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

Deletion Map of *Triticum aestivum* cv. Chinese Spring (Chromosome 6A)*

*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**

5AS-7/6AS-5 0.65 →

6AS1-0.35-0.65 →

6AS-1 0.35 →

C-6AS1-0.35 →

C →

C-C6A

C-6AL4-0.55 →

4BL-5/6AL-4 0.55 →

6AL4-0.55-0.90 →

*6AL-2 0.89
6AL-8 0.90 →

6AL8-0.90-1.00 →

* Normal 6AL in this line

6A

6AS5-0.65-1.00

CNL014BE490604-3	6.0e-12	Arabidopsis thaliana AT4g17600\dl4835w gene, complete (	6.0e-49	hypothetical protein - Arabidopsis thaliana
CNL023BF292168-3,4	0	Oryza sativa calcium-dependent protein kinase (CDPK1) m	e-129	(AF194413) calcium-dependent protein kinase [Oryza sativ
CNL023BF483150-3	9.0e-97	Wheat mRNA for ubiquitin	1.0e-26	(AF093504) tetra-ubiquitin [Saccharum hybrid cultivar H32-8
KSU012BE442721-3	6.0e-06	Arabidopsis thaliana putative MtN3 protein (MQM1.8\At5g	4.0e-32	(AF151726) putative MtN3-like protein [Dianthus caryophyll
KSU012BE443401-9	4.0e-63	Hordeum vulgare mRNA for hypothetical protein, clone RG	3.0e-84	(AC003672) putative heme A:farnesyltransferase [Arabido
KSU012BE490604-3	6.0e-12	Arabidopsis thaliana AT4g17600\dl4835w gene, complete (	6.0e-49	hypothetical protein - Arabidopsis thaliana
KSU019BE490365-2	9.0e-67	Z.mays CHX mRNA	2.0e-81	CALNEXIN HOMOLOG PRECURSOR
KSU019BE490584-2,7,8	0	Triticum aestivum chlorophyll a\/b-binding protein WCAB p	2.0e-77	(U73218) chlorophyll a\/b-binding protein WCAB precursor
KSU019BE494189-2	0	Hordeum vulgare mRNA for BAX inhibitor 1 (pBI-1 gene)	2.0e-75	(AJ290421) BAX inhibitor 1 [Hordeum vulgare]
KSU024BE500768-4	e-105	Hordeum vulgare partial mRNA for small GTP-binding prot	7.0e-43	(AF250327) small GTP-binding protein RACBP [Oryza sativa
KSU027BE495217-3	3.0e-04	Arabidopsis thaliana 15.9 kDa subunit of RNA polymerase I	1.0e-43	(AF016511) 15.9 kDa subunit of RNA polymerase II [Arabido
NDS021BG406149-1,3	0.23	Rattus norvegicus Ste-20 related kinase SPAK mRNA, com	0.2	HISTONE H2B.3, SPERM
NDS021BG313246-3	e-113	Triticum aestivum mRNA for beta-fructosidase, partial CDS	2.0e-64	probable vacuolar hydrolase (EC 3.2.1.-) - wheat (fragment
TTU047BE445952-2	1.0e-80	Hordeum vulgare mRNA for ribosomal like-protein, clone I	2.0e-60	(AP001389) ESTs AU077873(S1878),D40121(S1878) correspo
TTU047BE495913-2	0.011	Mus musculus 1 BAC RP23-337F12 (Roswell Park Cancer In	1.0e-11	hypothetical protein - garden asparagus
UCD017BE488501-2,6	0	Triticum aestivum cell wall invertase (IVR3) mRNA, partial (	1.0e-61	beta-fructofuranosidase (EC 3.2.1.26), cell wall - wheat (fra
UCD029BF482700-2	e-133	Oryza sativa subsp. indica UDP-glucose pyrophosphorylas	1.0e-78	(AF249880) UDP-glucose pyrophosphorylase [Oryza sativa
UCD037BE498352-2	0	Hordeum vulgare HSP70 mRNA, complete cds	e-113	dnaK-type molecular chaperone HSP70 - barley
UCD037BE498351-2	1.0e-25	Arabidopsis thaliana putative hydroxypyruvate reductase (	4.0e-76	GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYP
UCW016BE496826-1	4.0e-89	Zea mays L-FNRII mRNA for ferredoxin, complete cds	8.0e-59	FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR)
UMN013BE442933-2	3.0e-17	Orobanche ramosa NADPH-dependent mannose 6-phosph	4.0e-68	(AC006841) putative NADPH dependent mannose 6-phosph
UNL044BF483580-6	2.0e-06	Solanum tuberosum SRE1b (sre1b) mRNA, complete cds		

6AS1-0.35-0.65

CNL001BE426401-6	0.39	Arabidopsis thaliana chromosome II section 207 of 255 of t	2.0e-77	(AC069472) unknown protein\; 3293-1369 [Arabidopsis thali
KSU002BE426401-3,6	0.39	Arabidopsis thaliana chromosome II section 207 of 255 of t	2.0e-77	(AC069472) unknown protein\; 3293-1369 [Arabidopsis thali
KSU012BE442576-2	2.0e-12	Mucor racemosus p-glycoprotein gene, complete cds	1.0e-55	(AP002051) multidrug resistance p-glycoprotein [Arabidop
KSU019BE499002-7	0	Barley mRNA for dehydrin (dhn17)	2.0e-14	DEHYDRIN DHN3 (B17)
KSU024BE499711-5	0.083	Homo sapiens clone RP11-355K7, complete sequence	3.0e-56	(AF367323) AT5g27410\F21A20_120 [Arabidopsis thaliana]
KSU027BF482563-8	5.0e-12	Oryza sativa lipoxygenase (CM-LOX1) mRNA, partial cds	5.0e-30	probable lipoxygenase (EC 1.13.11.12) (clone H1) - potato
KSU027BF482824-2	0.006	Datisca glomerata thiosulfate sulfurtransferase (TST) mR	4.0e-39	(AF109156) thiosulfate sulfurtransferase [Datisca glomerat
KSU038BE445201-2	0.39	Arabidopsis thaliana AT3g57880\T10K17_90 gene, complet	7.0e-53	chorismate mutase CM2 - Arabidopsis thaliana
TTU047BE446153-2,4	0.32	Shigella flexneri virulence plasmid pWR501, complete seq	7.0e-39	(AF370140) unknown protein [Arabidopsis thaliana]
UCD017BE488501-4	0	Triticum aestivum cell wall invertase (IVR3) mRNA, partial (	1.0e-61	beta-fructofuranosidase (EC 3.2.1.26), cell wall - wheat (fra
UCD037BE488206-3	7.0e-64	Oryza sativa putative cycloartenol synthase (CAS1) mRNA,	1.0e-50	(AF169966) putative cycloartenol synthase [Oryza sativa]
UCW001BE398695-5	0.18	Influenza A virus (A\Swine\Indiana\9K035\99 (H1N2)) polymer	ase subunit PB2 (PB2) gene, complete cds	
UCW001BE399163-6	4.0e-12	(wU2.1)=U2 snRNA [Triticum aestivum=wheat, snRNA, 194 (	5.6	hypothetical protein F14F4.1 - Caenorhabditis elegans tran
UCW001BE399996-6	7.0e-58	Triticum aestivum mRNA for alpha-gliadin storage protein,	6.0e-10	(AJ133605) alpha-gliadin [Triticum aestivum]
UCW016BE637738-4	2.0e-20	Arabidopsis thaliana putative clathrin assembly protein	8.0e-52	(AC005169) putative clathrin assembly protein [Arabidopsi
UMC001BE399996-6,7	7.0e-58	Triticum aestivum mRNA for alpha-gliadin storage protein,	6.0e-10	(AJ133605) alpha-gliadin [Triticum aestivum]
UMC015BE426174-4	9.0e-30	Nicotiana tabacum mRNA for beta-1,2-N-acetylglucosaminy	e-102	(Y16832) alpha-1,3-mannosyl-glycoprotein beta-1,2-N-acety
UMC015BE606541-2	0.32	Homo sapiens 12p13.3 BAC RPCI3-488H23 (Roswell Park Ca	2.0e-32	(AB024034) DNA-damage inducible protein DDI1-like [Arabic
UNL048BE445603-2	0.42	Arabidopsis thaliana chromosome 1 BAC F17J6 genomic s	2.0e-92	(AC012561) Unknown protein [Arabidopsis thaliana]
UNL048BE592027-3	5.0e-09	Arabidopsis thaliana DNA chromosome 4, BAC clone F18A	1.0e-46	(AP002968) putative cytochrome P450 [Oryza sativa]
UNL053BF475080-3,6	0	Zea mays translation initiation factor eIF-4A mRNA, compl	e-113	EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) (EIF4A)
UNL053BG275060-4	8.0e-05	Arabidopsis thaliana AIM1 protein (AIM1) gene, complete (	2.0e-51	AIM1 protein - Arabidopsis thaliana

C-6AS1-0.35

KSU001BE406602-4	2.0e-16	Zea mays 40S ribosomal protein S24 mRNA, complete cds	3.0e-19	(AF298769) 40S ribosomal protein S24 [Zea mays]
KSU012BE405809-3	6.0e-06	Genomic sequence for Arabidopsis thaliana BAC F1K23 frc	1.0e-51	(AC007508) F1K23.1 [Arabidopsis thaliana]
KSU012BE406474-4	2.0e-44	Rice mRNA for 40S subunit ribosomal protein, complete cc	7.0e-26	40S RIBOSOMAL PROTEIN S21
KSU012BE406602-4	2.0e-16	Zea mays 40S ribosomal protein S24 mRNA, complete cds	3.0e-19	(AF298769) 40S ribosomal protein S24 [Zea mays]
KSU019BE422743-1	2.0e-61	Zea mays brittle-1 protein (bt1) mRNA, complete cds	6.0e-28	BRITTLE-1 PROTEIN PRECURSOR
KSU019BE445239-6	e-125	Oryza sativa mRNA for 26S proteasome ATPase subunit R(	1.0e-67	(AB033357) 26S proteasome regulatory particle triple-A AT
KSU024BE606502-1	0.11	Human DNA sequence from clone RP1-130E4 on chromoso	0.83	pleckstrin homology domain-containing, family A (phosph
NDS043BF291907-1	0.069	Homo sapiens angiopoietin-related protein 5 (ARP5), mRN	5.0e-38	(U83179) unknown [Arabidopsis thaliana] unknown protein
NDS043BF293402-4	0.02	Drosophila melanogaster, chromosome 3R, region 95E-95I	1.0e-17	(AB018109) gene_idX17H15.6-unknown protein [Arabidops
NDS043BG274742-1	7.0e-37	Solanum tuberosum mRNA for plastidic ATP\ADP-transpo	6.0e-61	(AP002910) putative plastidic ATP\ADP-transporter [Oryza
TTU025BE406602-4	2.0e-16	Zea mays 40S ribosomal protein S24 mRNA, complete cds	3.0e-19	(AF298769) 40S ribosomal protein S24 [Zea mays]
TTU025BE490604-3	6.0e-12	Arabidopsis thaliana AT4g17600\dl4835w gene, complete (	6.0e-49	hypothetical protein - Arabidopsis thaliana
UCD001BE403519-1	7.0e-09	Arabidopsis thaliana chromosome II section 144 of 255 of t	1.0e-70	(AC006053) hypothetical protein [Arabidopsis thaliana]
UCD029BE500818-3	4.0e-13	Arabidopsis thaliana mRNA for thiosulfate sulfurtransfera	5.0e-55	(AF109156) thiosulfate sulfurtransferase [Datisca glomerat
UCD037BE606884-2	0.039	Sorghum bicolor cytochrome P450 CYP71E1 (CYP71E1) mR	6.0e-23	(AP002968) putative cytochrome P450 [Oryza sativa]
UCW016BE497170-1	2.0e-76	Oryza sativa OsRPT1 mRNA for 26S proteasome regulatory	2.0e-94	(AB033535) 26S proteasome regulatory particle triple-A AT
UCW039BE445667-1	1.0e-09	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	3.0e-24	(AB026653) protein kinase-like protein [Arabidopsis thalia
UMN013BE444631-2	1.3	Mesorhizobium loti, complete genome	2.0e-36	(AB025639) dehydrogenase-like protein [Arabidopsis thali
UNL036BE518418-3	7.0e-09	Mus musculus, Sin3-associated polypeptide 18, clone MGC	5.0e-42	PROBABLE SIN3 ASSOCIATED POLYPEPTIDE P18

C-6AL4-0.55

CNL023BF291714-1	0	Oryza sativa chloroplast translational elongation factor Tu	1.0e-74	(AF145053) chloroplast translational elongation factor Tu [(
CNL031BE498480-3	0	Triticum aestivum cytosolic glyceraldehyde-3-phosphate (	2.0e-92	(AF251217) cytosolic glyceraldehyde-3-phosphate dehydro
CNL031BF202032-4	1.0e-12	A.thaliana mRNA for 12-oxo-phytodienoate reductase	9.0e-62	probable 12-oxophytodienoate reductase (EC 1.3.1.42) CPR
CNL031BF474511-2	1.0e-04	Arabidopsis thaliana IAA2 (MXC7.6) mRNA, complete cds	2.0e-21	(AF123509) Nt-iaa4.1 deduced protein [Nicotiana tabacum]
CSU057BE403422-3	2.0e-04	Arabidopsis thaliana genomic DNA, chromosome 5, TAC cl	6.0e-52	(AB024032) contains similarity to pyridoxamine 5-phosphat
KSU001BE443706-2	2.0e-06	Secale cereale mRNA for catalase	0.19	CATALASE ISOZYME 2
KSU001BE443951-1,5	9.0e-36	Triticum aestivum clone pEMB27 transposon Tn1721 homo	2.0e-48	hypothetical protein T14P8.6 - Arabidopsis thaliana [Arabid
KSU012BE403421-2	5.0e-24	Maize gamma zein mRNA, partial cds	8.0e-55	(AF140219) nuclear cap-binding protein\; CBP20 [Arabidops
KSU012BE404354-3	6.0e-34	Arabidopsis thaliana mRNA for Succinyl-CoA-ligase beta su	2.0e-55	succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) beta chair
KSU012BE442608-2	6.0e-12	P.sativum PHSP1 mRNA for HSP70	3.0e-70	HEAT SHOCK 70 KD PROTEIN, MITOCHONDRIAL PRECURSOR
KSU024BE500104-3	0.1	Drosophila melanogaster genomic scaffold 142000013360	2.0e-08	(D21013) ORF [Lilium longiflorum]
KSU027BE404912-2,5,6	2.0e-83	Zea mays putative transcription repressor maize TRM pro	5.0e-79	(AF142322) putative transcription repressor maize TRM pr
KSU027BE517763-1	2.0e-05	Nicotiana plumbaginifolia partial mRNA for RNA Binding Pro	2.0e-06	RNA binding protein homolog - common tobacco (fragmen
KSU030BE489896-3	3.0e-14	Arabidopsis thaliana protein kinase (AFC2) mRNA, comple	2.0e-33	(AF234652) protein kinase MK5 [Mesembryanthemum crys
KSU030BE606591-1	1.0e-87	Zea mays lysine-ketoglutarate reductase\saccharopine d	8.0e-75	(AF003551) lysine-ketoglutarate reductase\saccharopine d
KSU038BE444256-1	9.0e-08	Arabidopsis thaliana DNA chromosome 5, BAC clone T4C1(	2.0e-65	(AL392145) alcohol dehydrogenase-like protein [Arabidopsi
NDS018BE404354-2	6.0e-34	Arabidopsis thaliana mRNA for Succinyl-CoA-ligase beta su	2.0e-55	succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) beta chair
NDS021BE607043-1,5	0.022	Arabidopsis thaliana gamma-tocopherol methyltransferas	3.0e-65	(AF104220) gamma-tocopherol methyltransferase [Arabido
NDS043BE406590-1	0.14	Homo sapiens chromosome 5 clone RP11-317O24, comple	2.0e-24	(AC006569) putative NADH-ubiquinone oxireductase [Arabi
NDS043BE498704-1	5.0e-40	S.tuberosum mRNA for aconitase\aconitate hydratase	2.0e-85	ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-L
NDS043BF293263-7	0	Barley alpha-amylase type B isozyme mRNA, complete cds	1.0e-99	ALPHA-AMYLASE TYPE B ISOZYME PRECURSOR (1,4-ALPHA-
UCD001BE405852-2	1.4	Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome	2.0e-13	(AB035183) N-hydroxycinnamoyl\benzoyltransferase [Ipom
UCD001BE406502-1,2	0.59	Drosophila melanogaster, chromosome 4, region 101F-102F, BAC clone BAC80\4K08, complete sequence		
UCD017BE405809-3	6.0e-06	Genomic sequence for Arabidopsis thaliana BAC F1K23 frc	1.0e-51	(AC007508) F1K23.1 [Arabidopsis thaliana]
UCD017BE408221-2	1.0e-55	Oryza sativa mRNA for S-adenosylmethionine decarboxyla	4.0e-58	(AJ251899) S-adenosylmethionine decarboxylase 2 [Oryza
UCD029BE426413-3	0	Zea mays mRNA for adenosine kinase, putative	2.0e-91	(AJ011281) adenosine kinase [Zea mays]
UCD029BE425967-1,4	2.0e-30	A.thaliana mRNA for ATH1 protein kinase	3.0e-89	(AB009052) protein kinase ATH1 [Arabidopsis thaliana]
UCD037BE497800-7	5.0e-15	Arabidopsis thaliana AT5g50430\MXI22_15 mRNA, complete	2.0e-54	(AB012248) ubiquitin conjugating enzyme-like protein [Ara
UCW016BE518349-1	0	Triticum aestivum plasma membrane intrinsic protein 2 (f	6.0e-73	(AF139815) plasma membrane intrinsic protein 2 [Triticum
UCW020BE518103-4	2.0e-21	Pyrus pyrifolia mRNA for senescencs-related protein, com	7.0e-78	(AB014457) senescencs-related protein [Pyrus pyrifolia]
UCW020BF473461-1,4	e-101	Oryza sativa ONIT4 mRNA for nitrilase-like protein, comple	3.0e-73	(AB027054) nitrilase-like protein [Oryza sativa]
UMN013BE443744-2,4	1.0e-74	Oryza sativa genomic DNA fragment, chromosome 2	1.0e-70	(AJ307662) putative protein [Oryza sativa]
UNL036BE496986-1	2.0e-39	Glycine max geranylgeranyl hydrogenase (Ggh) and nodul	2.0e-80	(AF068686) geranylgeranyl hydrogenase [Glycine max]
UNL036BE518064-5	9.0e-05	M.crystallinum mRNA for ribosomal protein YL16	1.0e-48	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE)
UNL036BF474493-4,5	0.4	Pseudomonas aeruginosa PA01, section 37 of 529 of the c	4.0e-75	pescadillo-like protein - Arabidopsis thaliana

6AL4-0.55-0.90

CNL001BE406407-3	0.003	Zea mays enolase (eno2) mRNA, complete cds	0.045	(AE003595) CG14563 gene product [Drosophila melanogast
CNL01 4BE490226-3	3.0e-14	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	7.0e-77	(AP000419) zinc metalloprotease (insulinase family) [Arabi
CNL031BE637311-2	0	Hordeum vulgare acetohydroxyacid synthase (AHAS) mRN	3.0e-77	(AF039600) acetohydroxyacid synthase [Hordeum vulgare]
CNL031BE637911-3	6.0e-08	Arabidopsis thaliana mRNA for receiver-like protein 4	7.0e-16	(AB062095) response regulator 9 [Zea mays]
CSU046BE443342-4	0.002	Arabidopsis thaliana chromosome I BAC F17F16 genomic (	1.0e-25	(AC051629) Unknown protein [Arabidopsis thaliana]
KSU001BE406407-2	0.003	Zea mays enolase (eno2) mRNA, complete cds	0.045	(AE003595) CG14563 gene product [Drosophila melanogast
KSU001BE442908-5	9.0e-14	Zea mays beta-expansin 4 (exp8\4) mRNA, complete cds	2.0e-07	(AF332177) beta-expansin 4 [Zea mays]
KSU001BE443899-2	7.0e-80	Oryza sativa inorganic pyrophosphatase (IPP) mRNA, comp	4.0e-42	(AF093629) inorganic pyrophosphatase [Oryza sativa]
KSU002BE406380-1	0.23	Homo sapiens 12 BAC RP11-173C20 (Roswell Park Cancer I	2.9	nidogen 2\; nidogen 2 (osteonidogen) [Homo sapiens]
KSU012BE404385-4	e-170	Zea mays golgi associated protein se-wap41 mRNA, comp	e-108	(AF294725) reversibly glycosylated polypeptide [Oryza sati
KSU012BE490226-3	3.0e-14	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	7.0e-77	(AP000419) zinc metalloprotease (insulinase family) [Arabi
KSU019BE442610-1	0	Triticum aestivum fimbrin\plastin-like mRNA, partial cds	0.004	SPERM HISTONE P2 PRECURSOR (PROTAMINE P2)
KSU019BE442611-1	3.0e-05	Zea mays flavanone 3-beta-hydroxylase (fht) mRNA, compl	5.0e-45	(AB005241) leucoanthocyanidin dioxygenase-like protein [A
KSU024BE497888-1,5	1.0e-28	Rice mRNA for F1-ATPase (480 gene), partial sequence	9.0e-34	ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
KSU024BE500453-4	7.0e-29	Z.mays mRNA for HMGc1 protein	1.0e-26	high mobility group protein HMGc1 - maize
KSU024BE500686-4,7	1.0e-04	G.hirsutum mRNA for omega-6 desaturase	1.0e-13	omega-6 fatty acid desaturase (EC 1.14.99.-) - parsley
KSU027BE490147-1	4.0e-60	Zantedeschia aethiopica geranylgeranyl reductase mRNA,	1.0e-94	(AF068686) geranylgeranyl hydrogenase [Glycine max]
KSU027BF485173-1	3.0e-63	Oryza sativa small zinc finger-like protein (TIM13) mRNA, c	1.0e-13	MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE
KSU030BE403397-2,3	4.0e-87	Zea mays tonoplast membrane integral protein ZmTIP2-3	6.0e-70	(AJ307662) putative aquaporin [Oryza sativa]
KSU030BF483643-3,4	e-134	Zea mays pyruvate dehydrogenase E1 alpha subunit RNA,	e-109	(AF063911) pyruvate dehydrogenase E1 alpha subunit [Zea
KSU035BE403397-4,5	4.0e-87	Zea mays tonoplast membrane integral protein ZmTIP2-3	6.0e-70	(AJ307662) putative aquaporin [Oryza sativa]
KSU035BE403577-2	1.0e-40	H.vulgare mRNA for cytoplasmic glutamine synthetase	4.0e-10	(AF003197) glutamine synthetase [Hevea brasiliensis]
KSU035BE404608-1	5.0e-19	Alfalfa nucleic acid binding protein (alfin-1) mRNA, complet	2.0e-58	nucleic acid binding protein [imported] - rice
KSU035BE497213-2	3.0e-70	Oryza sativa H protein subunit of glycine decarboxylase m	1.0e-75	(AC025296) putative glycine decarboxylase subunit [Oryza
NDS001BE443899-2	7.0e-80	Oryza sativa inorganic pyrophosphatase (IPP) mRNA, comp	4.0e-42	(AF093629) inorganic pyrophosphatase [Oryza sativa]
NDS018BE405016-4	e-105	Oryza sativa germin-like protein 4 (GER4) mRNA, complete	2.0e-70	probable germin protein 4 - rice
NDS043BE403152-4	6.0e-30	Potato pyrophosphate-fructose 6-phosphate 1-phosphotr	2.0e-53	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRA
TTU025BE490226-3	3.0e-14	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	7.0e-77	(AP000419) zinc metalloprotease (insulinase family) [Arabi
TTU047BE494616-1	0.34	Homo sapiens BAC clone GS1-308H5 from 7p13-p11.2, com	8.0e-25	(AC074360) hypothetical protein [Arabidopsis thaliana]
UCD028BE426214-1	0	T.turgidum mRNA for ADP\ATP carrier	4.0e-97	(X80023) ATP\ADP carrier protein [Triticum turgidum]
UCD037BE442546-2	3.0e-05	Genomic sequence for Arabidopsis thaliana BAC F2E2 fror	5.0e-35	(U84926) HTGP5 [Nicotiana tabacum]
UCD037BE488319-2	0.36	Human DNA sequence from clone 194O8 on chromosome	2.0e-24	one helix protein (OHP) - Arabidopsis thaliana
UMC055BF484678-8	2.0e-58	Oryza sativa genomic DNA, chromosome 1, PAC clone:P0 4	1.0e-84	(AC069471) sphingosine-1-phosphate lyase, putative [Arab
UMN013BE443929-1	1.0e-06	Arabidopsis thaliana chromosome I BAC T14N5 genomic s	7.0e-56	hypothetical protein T14N5.5 - Arabidopsis thaliana
UNL001BE442908-3	9.0e-14	Zea mays beta-expansin 4 (exp8\4) mRNA, complete cds	2.0e-07	(AF332177) beta-expansin 4 [Zea mays]
UNL044BF482687-3	0.088	Halobacterium sp. NRC-1 section 107 of 170 of the complet	2.0e-11	(AC002423) T23E23.20 [Arabidopsis thaliana]

6AL8-0.90-1.00

CNL001BE405516-10	3.0e-05	Oryza sativa genomic DNA, chromosome 1, PAC clone:P0 4	1.0e-58	(AB019229) cucumisin-like serine protease\; subtilisin-like
CSU057BE490152-2	3.0e-23	Zea mays clone ZmMYB2 R2R3MYB-domain protein mRN	9.0e-50	(AC007894) Strong similarity to M4 protein gb Arabidopsis
CSU058BE518379-2	6.0e-12	Arabidopsis thaliana NBD-like protein (POP) mRNA, comple	1.0e-50	(AF127664) NBD-like protein [Arabidopsis thaliana]
KSU001BE403154-3	4.7	Arabidopsis thaliana chromosome 1 BAC T2J15 genomic s	2.0e-12	(AC012395) putative RING zinc finger protein [Arabidopsis t
KSU001BE443703-2	0.005	Human DNA sequence from clone RP11-33B C15 on chromo	1.4	(AE003826) CG7741 gene product [Drosophila melanogaste
KSU001BE444363-3,4	0.4	Human DNA sequence from clone RP11-92G12 on chromos	1.7	(U15208) chemokine receptor [Mus musculus]
KSU002BE403221-1	3.0e-32	Oryza sativa genomic DNA, chromosome 1, PAC clone:P0	7.0e-69	hypothetical protein F41.8 - Arabidopsis thaliana
KSU002BE405516-5,7	3.0e-05	Oryza sativa genomic DNA, chromosome 1, PAC clone:P0 4	1.0e-58	(AB019229) cucumisin-like serine protease\; subtilisin-like
KSU002BE425207-8	8.0e-08	Nicotiana tabacum (clone: L24-2) chloroplast ribosomal pr	3.0e-36	(AB016879) 50S ribosomal protein L24, chloroplast precurs
KSU012BE403564-2	7.0e-06	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L2	1.0e-79	splicing factor 3b, subunit 2, 145kD\; spliceosome associat
KSU012BE403950-2	1.0e-04	Genomic sequence for Arabidopsis thaliana BAC F1N19 frc	e-100	(AC009519) F1N19.11 [Arabidopsis thaliana]
KSU012BE407066-2	0.067	Hordeum vulgare mRNA for hypothetical protein	5.0e-22	(AC005322) ESTs gb|H36249| gb this gene. [Arabidopsis tha
KSU012BE490200-1	5.0e-77	Zea mays ribosomal protein L29 (L29) mRNA, complete cd	2.0e-41	(AF147725) ribosomal protein L29 [Zea mays]
KSU019BE498785-5	1.0e-06	Mycobacterium smegmatis adhC gene for alcohol dehydr	3.0e-32	PROBABLE MANNITOL DEHYDROGENASE (NAD-DEPENDENT M.
KSU019BE499002-1,2,5,6,8	0	Barley mRNA for dehydrin (dhn17)	2.0e-14	DEHYDRIN DHN3 (B17)
KSU024BE498892-3	5.0e-06	Arabidopsis thaliana unknown protein (AT4g38340) mRNA,	2.0e-65	(AC005724) putative diacylglycerol kinase [Arabidopsis tha
KSU024BE500840-4,6	1.0e-39	Oryza sativa chromosome 3 BAC OSJNBa0026A15 genomic	1.0e-58	(AC084404) putative translation initiation factor [Oryza sativ
KSU035BE404596-1	1.5	Homo sapiens chromosome 15 clone RP11-473C18 map 15	1.0e-43	herbicide safener binding protein 1 - maize
KSU035BE406840-3	3.0e-04	Lolium perenne caffeic acid O-methyltransferase (OMT2) (	6.0e-48	caffeic acid O-methyltransferase-like protein - Arabidopsis
KSU035BE497099-1	0.091	Homo sapiens chromosome 21 segment HS21C102	4.0e-41	(Y08726) MtN3 [Medicago truncatula]
KSU038BE442605-4,8	0.83	Streptomyces coelicolor cosmid D31	6.0e-31	(AC005896) nodulin-like protein [Arabidopsis thaliana]
KSU038BE442681-1	0.026	Arabidopsis thaliana chromosome II section 127 of 255 of t	5.0e-54	(AJ011892) cyclin D2.1 protein [Nicotiana tabacum]
KSU038BE443643-2,3	3.0e-08	Lolium rigidum clone Lol-2 putative cytochrome P450 mRN	3.0e-48	CYTOCHROME P450 89A2 (CYPLXXXIX) (ATH 6-1)
KSU038BE443711-2	1.4	Oryza sativa genomic DNA, chromosome 1, PAC clone:P0 4	3.0e-23	(AP002543) glycolate oxidase subunit D-like\; D-lactate deh
KSU038BE444279-2	5.4	Human DNA sequence from clone RP11-442.H7 on chromo	6.0e-06	(AF201456) NAC2 [Arabidopsis thaliana]
TTU025BE403950-2	1.0e-04	Genomic sequence for Arabidopsis thaliana BAC F1N19 frc	e-100	(AC009519) F1N19.11 [Arabidopsis thaliana]
UCD001BE443703-2	0.005	Human DNA sequence from clone RP11-33B C15 on chromo	1.4	(AE003826) CG7741 gene product [Drosophila melanogaste
UCD017BE494057-2	1.0e-19	Arabidopsis thaliana chromosome 1 BAC T24D18 sequenc	4.0e-34	(AC010924) Contains similarity to gb TMS1d from Drosophi
UCD029BE606671-1	1.0e-04	Triticum aestivum WESR1 mRNA, partial sequence	4.0e-54	MTN3-like protein - Arabidopsis thaliana
UMC040BE598638-11	0	T.aestivum rab15B mRNA	1.0e-16	rab15B protein - wheat
UNL002BE500158-1	0.35	Sorghum bicolor clone Sor2 unknown gene	1.0e-30	(AC087926) Putative MLA6 protein [Oryza sativa]
UNL002BE538124-3	0.32	Homo sapiens chromosome 17, clone hRPK.15_K_2, compl	7.0e-19	resistance protein RPP13 [imported] - Arabidopsis thaliana
UNL002BF199788-4	6.0e-80	Hordeum vulgare NBS-LRR type resistance protein (b7) ge	4.0e-43	NBS-LRR type resistance protein - barley (fragment)
UNL048BE495143-3,5	3.0e-08	Arabidopsis thaliana chromosome II section 109 of 255 of t	5.0e-48	(AL161576) putative protein [Arabidopsis thaliana]
UNL053BF293956-1,5	0.005	Homo sapiens chromosome 18 clone RP11-245A17, compl	3.0e-64	(AC020889) T1H15.3 [Arabidopsis thaliana] deaminase from
UNL053BF475120-2	1.0e-17	Oryza sativa genomic DNA, chromosome 1, PAC clone:P0 4	5.0e-29	(AC016829) putative GDSL-motif lipase\acylhydrolase [Aral

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