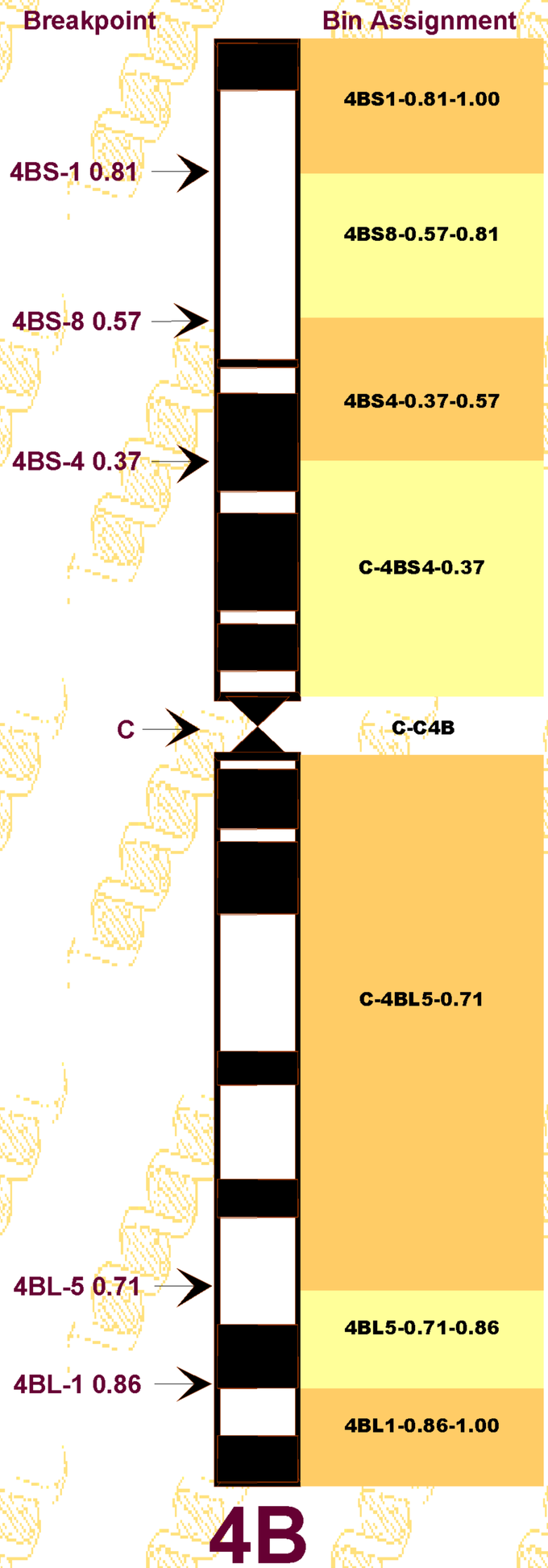
The Structure and Function of the Expressed Portion of the Wheat Genomes

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

*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

4BS1-0.81-1.00

CNL001BE405581-6	2.0e-06	Arabidopsis thaliana chromosome II section 201 of 255 of t	1.0e-23	(AC006922) unknown protein [Arabidopsis thaliana]
CNL001BE406616-3	7.0e-19	Zea mays seven transmembrane protein Mlo4 mRNA, corr	1.0e-23	(AY029315) seven transmembrane protein Mlo4 [Zea mays
CNL023BE405218-7	0	T.aestivum mRNA 1 for cathepsin B (2529)	e-120	cathepsin B-like cysteine proteinase (EC 3.4.22..) - wheat (t
CNL023BE405625-2,4,7	3.0e-51	Oryza sativa chromosome 3 BAC OSJNBa0018H01 genomic	3.0e-72	(AC087181) putative glutathione S-transferase [Oryza sativ
CNL023BG263307-2	0	Triticum aestivum COP alpha homolog mRNA, partial cds	1.0e-73	(AC082645) putative alpha-coat protein [Oryza sativa]
CNL031BG263898-1	2.0e-20	Chlamydomonas reinhardtii 60S ribosomal protein L10a m	3.0e-24	(AB007651) 60S ribosomal protein L10A [Arabidopsis thalia
CSU001BE405581-5	2.0e-06	Arabidopsis thaliana chromosome II section 201 of 255 of t	1.0e-23	(AC006922) unknown protein [Arabidopsis thaliana]
CSU102BE406462-2	0.71	Lolium perenne clone 8 gibberellin 20-oxidase mRNA, corr	2.0e-22	hypothetical protein Hfflk - Arabidopsis thaliana (fragment
KSU001BE403860-5	3.0e-10	Oryza sativa microsatellite MRG5838 containing (TCT)X14, c	7.0e-30	(AF198054) HAC1 [Arabidopsis thaliana]
KSU001BE406616-4	7.0e-19	Zea mays seven transmembrane protein Mlo4 mRNA, corr	1.0e-23	(AY029315) seven transmembrane protein Mlo4 [Zea mays
KSU002BE405581-7	2.0e-06	Arabidopsis thaliana chromosome II section 201 of 255 of t	1.0e-23	(AC006922) unknown protein [Arabidopsis thaliana]
KSU012BE406438-2	2.0e-07	Arabidopsis thaliana chromosome II section 86 of 255 of th	8.0e-14	(AF116752) seed maturation protein PM23 [Glycine max]
KSU012BE406450-2	3.0e-07	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-51	(U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsi
KSU024BE498699-2	0	Hordeum vulgare mRNA for endo-1,4-beta-glucanase Cel1,	7.0e-90	(AB040769) endo-1,4-beta-glucanase Cel1 [Hordeum vulgar
KSU024BF484585-2	0	Bromus inermis putative cytosolic phosphoglucomutase r	4.0e-94	PHOSPHOGLUCOMUTASE, CYTOPLASMIC (GLUCOSE PHOSPH
KSU024BF484620-2	5.0e-71	Solanum tuberosum methionine synthase (MS) mRNA, co	1.0e-61	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYS
KSU027BE403491-1	0.004	Hordeum vulgare 32 kDa protein (JRG1.2) gene, complete c	2.0e-20	benzothiadiazole-induced protein (clone WCI-1) - wheat
KSU027BE406676-6,11	3.0e-96	Triticum aestivum germin protein precursor, mRNA, comp	2.0e-40	GERMIN GF-2.8 PRECURSOR
KSU030BE490281-2	0	Avena nuda actin 1 gene, complete cds	4.0e-96	actin 1 [imported] - small naked oat
KSU035BE403268-6,10,11	e-152	Triticum aestivum metallothionein-like protein (wali1) mR	4.0e-12	METALLOTHIONEIN-LIKE PROTEIN 1
KSU035BE403348-9,10	0.058	Streptomyces coelicolor cosmid 9C5	2.0e-08	nucleoid DNA-binding protein cnd41-like protein - Arabidop
KSU035BE403438-6,10,11	0.069	Human DNA sequence from clone RP1-101A2 on chromosc	5.0e-07	(AB007648) contains similarity to ABA-responsive protein-
KSU035BE403439-6,10,11	1.0e-74	Panicum miliaceum mRNA for 2-oxoglutarate\/malate trans	1.0e-61	2-oxoglutarate\/malate translocator (clone OMT103), mitocl
KSU035BE403721-5	4.0e-53	Oryza sativa beta-glucosidase mRNA, nuclear gene encodi	2.0e-77	beta-glucosidase BGQ60 precursor - barley
KSU035BE496999-1	0	Hordeum vulgare mRNA for alpha-tubulin 3	7.0e-74	TUBULIN ALPHA-3 CHAIN
KSU035BE497366-6,10,11	2.0e-27	Oryza sativa subsp. japonica clone S14511 putative glutathi	6.0e-09	(AF309376) putative glutathione S-transferase OsGSTU6 [Oz
KSU038BE444890-1	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
KSU038BE445831-1	0.31	Human DNA sequence from clone RP11-515J24 on chromo	3.0e-17	(AF232008) beta-glucosidase aggregating factor precursor
NDS034BE403491-1	0.004	Hordeum vulgare 32 kDa protein (JRG1.2) gene, complete c	2.0e-20	benzothiadiazole-induced protein (clone WCI-1) - wheat
NDS038BE498602-4	0	T.aestivum mRNA for germin-like protein 4, partial	6.0e-35	(Y14203) oxalate oxidase [Hordeum vulgare]
UCD017BE488619-3	4.0e-27	Hordeum vulgare high light-induced mRNA for putative lec	3.0e-08	(AJ237754) putative lectin [Hordeum vulgare]
UCW039BE405592-5,11	0	Hordeum vulgare CM 72 germin subunit mRNA, complete	1.0e-87	GERMIN GF-2.8 PRECURSOR
UMC015BE590748-2	0	Barley embryo globulin (BEG1) mRNA, complete cds	6.0e-69	globulin Beg1 precursor - barley
UMC032BF291740-1	6.0e-25	Spinacia oleracea phosphoethanolamine N-methyltransfer	2.0e-81	(AB019238) methyl transferase-like protein [Arabidopsis th
UNL044BG263624-1	4.0e-04	Homo sapiens 11 beta-hydroxysteroid dehydrogenase 2 (HSD11B2) gene, complete cds		

4BS8-0.57-0.81

KSU002BE425993-6	e-154	Oryza sativa chromosome 3 BAC OSJNBa0040E01 genomic	1.0e-68	(AC079887) putative UDP-glucose dehydrogenase [Oryza s
KSU012BE403761-3	1.0e-72	Hordeum vulgare mRNA for alpha-keto acid dehydrogenas	e-102	(AL391712) branched-chain alpha keto-acid dehydrogenas
KSU012BE406875-1	9.0e-26	Zea mays ABA- and ripening-inducible-like protein mRNA,	1.3	probable serine\/threonine-specific protein kinase (EC 2.7.
KSU012BE490685-1	0.062	Cercocebus torquatus interleukin-1 beta (IL-1 beta) mRNA	1.0e-23	(AC012328) putative NADP-dependent oxidoreductase [Ara
KSU035BE497446-3	7.0e-73	Hordeum vulgare gene for CP29 precursor for core chloro	2.0e-56	chlorophyll a\/b-binding protein CP29 precursor - barley pr
KSU035BE497510-7,8	e-139	Avena sativa vacuolar H+-ATPase 16 kDa proteolipid subun	3.0e-42	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT oat
UCD037BE499456-2	0	H.vulgare mRNA for seed protein B32E	1.0e-46	seed protein B32E - barley (fragment)
UCW016BE403761-3	1.0e-72	Hordeum vulgare mRNA for alpha-keto acid dehydrogenas	e-102	(AL391712) branched-chain alpha keto-acid dehydrogenas
UCW016BE406875-1	9.0e-26	Zea mays ABA- and ripening-inducible-like protein mRNA,	1.3	probable serine\/threonine-specific protein kinase (EC 2.7.
UCW039BE405358-1	0.026	H.vulgare L. mRNA for flavonoid 7-O-methyltransferase	5.0e-31	catechol O-methyltransferase (EC 2.1.1.6) - barley
UMC015BE590976-5	0	Hordeum vulgare mRNA for formate dehydrogenase, com	3.0e-98	(D88272) formate dehydrogenase [Hordeum vulgare]
UMN013BE443232-3	2.0e-14	Lily mRNA for ORF, partial cds	4.0e-77	hypothetical protein T11I11.100 - Arabidopsis thaliana
UMN013BE443580-3,4	2.0e-24	Gossypium hirsutum GhCAP mRNA for adenylyl cyclase as	2.0e-76	(AB014884) adenylyl cyclase associated protein [Gossypiu
UNL002BF474165-2,5	1.1	Homo sapiens clone RP11-551D18, complete sequence	7.0e-08	(AB007645) gb|AAF67766.1~gene_id:K8K14.12~similar to uni

4BS4-0.37-0.57

CNL014BE444858-2	7.0e-15	Sequence of BAC F19K23 from Arabidopsis thaliana chrom	4.0e-66	(AC009525) Unknown protein [Arabidopsis thaliana]
KSU002BE406618-1	0.75	Deinococcus radiodurans R1 section 220 of 229 of the com	5.0e-28	(AB056451) CPRD49 [Vigna unguiculata]
KSU012BE403622-4,9	2.0e-09	Sequence of BAC F7H2 from Arabidopsis thaliana chromos	7.0e-95	(AC018849) unknown protein\; 52184-57536 [Arabidopsis th
KSU012BE403789-1,5	3.0e-05	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	8.0e-28	(AB016890) contains similarity to elongin C~gene_id:MNC1
KSU019BE403569-2	2.0e-27	Oryza sativa microsatellite MRG2726 containing (GA)X16, g	1.0e-78	(AC003970) Similar to ATP-citrate-lyase [Arabidopsis thalia
KSU027BE517725-1	5.0e-15	Lilium longiflorum lipid transfer protein precursor (LTP) m	2.0e-13	basic protein 1B, WBP1B-lipid transfer protein homolog [Ti
KSU030BE406580-3	3.0e-28	Oryza sativa OsUCP2 gene for uncoupling protein, complet	7.0e-52	(AB049998) uncoupling protein [Oryza sativa]
KSU035BE403770-1	3.0e-05	Mus musculus short stature homeobox 2 (Shox2), mRNA	5.0e-68	(AF117335) succinic semialdehyde dehydrogenase [Arabid
KSU035BE404401-4	0	T.aestivum mRNA for obtusifoliol 14-alpha-demethylase (C	4.0e-61	probable obtusifoliol 14-alpha-demethylase CYP51 - wheat
KSU035BE497184-2	4.0e-04	Arabidopsis thaliana chromosome II section 166 of 255 of t	5.0e-58	(AC004561) putative C-4 sterol methyl oxidase [Arabidopsi
KSU035BE497324-3	3.0e-11	Hordeum vulgare rubisco activase genes,complete cds	5.2	(AE003719) CG7397 gene product [Drosophila melanogaste
UMC015BE606474-5	5.0e-62	Glycine max clathrin heavy chain mRNA, complete cds	2.0e-95	(AC074395) clathrin heavy chain, putative [Arabidopsis thal

C-4BS4-0.37

KSU001BE443755-14	0.007	Dictyostelium discoideum nucleoside diphosphate kinase	6	(AF202730) Niemann-Pick type C1 disease protein [Oryctola
KSU002BE406512-2	0.044	Drosophila melanogaster, chromosome 2R, region 50C-50	2.0e-15	(AB010069) contains similarity to RNA binding protein~gen
KSU027BF202969-2	2.0e-87	Oryza sativa cystathionine gamma-synthase (CGS1) mRNA	3.0e-54	O-succinylhomoserine (thiol)-lyase (EC 4.2.99.9) 1 - maize
KSU035BE497635-2	0.38	Taeniopygia guttata SWS2 opsin mRNA, complete cds	4.0e-09	(X93159) ribosomal protein S5 [Spinacia oleracea]
KSU038BE443596-4	0	Hordeum vulgare (cv. Bomi) B120 mRNA	9.0e-45	B120 protein - barley
TTU047BE444811-3	6.0e-49	Sorghum bicolor BAC clone 25.M19, complete sequence	2.0e-86	(AF114171) H beta 58 homolog [Sorghum bicolor]
UCD037BE499948-2	4.0e-04	Homo sapiens glutamate rich WD repeat protein GRWD (GE	1.0e-40	(AC005917) putative WD-40 repeat protein [Arabidopsis tha
UCW020BE591320-1	4.0e-22	Nicotiana tabacum WERBP-1 mRNA, complete cds	2.0e-33	hypothetical protein T5F17.60 - Arabidopsis thaliana
UMN013BE443291-2	1.0e-25	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-96	(AP003143) putative neutral invertase [Oryza sativa]
UMN013BE443537-4,6	2.0e-05	Lilium longiflorum potential thioredoxin mRNA, complete	7.0e-46	thioredoxin homolog F22O13.5 - Arabidopsis thaliana

C-4BL5-0.71

CNL001BE426317-2	1.5	Sphingomonas aromaticivorans plasmid pNL1, complete s	4.0e-37	hypothetical protein F12L6.13 - Arabidopsis thaliana
CNL014BE445427-2	3.0e-05	Arabidopsis thaliana chromosome II section 143 of 255 of t	8.0e-62	(AC006300) unknown protein [Arabidopsis thaliana]
CNL031BF428799-3	e-142	Oryza sativa GAD mRNA for glutamate decarboxylase, com	e-108	(AF020425) glutamate decarboxylase isozyme 1 [Nicotiana t
KSU001BE443755-10	0.007	Dictyostelium discoideum nucleoside diphosphate kinase	6	(AF202730) Niemann-Pick type C1 disease protein [Oryctola
KSU002BE426317-2	1.5	Sphingomonas aromaticivorans plasmid pNL1, complete s	4.0e-37	hypothetical protein F12L6.13 - Arabidopsis thaliana
KSU019BE498350-1	9.0e-06	Solanum tuberosum spliceosomal protein (U2B) mRNA, co	8.0e-11	small nuclear ribonucleoprotein U2B'' - potato
KSU019BE495116-1	0	Triticum aestivum eIF-2 beta subunit mRNA, complete cds	1.0e-88	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUB
KSU024BF202695-3	3.0e-19	Oryza sativa peroxidase (POX22.3) mRNA, complete cds	6.0e-31	peroxidase (EC 1.11.1.7) 2 precursor - wheat
KSU024BF202706-1,2	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
KSU024BF485396-1	1.0e-25	Nicotiana tabacum GDP dissociation inhibitor (GDI) mRNA, c	2.0e-77	GDP dissociation inhibitor - common tobacco
KSU027BE426016-1	0	Triticum aestivum vacuolar targeting receptor bp-80 mRN	1.0e-93	(AF161719) vacuolar targeting receptor bp-80 [Triticum aes
KSU030BE497108-2	1.0e-22	A.thaliana mRNA for stromal ascorbate peroxidase	4.0e-40	(AB022273) thylakoid-bound ascorbate peroxidase [Nicotia
KSU030BF485011-3	0.066	Tacca chantieri MADS box containing protein PI mRNA, par	0.003	(AC067974) Contains similarity to a hypothetical protein F2
KSU035BE497610-3	e-120	Hordeum vulgare mRNA for ascorbate peroxidase	1.0e-34	(AJ000223) ascorbate peroxidase [Hordeum vulgare]
KSU038BE442811-2	3.0e-11	Oryza sativa chromosome unknown BAC clone OSJNBa00	1.0e-15	(AB046954) pseudo-response regulator 7 [Arabidopsis tha
KSU038BE443190-2	0.093	Homo sapiens genomic DNA, chromosome 21q, section 58	2.0e-24	(AB026636) contains similarity to similar to ubiquitin conju
KSU038BE443191-11	e-115	Triticum aestivum 70 kDa heat shock protein (TaHSP70d) r	2.0e-62	dnaK-type molecular chaperone hsp70 - rice (fragment)
KSU038BE443973-1	4.0e-04	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	3.0e-45	(AB005248) glucosyltransferase-like protein [Arabidopsis t
KSU038BE446076-1,2	0	Triticum aestivum MAP kinase homolog (WCK-1) mRNA, co	1.0e-64	mitogen-activated protein kinase 1 homolog (clone Asplk9
NDS018BE404963-3,5,6	5.0e-22	Brassica napus mRNA for acyl-carrier protein] S-malonyltr	1.0e-86	probable [acyl-carrier-protein] S-malonyltransferase (EC 2
NDS043BG274947-2	0.025	Hordeum vulgare partial mRNA for lectin, clone 4B1017	6.0e-24	(AB016880) contains similarity to disease resistance respo
TTU047BE405190-3	5.9	Homo sapiens chromosome 10 clone RP11-77G23, comple	1.0e-53	(AF169021) seed maturation protein PM36 [Glycine max]
TTU047BE446061-1	3.0e-20	Arabidopsis thaliana chromosome 3 BAC T2E22 genomic s	5.0e-48	(AC069474) nascent polypeptide associated complex alpha
UCD037BE443253-2	2.0e-08	Arabidopsis thaliana ABC transporter-like protein (T1E22_	6.0e-51	ABC transporter-like protein - Arabidopsis thaliana
UMC032BG314130-3	3.0e-76	Arabidopsis thaliana beta-adaptin-like protein C mRNA, pa	e-101	beta-adaptin homolog F16G20.160 - Arabidopsis thaliana
UMC040BE590942-3	2.0e-17	N.tabacum mRNA for LIM-domain protein	2.0e-44	probable transcription factor SF3 - common tobacco
UNL048BE605229-4	1.0e-61	Rice mRNA for low molecular weight heat shock protein, c	5.0e-15	17.4 KD CLASS I HEAT SHOCK PROTEIN

4BL5-0.71-0.86

CNL014BE444731-3	0	Hordeum vulgare Harrington haemoglobin apoprotein (hb)	8.0e-88	NONLEGUME HEMOGLOBIN
TTU047BE405064-2,3,7	1.3	Pseudomonas aeruginosa PAO1, section 328 of 529 of the	3.0e-49	(AC007767) Strong similarity to an unknown protein F19D1
UMC032BF145459-1	5.0e-68	Oryza sativa subsp. indica serine\/threonine protein phosp	6.0e-39	male sterility protein 2 - rape

4BL1-0.86-1.00

CNL014BE424255-1	6.0e-09	Genomic sequence for Arabidopsis thaliana BAC T25N20 fi	2.0e-65	probable transport protein - Arabidopsis thaliana
CNL014BE591172-1	e-132	Oryza sativa phytoene desaturase precursor (Pds) mRNA,	4.0e-77	PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESAT
CSU001BE406335-1	0.87	Homo sapiens sema domain, immunoglobulin domain (Ig)	2.0e-41	(AC079279) unknown protein [Arabidopsis thaliana]
CSU001BE444616-4,5	0.006	Human DNA sequence from clone RP1-211D12 on chromos	7.0e-32	(AC051633) putative ubiquitin protein [Oryza sativa]
CSU046BE444458-2	1.0e-07	Oryza sativa chromosome 10 clone nbxb0094K20, complet	4.0e-15	hypothetical protein (clone NF22) - common tobacco
KSU001BE444334-1	e-125	Triticum aestivum delta-24-sterol methyltransferase (TA-1	9.0e-24	(U60755) delta-24-sterol methyltransferase [Triticum aesti
KSU001BE444421-2	0.09	Homo sapiens chromosome 5 clone RP11-138C1, complete sequence		
KSU001BE444473-3,4	0.016	Drosophila melanogaster genomic scaffold 142000013386	2.0e-23	(AC084763) hypothetical protein [Oryza sativa]
KSU012BE403305-1	5.0e-19	Oryza sativa chromosome 10 BAC OSJNBa0001O14 genomi	6.0e-74	(AC025783) putative protein phosphatase 2C [Oryza sativa]
KSU012BE490658-1	e-104	Eleusine indica alpha-tubulin 2 (TUA2) mRNA, complete cds	1.0e-65	TUBULIN ALPHA-2 CHAIN (ALPHA-2 TUBULIN)
KSU019BE497134-3,5	8.0e-17	Hordeum vulgare genomic DNA fragment\; clone MWG0934	6.0e-55	(AC012563) putative trehalose-6-phosphate synthase\; 468
KSU024BE497808-1	0	Wheat histone H4 gene	9.0e-40	histone H4 [Triticum aestivum]
KSU024BE498038-5	0	Triticum aestivum p34cdc2 (cdc2TaA) mRNA, complete cds	e-125	(U23409) p34cdc2 [Triticum aestivum]
KSU024BE606476-4	0.34	Homo sapiens BAC clone RP11-251G23 from 7, complete se	0.28	MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MAR
KSU024BE638039-3	2.0e-11	Arabidopsis thaliana At1g69340\/F10D13.28 mRNA, complete	6.0e-61	(AC073178) unknown protein [Arabidopsis thaliana]
KSU027BE590745-1	0	Hordeum vulgare cultivar Franklin beta-amylase mRNA, pa	e-109	(D21349) beta-amylase [Hordeum vulgare]
KSU027BF482595-1	0	Oryza sativa rCOP11 protein (rCOP11) mRNA, complete cds	e-105	(AF160880) constitutive photomorphogenic 11 [Oryza sativ
KSU027BF484401-3	7.0e-64	Genomic Sequence for Oryza sativa, Nipponbare strain, clo	5.0e-15	(AB016893) emb|CAB61744.1~gene_id:MYB9.17~similar to u
KSU030BE499019-2	2.0e-67	Arabidopsis thaliana Ser\/Thr protein phosphatase mRNA,	6.0e-84	SERINE\/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALY
KSU030BF201003-2	0.29	Dictyostelium discoideum C-module-binding factor (cbfA)	0.36	(AC006264) hypothetical protein [Arabidopsis thaliana]
KSU030BF482216-3	8.0e-24	Arabidopsis thaliana CAF protein (CAF) mRNA, complete c	2.0e-75	(AF292940) short integuments 1 [Arabidopsis thaliana]
KSU035BE403378-3	0.081	Homo sapiens BAC clone GS1-286B23 from 7q21.1-q21.3, c	5.0e-38	(AC069380) putative transcription regulatory protein [Oryz
KSU035BE404665-3	0.006	Homo sapiens suppressor of Ty (S.cerevisiae) 5 homolog	2.0e-25	(AL161577) signal recognition particle receptor-like protei
KSU035BE406989-2,4	1.0e-11	Zea mays herbicide safener binding protein (SBP1) mRNA,	2.0e-25	herbicide safener binding protein 1 - maize
KSU035BE497160-2	e-133	Oryza sativa ribulose-5-phosphate-3-epimerase (RPE) mR	4.0e-63	RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR (PENTOSE-
KSU035BE517664-1	0.088	Synechococcus sp. gene for ribosomal proteins, complet	8.0e-54	50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (
KSU038BE444566-3	0.006	Arabidopsis thaliana putative DNA-binding protein (T20K12	2.0e-13	(AF123265) remorin 1 [Lycopersicon esculentum]
KSU038BE444757-4,7	4.0e-05	Oryza sativa chromosome 10 clone nbxb0040P18, complet	2.0e-76	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CON
NDS001BE442582-1	0.42	Microtus arvalis smc4 gene for SMC4 protein, exons 1-19	6.0e-26	(AC004135) T17H7.16 [Arabidopsis thaliana]
NDS001BE444334-1	e-125	Triticum aestivum delta-24-sterol methyltransferase (TA-1	9.0e-24	(U60755) delta-24-sterol methyltransferase [Triticum aesti
NDS018BE426767-3	1.0e-07	Arabidopsis thaliana BAC T1M15	3.0e-62	(AF154423) putative beta-galactosidase [Lycopersicon esc
NDS021BF201470-4	e-167	Zea mays unconventional myosin heavy chain (MYO1) mR	4.0e-83	unconventional myosin heavy chain - maize
NDS021BF472975-4	4.0e-72	Hordeum vulgare cell division cycle protein 48 (CDC48) mR	e-107	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CON
NDS021BF473020-7	0	Oryza sativa MAP kinase kinase 1 mRNA, complete cds	1.0e-98	protein kinase MEK1 (EC 2.7.1..) - maize
NDS034BE403814-2	0.34	Oryza sativa chromosome 10 BAC OSJNBa0010C11 genomi	6.0e-48	(AC069380) putative dioxygenase [Oryza sativa]
NDS034BE403881-3	0.11	Glycine max putative purple acid phosphatase precursor (	1.0e-79	(AF236109) putative purple acid phosphatase precursor [P
NDS034BE470946-4	0	Hordeum vulgare mRNA for allene oxide synthase (aos2 g	1.0e-94	(AJ251304) allene oxide synthase [Hordeum vulgare]
NDS034BE499019-1	2.0e-67	Arabidopsis thaliana Ser\/Thr protein phosphatase mRNA,	6.0e-84	SERINE\/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALY
NDS034BF201003-2	0.29	Dictyostelium discoideum C-module-binding factor (cbfA)	0.36	(AC006264) hypothetical protein [Arabidopsis thaliana]
NDS043BF293366-2	1.2	Genomic Sequence for Oryza sativa, Nipponbare strain, clo	7.0e-11	(AF245482) OSE3 [Oryza sativa]
UCD017BE490291-1	0	Triticum aestivum cold acclimation protein WCOR615 (Wco	8.0e-85	cold acclimation protein WCOR615 - wheat
UCD017BE494988-1	7.0e-19	Oryza sativa genomic DNA, chromosome 6, PAC clone:P06-	6.0e-30	(AP001129) ESTs AU029380(C30287),D49277(S16474) corresp
UCD028BE498551-8,19,22	2.0e-36	Oryza sativa poly(A)-binding protein gene, partial cds	5.0e-35	(AF153689) poly(A)-binding protein [Oryza sativa]
UCD029BG263563-3	3.0e-08	Nicotiana tabacum anther ethylene-upregulated protein EF	4.0e-52	(AF096268) ER66 protein [Lycopersicon esculentum]
UCD029BG273991-3	0.006	Genomic Sequence for Oryza sativa, Nipponbare strain, clo	2.0e-23	hypothetical protein F13G24.170 - Arabidopsis thaliana
UCD037BE489586-4	0	Triticum aestivum gamma-type tonoplast intrinsic protein	7.0e-28	tonoplast intrinsic protein gamma - barley
UCD037BF201181-1	0.097	Human polymorphic loci in Xq28	3.0e-11	(AC007134) putative sugar transporter [Arabidopsis thalia
UCW016BE424208-1	0	T.aestivum mRNA for CM 17 protein	6.0e-71	alpha-amylase inhibitor, tetrameric, chain CM17 precursor
UCW016BE518014-2	7.0e-33	Oryza sativa chromosome 3 BAC OSJNBb0022E02 genomic	1.0e-32	(AC087797) putative phospholipase [Oryza sativa]
UCW020BE403628-5	1.5	Xenopus laevis receptor protein tyrosine phosphatase de	1.0e-13	(AB017061) anthranilate N-benzoyltransferase [Arabidopsi
UCW020BF473204-3	6.0e-06	Arabidopsis thaliana transcription factor CRC mRNA, comp	2.0e-22	(AF132606) transcription factor CRC [Arabidopsis thaliana]
UCW039BE444393-10	6.0e-12	Arabidopsis thaliana unknown protein (At2g23810) mRNA,	6.0e-31	(AF082030) senescence-associated protein 5 [Hemerocalli
UMC015BE426266-3	6.0e-86	Oryza sativa mRNA for ribonuclease, partial cds, clone:E11	1.0e-65	ribonuclease (EC 3.1.-.-) - barley
UMC015BE426767-3	1.0e-07	Arabidopsis thaliana BAC T1M15	3.0e-62	(AF154423) putative beta-galactosidase [Lycopersicon esc
UMC032BE426410-1	5.0e-28	Oryza sativa genomic DNA, chromosome 6, BAC clone:OSJ	6.0e-65	(AF233342) DNA-binding protein p24 [Solanum tuberosum]
UMC040BE590589-4,5	e-145	Hordeum vulgare Bmy1 gene for Sd1 beta-amylase, compl	1.0e-52	(D21349) beta-amylase [Hordeum vulgare]
UMC040BF474251-6	0	Triticum aestivum mRNA for PR-1.1 protein	7.0e-57	(AJ007348) pathogenisis-related protein 1.1 [Triticum aest
UMC040BF474257-7	0.1	S.pombe chromosome II cosmid c5H6	4.0e-13	probable serine\/threonine-specific protein kinase T20F6.1
UMN013BE442995-1,5	1.0e-35	Cucumis melo mitochondrial processing peptidase beta s	6.0e-86	(AF363285) mitochondrial processing peptidase [Aviceni
UNL001BE444421-1	0.09	Homo sapiens chromosome 5 clone RP11-138C1, complete sequence		
UNL001BE444473-1,2	0.016	Drosophila melanogaster genomic scaffold 142000013386	2.0e-23	(AC084763) hypothetical protein [Oryza sativa]
UNL002BE425301-1	6.0e-74	Avena fatua 40S ribosomal protein S3A mRNA, partial cds	7.0e-46	40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
UNL002BE444616-4,5	0.006	Human DNA sequence from clone RP1-211D12 on chromos	7.0e-32	(AC051633) putative ubiquitin protein [Oryza sativa]
UNL036BE518134-3	7.0e-09	Trypanosoma brucei putative DEAD box RNA helicase HEL6	3.0e-76	(AB010259) DRH1 [Arabidopsis thaliana]
UNL036BE518255-2	e-106	Z.mays CPN4 gene encoding mitochondrial chaperonin-60	1.0e-80	CHAPERONIN CPN60-1, MITOCHONDRIAL PRECURSOR (HSP60
UNL036BE637560-1	0	T.aestivum Rrt-1 mRNA for CMx	3.0e-52	trypsin inhibitor CMx precursor (clones pCMx1 and pCMx3
UNL036BF200627-3	9.0e-62	Zea mays mRNA for Toc34-1 protein (toc34A gene)	8.0e-22	(AJ271049) Toc34-2 protein [Zea mays]
UNL036BF200656-2	0.61	Homo sapiens, Similar to thiosulfate sulfurtransferase (rh	2.0e-06	(AF156782) nod factor binding lectin-nucleotide phosphoh
UNL044BG263172-2	9.0e-11	Arabidopsis thaliana chromosome II section 141 of 255 of t	1.0e-73	clpB heat shock protein-like - Arabidopsis thaliana
UNL044BG312582-2	e-100	Hordeum vulgare DNA for chromosome 4H	6.0e-53	ribophorin I homolog - barley (fragment)
UNL048BE591739-2	2.0e-64	Genomic Sequence for Oryza sativa, Nipponbare strain, clo	3.0e-36	(AP000600) gb|AAC25523.1~gene_id:MAG2.20~similar to uni
UNL053BF293541-4	3.0e-04	Homo sapiens 12q24 PAC RPCI1-46F2 (Roswell Park Cance	5.0e-15	(AF370143) putative cysteinyl-tRNA synthetase [Arabidopsi

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