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

Deletion Map of *Triticum aestivum* cv. Chinese Spring (Chromosome 1B)*

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.

Breakpoint / **Bin Assignment**

Breakpoint	Bin Assignment
	1BS.sat18-0.50-1.00
4DL-9/1BS-18 0.50	1BS.sat19-0.31-0.50
6DS-4/1BS-19 0.31	1BS.sat-0.31
7DL-3/1BS-2 1.06	1BS9-0.84-1.06
1BS-9 0.84	1BS10-0.50-0.84
1BS-10 0.50	C-1BS10-0.50
C	C-C1B
	C-1BL6-0.32
1BL-6 0.32	1BL6-0.32-0.47
1BL-1 0.47	1BL1-0.47-0.69
6AL-8/1BL-2 0.69	1BL2-0.69-0.83
5AS-10/1BL-3 0.83	1BL3-0.83-1.00

1B

1BS.sat18-0.50-1.00

CNL001BE406612-1	2.0e-22	Oryza sativa chromosome 5 clone P0574H01, complete seq	2.0e-08	cysteine proteinase (EC 3.4.22.-) F23E12.90 - Arabidopsis th
CNL014BE406450-2	3.0e-07	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-51	(U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsi
CNL014BE445204-1,3	3.0e-18	Hordeum vulgare beta-D-glucan exohydrolase isoenzyme	3.7	(AC074110) hypothetical protein [Arabidopsis thaliana]
CNL031BE637568-2	7.0e-08	A.sativa seed storage protein gene, complete cds	9.0e-21	avenin precursor - oat
KSU001BE399288-4,6	0.078	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIG10		
KSU012BE406438-3,5	2.0e-07	Arabidopsis thaliana chromosome II section 86 of 255 of th	8.0e-14	(AF116752) seed maturation protein PM23 [Glycine max]
KSU012BE406450-3,5	3.0e-07	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-51	(U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsi
KSU012BE442682-3,4,5,6,7	1.0e-28	H.vulgare chymotryposin inhibitor-2 gene		
KSU012BE443401-2,4,7	4.0e-63	Hordeum vulgare mRNA for hypothetical protein, clone RG	3.0e-84	(AC003672) putative heme A: farnesyltransferase [Arabido
KSU019BE426701-5	2.0e-20	Oryza sativa OsIF1-1 mRNA for F1F0-ATPase inhibitor prote	8.0e-13	(AB029059) F1F0-ATPase inhibitor protein [Oryza sativa]
KSU024BE500104-2	0.1	Drosophila melanogaster genomic scaffold 1420000133860	2.0e-08	(D21813) ORF [Lilium longiflorum]
KSU027BE490041-1	0.006	Petunia x hybrida PHAP2A protein (Ap2A) mRNA, complete	1.0e-32	(AF134116) APETALA2 protein homolog HAP2 [Hyacinthus c
KSU027BE517941-3	2.0e-23	Hordeum vulgare partial mRNA for putative proteinase inh	4.0e-20	(AJ250663) putative proteinase inhibitor [Hordeum vulgare
KSU027BE590674-2,3	0	T.aestivum Glu-B3 gene	5.0e-31	glutenin low molecular weight - wheat (fragment)
KSU027BF482663-4,5,6,11	5.0e-12	Oryza sativa lipoxygenase (CM-LOX1) mRNA, partial cds	5.0e-30	probable lipoxygenase (EC 1.13.11.12) (clone H1) - potato
KSU030BE606926-4,6	0.49	Homo sapiens unconventional myosin (MYO15) gene, part	1.0e-19	(AC013483) putative GTPase activator protein [Arabidopsis
KSU030BG313350-1	3.0e-17	A.thaliana mRNA for CaLB protein	9.0e-91	CaLB protein - Arabidopsis thaliana
KSU035BE404740-6,12	0.024	Homo sapiens chromosome 5, BAC clone 45m2 (LBNL H14	6.0e-61	(AB016893) 26S proteasome p55 protein-like [Arabidopsis
KSU038BE444890-2	3.0e-11	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	4.0e-59	probable 12-oxophytodienoate reductase (EC 1.3.1.42) - Ma
TTU025BE406438-3	2.0e-07	Arabidopsis thaliana chromosome II section 86 of 255 of th	8.0e-14	(AF116752) seed maturation protein PM23 [Glycine max]
TTU025BE406450-3	3.0e-07	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-51	(U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsi
TTU047BE405648-1	e-114	Zea mays mus1 gene, exons 1-13	e-102	DNA MISMATCH REPAIR PROTEIN MSH2 (MUS1)
UCD029BE637553-3,4,5,6,8,9,10,11,12,14,16	0.001	Plasmodium falciparum ADA2-like protein gene, partial cds		
UCD037BE443103-1	1.8	Arabidopsis thaliana DNA chromosome 4, BAC clone F20B	2.0e-23	DNA-BINDING PROTEIN HEXBP (HEXAMER-BINDING PROTEIN)
UCW020BE494541-1,3	0.26	Oryza sativa GS gene for cytosolic glutamine synthetase, complete cds		
UMC040BE590575-2,4,5,10	3.0e-47	Triticum aestivum omega gliadin pseudogene, complete s	2.1	cytochrome c oxidase subunit 1 [Tetrahymena pyriformis]
UMC040BE591042-4	e-163	Hordeum vulgare plasma membrane associated protein (p	1.0e-65	(AF218627) plasma membrane associated protein [Hordeu
UNL002BE405778-1,3	e-120	Hordeum vulgare genomic sequence, clone BAC 711N16, is	2.0e-65	(AY009938) Mla1 [Hordeum vulgare]
UNL002BE498831-3,4	1.0e-10	Triticum aestivum cyst nematode resistance gene candid	3.0e-40	probable cyst nematode resistance gene - wheat (fragme
UNL002BE518223-4	3.0e-63	Hordeum vulgare NBS-LRR type resistance protein (b6) ge	2.0e-46	(AB019240) RPR1h [Oryza sativa]
UNL002BF474204-2,3	3.0e-05	Triticum aestivum cyst nematode resistance gene candid	5.0e-37	probable cyst nematode resistance gene - wheat (fragme
UNL002BF475048-2	3.0e-09	Oryza sativa mRNA for RPR1h, complete cds	3.0e-34	(AB019186) RPR1 [Oryza sativa]
UNL002BF483881-3,4	0.36	Homo sapiens clone RP11-350H1 from 7p14-15, complete s	3.0e-32	probable cyst nematode resistance gene - wheat (fragme
UNL048BF428925-1,2,4,5	4.0e-07	Arabidopsis thaliana chromosome III P1 MGH6 genomic se	3.0e-67	ELONGATION FACTOR 2 (EF-2)

1BS.sat19-0.31-0.50

UCW001BE399288-2	0.078	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIG10		

1BS.sat-0.31

CNL014BE445121-2	7.0e-21	Brassica juncea mRNA for gamma-glutamylcysteine synth	2.0e-79	GLUTAMATE--CYSTEINE LIGASE, CHLOROPLAST PRECURSOI

1BS9-0.84-1.06

TTU047BE494321-7	3.0e-38	Daucus carota mRNA for P40-like protein, complete cds	7.0e-38	40S RIBOSOMAL PROTEIN SA (P40)
UCD028BE426663-4	e-139	Oryza sativa DHAR1 mRNA for GSH-dependent dehydroasc	e-100	(AB037970) GSH-dependent dehydroascorbate reductase 1
UCD037BG263028-2,3	e-105	Rice mRNA for aspartic proteinase, complete cds	3.0e-85	ASPARTIC PROTEINASE PRECURSOR
UMC015BE426274-1	3.0e-75	Hordeum vulgare mRNA for hypothetical protein, partial, cl	1.0e-50	(AB007627) homeobox gene [Oryza sativa]
UMC015BE426301-1	4.0e-65	Oryza sativa chromosome 4 BAC H332 genomic sequence	1.0e-80	(AL117264) zwh21.1 [Oryza sativa]
UNL036BE497177-3	4.0e-16	Brassica juncea mRNA for gamma-glutamylcysteine synth	2.0e-67	GLUTAMATE--CYSTEINE LIGASE, CHLOROPLAST PRECURSOI

1BS10-0.50-0.84

CNL001BE426257-3	7.0e-27	Oryza sativa chromosome 5 clone P0001A07, complete seq	1.0e-85	(AC084218) similar to Pisum sativum methylenetetrahydro
CNL014BE444328-6	5.0e-13	Genomic Sequence For Oryza sativa, Nipponbare Strain, Cl	7.0e-36	PEROXIDASE
CSU001BE426257-3	7.0e-27	Oryza sativa chromosome 5 clone P0001A07, complete seq	1.0e-85	(AC084218) similar to Pisum sativum methylenetetrahydro
CSU001BE426488-3	5.0e-16	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7	7.0e-95	argininosuccinate synthase (EC 6.3.4.5) - Arabidopsis thali
CSU046BE443071-1	9.0e-27	Oryza sativa chromosome 5 clone P0431G05, complete seq	2.0e-87	hypothetical protein F26K9.30 - Arabidopsis thaliana
CSU046BE444859-4	7.0e-40	Oryza sativa chromosome 5 clone P0431G05, complete seq	1.0e-86	probable protein disulfide-isomerase (EC 5.3.4.1) precurso
CSU057BE489895-1	3.0e-11	Arabidopsis thaliana putative serine protease (F17A22.33\	1.0e-90	(AC005309) putative serine protease [Arabidopsis thaliana
KSU001BE443755-1	0.007	Dictyostelium discoideum nucleoside diphosphate kinase	6	(AF202730) Niemann-Pick type C1 disease protein [Oryctola
KSU002BE425354-1	1.1	Arabidopsis thaliana DNA chromosome 3, BAC clone T6L1	1.0e-42	hypothetical protein T11I11.70 - Arabidopsis thaliana
KSU002BE426257-3	7.0e-27	Oryza sativa chromosome 5 clone P0001A07, complete seq	1.0e-85	(AC084218) similar to Pisum sativum methylenetetrahydro
KSU012BE403153-3,5	e-148	Avena fatua mRNA for VIP2 protein (vip2 gene)	4.0e-61	(AJ251051) VIP2 protein [Avena fatua]
KSU012BE403553-3	7.0e-39	Oryza sativa chromosome 4 BAC q3037-207F1 complete ge	6.0e-50	(AJ245900) CAA303716.1 protein [Oryza sativa]
KSU012BE403867-3	2.0e-71	Sorghum bicolor pathogenesis-related protein (PR-10) mR	2.0e-51	pathogenesis-related protein - sorghum
KSU012BE490643-5	1.0e-49	Hordeum vulgare mRNA for vacuolar membrane proton-tr	8.0e-12	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTO
UCD001BE406512-1	0.044	Drosophila melanogaster, chromosome 2R, region 50C-50	2.0e-15	(AB010069) contains similarity to RNA binding protein~gen
UCW003BE590695-1	2.0e-91	H.vulgare gene encoding serine carboxypeptidase II, CP-M	3.0e-85	Chain B, Structural Basis For Light Acitvation Of A Chloropl
UCW003BE590760-1	2.0e-85	Hordeum vulgare glucose and ribitol dehydrogenase hom	4.0e-21	glucose and ribitol dehydrogenase homolog - barley
UCW016BE590695-1	2.0e-91	H.vulgare gene encoding serine carboxypeptidase II, CP-M	3.0e-85	Chain B, Structural Basis For Light Acitvation Of A Chloropl
UCW016BE590760-1	2.0e-85	Hordeum vulgare glucose and ribitol dehydrogenase hom	4.0e-21	glucose and ribitol dehydrogenase homolog - barley
UCW020BE499900-4	4.0e-44	Arabidopsis thaliana AT3g52990\F8J2_160 mRNA, complete	1.0e-85	pyruvate kinase-like protein - Arabidopsis thaliana
UCW026BE498820-3	0	Oryza sativa mRNA for importin alpha 1b, complete cds	e-102	(AB024311) importin alpha 1b [Oryza sativa]
UCW026BG262247-2	5.0e-62	Oryza sativa 2-oxoglutarate\malate translocator mRNA, pa	e-102	2-oxoglutarate\malate translocator (clones OMT134 and Ol
UCW039BE443797-3	8.0e-52	Oryza sativa genomic DNA, chromosome 1, PAC clone:P05	2.0e-34	(AB012245) 26S proteasome subunit-like protein [Arabidop

C-1BS19-0.31

UCD001BE406516-2	2.0e-26	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	2.0e-64	(AP003244) casein kinase-like protein [Oryza sativa]
UCD001BE442851-3	0.11	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-639F2 of library RPCI-11 from chromosome 14 of Homo sapi		
UCD001BE444294-5	0.36	Caenorhabditis elegans cosmid C08G9	5.0e-45	(AB024035) gb|AAD55473.1~gene_id:MHM17.18~similar to u

C-1BS10-0.50

KSU001BE442851-2	0.11	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-639F2 of library RPCI-11 from chromosome 14 of Homo sapi		
KSU012BE443430-2	2.0e-05	Arabidopsis thaliana RNA polymerase II 13.6 kDa subunit (A	1.0e-47	DNA-DIRECTED RNA POLYMERASE II 13.6 KDA POLYPEPTIDE A
KSU019BE406901-1,5	1.0e-15	Oryza sativa genomic DNA, chromosome 1, PAC clone:P05	1.0e-31	(AP002869) putative lipase homolog [Oryza sativa]
KSU024BE499250-2	e-135	Rice mRNA for GTP binding protein	4.0e-79	RAS-RELATED PROTEIN RGP2 (GTP-BINDING REGULATORY PR
KSU027BF202643-4	1.0e-28	Oryza sativa chromosome 10 clone nbxb0045B21, complete	1.0e-46	(AB026644) prolyl 4-hydroxylase alpha subunit-like protein
KSU035BE497372-2	1.0e-05	Hordeum vulgare mRNA for expressed sequence tag	4.0e-45	(AC011620) putative serine\threonine protein phosphatase
KSU038BE489323-4	0.086	Arabidopsis thaliana DNA chromosome 3, BAC clone F1P2	9.0e-15	(AF247646) transposase [Zea mays]
NDS001BE442851-3	0.11	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-639F2 of library RPCI-11 from chromosome 14 of Homo sapi		
TTU047BE494680-4	9.0e-05	Arabidopsis thaliana AT4g37830\T28I19_110 mRNA, comple	2.0e-24	hypothetical protein T28I19.110 - Arabidopsis thaliana
UCD029BE604047-3	3.0e-04	Arabidopsis thaliana unknown protein (F5D14.17) mRNA, c	1.0e-29	(AF334723) unknown protein [Arabidopsis thaliana]

C-1BL6-0.32

CNL023BE405613-6	0	T.aestivum beta glucanase mRNA, complete CDS	e-106	(Z22873) beta glucanase [Triticum aestivum]
CNL031BE404005-2	0.29	Lactuca sativa resistance protein candidate RGC2A (RGC2A	4.0e-17	(AC007134) unknown protein [Arabidopsis thaliana]
CNL031BE405692-8	7.0e-49	Zea mays glutathione S-transferase GST 42 mRNA, partial	2.0e-54	(AF244707) glutathione S-transferase GST 42 [Zea mays]
CSU046BE444527-2	0.094	Pestivirus type 1 cytopathic genomic RNA, complete genom	1.0e-41	hypothetical protein T27E13.16 - Arabidopsis thaliana thalia
CSU058BE518358-1	1.0e-15	Arabidopsis thaliana genomic DNA, chromosome 5, BAC cl	1.0e-62	(AB028605) protein kinase-like protein [Arabidopsis thaliar
CSU058BE518403-2	0	Lophopyrum elongatum protein serine\threonine kinase	4.0e-30	(AF131222) protein serine\threonine kinase [Lophopyrum
KSU001BE442924-2	0.007	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K6M13		
KSU024BE500081-4,5,6	1.0e-07	Arabidopsis thaliana genomic DNA, chromosome 5, BAC cl	2.0e-71	(AP002029) N-glyceraldehyde-2-phosphotransferase-like [A
KSU024BE500310-2	4.0e-59	Oryza sativa chromosome 10 BAC OSJNBa0003O19 genomi	2.0e-57	(AC060755) unknown protein [Oryza sativa]
KSU024BE606502-2,4	0.11	Human DNA sequence from clone RP1-130E4 on chromoso	0.83	pleckstrin homology domain-containing, family A (phosph
KSU035BE403404-6	9.0e-22	Catharanthus roseus PAPS-reductase-like protein (par2ne	8.0e-42	(U63784) PAPS-reductase-like protein [Catharanthus roseu
KSU035BE403420-3	8.0e-30	Oryza sativa chromosome 10 BAC OSJNBb0011A08 genomi	3.0e-62	(AC034258) putative thiolase [Oryza sativa]
KSU035BE497107-1,6	5.0e-47	Oryza sativa chromsome 9 clone PAC0645D04, complete s	7.0e-84	RAS-RELATED PROTEIN RAB11D
KSU035BE497584-4	e-123	Z.mays CPNB gene encoding mitochondrial chaperonin-60	2.0e-52	CHAPERONIN CPN60-2, MITOCHONDRIAL PRECURSOR (HSP60
KSU035BE497600-3	0.045	Nicotiana tabacum mRNA for ethylene responsive element	4.0e-17	transcription factor DREB2A, drought induced [validated] - .
KSU038BE444094-3,4	0.09	Human DNA sequence from clone 1045J21 on chromosom	3.0e-61	(AJ238212) glutamine synthetase I [Medicago truncatula]
KSU038BE444638-5	0.34	Human DNA sequence from clone RP11-300B2 on chromos	3.0e-23	POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE 2
KSU038BE446010-1	2.0e-52	Oryza sativa chromosome 10 BAC OSJNBa0079L16 genomi	2.0e-62	(AB004568) cyanase [Arabidopsis thaliana]
UCD017BE494376-3	2.0e-39	Rice mRNA for Cytochrome b5	1.0e-57	(AC025296) putative cytochrome [Oryza sativa]
UCD017BE494853-1,2	5.0e-09	Oryza sativa putative lipid transfer protein (Ltp-2) gene, co	2.0e-22	probable lipid transfer protein - rice
UCD028BE497109-3	2.0e-76	Hordeum vulgare RNase S-like protein precursor (rsh1) ge	4.0e-68	(AF182197) RNase S-like protein precursor [Hordeum vulga
UCW039BE446312-2	0	Wheat (clone p28-1) initiation factor isozyme 4F p82 subun	2.0e-42	EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (
UMC040BF474511-4	1.0e-04	Arabidopsis thaliana IAA2 (MXC7.6) mRNA, complete cds	2.0e-21	(AF123509) Nt-iaa4.1 deduced protein [Nicotiana tabacum]
UMC055BF482555-2,5	3.0e-04	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	1.0e-29	(AB025631) contains similarity to transcription factor CA15
UMN013BE442876-1	2.0e-49	Oryza sativa clone riceipp2 isopentenyl pyrophosphate:dir	1.0e-75	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) 1 - C
UMN013BE443531-1	4.0e-38	S.tuberosum LAP mRNA for leucine aminopeptidase	4.0e-81	leucyl aminopeptidase (EC 3.4.11.1) - parsley (fragment)
UMN013BE444505-1	0.38	Human DNA sequence from clone RP11-473L1 on chromos	9.0e-25	(AC051629) Unknown protein [Arabidopsis thaliana]
UNL036BE518393-4,5,6,7	e-119	Oryza sativa chromosome 10 BAC OSJNBa0006L06 genomi	7.0e-71	(AF334838) ribosomal protein L17 [Castanea sativa]

1BL6-0.32-0.47

CSU001BE442858-3	1.3	Homo sapiens chromosome 19, cosmid R27216 (LLNLR-23	4.0e-05	(X98316) peroxidase [Arabidopsis thaliana]
KSU012BE352628-2	2.0e-37	Oryza sativa chromosome 10 BAC OSJNBb0089A17 genomi	2.0e-85	(AC079890) unknown protein [Oryza sativa]
KSU012BE403956-2	2.0e-79	Zea mays beta-expansin 8 (expB8) mRNA, complete cds	2.0e-65	(AF261272) beta-expansin [Oryza sativa]
KSU012BE442716-1	e-108	A.sativa (Pewi) ASTCP-K19 mRNA for t complex polypeptid	4.0e-92	T complex protein [Cucumis sativus]
KSU035BE407013-1	0.28	Caulobacter crescentus section 121 of 359 of the complet	4.0e-44	(AB012239) autophagocytosis protein AUT1-like [Arabidops
KSU038BE444757-6	4.0e-65	Oryza sativa chromosome 10 clone nbxb0046P18, complete	2.0e-76	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CON
NDS034BE490430-2,5	6.0e-23	Oryza sativa chromosome 10 BAC OSJNBa0027P10 genomi	1.0e-10	(AC084763) putative casein kinase II beta subunit [Oryza sa
UCW016BE517774-1	6.0e-73	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-32	(AP003244) putative ethylene-responsive RNA helicase [Or
UCW016BE518309-1,2,3	4.0e-07	M.sativa mRNA for cdc2 kinase homologue, cdc2MsC	3.0e-84	cdc2-like protein kinase cdc2MsC - alfalfa
UCW039BE405167-2	2.0e-64	Zea mays ubiquitin-conjugating enzyme mRNA, partial cds	3.0e-73	E2 ubiquitin-conjugating-like enzyme Ahus5 - Arabidopsis
UMC040BE606632-10	1.0e-98	Hordeum vulgare cv. Haisa mRNA for MCB1 protein	3.0e-31	(AJ303354) MCB1 protein [Hordeum vulgare]
UNL036BE590719-3	1.0e-37	Triticum aestivum cold-responsive LEA\RAB-related COR	2.0e-51	LEA protein - rice

1BL1-0.47-0.69

CNL014BE445113-3	1.0e-95	Sorghum bicolor cytochrome P450 CYP98A1 (CYP98A1) mR	6.0e-52	CYTOCHROME P450 98A1
CSU057BE490064-2,3	6.0e-15	Arabidopsis thaliana genomic DNA, chromosome 3, TAC cl	1.0e-66	(AB028608) phospholipase D-like protein [Arabidopsis thal
KSU001BE398611-4,5	0.096	Drosophila melanogaster maroon-like protein (mal) gene,	0.35	(AE003708) ldlCp gene product [Drosophila melanogaster]
KSU001BE443789-3	0.23	Homo sapiens spindlin (SPIN), mRNA		
KSU002BE405581-2,5	2.0e-06	Arabidopsis thaliana chromosome II section 201 of 255 of	7.0e-23	(AC006922) unknown protein [Arabidopsis thaliana]
KSU002BE406605-1	0.15	Drosophila melanogaster, chromosome 3R, region 98A-98	0.2	HYPOTHETICAL 113.1 KD PROTEIN T28D9.7 IN CHROMOSOME
KSU002BE426488-1	5.0e-16	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7	7.0e-95	argininosuccinate synthase (EC 6.3.4.5) - Arabidopsis thali
KSU012BE442818-4	4.0e-10	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	4.0e-71	(AP000604) contains similarity to unknown protein~gb|AAF
KSU012BE442876-1	2.0e-49	Oryza sativa clone riceipp2 isopentenyl pyrophosphate:dir	1.0e-75	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) 1 - C
KSU019BE405414-2,4	1.0e-09	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	8.0e-60	(AC009853) unknown protein [Arabidopsis thaliana]
KSU019BE444620-2	e-142	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	5.0e-84	(AP002522) hypothetical protein [Oryza sativa]
KSU019BE495150-5	1.0e-99	Zea mays cytochrome b5 reductase (NFR) mRNA, complete	2.0e-73	(AF077372) cytochrome b5 reductase [Zea mays]
KSU024BE497808-4	0	Wheat histone H4 gene	9.0e-40	histone H4 [Triticum aestivum]
KSU024BF202735-3	2.0e-07	Oryza sativa protein phosphatase 2A 55 kDa B regulatory subunit gene, complete cds		
KSU027BE495028-4	e-147	Oryza sativa calmodulin (CaM2) mRNA, complete cds	5.0e-72	(X65016) calmodulin [Oryza sativa]
KSU030BE637473-2	e-115	Triticum aestivum secretory protein (WAS-2) mRNA, comp	1.0e-42	(AF079526) secretory protein [Triticum aestivum]
KSU030BF200980-2	3.0e-57	Zea mays translation initiation factor GOS2 (TIF) mRNA, cor	4.0e-54	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PRO
KSU035BE404723-1	1.2	Homo sapiens 12p BAC RP11-625L16 (Roswell Park Cancer	2.0e-29	(Z99707) RNA-binding like protein [Arabidopsis thaliana]
KSU035BE406918-4,5	2.0e-11	Oryza sativa subsp. indica putative aldehyde dehydrogena	5.0e-45	(AC074228) aldehyde dehydrogenase, putative [Arabidopsi
KSU035BE406943-7	5.0e-45	Oryza sativa mRNA for elongation factor 1B gamma, compl	8.0e-35	ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA) (EEF-1B GAM
KSU035BE406977-2,4,6,9,10,11	e-117	H.vulgare ids-1 mRNA	1.0e-17	(D50641) plant metallothionein-like protein [Hordeum vulga
KSU035BE496824-1	0.021	Caenorhabditis elegans cosmid B0496, complete sequenc	1.0e-36	(AB023036) contains similarity to endo-1,3-1,4-beta-D-gluca
KSU038BE443905-2	0.43	Drosophila melanogaster, chromosome 2L, region 37D, BA	4.0e-26	pit2 protein (clone pAL141), Pi starvation induced - commo
KSU038BE443930-3	3.0e-72	Saccharum officinarum pyruvate orthophosphate dikinase	5.0e-40	(M58656) pyruvate,orthophosphate dikinase [Zea mays]
KSU038BE445834-3,4	0.85	Arabidopsis thaliana BAC F7K24	3.0e-13	(AB017067) TMV resistance protein-like [Arabidopsis thali
KSU038BE446240-3	e-157	Oryza sativa GDP dissociation inhibitor protein OsGDI2 (Os	2.0e-87	GDP dissociation inhibitor protein - rice
NDS001BE405594-1	0.12	Homo sapiens chromosome 5 clone CTB-2J5, complete se	2.2	probable regulatory protein - Streptomyces coelicolor A3(
NDS018BE404147-1	1.0e-15	Pisum sativum nucleoside diphosphate kinase (ndpk) mR	2.0e-21	hypothetical protein T32A16.70 - Arabidopsis thaliana
NDS018BE404880-1,2	3.0e-05	N.crassa mRNA for mitochondrial 12 kD subunit of NADH:ub	1.0e-30	probable acyl carrier protein T8F5.6 - Arabidopsis thaliana
NDS034BE403158-3,5	4.0e-87	H.vulgare Bsi1 gene for putative protease inhibitor	5.0e-36	wheat aluminum induced protein wali 5 - wheat
NDS034BE470696-2	0.005	Arabidopsis thaliana mRNA for 2-oxoglutarate dehydrogen	3.0e-25	(AB010071) 2-oxoglutarate dehydrogenase E2 subunit [Aral
NDS034BF200980-2	3.0e-57	Zea mays translation initiation factor GOS2 (TIF) mRNA, cor	4.0e-54	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PRO
NDS043BF292349-3,4	0.016	Zea mays clone tac_919.27 Ac insertion site sequence	1.0e-33	(AC012654) Strong similarity to the putative GDSL-motif co
NDS043BG274942-3	0.025	Homo sapiens nerve growth factor receptor (TNFR superf	5.0e-25	(AP001299) gene_id:F4B12.9~unknown protein [Arabidopsi
TTU025BE490592-1	2.0e-42	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	9.0e-76	(AP003053) putative malate dehydrogenase [Oryza sativa]
UCD001BE405594-1	0.12	Homo sapiens chromosome 5 clone CTB-2J5, complete se	2.2	probable regulatory protein - Streptomyces coelicolor A3(
UCD001BE406605-6	0.15	Drosophila melanogaster, chromosome 3R, region 98A-98	0.2	HYPOTHETICAL 113.1 KD PROTEIN T28D9.7 IN CHROMOSOME
UCD001BE443789-3	0.23	Homo sapiens spindlin (SPIN), mRNA		
UCD001BE444378-1	6.0e-09	Arabidopsis thaliana genomic DNA, chromosome 3, TAC cl	1.0e-53	hypothetical protein T24A18.30 - Arabidopsis thaliana
UCD029BE517991-2	1.0e-04	A.thaliana rpl1 gene	2.0e-29	(X90855) L1 protein [Arabidopsis thaliana]
UCD029BF483378-8	e-110	Oryza sativa OsPAG1 mRNA for alpha 7 subunit of 20S prot	3.0e-87	PROTEASOME SUBUNIT ALPHA TYPE 3 (20S PROTEASOME AL
UCD029BF483456-2	2.0e-80	Arabidopsis thaliana AT3g62830\F26K9_260 gene, complet	e-109	dTDP-glucose 4-6-dehydratase homolog T30B22.4 - Arabid
UCD037BE443332-1	5.0e-10	Arabidopsis thaliana unknown protein (AT4g21860) mRNA,	6.0e-45	(AF360341) unknown protein [Arabidopsis thaliana]
UCD037BE488529-4	1.4	Homo sapiens chromosome 5 clone CTD-2213L16, comple	5.0e-55	(AC006434) F10A5.27 [Arabidopsis thaliana] subunit [Arabic
UCW020BE404660-3	e-170	Zea mays ubiquitin conjugating enzyme (UBC) mRNA, com	6.0e-85	(AF034946) ubiquitin conjugating enzyme [Zea mays]
UMC032BF291740-4,6	6.0e-25	Spinacia oleracea phosphoethanolamine N-methyltransfer	2.0e-81	(AB019230) methyl transferase-like protein [Arabidopsis th
UMN013BE443722-4	1.0e-06	Hordeum vulgare (cv. Bomi) B12D mRNA	9.0e-30	hypothetical protein T24C20.20 - Arabidopsis thaliana
UNL002BF473313-1	1.0e-06	Hordeum vulgare NBS-LRR type resistance protein (b7) ge	3.0e-39	NBS-LRR type resistance protein - barley (fragment)
UNL044BF482786-3	0.32	Caenorhabditis elegans transmembrane cell adhesion rec	5.0e-32	(AC009519) F1N19.9 [Arabidopsis thaliana]
UNL044BF483820-2	2.0e-17	Rice gene for ferredoxin, complete cds	1.0e-14	ferredoxin [2Fe-2S], root - rice
UNL048BE445579-3	1.2	Streptomyces antibioticus putative 3-ketoreductase (oleW	1.0e-53	(AF002109) unknown protein [Arabidopsis thaliana]

1BL2-0.69-0.83

CSU102BE406562-4	0.96	Sus scrofa large white\landrace cross myosin heavy chain mRNA, partial cds		
KSU001BE406602-8	2.0e-16	Zea mays 40S ribosomal protein S24 mRNA, complete cds	3.0e-19	(AF298769) 40S ribosomal protein S24 [Zea mays]
KSU001BE443720-1	0.024	Homo sapiens BAC clone RP11-235I1 from Y, complete sec	9.0e-18	(AC010926) protein phosphatase 2C (AtP2C-HA)\; 19519-176
KSU001BE444305-3	0.026	Staphylococcus aureus serine protease spl operon, comp	4.0e-15	(AJ276270) hypothetical protein [Cicer arietinum]
KSU001BE444359-3,5,7	2.0e-06	Arabidopsis thaliana chromosome III BAC F3E22 genomic s	3.0e-37	(AC023912) unknown protein [Arabidopsis thaliana]
KSU002BE403217-3	0.24	Arabidopsis thaliana chromosome II section 191 of 255 of	3.0e-23	multidrug-resistance protein homolog T29F13.13 - Arabido
KSU002BE405200-1	1.5	Homo sapiens chromosome 5 clone CTB-70H11, complete	8.1	testis expressed sequence 14 [Homo sapiens]
KSU012BE403322-4	0.66	Homo sapiens excision repair cross-complementing rode	4.0e-07	(AB016886) emb|CAB71043.1~gene_id:MCA23.10~strong sir
KSU027BE590822-1	2.0e-24	Citrus sinensis mRNA for ACC synthase (acs-1 gene)	2.0e-59	peptidylprolyl isomerase (EC 5.2.1.8) F23F1.12 - Arabidopsi
KSU038BE442699-1	4.0e-53	Rice mRNA for q group of receptor for activated C-kinase,	2.0e-42	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
KSU038BE445134-1,6	0.017	Caenorhabditis elegans cosmid F21H11, complete sequen	4.0e-37	(AC008030) Similar to apoptosis related protein 19 [Arabid
UCD028BE490596-3	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
UCD028BF146193-4	0.005	Rhodobacter sphaeroides strain 2.4.1T quinol oxidase sub	5.0e-42	hypothetical protein F9D16.100 - Arabidopsis thaliana
UCD028BF202674-3	1.0e-10	Oryza sativa chromosome 10 BAC OSJNBa0010C11 genomi	5.0e-13	(AC055769) zinc-finger protein, putative\; 7043-7771 [Arabid
UCD029BE426097-6,10	2.0e-61	Arabidopsis thaliana AT5g08290\F8L15_20 gene, complete	9.0e-78	(AL392174) putative protein [Arabidopsis thaliana] thaliana]
UMC040BF474284-3	0	T.aestivum VDAC2 mRNA for voltage dependent anion cha	3.0e-61	porin VDAC2 - wheat (fragment)
UMC055BG263233-1	e-147	Oryza sativa OsFEN-1 mRNA for FEN-1, complete cds	8.0e-86	(AB021666) FEN-1 [Oryza sativa]
UNL001BE444359-2,5	2.0e-06	Arabidopsis thaliana chromosome III BAC F3E22 genomic s	3.0e-37	(AC023912) unknown protein [Arabidopsis thaliana]
UNL036BE518221-3	1	Homo sapiens 12q BAC RP11-848D3 (Roswell Park Cancer I	1.0e-29	(AB022330) nClpP5 [Arabidopsis thaliana] gb|AB022330 and
UNL053BF293953-4	3.0e-20	Selaginella lepidophylla trehalose-6-phosphate synthase r	3.0e-77	(Y08568) trehalose-6-phosphate synthase [Arabidopsis tha

1BL2-0.69-1.00

UCD017BE494527-4	0.24	Caenorhabditis elegans cosmid C38H2, complete sequenc	5.0e-10	(AC079676) phosphoethanolamine N-methyltransferase, pu

1BL3-0.83-1.00

CNL001BE403217-5	0.24	Arabidopsis thaliana chromosome II section 191 of 255 of	3.0e-23	multidrug-resistance protein homolog T29F13.13 - Arabido
CNL014BE490592-1	2.0e-42	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	9.0e-76	(AP003053) putative malate dehydrogenase [Oryza sativa]
CSU101BE490707-3	0.95	Homo sapiens mRNA\; cDNA DKFZp434P1414 (from clone DKFZp434P1414)\; complete cds		
KSU012BE490592-1	2.0e-42	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	9.0e-76	(AP003053) putative malate dehydrogenase [Oryza sativa]
KSU019BE500394-7	2.0e-21	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	3.0e-51	(AP002744) putative late embryogenesis abundant protein
KSU038BE446672-2	0.28	Vigna mungo yellow mosaic virus B component DNA, com	6.0e-50	(AP000836) ESTs AU068544(C30430),C98487(E0325),D23445(C
NDS043BG274687-4	1.0e-06	Vibrio cholerae chromosome II, section 62 of 93 of the cor	7.0e-59	PROBABLE UDP-GLUCOSE 4-EPIMERASE AT4G23920 (GALACT
UCW026BG263358-2	5.0e-40	Hordeum vulgare var. distichum soluble inorganic pyroph	1.0e-73	(AC007323) T25K16.5 [Arabidopsis thaliana]
UMC015BE426661-2	5.0e-07	Hordeum vulgare genomic DNA fragment\; clone MWG0952	3.0e-91	(AP002897) putative CTP synthase [Oryza sativa]
UMC032BF483595-3	2.0e-08	Triticum aestivum PST19 (Pst19), LRR19 (Lrr19), TAK19-1 (Tak19-1), and LRK19 (Lrk19) genes, complete cds		
UMC040BE590637-1,2	0.084	Cicer arietinum mRNA for cytochrome P450 (cyp93C3 gene	2.0e-30	(AJ296346) cytochrome P450 [Solanum tuberosum]
UNL002BE605005-1	1.1	Homo sapiens Chromosome 11q12.2 PAC clone pDJ52b24	8.0e-09	(AB013451) NBS-LRR type resistance gene [Oryza sativa]
UNL036BE518048-1	9.0e-33	Cicer arietinum partial mRNA for MAP kinase protein	6.0e-96	(AC006931) putative MAP kinase [Arabidopsis thaliana]
UNL036BF200636-5	0.01	Andira aubletii clone CwB12-II microsatellite sequence	3.0e-08	peptidylprolyl isomerase (EC 5.2.1.8), microsomal - maize

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