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

Deletion Map of *Triticum aestivum* cv. Chinese Spring (Chromosome 4A)*

*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:

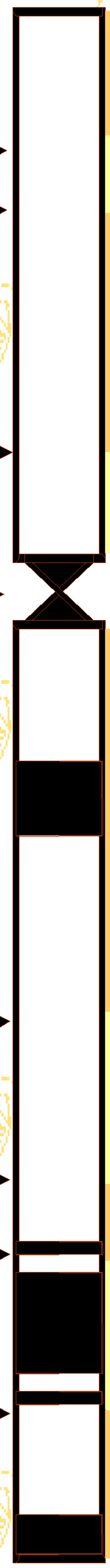
Bin Identity

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**



3BS-8/ 4AS-3 0.76 →
4AS-4 0.63 →
4AS-1 0.20 →
C →
4AL-12 0.43 →
4AL-13 0.59 →
3DS-6/4AL-11, 4AL-5 0.66 →
4AL-4 0.80 →

4AS3-0.76-1.00
4AS4-0.63-0.76
4AS1-0.20-0.63
C-4AS1-0.20
C-C4A
C-4AL12-0.43
4AL12-0.43-0.59
4AL13-0.59-0.66
4AL5-0.66-0.80
4AL4-0.80-1.00

4A

4AS3-0.76-1.00

CNL014BE490790-1	0.015	Genomic Sequence For Arabidopsis thaliana Clone T1G16	2.0e-18	(AF160912) BcDNA.LD06837 [Drosophila melanogaster]
CNL031BF428799-6	e-142	Oryza sativa GAD mRNA for glutamate decarboxylase, com	e-108	(AF020425) glutamate decarboxylase isozyme 1 [Nicotiana
KSU012BE490658-3	e-104	Eleusine indica alpha-tubulin 2 (TUA2) mRNA, complete cds	1.0e-65	TUBULIN ALPHA-2 CHAIN (ALPHA-2 TUBULIN)
KSU019BE494848-2	1.0e-71	Arabidopsis thaliana cell division cycle protein (CDC48) mR	5.0e-94	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG [Arabidopsis t
KSU019BE497134-1	8.0e-17	Hordeum vulgare genomic DNA fragment\; clone MWG0934	6.0e-55	(AC012563) putative trehalose-6-phosphate synthase\; 468
KSU027BF484401-4	7.0e-64	Genomic Sequence for Oryza sativa, Nipponbare strain, clo	5.0e-15	(AB016893) emb|CAB61744.1~gene_id:MYH9.17~similar to u
KSU030BE497108-3	1.0e-22	A.thaliana mRNA for stromal ascorbate peroxidase	4.0e-40	(AB022273) thylakoid-bound ascorbate peroxidase [Nicotia
KSU030BE499019-1	2.0e-67	Arabidopsis thaliana Ser\/Thr protein phosphatase mRNA,	6.0e-84	SERINE\/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALY
KSU030BF201003-3	0.29	Dictyostelium discoideum C-module-binding factor (cbfA)	0.36	(AC006264) hypothetical protein [Arabidopsis thaliana]
KSU035BE497160-3	e-133	Oryza sativa ribulose-5-phosphate-3-epimerase (RPE) mRN	4.0e-63	RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR (PENTOSE-
KSU035BE517664-3	0.088	Synechococcus sp. gene for ribosomal proteins, complet	8.0e-54	50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (
KSU038BE444757-2	4.0e-65	Oryza sativa chromosome 10 clone nbxb0046P18, complet	2.0e-76	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CON
UCD037BE497989-1,4	4.0e-10	L.esculentum chorismate synthase 2 precursor	3.0e-72	CHORISMATE SYNTHASE 1, CHLOROPLAST PRECURSOR (5-EI
UCD037BF201181-2	0.097	Human polymorphic loci in Xq28	3.0e-11	(AC007134) putative sugar transporter [Arabidopsis thaliar
UCW020BE403628-4,6	1.5	Xenopus laevis receptor protein tyrosine phosphatase de	1.0e-13	(AB017061) anthranilate N-benzoyltransferase [Arabidopsis
UMC015BE426767-1	1.0e-07	Arabidopsis thaliana BAC T1M15	3.0e-62	(AF154423) putative beta-galactosidase [Lycopersicon esc
UMC015BE590579-3	3.0e-17	Arabidopsis thaliana putative zinc finger protein (AT4g314	3.0e-34	hypothetical protein F8F16.240 - Arabidopsis thaliana
UMC040BF474257-5	0.1	S.pombe chromosome II cosmid c646	4.0e-13	probable serine\/threonine-specific protein kinase T20F6.
UMN013BE442995-2,3	1.0e-35	Cucumis melo mitochondrial processing peptidase beta s	6.0e-86	(AF363285) mitochondrial processing peptidase [Avicennia
UNL002BE445244-4	0.1	Lycopersicon esculentum disease resistance protein I2 (I	1.0e-18	NBS-LRR type resistance protein - rice (fragment)
UNL002BF473052-1	2.0e-30	Oryza sativa chromosome 10 clone nbxb0046P18, complet	1.0e-47	CDC48-like protein - Arabidopsis thaliana
UNL036BE518074-1	3.0e-87	Rice mRNA for ribosomal protein S12 (320 gene), partial se	3.0e-51	40S RIBOSOMAL PROTEIN S23 (S12)
UNL036BE518134-1,2	7.0e-09	Trypanosoma brucei putative DEAD box RNA helicase HEL6	3.0e-76	(AB010259) DRH1 [Arabidopsis thaliana]
UNL036BF200627-2	9.0e-62	Zea mays mRNA for Toc34-1 protein (toc34A gene)	8.0e-22	(AJ271049) Toc34-2 protein [Zea mays]

4AS4-0.63-1.00

CNL001BE426317-3,5	1.5	Sphingomonas aromaticivorans plasmid pNL1, complete s	4.0e-37	hypothetical protein F12L6.13 - Arabidopsis thaliana

4AS4-0.63-0.76

CNL001BE406616-4	7.0e-19	Zea mays seven transmembrane protein Mlo4 mRNA, com	1.0e-23	(AY029315) seven transmembrane protein Mlo4 [Zea mays
CNL014BE591172-6	e-132	Oryza sativa phytoene desaturase precursor (Pds) mRNA,	4.0e-77	PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATU
KSU002BE426317-3	1.5	Sphingomonas aromaticivorans plasmid pNL1, complete s	4.0e-37	hypothetical protein F12L6.13 - Arabidopsis thaliana
KSU024BF485396-3,4	1.0e-25	Nicotiana tabacum GDP dissociation inhibitor (GDI) mRNA, c	2.0e-77	GDP dissociation inhibitor - common tobacco
KSU027BE426016-3	0	Triticum aestivum vacuolar targeting receptor bp-80 mRNA	1.0e-83	(AF161719) vacuolar targeting receptor bp-80 [Triticum aes
KSU035BE497618-2	e-120	Hordeum vulgare mRNA for ascorbate peroxidase	1.0e-34	(AJ000223) ascorbate peroxidase [Hordeum vulgare]
KSU038BE442811-3	3.0e-11	Oryza sativa chromosome unknown BAC clone OSJNBa004	1.0e-15	(AB046954) pseudo-response regulator 7 [Arabidopsis tha
KSU038BE446076-3,6,7	0	Triticum aestivum MAP kinase homolog (WCK-1) mRNA, cc	1.0e-64	mitogen-activated protein kinase 1 homolog (clone Aspk9
NDS018BE426767-1	1.0e-07	Arabidopsis thaliana BAC T1M15	3.0e-62	(AF154423) putative beta-galactosidase [Lycopersicon esc
NDS034BE490602-3	0	T.aestivum mRNA for germin-like protein 4, partial	6.0e-35	(Y14203) oxalate oxidase [Hordeum vulgare]
UMC015BE426266-1	6.0e-86	Oryza sativa mRNA for ribonuclease, partial cds, clone:E11	1.0e-65	ribonuclease (EC 3.1.-.-) - barley
UMN013BE442961-2	1.0e-16	Arabidopsis thaliana chromosome 1 BAC F22G10 genomic	3.0e-98	(AC007260) Similar to dTDP-D-glucose 4,6-dehydratase [Ara
UNL002BE425301-3	6.0e-74	Avena fatua 40S ribosomal protein S3A mRNA, partial cds	7.0e-46	40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
UNL048BE605229-6	1.0e-61	Rice mRNA for low molecular weight heat shock protein, c	5.0e-15	17.4 KD CLASS I HEAT SHOCK PROTEIN

4AS1-0.20-0.63

CNL001BE406512-4	0.044	Drosophila melanogaster, chromosome 2R, region 50C-50	2.0e-15	(AB010069) contains similarity to RNA binding protein~gen
CNL014BE490658-4	e-104	Eleusine indica alpha-tubulin 2 (TUA2) mRNA, complete cds	1.0e-65	TUBULIN ALPHA-2 CHAIN (ALPHA-2 TUBULIN)
CNL023BG262664-3	0.024	Acanthamoeba castellanii myosin heavy chain (HMWMI) ge	2.0e-46	(AC067971) Contains similarity to an unknown protein F7A
KSU002BE406512-3	0.044	Drosophila melanogaster, chromosome 2R, region 50C-50	2.0e-15	(AB010069) contains similarity to RNA binding protein~gen
KSU012BE403867-5	2.0e-71	Sorghum bicolor pathogenesis-related protein (PR-10) mR	2.0e-51	pathogenesis-related protein - sorghum
KSU024BF202695-1	3.0e-19	Oryza sativa peroxidase (POX22.3) mRNA, complete cds	6.0e-31	peroxidase (EC 1.11.1.7) 2 precursor - wheat
KSU030BF485011-2	0.066	Tacca chantieri MADS box containing protein PI mRNA, part	0.003	(AC067971) Contains similarity to a hypothetical protein F2
KSU038BE443190-1	0.093	Homo sapiens genomic DNA, chromosome 21q, section 58	2.0e-24	(AB026636) contains similarity to similar to ubiquitin conju
KSU038BE443973-2	4.0e-04	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	3.0e-45	(AB005248) glucosyltransferase-like protein [Arabidopsis
NDS001BE443995-2	1.6	Homo sapiens 12 BAC RP11-547C5 (Roswell Park Cancer In	4.0e-71	(AC079281) unknown protein [Arabidopsis thaliana]
NDS018BE404835-4	e-120	Zea mays strain W64A x A182E putative cytosolic 6-phosph	2.0e-80	phosphogluconate dehydrogenase (decarboxylating) (EC 1
UCD001BE406324-12,13	3.0e-15	Zea mays seven transmembrane protein Mlo7 mRNA, com	1.0e-06	MLO PROTEIN HOMOLOG 1 (ATMLO-H1)
UCD001BE406512-2	0.044	Drosophila melanogaster, chromosome 2R, region 50C-50	2.0e-15	(AB010069) contains similarity to RNA binding protein~gen
UCD001BE444330-1	0.006	Human DNA sequence from clone RP4-687J17 on chromos	0.03	(AC005499) hypothetical protein [Arabidopsis thaliana]
UCD037BE443253-4	2.0e-08	Arabidopsis thaliana ABC transporter-like protein (T1E22_	6.0e-51	ABC transporter-like protein - Arabidopsis thaliana
UCD037BE489400-2	0.006	Human chromosome 14 DNA sequence BAC R-1126O17 of l	9.0e-07	(AC069473) GTPase, putative\; 34281-30152 [Arabidopsis th
UCW020BE591320-3	4.0e-22	Nicotiana tabacum WERBP-1 mRNA, complete cds	2.0e-33	hypothetical protein T5F17.60 - Arabidopsis thaliana
UMC040BG262345-4	e-138	Oryza sativa pyruvate decarboxylase 2 (Pdc2) mRNA, comp	4.0e-80	PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC)
UMN013BE443291-1	1.0e-25	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-96	(AP003143) putative neutral invertase [Oryza sativa]
UMN013BE443537-2	2.0e-05	Lilium longiflorum potential thioredoxin mRNA, complete	7.0e-46	thioredoxin homolog F22O13.5 - Arabidopsis thaliana
UNL053BF293261-2,4,5	1.1	Homo sapiens chromosome 16 clone RP11-328J14, comple	5.0e-24	helicase-like protein - Arabidopsis thaliana
UNL053BG313633-1	e-136	Oryza sativa mRNA for putative phospholipid hydroperoxid	4.0e-87	(AJ270955) putative phospholipid hydroperoxide glutathion

C-4AS1-0.20

TTU047BE405190-2	5.9	Homo sapiens chromosome 10 clone RP11-77G23, comple	1.0e-53	(AF169021) seed maturation protein PM36 [Glycine max]
TTU047BE446061-3	3.0e-20	Arabidopsis thaliana chromosome 3 BAC T2E22 genomic s	5.0e-48	(AC069474) nascent polypeptide associated complex alpha
UNL002BF484266-3	8.0e-05	Hordeum vulgare genomic sequence, clone BAC 80H14, is	2.0e-29	(AJ302292) MLA6 protein [Hordeum vulgare]

C-4AL12-0.43

CNL001BE406618-3	0.75	Deinococcus radiodurans R1 section 220 of 229 of the com	5.0e-28	(AB056451) CPRD49 [Vigna unguiculata]
CSU001BE406618-1	0.75	Deinococcus radiodurans R1 section 220 of 229 of the com	5.0e-28	(AB056451) CPRD49 [Vigna unguiculata]
KSU002BE406618-3	0.75	Deinococcus radiodurans R1 section 220 of 229 of the com	5.0e-28	(AB056451) CPRD49 [Vigna unguiculata]
KSU012BE403622-5,10	2.0e-09	Sequence of BAC F7H2 from Arabidopsis thaliana chromos	7.0e-95	(AC018849) unknown protein\; 52184-57536 [Arabidopsis th
KSU012BE403789-2,6	3.0e-05	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	8.0e-28	(AB016890) contains similarity to elongin C~gene_id:MNC17
KSU024BF202706-5	9.0e-81	Oryza sativa OsPAE1 mRNA for alpha 5 subunit of 20S prote	2.0e-37	PROTEASOME SUBUNIT ALPHA TYPE 5 (20S PROTEASOME AL
KSU027BE406676-3,5	3.0e-96	Triticum aestivum germin protein precursor, mRNA, comp	2.0e-40	GERMIN GF-2.8 PRECURSOR
KSU027BF202969-1	2.0e-87	Oryza sativa cystathionine gamma-synthase (CGS1) mRNA	3.0e-54	O-succinylhomoserine (thiol)-lyase (EC 4.2.99.9) 1 - maize
KSU030BE406580-1	3.0e-28	Oryza sativa OsUCP2 gene for uncoupling protein, complet	7.0e-52	(AB049998) uncoupling protein [Oryza sativa]
KSU035BE403268-3	e-152	Triticum aestivum metallothionein-like protein (wali1) mR	4.0e-12	METALLOTHIONEIN-LIKE PROTEIN 1
KSU035BE403348-3	0.058	Streptomyces coelicolor cosmid 9C5	2.0e-08	nucleoid DNA-binding protein cnd41-like protein - Arabidop
KSU035BE403438-3	0.069	Human DNA sequence from clone RP1-101A2 on chromosc	5.0e-07	(AB007648) contains similarity to ABA-responsive protein~
KSU035BE403439-3	1.0e-74	Panicum miliaceum mRNA for 2-oxoglutarate\/malate trans	1.0e-61	2-oxoglutarate\/malate translocator (clone OMT103), mitocl
KSU035BE403770-4	3.0e-05	Mus musculus short stature homeobox 2 (Shox2), mRNA	5.0e-68	(AF117335) succinic semialdehyde dehydrogenase [Arabid
KSU035BE497184-1	4.0e-04	Arabidopsis thaliana chromosome II section 166 of 255 of t	5.0e-58	(AC004561) putative C-4 sterol methyl oxidase [Arabidopsi
KSU035BE497324-2	3.0e-11	Hordeum vulgare rubisco activase genes,complete cds	5.2	(AE003719) CG7397 gene product [Drosophila melanogaste
KSU035BE497366-3	2.0e-27	Oryza sativa subsp. japonica clone S14511 putative glutath	6.0e-09	(AF309376) putative glutathione S-transferase OsGSTU6 [O
KSU035BE497635-3	0.38	Taeniopygia guttata SWS2 opsin mRNA, complete cds	4.0e-09	(X93159) ribosomal protein S5 [Spinacia oleracea]
NDS018BE404963-1	5.0e-22	Brassica napus mRNA for acyl-carrier protein] S-malonyltr	1.0e-86	probable [acyl-carrier-protein] S-malonyltransferase (EC 2
NDS034BE403881-2	0.11	Glycine max putative purple acid phosphatase precursor (	1.0e-79	(AF236109) putative purple acid phosphatase precursor [P
NDS034BE470946-2	0	Hordeum vulgare mRNA for allene oxide synthase (aos2 g	1.0e-94	(AJ251304) allene oxide synthase [Hordeum vulgare]
UCD001BE443755-8	0.007	Dictyostelium discoideum nucleoside diphosphate kinase	6	(AF202730) Niemann-Pick type C1 disease protein [Oryctol
UCD017BE403622-4,8	2.0e-09	Sequence of BAC F7H2 from Arabidopsis thaliana chromos	7.0e-95	(AC018849) unknown protein\; 52184-57536 [Arabidopsis th
UCD017BE403789-4,8	3.0e-05	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	8.0e-28	(AB016890) contains similarity to elongin C~gene_id:MNC17
UCD017BE494281-9	e-164	H.vulgare mRNA for putative zinc finger protein	4.0e-36	(X85544) putative zinc finger protein [Hordeum vulgare]
UCD037BE499131-9	6.0e-73	O.sativa RAc2 gene for actin	2.0e-55	ACTIN 1
UCD037BE499948-1	4.0e-04	Homo sapiens glutamate rich WD repeat protein GRWD (GF	1.0e-40	(AC005917) putative WD-40 repeat protein [Arabidopsis tha
UCW016BE517645-1	1.0e-34	Nicotiana plumbaginifolia mRNA for U2 snRNP auxiliary fact	3.0e-90	(Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana
UMN013BE443038-5	2.0e-94	Hordeum vulgare thaumatin-like protein TLP8 mRNA, com	1.0e-18	(AF355458) thaumatin-like protein TLP8 [Hordeum vulgare]
UNL001BE443412-1	4.4	Homo sapiens BAC clone RP11-319A7 from 2, complete se	1.4	(AF207842) Pi-ta protein [Oryza sativa]
UNL044BG263544-5	4.0e-04	Cruznema tripartitum large subunit RNA polymerase II mR	1.0e-47	DNA-directed RNA polymerase I 190K chain homolog F15B8

4AL12-0.43-0.59

CNL001BE406616-2	7.0e-19	Zea mays seven transmembrane protein Mlo4 mRNA, com	1.0e-23	(AY029315) seven transmembrane protein Mlo4 [Zea mays
CNL023BE405218-8	0	T.aestivum mRNA 1 for cathepsin B (2529)	e-120	cathepsin B-like cysteine proteinase (EC 3.4.22.-) - wheat (
CNL031BF428799-10	e-142	Oryza sativa GAD mRNA for glutamate decarboxylase, com	e-108	(AF020425) glutamate decarboxylase isozyme 1 [Nicotiana
KSU001BE403860-3	3.0e-10	Oryza sativa microsatellite MRG5838 containing (TCT)X14,	7.0e-30	(AF198054) NAC1 [Arabidopsis thaliana]
KSU001BE406602-6	2.0e-16	Zea mays 40S ribosomal protein S24 mRNA, complete cds	3.0e-19	(AF298769) 40S ribosomal protein S24 [Zea mays]
KSU001BE406616-3	7.0e-19	Zea mays seven transmembrane protein Mlo4 mRNA, com	1.0e-23	(AY029315) seven transmembrane protein Mlo4 [Zea mays
KSU002BE425993-2	e-154	Oryza sativa chromosome 3 BAC OSJNBa0040E01 genomic	1.0e-68	(AC079887) putative UDP-glucose dehydrogenase [Oryza s
KSU012BE406602-7	2.0e-16	Zea mays 40S ribosomal protein S24 mRNA, complete cds	3.0e-19	(AF298769) 40S ribosomal protein S24 [Zea mays]
KSU012BE406875-2	9.0e-26	Zea mays ABA- and ripening-inducible-like protein mRNA,	1.3	probable serine\/threonine-specific protein kinase (EC 2.7.
KSU012BE490685-2,3,4	0.062	Cercocebus torquatus interleukin-1 beta (IL-1 beta) mRNA	1.0e-23	(AC012328) putative NADP-dependent oxidoreductase [Ara
KSU024BE498699-1	0	Hordeum vulgare mRNA for endo-1,4-beta-glucanase Cel1,	7.0e-90	(AB040769) endo-1,4-beta-glucanase Cel1 [Hordeum vulgar
KSU027BE517725-2	5.0e-15	Lilium longiflorum lipid transfer protein precursor (LTP) n	2.0e-13	basic protein 1B, WBP1B=lipid transfer protein homolog [T
KSU030BE490281-3	0	Avena nuda actin 1 gene, complete cds	4.0e-96	actin 1 [imported] - small naked oat
KSU035BE404401-1	0	T.aestivum mRNA for obtusifoliol 14-alpha-demethylase (C	4.0e-61	probable obtusifoliol 14-alpha-demethylase CYP51 - wheat
KSU035BE496999-2	0	Hordeum vulgare mRNA for alpha-tubulin 3	7.0e-74	TUBULIN ALPHA-3 CHAIN
KSU035BE497446-2	7.0e-73	Hordeum vulgare gene for CP29 precursor for core chloro	2.0e-56	chlorophyll a\/b-binding protein CP29 precursor - barley pr
KSU035BE497510-4	e-139	Avena sativa vacuolar H+-ATPase 16 kDa proteolipid subun	3.0e-42	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT oat
UCW016BE406875-2	9.0e-26	Zea mays ABA- and ripening-inducible-like protein mRNA,	1.3	probable serine\/threonine-specific protein kinase (EC 2.7.
UCW039BE405350-3	0.026	H.vulgare L. mRNA for flavonoid 7-O-methyltransferase	5.0e-31	catechol O-methyltransferase (EC 2.1.1.6) - barley
UMC040BE637573-4	3.0e-23	Oryza sativa nucleic acid binding protein mRNA, complete	5.0e-56	probable nucleic acid binding protein - rice
UMN013BE443500-2	2.0e-24	Gossypium hirsutum GhCAP mRNA for adenylyl cyclase as	2.0e-76	(AB014884) adenylyl cyclase associated protein [Gossypiu

4AL13-0.59-0.66

CNL014BE490658-8	e-104	Eleusine indica alpha-tubulin 2 (TUA2) mRNA, complete cds	1.0e-65	TUBULIN ALPHA-2 CHAIN (ALPHA-2 TUBULIN)
CNL031BG263898-3	2.0e-20	Chlamydomonas reinhardtii 60S ribosomal protein L10a m	3.0e-24	(AB007651) 60S ribosomal protein L10A [Arabidopsis thalia
KSU001BE443794-3	0.064	Human DNA sequence from clone RP3-393K13 on chromos	5.9	(AE003500) CG8184 gene product [Drosophila melanogaste
KSU012BE404468-2	1.0e-07	Drosophila melanogaster, chromosome 2L, region 21D-21E	2.0e-52	(AC010556) putative transcription factor BTF3 (RNA polyme
KSU024BE499664-8	0	Maize gene for beta 1 tubulin	1.0e-96	TUBULIN BETA-1 CHAIN
KSU024BF484620-1	5.0e-71	Solanum tuberosum methionine synthase (MS) mRNA, co	1.0e-61	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYS
KSU027BE406676-8	3.0e-96	Triticum aestivum germin protein precursor, mRNA, comp	2.0e-40	GERMIN GF-2.8 PRECURSOR
KSU030BE498573-1	e-107	Zea mays protein kinase AKINbetagamma-1 mRNA, compl	4.0e-81	(AF276086) protein kinase AKINbetagamma-2 [Zea mays]
KSU035BE403721-1	4.0e-53	Oryza sativa beta-glucosidase mRNA, nuclear gene encodi	2.0e-77	beta-glucosidase BGQ60 precursor - barley
KSU035BE497238-4,5,6	e-102	Zea mays variety BMS prohibitin (PHB4) mRNA, complete c	2.0e-59	(AF236368) prohibitin [Zea mays]
NDS021BF473020-4	0	Oryza sativa MAP kinase kinase 1 mRNA, complete cds	1.0e-98	protein kinase MEK1 (EC 2.7.1.-) - maize
NDS034BE498573-3,4,6	e-107	Zea mays protein kinase AKINbetagamma-1 mRNA, compl	4.0e-81	(AF276086) protein kinase AKINbetagamma-2 [Zea mays]
UCD001BE406335-2	0.87	Homo sapiens sema domain, immunoglobulin domain (Ig)	2.0e-41	(AC079279) unknown protein [Arabidopsis thaliana]
UCD001BE443951-1	9.0e-36	Triticum aestivum clone pEMB27 transposon Tn1721 homo	2.0e-48	hypothetical protein T14P8.6 - Arabidopsis thaliana [Arabid
UCD028BE426203-2	0.36	Nicotiana tabacum cultivar Xanthi arginine decarboxylase 1	1.0e-33	(AC007727) ESTs gb|N96028, gb|F14286, gb|T20680, gb|F1444
UMC015BE590748-3	0	Barley embryo globulin (BEG1) mRNA, complete cds	6.0e-69	globulin Beg1 precursor - barley
UMC040BE637594-6	1.5	Pseudomonas aeruginosa PA01, section 225 of 529 of the	3.0e-47	glutamyl aminopeptidase homolog F4I10.20 - Arabidopsis t
UNL002BE403251-3,5	0.28	Bacillus anthracis virulence plasmid PX01, complete seque	1.0e-16	(AP001073) Similar to Disease resistance gene homolog 9N
UNL002BE426789-2,8	0.007	Cricetulus griseus mRNA for RNA polymerase II largest su	4.0e-41	(AF158634) Vrga1 [Aegilops ventricosa]
UNL002BE426790-2,8	0.39	Bos taurus blue cone pigment protein mRNA, complete cd	1.0e-09	(AF114171) disease resistance protein RPM1 homolog [Sor

4AL5-0.66-0.80

KSU001BE444339-1	1.4	Drosophila melanogaster genomic scaffold 1420000133860	3.5	(AF264760) cAMP-dependent protein kinase [Neurospora c
KSU002BE403518-1	1.0e-65	Oryza sativa Ca2+ sensitive 3'(2'),5-diphosphonucleoside 3	2.0e-70	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHO
KSU012BE442812-1	8.0e-30	Oryza sativa putative zinc finger protein mRNA, complete c	1.0e-61	(AP000399) ESTs AU077984(C62969),D41648(S4289), AU06358
KSU019BE494320-4	1.0e-62	Zea mays calreticulin (CRT) mRNA, complete cds	1.0e-51	CALRETICULIN PRECURSOR
KSU019BE606973-2	2.0e-71	Oryza sativa genomic DNA, chromosome 6, BAC clone:OSJ	e-106	(AP000399) EST AU056133(S20320) corresponds to a region
KSU024BE499599-1	5.0e-13	Vigna unguiculata phosphatidic acid phosphatase alpha m	8.0e-88	(AC007591) Contains similarity to gb acid phosphatase alpl
KSU024BE638039-2	2.0e-11	Arabidopsis thaliana At1g69340\/F10D13.28 mRNA, complet	6.0e-21	(AC073178) unknown protein [Arabidopsis thaliana]
KSU030BE403710-2	0.001	Arabidopsis thaliana AT3g62110 (AT3g62110\/T17J13_70) m	3.0e-53	(AF324992) AT3g62110 [Arabidopsis thaliana]
KSU030BF474862-1	2.0e-76	Oryza sativa OSKgamma mRNA for shaggy-related protein	1.0e-95	(AP001278) ESTs C22403(C50132),C22404(C50132) correspo
KSU035BE403256-1,5,6	4.0e-04	Arabidopsis thaliana galactose kinase (GAL1) mRNA, comp	2.0e-67	GALACTOKINASE (GALACTOSE KINASE)
KSU035BE404434-1	e-114	Lycopersicon esculentum elongation factor 2 mRNA, parti	2.0e-96	ELONGATION FACTOR 2 (EF-2)
KSU035BE404740-1	0.024	Homo sapiens chromosome 5, BAC clone 45m2 (LBNL H14	6.0e-61	(AB016893) 26S proteasome p55 protein-like [Arabidopsis
NDS034BE403826-2	e-170	L.temulentum mRNA for histone H3	2.0e-71	HISTONE H3.2, MINOR predicted gene.\; Similar to histone H
UCD001BE403518-1	1.0e-65	Oryza sativa Ca2+ sensitive 3'(2'),5-diphosphonucleoside 3	2.0e-70	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHO
UCD001BE444339-1	1.4	Drosophila melanogaster genomic scaffold 1420000133860	3.5	(AF264760) cAMP-dependent protein kinase [Neurospora c
UCD028BE498551-18	2.0e-36	Oryza sativa poly(A)-binding protein gene, partial cds	5.0e-35	(AF153689) poly(A)-binding protein [Oryza sativa]
UCD028BG274817-2,4,7,8,10,11	1.0e-04	Arabidopsis thaliana galactose kinase (GAL1) mRNA, comp	3.0e-96	GALACTOKINASE (GALACTOSE KINASE)
UCD029BG263563-2,5	3.0e-08	Nicotiana tabacum anther ethylene-upregulated protein ER	4.0e-52	(AF096260) ER66 protein [Lycopersicon esculentum]
UCD037BE443044-1	2.0e-29	Oryza sativa genomic DNA, chromosome 6, clone:P0535G0	4.0e-42	(AP000399) ESTs AU077984(C62969),D41648(S4289), AU06358
UCD037BE489586-1	0	Triticum aestivum gamma-type tonoplast intrinsic protein	7.0e-28	tonoplast intrinsic protein gamma - barley
UCD037BE606838-2	2.0e-05	Wheat mRNA for protein H2B-6, complete cds	4.0e-29	hypothetical protein F6E13.19 - Arabidopsis thaliana [Arabi
UCW039BE446195-2	0.39	Pyricularia grisea chromosome 7 clone BAC 6J18, genomi	3.0e-39	(X99923) male sterility 2-like protein [Arabidopsis thaliana]
UMC032BE426032-2	1.0e-12	Cicer arietinum mRNA for putative cytidine or deoxycytidyl	3.0e-57	(AJ006764) putative deoxycytidylate deaminase [Cicer arie
UMC040BE590763-3	e-126	Hordeum vulgare peroxidase BP 1 (Prx5) mRNA, complete	6.0e-45	peroxidase (EC 1.11.1.7) BP1 precursor - barley
UNL002BE492524-3,4	2.0e-41	Zea mays eukaryotic translation initiation factor 3 large su	2.0e-49	(AP002487) putative eukaryotic translation initiation factor
UNL036BF200529-4	0.32	Human chromosome 14 DNA sequence BAC R-689J19 of lit	1.0e-47	(AF223949) amidase [Arabidopsis thaliana]
UNL044BF484166-4	0.006	Homo sapiens chromosome 4q35 BAC clones RPCI-11-463	7.0e-18	(AB006698) gene_id:MCL19.8~pir||T27174~similar to unknov
UNL044BG263544-3	4.0e-04	Cruznema tripartitum large subunit RNA polymerase II mR	1.0e-47	DNA-directed RNA polymerase I 190K chain homolog F15B8
UNL053BF293541-3	3.0e-04	Homo sapiens 12q24 PAC RPCI1-46F2 (Roswell Park Cance	5.0e-15	(AF370143) putative cysteinyl-tRNA synthetase [Arabidopsi
UNL053BG274908-3,4,5,6	e-101	Lolium rigidum 5-enolpyruvylshikimate 3-phosphate syntl	8.0e-46	(AB016765) 3-phosphoshikimate 1-carboxyvinyltransferase

4AL11-0.66-0.80

KSU030BG314423-4,5	1.1	Bifidobacterium longum Na+\/H+ antiporter (nhaB), cytosine	0.001	(AF049920) PGPS\/D4 [Petunia x hybrida]

4AL4-0.80-1.00

CNL014BE489999-3,8	5.0e-93	Rice mRNA for T complex polypeptide, partial sequence	7.0e-89	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CC
CNL014BE490790-2	0.015	Genomic Sequence For Arabidopsis thaliana Clone T1G16	2.0e-18	(AF160912) BcDNA.LD06837 [Drosophila melanogaster]
KSU001BE442648-4	2.0e-18	Oryza sativa genomic DNA, chromosome 1, PAC clone:P06	7.0e-45	(AP003047) hypothetical protein [Oryza sativa]
KSU001BE443412-4	4.4	Homo sapiens BAC clone RP11-319A7 from 2, complete se	1.4	(AF207842) Pi-ta protein [Oryza sativa]
KSU001BE444470-8	2.0e-89	Hordeum vulgare genomic DNA fragment\; clone MWG0866	8.0e-87	(AB016885) protein kinase-like protein [Arabidopsis thaliar
KSU012BE406897-3	4.0e-34	Arabidopsis thaliana AT4g22310 (AT4g22310\/T10I14_140) m	5.0e-47	hypothetical protein T10I14.140 - Arabidopsis thaliana
KSU012BE443444-2	1.0e-53	Oryza sativa geneomic DNA, chromosome 6, PAC clone:P0	2.0e-45	(AP001552) ESTs AU032452(S10068),C23571(S10068) corresp
KSU012BE489999-2,5,8	5.0e-93	Rice mRNA for T complex polypeptide, partial sequence	7.0e-89	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CC
KSU012BE490790-2,9	0.015	Genomic Sequence For Arabidopsis thaliana Clone T1G16	2.0e-18	(AF160912) BcDNA.LD06837 [Drosophila melanogaster]
KSU024BE498428-1,5	e-141	Zea mays sucrose synthase (Sus1) mRNA, complete cds	2.0e-85	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFER
KSU024BE499049-7	0	Zea mays strain W64A x A182E putative cytosolic 6-phosph	e-116	phosphogluconate dehydrogenase (decarboxylating) (EC 1
KSU030BE490186-2,5	5.0e-24	Oryza sativa subsp. japonica clone C2421_1A putative gluta	3.0e-37	(AF309379) putative glutathione S-transferase OsGSTU3 [O
KSU030BE606678-2	0	Wheat mRNA coding for chloroform\/methanol-soluble (CM	1.0e-75	ALPHA-AMYLASE\/TRYPSIN INHIBITOR CM2 PRECURSOR (CHI
KSU035BE497624-1	0.5	Bovine herpesvirus type 1.1, complete genome	6.0e-06	(AP001168) ESTs C26000(C11448),AU082130(C11448) corres
KSU038BE443120-1	3.0e-10	Oryza sativa geneomic DNA, chromosome 6, PAC clone:P0	4.0e-07	(AP001552) EST AU082058(C12976) corresponds to a region
NDS018BE405013-2	0	Wheat ubiquitin carrier protein (E2) mRNA, complete cds	7.0e-87	UBIQUITIN-CONJUGATING ENZYME E2-23 KD (UBIQUITIN-PROT
NDS034BE403710-2	0.001	Arabidopsis thaliana AT3g62110 (AT3g62110\/T17J13_70) m	3.0e-53	(AF324992) AT3g62110 [Arabidopsis thaliana]
NDS043BG274929-2,3	1.2	Deinococcus radiodurans plasmid MP1, complete sequen	2.0e-17	jacalin homolog - barley vulgare]
TTU025BE489999-3	5.0e-93	Rice mRNA for T complex polypeptide, partial sequence	7.0e-89	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CC
TTU025BE490790-3	0.015	Genomic Sequence For Arabidopsis thaliana Clone T1G16	2.0e-18	(AF160912) BcDNA.LD06837 [Drosophila melanogaster]
UCD037BE443129-4,6,8	1.0e-53	Oryza sativa geneomic DNA, chromosome 6, PAC clone:P0	6.0e-54	(AP001552) ESTs AU032452(S10068),C23571(S10068) corresp
UCW020BG262472-3	0.005	Dictyostelium discoideum gene for AmiB, complete cds	4.0e-15	AVENIN-3 PRECURSOR (PROLAMIN)
UMC040BE590484-4	4.0e-04	A.sativa avenin mRNA, complete cds	9.0e-16	avenin-3 - oat Narymsky 943, Peptide, 201 aa]
UNL001BE442648-1	2.0e-18	Oryza sativa genomic DNA, chromosome 1, PAC clone:P06	7.0e-45	(AP003047) hypothetical protein [Oryza sativa]
UNL001BE443412-2,6	4.4	Homo sapiens BAC clone RP11-319A7 from 2, complete se	1.4	(AF207842) Pi-ta protein [Oryza sativa]
UNL001BE444421-2,3	0.09	Homo sapiens chromosome 5 clone RP11-138C1, complete sequence		
UNL001BE444470-5	2.0e-89	Hordeum vulgare genomic DNA fragment\; clone MWG0866	8.0e-87	(AB016885) protein kinase-like protein [Arabidopsis thaliar
UNL002BE444404-3,4,5	3.0e-04	Oryza sativa genomic DNA, chromosome 6, clone:OSJ	5.0e-17	(AP001168) Similar to gene for Pib (AB013448) [Oryza sativa
UNL002BE497251-2	0.1	Human DNA sequence from clone RP1-45N11 on chromoso	4.0e-13	(AY009938) Mla1 [Hordeum vulgare]
UNL002BF201403-4	0.064	Human DNA sequence from clone RP11-419N10 on chromo	2.0e-06	(AP001168) Similar to gene for Pib (AB013448) [Oryza sativa
UNL036BE518255-3	e-106	Z.mays CPNA gene encoding mitochondrial chaperonin-60	1.0e-80	CHAPERONIN CPN60-1, MITOCHONDRIAL PRECURSOR (HSP60
UNL036BE606874-2	0	Triticum aestivum granule-bound starch synthase I (Wx-Dl	1.0e-58	(AB019624) starch synthase (GBSSI) [Triticum aestivum] ta
UNL036BG262302-3	0.023	Helobdella robusta homeodomain protein LOX5 (Lox5) mR	3.0e-16	avenin N9 - oat
UNL044BF482786-2	0.32	Caenorhabditis elegans transmembrane cell adhesion rec	5.0e-32	(AC009519) F1N19.9 [Arabidopsis thaliana]

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