeae gene for reductase, partial cds	2.0e-22	(AC078891) Putative NADPH-dependent oxidoreductase [Or
KSU027BF478600-1	8.0e-24	Mesembryanthemum crystallinum cytosolic ascorbate pe	5.0e-45	L-ascorbate peroxidase (EC 1.11.1.11), glyoxysomal - uplan
KSU030BE404899-2	2.0e-36	Arabidopsis thaliana AT5g11200\/F2I11_90 mRNA, complete	1.0e-85	(AF378868) AT5g11200\/F2I11_90 [Arabidopsis thaliana]
KSU035BE404540-1,2	3.0e-29	S.tuberosum (Desiree) cyc1 II mRNA. for cytochrome c1	2.0e-49	(AP000381) ubiquinol-cytochrome c1 reductase cytochrom
KSU035BE404728-1	0.25	Human cosmid Xq28_IA649, complete sequence [Homo sa	4.0e-33	(Y15367) MtN19 [Medicago truncatula]
KSU035BE406976-2,4	2.0e-55	Oryza sativa mRNA for spermidine synthase 1 (spdSyn1 g	1.0e-76	SPERMIDINE SYNTHASE 1 (PUTRESCINE AMINOPROPYLTRANS
KSU038BE442797-4	4.0e-04	Arabidopsis thaliana chromosome 1 BAC F24D7 genomic s	5.0e-50	(AC009999) Contains similarity to Ariadne-2 protein from D
KSU038BE444769-1	0.087	Sequence of BAC F7H2 from Arabidopsis thaliana chromos	4.0e-35	(AC034256) Contains similarity to RP42 from Mus musculu
NDS021BE494078-2	1.2	Oryza sativa chromosome 10 BAC OSJNBa0001O14 genomi	2.1	claudin 18 [Homo sapiens]
NDS043BF293124-1	4.0e-04	Volvox carteri f. nagariensis clone G32 unknown mRNA	7.0e-35	(AC006220) unknown protein [Arabidopsis thaliana]
NDS043BG605575-2	0	T.aestivum L mRNA for histone H2B	4.0e-43	HISTONE H2B
UCD029BE497604-1	4.0e-13	Pisum sativum poly(A) polymerase mRNA, nuclear gene e	6.0e-58	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST F
UCW016BE496839-2,6	3.0e-87	Triticum aestivum WESR2 mRNA, partial sequence	4.0e-36	hypothetical protein F8F16.160 - Arabidopsis thaliana
UCW020BE591865-1	2.0e-04	Nicotiana tabacum wound inducive mRNA , complete cds	4.0e-45	(AB009885) wound inducive gene [Nicotiana tabacum]
UMC040BE637511-9	2.0e-15	Z.mays ABP1 mRNA for actin-depolymerizing factor	6.0e-46	actin-depolymerizing factor 3 - maize
UMC040BG262287-6	e-159	Hordeum vulgare HVA\/68 mRNA for vacuolar proton-ATPa	1.0e-62	(AB032840) vacuolar proton-ATPase [Hordeum vulgare]
UNL044BG263859-2,4	0.12	Leishmania major chromosome 35 clone L1905 strain Frie	3.0e-14	hypothetical protein - Arabidopsis thaliana

C-7DL5-0.30

KSU012BE403622-2,6	2.0e-09	Sequence of BAC F7H2 from Arabidopsis thaliana chromos	7.0e-95	(AC018849) unknown protein\; 52184-57536 [Arabidopsis th
KSU024BE498418-1	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
KSU024BE498849-2	1.0e-34	Arabidopsis thaliana RNA recognition motif-type RNA-bindi	7.0e-60	(AC017118) F6N18.17 [Arabidopsis thaliana]
KSU030BF483454-2	0.42	Genomic Sequence for Oryza sativa, Nipponbare strain, clo	4.0e-13	(AF030386) NOI protein [Arabidopsis thaliana]
NDS018BE404240-1	7.0e-34	T.aestivumn (subclone pAWJL175) AWJL175 gene	1.0e-04	(AF133839) papain-like cysteine protease [Sandersonia aur
UCD037BE638123-3	e-142	Oryza sativa mRNA for succinate dehydrogenase iron-prot	6.0e-74	(AJ012374) iron sulfur subunit of succinate dehydrogenase
UCW039BE446052-2	0.78	Rattus norvegicus antioxidant enzyme B166 mRNA, comple	6.0e-08	(AJ291817) expansin [Cicer arietinum]
UMN013BE444179-1,7	e-136	Oryza sativa GDP dissociation inhibitor protein OsGDI2 (Os	6.0e-64	GDP dissociation inhibitor protein - rice
UNL002BF473119-1,3	0	Triticum aestivum Cu\/Zn superoxide dismutase (SOD1.2)	6.0e-62	superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 2, chloroplast -

7DL5-0.30-0.61

CNL014BE490790-5	0.015	Genomic Sequence For Arabidopsis thaliana Clone T1G16	2.0e-18	(AF160912) BcDNA.LD06837 [Drosophila melanogaster]
CNL031BE403423-6	4.0e-06	Arabidopsis thaliana timing of CAB expression 1 protein (TOC1) mRNA, complete cds		
CSU001BE405498-2,4	4.0e-06	Oryza sativa genomic DNA, chromosome 1, PAC clone:P0001B06		
CSU058BF200526-2,3	3.0e-05	Oryza sativa genomic DNA, chromosome 4, BAC clone:H02	2.0e-11	(AC023628) Similar to UTP-glucose glucosyltransferases [
KSU001BE444301-2	1.5	Arabidopsis thaliana chromosome I BAC F25I16 genomic s	0.24	(AE003581) Chd1 gene product [Drosophila melanogaster]
KSU012BE442619-2	5.0e-09	Arabidopsis thaliana chromosome 1 BAC T6J19 genomic s	8.0e-28	copper homeostasis factor [imported] - Arabidopsis thalia
KSU012BE443436-2	e-151	Oryza sativa genomic DNA, chromosome 2, clone:P0437H0	3.0e-95	(AP000366) Similar to maize transposon MuDR mudrA-like
KSU019BE445239-4	e-125	Oryza sativa mRNA for 26S proteasome ATPase subunit Rp	1.0e-67	(AB033537) 26S proteasome regulatory particle triple-A AT
KSU019BE498785-8	1.0e-06	Mycobacterium smegmatis adhC gene for alcohol dehydr	3.0e-32	PROBABLE MANNITOL DEHYDROGENASE (NAD-DEPENDENT M.
KSU027BE490007-4	e-150	Oryza sativa mRNA for glyoxalase I, complete cds	6.0e-90	(AB017042) glyoxalase I [Oryza sativa]
KSU027BF482769-2	0	Lolium perenne caffeic acid O-methyltransferase (OMT3)	2.0e-87	(AF033538) caffeic acid O-methyltransferase\; LPOMT1 [Lol
KSU035BE403740-3,4,5	8.0e-09	Arabidopsis thaliana AT4g13360\/T9E8_100 mRNA, complete	2.0e-75	3-hydroxyisobutyryl-coenzyme A hydrolase homolog T9E8
KSU035BE406937-4	1.2	S.pombe chromosome II cosmid c3B8	3.0e-22	(AF096247) ethylene-responsive elongation factor EF-Ts pr
KSU035BE406943-4	5.0e-45	Oryza sativa mRNA for elongation factor 1B gamma, compl	8.0e-35	ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA) (EEF-1B GA
KSU038BE446029-2	5.0e-06	Oryza sativa copper chaperone homolog CCH mRNA, comp	8.0e-28	copper homeostasis factor [imported] - Arabidopsis thalia
NDS021BF201644-3	0.9	Oryza sativa chromosome 4 BAC q3037-207F1 complete ge	1.7	BALBIANI RING PROTEIN 3 PRECURSOR
UCD017BE488670-1	1.0e-53	Oryza sativa partial mRNA for putative aminopropyltransfe	6.0e-51	(AJ251302) putative aminopropyltransferase [Oryza sativa]
UCD029BF485273-3	8.0e-14	Arabidopsis thaliana IAA9 (F6H11.210) mRNA, complete cds	1.0e-34	phytochrome-associated protein PAP2 - Arabidopsis thalia
UCD037BE443010-6	3.0e-82	Oryza sativa mRNA for adenylate kinase-a, complete cds	1.0e-53	ADENYLATE KINASE A (ATP-AMP TRANSPHOSPHORYLASE)
UCW016BE497215-2	e-119	Zea mays thiamine biosynthetic enzyme (thi1-1) mRNA, co	6.0e-60	THIAZOLE BIOSYNTHETIC ENZYME 1-2, CHLOROPLAST PREC
UMC040BE590568-2,4	9.0e-78	Oryza sativa signal recognition particle 19 kDa protein sub	2.0e-29	SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19) [Ory
UMN013BE442619-2	5.0e-09	Arabidopsis thaliana chromosome 1 BAC T6J19 genomic s	8.0e-28	copper homeostasis factor [imported] - Arabidopsis thalia
UMN013BE443312-3	2.0e-08	Sequence of BAC T2D23 from Arabidopsis thaliana chrom	1.0e-62	(AF253474) acyl-CoA oxidase [Arabidopsis thaliana]

7DL2-0.61-0.82

CNL014BE423703-16	7.0e-27	Oryza sativa Ub-CEP52-2 gene for ubiquitin fused to riboso	1.0e-32	(AF285859) ubiquitin-like protein [Wuchereria bancrofti]
CNL014BE444328-7	5.0e-13	Genomic Sequence For Oryza sativa, Nipponbare Strain, Cl	7.0e-36	PEROXIDASE
CNL023BF483150-11	9.0e-97	Wheat mRNA for ubiquitin	1.0e-26	(AF093504) tetra-ubiquitin [Saccharum hybrid cultivar H32-8
CSU001BE425207-4	8.0e-08	Nicotiana tabacum (clone: L24-2) chloroplast ribosomal pro	3.0e-36	(AB016879) 50S ribosomal protein L24, chloroplast precurs
CSU057BE490023-4	1.0e-19	Arabidopsis thaliana genomic DNA, chromosome 3, BAC cl	1.0e-98	(AP001298) contains similarity to the auxin-independent gr
CSU058BE518447-1	1.0e-04	T.repens mRNA for cyanogenic beta-glucosidase (linamar	2.0e-52	(AB016879) beta-glucosidase [Arabidopsis thaliana]
KSU001BE403860-9,10	3.0e-10	Oryza sativa microsatellite MRG5838 containing (TCT)X14,	7.0e-30	(AF198054) NAC1 [Arabidopsis thaliana]
KSU001BE442572-3	5.0e-19	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	8.0e-87	(AB024036) contains similarity to EH domain containing pro
KSU001BE442845-2	1.1	Drosophila melanogaster, chromosome 2R, region 45E1-4	1.0e-51	pitrilysin (EC 3.4.24.55) - garden pea
KSU002BE425207-9	8.0e-08	Nicotiana tabacum (clone: L24-2) chloroplast ribosomal pro	3.0e-36	(AB016879) 50S ribosomal protein L24, chloroplast precurs
KSU019BE443559-3	7.0e-06	Arabidopsis thaliana unknown protein (F6F3.4) mRNA, com	2.0e-19	(AC023628) Unknown protein [Arabidopsis thaliana]
KSU024BF484707-1	0.37	Homo sapiens chromosome 3, olfactory receptor pseudo	6.0e-08	(AB023042) gene_id:MUL3.13~pir||T04254~similar to unknow
KSU024BG274853-1	9.0e-57	Arabidopsis thaliana zinc dependent protease (VAR2) mR	6.0e-57	(AJ012165) chloroplast protease [Capsicum annuum]
KSU030BE518357-2,4	3.0e-60	Oryza sativa subsp. japonica clone S4892 putative glutathic	5.0e-55	(AF309381) putative glutathione S-transferase OsGSTZ1 [O
KSU035BE404434-2	e-114	Lycopersicon esculentum elongation factor 2 mRNA, parti	2.0e-96	ELONGATION FACTOR 2 (EF-2)
KSU038BE489323-7	0.086	Arabidopsis thaliana DNA chromosome 3, BAC clone F1P2	9.0e-15	(AF247646) transposase [Zea mays]
NDS001BE443753-2	1.3	Tauraco erythrolophus cytochrome b gene, partial cds\; mitochondrial gene for mitochondrial product		
NDS021BE406148-2	8.0e-14	Arabidopsis thaliana cyclophilin (ROC7) mRNA, complete c	4.0e-44	cyclophilin CYP5 [imported] - Arabidopsis thaliana
UCD001BE442572-2,6	5.0e-19	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	8.0e-87	(AB024036) contains similarity to EH domain containing pro
UCD017BE488496-3	0	Hordeum vulgare Mg-chelatase subunit (Xantha-h) mRNA,	1.0e-47	protoporphyrin IX magnesium chelatase (EC 4.99.1.-) Xanth
UCW039BE405131-4	3.0e-57	Musa acuminata mRNA for unknown ripening-related prot	1.0e-75	(AB023034) ATP citrate lyase [Arabidopsis thaliana]
UMC015BE590741-1	0	T.aestivum 1b-c38 gene for HBP-1b (leucine zipper type tra	2.0e-20	probable 26S proteasome non-ATPase chain S5a [importe
UNL002BF199604-2	0.37	Caenorhabditis elegans cosmid C09G4, complete sequen	2.0e-08	hypothetical protein T29F13.4 - Arabidopsis thaliana
UNL002BF200008-3	1.6	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt	2.0e-14	(AP001073) Similar to Oryza sativa gene for Pib. (AB013448)
UNL036BE497375-2,3	1.0e-07	Lycopersicon esculentum auxin-regulated IAA6 (IAA6) mR	1.0e-10	auxin-induced protein IAA9 - Arabidopsis thaliana
UNL036BE606874-3	0	Triticum aestivum granule-bound starch synthase I (Wx-Dl	1.0e-58	(AB019624) starch synthase (GBSSI) [Triticum aestivum] ta
UNL044BF485408-1	0.022	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA conti	9.0e-42	hypothetical protein - Arabidopsis thaliana
UNL044BG274514-6	e-147	Rice mRNA for ubiquitin protein fused to a ribosomal prote	2.0e-60	ubiquitin \/ ribosomal protein CEP52 - rice
UNL048BE446586-2	0.38	Drosophila melanogaster genomic scaffold 1420000133860	1.0e-24	(AC079041) unknown protein [Arabidopsis thaliana]
UNL048BE591273-3	0.087	Homo sapiens chromosome 3 clone RP11-127I14 map 3p,	2.0e-24	hypothetical protein T10K17.100 - Arabidopsis thaliana
UNL048BF428786-1	0.019	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence,	2.0e-46	(AC007060) T5I8.13 [Arabidopsis thaliana]
UNL053BF475000-1	0	Zea mays translation initiation factor eIF-4A mRNA, comple	e-113	EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) (EIF4A)

7DL3-0.82-1.00

CSU059BG604419-3,4,5	7.0e-14	Arabidopsis thaliana ISA1 gene	3.0e-52	(Y14404) putative arabinose kinase [Arabidopsis thaliana]
KSU012BE403180-1,6	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
KSU012BE404744-2	5.0e-06	Z.mays CYP71C4 mRNA for cytochrome P-450	2.0e-42	CYTOCHROME P450 71C4
KSU012BE490643-6	1.0e-49	Hordeum vulgare mRNA for vacuolar membrane proton-tr	8.0e-12	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTO
KSU019BE404737-3	6.0e-06	Arabidopsis thaliana chromosome III BAC F13E7 genomic	2.0e-77	(AB005242) S-adenosylmethionine:2-demethylmenaquinon
KSU038BE445506-2	1.0e-07	Oryza sativa genomic DNA, chromosome 6, clone:P0535G0	1.0e-46	(AC007127) putative protein kinase [Arabidopsis thaliana]
KSU038BE446244-5,9	0.091	Human DNA sequence from clone RP13-153N15 on chromo	2.0e-33	(AC037197) Putative hypersensitivity-related protein [Oryz
NDS018BE426274-8	3.0e-75	Hordeum vulgare mRNA for hypothetical protein, partial, cl	1.0e-50	(AB007627) homeobox gene [Oryza sativa]
UCD028BF291608-2	2.0e-64	Lupinus luteus ribosomal protein S14 (rps14) mRNA, comp	1.0e-66	40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
UCD029BE591469-3	0	Hordeum vulgare catalase 1 (CAT1) gene, partial cds	e-129	(AF021938) catalase 1 [Hordeum vulgare]
UCD037BE488895-1,3,6	0.38	Carex divisa internal transcribed spacer 1, partial sequenc	8.0e-10	(U63012) lectin precursor [Sophora japonica]
UCD037BE489651-2	2.0e-16	Hordeum vulgare mRNA for putative thiol protease, clone	0.027	probable cysteine proteinase (EC 3.4.22.-) - barley (fragme
UCW016BE604102-2	4.0e-63	A.thaliana mRNA for chloroplast FtsH protease	e-104	CELL DIVISION PROTEIN FTSH HOMOLOG, CHLOROPLAST PR
UMC015BE426680-10	0	Avena fatua ras-like small monomeric GTP-binding protei	7.0e-79	(AF084005) ras-like small monomeric GTP-binding protein
UNL036BE637476-2	0	Hordeum vulgare catalase (Cat1) mRNA, complete cds	1.0e-91	CATALASE ISOZYME 1
UNL053BF293421-5,7	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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