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

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

*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.

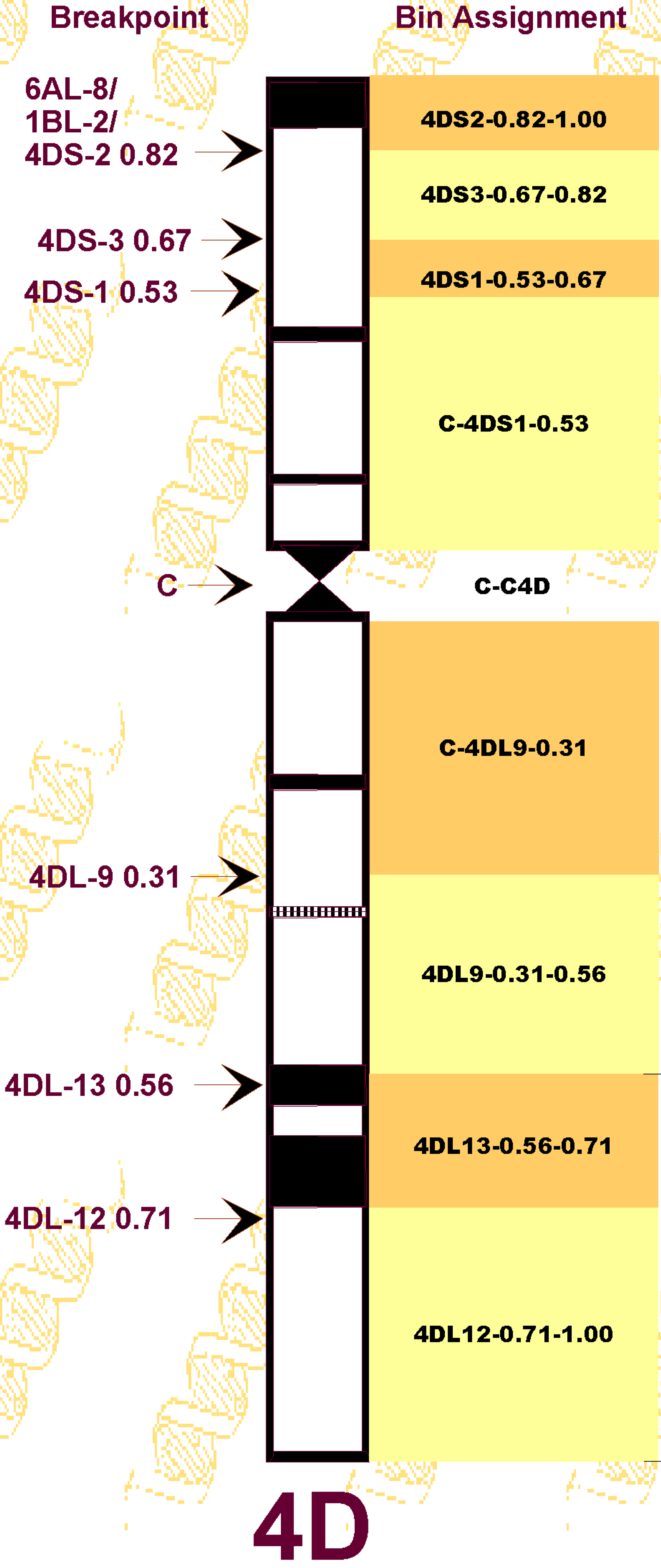
How to Interpret This Image:

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



4DS2-0.82-1.00

CSU001BE425993-2	e-154	Oryza sativa chromosome 3 BAC OSJNBa0040E01 genomic	1.0e-68	(AC079887) putative UDP-glucose dehydrogenase [Oryza s
CSU102BE406462-1	0.71	Lolium perenne clone 8 gibberellin 20-oxidase mRNA, com	2.0e-22	hypothetical protein H1flk - Arabidopsis thaliana (fragment
KSU001BE403860-2	3.0e-10	Oryza sativa microsatellite MRG5838 containing (TCT)X14,	7.0e-30	(AF198054) NAC1 [Arabidopsis thaliana]
KSU001BE406616-2	7.0e-19	Zea mays seven transmembrane protein Mlo4 mRNA, com	1.0e-23	(AY029315) seven transmembrane protein Mlo4 [Zea mays
KSU002BE425993-7	e-154	Oryza sativa chromosome 3 BAC OSJNBa0040E01 genomic	1.0e-68	(AC079887) putative UDP-glucose dehydrogenase [Oryza s
KSU024BE498699-3	0	Hordeum vulgare mRNA for endo-1,4-beta-glucanase Cel1,	7.0e-90	(AB040769) endo-1,4-beta-glucanase Cel1 [Hordeum vulgar
KSU024BF484620-3	5.0e-71	Solanum tuberosum methionine synthase (MS) mRNA, co	1.0e-61	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYS
KSU027BE403491-2	0.004	Hordeum vulgare 32 kDa protein (JRG1.2) gene, complete	2.0e-20	benzothiadiazole-induced protein (clone WCI-1) - wheat
KSU027BE406676-1,4,7,9,10,13	3.0e-96	Triticum aestivum germin protein precursor, mRNA, comp	2.0e-40	GERMIN GF-2.8 PRECURSOR
KSU030BE490281-1	0	Avena nuda actin 1 gene, complete cds	4.0e-96	actin 1 [imported] - small naked oat
KSU035BE403268-1,4,7,8,9,13	e-152	Triticum aestivum metallothionein-like protein (wali1) mR	4.0e-12	METALLOTHIONEIN-LIKE PROTEIN 1
KSU035BE403348-1,4,6,7,12	0.058	Streptomyces coelicolor cosmid 9C5	2.0e-08	nucleoid DNA-binding protein cnd41-like protein - Arabidop
KSU035BE403438-1,4,7,8,9,13	0.069	Human DNA sequence from clone RP1-101A2 on chromoso	5.0e-07	(AB007648) contains similarity to ABA-responsive protein~
KSU035BE403439-1,4,7,8,9,13	1.0e-74	Panicum miliaceum mRNA for 2-oxoglutarate\/malate trans	1.0e-61	2-oxoglutarate\/malate translocator (clone OMT103), mitoc
KSU035BE496999-3,5	0	Hordeum vulgare mRNA for alpha-tubulin 3	7.0e-74	TUBULIN ALPHA-3 CHAIN
KSU035BE497366-1,4,7,8,9,13	2.0e-27	Oryza sativa subsp. japonica clone S14511 putative glutath	6.0e-09	(AF309376) putative glutathione S-transferase OsGSTU6 [O
KSU038BE445831-2	0.31	Human DNA sequence from clone RP11-515J24 on chromo	3.0e-17	(AF232008) beta-glucosidase aggregating factor precursor
UCD037BE498476-3	4.0e-04	Arabidopsis thaliana dynamin-like GTP binding protein mR	1.0e-76	(AF180734) dynamin-like protein 5 [Arabidopsis thaliana]
UCW039BE405350-2	0.026	H.vulgare L. mRNA for flavonoid 7-O-methyltransferase	5.0e-31	catechol O-methyltransferase (EC 2.1.1.6) - barley
UCW039BE405592-8,9,13	0	Hordeum vulgare CM 72 germin subunit mRNA, complete	1.0e-87	GERMIN GF-2.8 PRECURSOR
UMC040BE637594-2	1.5	Pseudomonas aeruginosa PA01, section 225 of 529 of the	3.0e-47	glutamyl aminopeptidase homolog F4I10.20 - Arabidopsis t
UMN013BE443038-4,7,9	2.0e-94	Hordeum vulgare thaumatin-like protein TLP8 mRNA, comp	1.0e-18	(AF355458) thaumatin-like protein TLP8 [Hordeum vulgare]
UMN013BE443500-1	2.0e-24	Gossypium hirsutum GhCAP mRNA for adenylyl cyclase as	2.0e-76	(AB014884) adenylyl cyclase associated protein [Gossypiu
UNL002BF474165-3,4,6	1.1	Homo sapiens clone RP11-551D18, complete sequence	7.0e-08	(AB007645) gb|AAF67766.1~gene_id:K8K14.12~similar to unk
UNL036BE518074-3,4,7,8	3.0e-87	Rice mRNA for ribosomal protein S12 (320 gene), partial se	3.0e-51	40S RIBOSOMAL PROTEIN S23 (S12)
UNL044BG263624-2	4.0e-04	Homo sapiens 11 beta-hydroxysteroid dehydrogenase 2 (HSD11B2) gene, complete cds		

4DS3-0.67-0.82

CNL001BE406616-1	7.0e-19	Zea mays seven transmembrane protein Mlo4 mRNA, com	1.0e-23	(AY029315) seven transmembrane protein Mlo4 [Zea mays
CNL031BE498480-4	0	Triticum aestivum cytosolic glyceraldehyde-3-phosphate	2.0e-92	(AF251217) cytosolic glyceraldehyde-3-phosphate dehydro
CNL031BF428799-8	e-142	Oryza sativa GAD mRNA for glutamate decarboxylase, com	e-108	(AF020425) glutamate decarboxylase isozyme 1 [Nicotiana
KSU035BE403721-2,3	4.0e-53	Oryza sativa beta-glucosidase mRNA, nuclear gene encodi	2.0e-77	beta-glucosidase BGQ60 precursor - barley
KSU035BE497446-1	7.0e-73	Hordeum vulgare gene for CP29 precursor for core chloro	2.0e-56	chlorophyll a\/b-binding protein CP29 precursor - barley pr
NDS021BF473824-3	5.0e-10	Rattus norvegicus SMC (segregation of mitotic chromoso	3.0e-78	structural maintenance of chromosomes (SMC)-like prote
NDS034BE403491-2	0.004	Hordeum vulgare 32 kDa protein (JRG1.2) gene, complete	2.0e-20	benzothiadiazole-induced protein (clone WCI-1) - wheat
NDS034BE490602-6	0	T.aestivum mRNA for germin-like protein 4, partial	6.0e-35	(Y14203) oxalate oxidase [Hordeum vulgare]
UCD017BE488619-2,4	4.0e-27	Hordeum vulgare high light-induced mRNA for putative lec	3.0e-08	(AJ237754) putative lectin [Hordeum vulgare]
UCD037BE499456-1	0	H.vulgare mRNA for seed protein B32E	1.0e-46	seed protein B32E - barley (fragment)
UMC032BE425830-2	2.0e-58	S.tuberosum mRNA for glycine hydroxymethyltransferase	3.0e-99	glycine hydroxymethyltransferase (EC 2.1.2.1) F20D10.50 -
UMC040BE637573-3	3.0e-23	Oryza sativa nucleic acid binding protein mRNA, complete	5.0e-56	probable nucleic acid binding protein - rice

4DS1-0.53-0.67

CNL023BE405218-6	0	T.aestivum mRNA 1 for cathepsin B (2529)	e-120	cathepsin B-like cysteine proteinase (EC 3.4.22.-) - wheat
CNL023BE405585-3	3.0e-69	Oryza sativa abscisic acid- and stress-inducible protein (A	3.0e-09	abscisic acid- and stress-induced protein - rice sativa]
CNL023BE405625-5,6	3.0e-51	Oryza sativa chromosome 3 BAC OSJNBa0018H01 genomic	3.0e-72	(AC087181) putative glutathione S-transferase [Oryza sativ
CNL031BG263898-2	2.0e-20	Chlamydomonas reinhardtii 60S ribosomal protein L10a m	3.0e-24	(AB007651) 60S ribosomal protein L10A [Arabidopsis thalia
KSU027BE517725-3	5.0e-15	Lilium longiflorum lipid transfer protein precursor (LTP) m	2.0e-13	basic protein 1B, WBP1B=lipid transfer protein homolog [T
KSU035BE404401-2	0	T.aestivum mRNA for obtusifoliol 14-alpha-demethylase (C	4.0e-61	probable obtusifoliol 14-alpha-demethylase CYP51 - wheat
KSU035BE497510-1	e-139	Avena sativa vacuolar H+-ATPase 16 kDa proteolipid subun	3.0e-42	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT oat
UCD037BE443280-6,9	2.0e-36	Arabidopsis thaliana DNA chromosome 3, BAC clone T14D3	7.0e-35	(AB023032) ubiquitin-like protein [Arabidopsis thaliana]
UCD037BE499948-3	4.0e-04	Homo sapiens glutamate rich WD repeat protein GRWD (GR	1.0e-40	(AC005917) putative WD-40 repeat protein [Arabidopsis tha

C-4DS1-0.53

CNL001BE406618-2	0.75	Deinococcus radiodurans R1 section 220 of 229 of the com	5.0e-28	(AB056451) CPRD49 [Vigna unguiculata]
CNL014BE444858-3	7.0e-15	Sequence of BAC F19K23 from Arabidopsis thaliana chrom	4.0e-66	(AC009525) Unknown protein [Arabidopsis thaliana]
CSU046BE444458-1	1.0e-07	Oryza sativa chromosome 10 clone nbxb0094K20, complet	4.0e-15	hypothetical protein (clone NF22) - common tobacco
KSU002BE406618-2	0.75	Deinococcus radiodurans R1 section 220 of 229 of the com	5.0e-28	(AB056451) CPRD49 [Vigna unguiculata]
KSU012BE403622-7,8	2.0e-09	Sequence of BAC F7H2 from Arabidopsis thaliana chromos	7.0e-95	(AC018849) unknown protein\; 52184-57536 [Arabidopsis th
KSU012BE403789-3,4	3.0e-05	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	8.0e-28	(AB016890) contains similarity to elongin C~gene_id:MNC1
KSU030BE406580-2	3.0e-28	Oryza sativa OsUCP2 gene for uncoupling protein, complet	7.0e-52	(AB049998) uncoupling protein [Oryza sativa]
KSU035BE403770-2	3.0e-05	Mus musculus short stature homeobox 2 (Shox2), mRNA	5.0e-68	(AF117335) succinic semialdehyde dehydrogenase [Arabid
KSU035BE497184-3	4.0e-04	Arabidopsis thaliana chromosome II section 166 of 255 of	5.0e-58	(AC004561) putative C-4 sterol methyl oxidase [Arabidopsi
KSU035BE497324-1	3.0e-11	Hordeum vulgare rubisco activase genes,complete cds	5.2	(AE003719) CG7397 gene product [Drosophila melanogaste
KSU035BE497635-1	0.38	Taeniopygia guttata SWS2 opsin mRNA, complete cds	4.0e-09	(X93159) ribosomal protein S5 [Spinacia oleracea]
TTU047BE444811-2	6.0e-49	Sorghum bicolor BAC clone 25.M18, complete sequence	2.0e-86	(AF114171) H beta 58 homolog [Sorghum bicolor]
UCD001BE444378-2	6.0e-09	Arabidopsis thaliana genomic DNA, chromosome 3, TAC cl	1.0e-53	hypothetical protein T24A18.30 - Arabidopsis thaliana
UCD017BE403622-5,6	2.0e-09	Sequence of BAC F7H2 from Arabidopsis thaliana chromos	7.0e-95	(AC018849) unknown protein\; 52184-57536 [Arabidopsis th
UCD017BE403789-5,6	3.0e-05	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	8.0e-28	(AB016890) contains similarity to elongin C~gene_id:MNC1
UCD017BE489218-1	e-175	Triticum aestivum ribulose bisphosphate carboxylase act	6.0e-56	RIBULOSE BISPHOSPHATE CARBOXYLASE\/OXYGENASE ACTI
UCW016BE517645-2	1.0e-34	Nicotiana plumbaginifolia mRNA for U2 snRNP auxiliary fa	3.0e-90	(Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana
UNL048BE605184-2	e-160	Triticum aestivum beta 1,3-glucanase (Glc1) mRNA, compl	2.0e-51	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR ((1->3)-B

C-4DL9-0.31

CNL014BE444731-2	0	Hordeum vulgare Harrington haemoglobin apoprotein (hb)	8.0e-88	NONLEGUME HEMOGLOBIN
CNL023BG263307-3	0	Triticum aestivum COP alpha homolog mRNA, partial cds	1.0e-73	(AC082645) putative alpha-coat protein [Oryza sativa]
KSU001BE444339-9	1.4	Drosophila melanogaster genomic scaffold 1420000133860	3.5	(AF264760) cAMP-dependent protein kinase [Neurospora c
KSU024BF202706-3	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
KSU027BF202969-3	2.0e-87	Oryza sativa cystathionine gamma-synthase (CGS1) mRNA	3.0e-54	O-succinylhomoserine (thiol)-lyase (EC 4.2.99.9) 1 - maize
KSU038BE489882-3,5	0.24	Human DNA sequence from PAC 57A13 between markers	2.0e-16	(AB013389) contains similarity to ATP binding protein asso
TTU047BE405190-1	5.9	Homo sapiens chromosome 10 clone RP11-77G23, comple	1.0e-53	(AF169021) seed maturation protein PM36 [Glycine max]
TTU047BE446061-2	3.0e-20	Arabidopsis thaliana chromosome 3 BAC T2E22 genomic s	5.0e-48	(AC069474) nascent polypeptide associated complex alpha
UCD001BE444339-10	1.4	Drosophila melanogaster genomic scaffold 1420000133860	3.5	(AF264760) cAMP-dependent protein kinase [Neurospora c
UCD017BE494281-6	e-164	H.vulgare mRNA for putative zinc finger protein	4.0e-36	(X85544) putative zinc finger protein [Hordeum vulgare]
UNL048BE446344-1	3.0e-08	Arabidopsis thaliana chromosome I BAC F25I16 genomic s	3.0e-69	(AC006234) unknown protein [Arabidopsis thaliana]

4DL9-0.31-0.56

CNL001BE406616-5	7.0e-19	Zea mays seven transmembrane protein Mlo4 mRNA, com	1.0e-23	(AY029315) seven transmembrane protein Mlo4 [Zea mays
CNL001BE426317-1,4	1.5	Sphingomonas aromaticivorans plasmid pNL1, complete s	4.0e-37	hypothetical protein F12L6.13 - Arabidopsis thaliana
CNL014BE445427-3	3.0e-05	Arabidopsis thaliana chromosome II section 143 of 255 of	8.0e-62	(AC006300) unknown protein [Arabidopsis thaliana]
CNL014BE592047-4,5	2.0e-42	Oryza sativa chromosome 10 clone OSJNBb0012A20, comp	1.0e-64	(AB017069) endosomal protein-like [Arabidopsis thaliana]
KSU001BE444339-4	1.4	Drosophila melanogaster genomic scaffold 1420000133860	3.5	(AF264760) cAMP-dependent protein kinase [Neurospora c
KSU002BE406512-1	0.044	Drosophila melanogaster, chromosome 2R, region 50C-50	2.0e-15	(AB010069) contains similarity to RNA binding protein~gen
KSU002BE426317-1,4	1.5	Sphingomonas aromaticivorans plasmid pNL1, complete s	4.0e-37	hypothetical protein F12L6.13 - Arabidopsis thaliana
KSU012BE442706-2	3.0e-17	Arabidopsis thaliana chromosome II section 212 of 255 of	2.0e-73	P-glycoprotein-like - Arabidopsis thaliana
KSU019BE495116-2	0	Triticum aestivum eIF-2 beta subunit mRNA, complete cds	1.0e-88	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUB
KSU024BF202695-4,5	3.0e-19	Oryza sativa peroxidase (POX22.3) mRNA, complete cds	6.0e-31	peroxidase (EC 1.11.1.7) 2 precursor - wheat
KSU024BF485396-2	1.0e-25	Nicotiana tabacum GDP dissociation inhibitor (GDI) mRNA, c	2.0e-77	GDP dissociation inhibitor - common tobacco
KSU027BE426016-2	0	Triticum aestivum vacuolar targeting receptor bp-80 mRNA	1.0e-83	(AF161719) vacuolar targeting receptor bp-80 [Triticum aes
KSU030BE497108-1	1.0e-22	A.thaliana mRNA for stromal ascorbate peroxidase	4.0e-40	(AB022273) thylakoid-bound ascorbate peroxidase [Nicotia
KSU030BF201003-1	0.29	Dictyostelium discoideum C-module-binding factor (cbfA)	0.36	(AC006264) hypothetical protein [Arabidopsis thaliana]
KSU030BF485011-1	0.066	Tacca chantieri MADS box containing protein PI mRNA, part	0.003	(AC067971) Contains similarity to a hypothetical protein F2
KSU035BE497618-1	e-120	Hordeum vulgare mRNA for ascorbate peroxidase	1.0e-34	(AJ000223) ascorbate peroxidase [Hordeum vulgare]
KSU038BE442811-1	3.0e-11	Oryza sativa chromosome unknown BAC clone OSJNBa004	1.0e-15	(AB046954) pseudo-response regulator 7 [Arabidopsis tha
KSU038BE443190-3	0.093	Homo sapiens genomic DNA, chromosome 21q, section 58	2.0e-24	(AB026636) contains similarity to similar to ubiquitin conju
KSU038BE443191-12	e-115	Triticum aestivum 70 kDa heat shock protein (TaHSP70d) n	2.0e-62	dnaK-type molecular chaperone hsp70 - rice (fragment)
KSU038BE443973-3	4.0e-04	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	3.0e-45	(AB005248) glucosyltransferase-like protein [Arabidopsis t
KSU038BE446076-4,5	0	Triticum aestivum MAP kinase homolog (WCK-1) mRNA, c	1.0e-64	mitogen-activated protein kinase 1 homolog (clone Aspk9
NDS018BE404963-2,4	5.0e-22	Brassica napus mRNA for acyl-carrier protein] S-malonyltr	1.0e-86	probable [acyl-carrier-protein] S-malonyltransferase (EC 2
NDS034BE406617-1	0	Triticum aestivum mRNA for putative In2.1-like protein	5.0e-84	safener-induced In2.1-like protein - wheat
NDS034BF201003-1	0.29	Dictyostelium discoideum C-module-binding factor (cbfA)	0.36	(AC006264) hypothetical protein [Arabidopsis thaliana]
UCD001BE444339-5	1.4	Drosophila melanogaster genomic scaffold 1420000133860	3.5	(AF264760) cAMP-dependent protein kinase [Neurospora c
UCD037BE443253-1	2.0e-08	Arabidopsis thaliana ABC transporter-like protein (T1E22_	6.0e-51	ABC transporter-like protein - Arabidopsis thaliana
UCD037BE497989-2	4.0e-10	L.esculentum chorismate synthase 2 precursor	3.0e-72	CHORISMATE SYNTHASE 1, CHLOROPLAST PRECURSOR (5-E
UCW016BE496907-1	0.26	Drosophila melanogaster genomic scaffold 1420000133860	2.1	diaphanous 2 isoform 12C\; Diaphanous, Drosophila, homo
UCW016BE518014-1	7.0e-33	Oryza sativa chromosome 3 BAC OSJNBb0022E02 genomic	1.0e-32	(AC087797) putative phospholipase [Oryza sativa]
UCW020BE591320-2	4.0e-22	Nicotiana tabacum WERBP-1 mRNA, complete cds	2.0e-33	hypothetical protein T5F17.60 - Arabidopsis thaliana
UMC015BE426266-2	6.0e-86	Oryza sativa mRNA for ribonuclease, partial cds, clone:E11	1.0e-65	ribonuclease (EC 3.1.-.-) - barley
UMC040BE590942-2,4	2.0e-17	N.tabacum mRNA for LIM-domain protein	2.0e-44	probable transcription factor SF3 - common tobacco
UMN013BE442706-3	3.0e-17	Arabidopsis thaliana chromosome II section 212 of 255 of	2.0e-73	P-glycoprotein-like - Arabidopsis thaliana
UMN013BE442776-2	2.0e-06	Staphylococcus aureus subsp. aureus Mu50 genomic DNA	2.0e-63	(AC005896) putative glutamate\/ornithine acetyltransferase
UMN013BE442961-3	1.0e-16	Arabidopsis thaliana chromosome 1 BAC F22G10 genomic	3.0e-98	(AC007260) Similar to dTDP-D-glucose 4,6-dehydratase [Ara
UMN013BE442995-4,6	1.0e-35	Cucumis melo mitochondrial processing peptidase beta s	6.0e-86	(AF363285) mitochondrial processing peptidase [Avicennia
UMN013BE443291-3	1.0e-25	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-96	(AP003143) putative neutral invertase [Oryza sativa]
UMN013BE443537-3,5	2.0e-05	Lilium longiflorum potential thioredoxin mRNA, complete	7.0e-46	thioredoxin homolog F22O13.5 - Arabidopsis thaliana
UNL036BF200627-1	9.0e-62	Zea mays mRNA for Toc34-1 protein (toc34A gene)	8.0e-22	(AJ271049) Toc34-2 protein [Zea mays]
UNL048BE445453-1	0.005	Arabidopsis thaliana AT3g58180\/F9D24_90 mRNA, complete	1.0e-52	(AF372878) AT3g58180\/F9D24_90 [Arabidopsis thaliana]
UNL048BE591739-1	2.0e-64	Genomic Sequence for Oryza sativa, Nipponbare strain, cl	3.0e-36	(AP000600) gb|AAC25523.1~gene_id:MAG2.20~similar to un
UNL048BE605229-3,5,7,8	1.0e-61	Rice mRNA for low molecular weight heat shock protein, c	5.0e-15	17.4 KD CLASS I HEAT SHOCK PROTEIN

4DL13-0.56-0.71

CNL023BG262664-2	0.024	Acanthamoeba castellanii myosin heavy chain (HMWMI) ge	2.0e-46	(AC067971) Contains similarity to an unknown protein F7A
CNL031BF428799-2	e-142	Oryza sativa GAD mRNA for glutamate decarboxylase, com	e-108	(AF020425) glutamate decarboxylase isozyme 1 [Nicotiana
KSU001BE444421-1	0.09	Homo sapiens chromosome 5 clone RP11-138C1, complete sequence		
KSU001BE444473-1,2	0.016	Drosophila melanogaster genomic scaffold 1420000133860	2.0e-23	(AC084763) hypothetical protein [Oryza sativa]
KSU012BE490658-2	e-104	Eleusine indica alpha-tubulin 2 (TUA2) mRNA, complete cds	1.0e-65	TUBULIN ALPHA-2 CHAIN (ALPHA-2 TUBULIN)
KSU019BE443559-4	7.0e-06	Arabidopsis thaliana unknown protein (F6F3.4) mRNA, com	2.0e-19	(AC023628) Unknown protein [Arabidopsis thaliana]
KSU019BE497134-2,4	8.0e-17	Hordeum vulgare genomic DNA fragment\; clone MWG0934	6.0e-55	(AC012563) putative trehalose-6-phosphate synthase\; 468
KSU024BE498038-8,9	0	Triticum aestivum p34cdc2 (cdc2TaA) mRNA, complete cds	e-125	(U23409) p34cdc2 [Triticum aestivum]
KSU024BE499664-6	0	Maize gene for beta 1 tubulin	1.0e-96	TUBULIN BETA-1 CHAIN
KSU027BF482595-4	0	Oryza sativa rCOP11 protein (rCOP11) mRNA, complete cds	e-105	(AF160800) constitutive photomorphogenic 11 [Oryza sativa
KSU030BF482216-2	8.0e-24	Arabidopsis thaliana CAF protein (CAF) mRNA, complete c	2.0e-75	(AF292940) short integuments 1 [Arabidopsis thaliana]
KSU035BE403378-1	0.081	Homo sapiens BAC clone GS1-286B23 from 7q21.1-q21.3, c	5.0e-38	(AC069300) putative transcription regulatory protein [Oryza
KSU035BE404665-2	0.006	Homo sapiens suppressor of Ty (S.cerevisiae) 5 homolog	2.0e-25	(AL161577) signal recognition particle receptor-like protei
KSU035BE406989-5	1.0e-11	Zea mays herbicide safener binding protein (SBP1) mRNA,	2.0e-25	herbicide safener binding protein 1 - maize
KSU035BE517664-2,4	0.088	Synechococcus sp. gene for ribosomal proteins, complete	8.0e-54	50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (
KSU038BE444566-1	0.006	Arabidopsis thaliana putative DNA-binding protein (T20K12	2.0e-13	(AF123265) remorin 1 [Lycopersicon esculentum]
KSU038BE444757-1,3,5	4.0e-65	Oryza sativa chromosome 10 clone nbxb0046P18, complete	2.0e-76	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CON
NDS001BE443751-2	0.087	Cicer arietinum nodulin-35 gene	5.0e-05	(AF145657) BcDNA.GH10120 [Drosophila melanogaster]
NDS018BE405269-2	6.0e-12	Arabidopsis thaliana chromosome 1 BAC T12P18 genomic	3.0e-81	(AC010852) unknown protein\; 55304-53614 [Arabidopsis th
NDS021BE591292-2	e-152	Festuca rubra putative copper-inducible 35.6 kDa protein (	1.0e-63	(AF104258) putative copper-inducible 35.6 kDa protein [Fes
NDS021BF472975-1	4.0e-72	Hordeum vulgare cell division cycle protein 48 (CDC48) mR	e-107	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CON
NDS034BE470946-3,5	0	Hordeum vulgare mRNA for allene oxide synthase (aos2 g	1.0e-94	(AJ251304) allene oxide synthase [Hordeum vulgare]
NDS043BG274947-4	0.025	Hordeum vulgare partial mRNA for lectin, clone 4B10T7	6.0e-24	(AB016888) contains similarity to disease resistance respo
UCD029BG273991-1	0.006	Genomic Sequence for Oryza sativa, Nipponbare strain, cl	2.0e-23	hypothetical protein F13G24.170 - Arabidopsis thaliana
UCD037BF201181-3	0.097	Human polymorphic loci in Xq28	3.0e-11	(AC007134) putative sugar transporter [Arabidopsis thalia
UMC032BF145459-2	5.0e-68	Oryza sativa subsp. indica serine\/threonine protein phosp	6.0e-39	male sterility protein 2 - rape
UMC040BE590589-6	e-145	Hordeum vulgare Bmy1 gene for Sd1 beta-amylase, compl	1.0e-52	(D21349) beta-amylase [Hordeum vulgare]
UMC040BE591070-6	e-112	T.aestivum ltrl-2 mRNA for CMx	2.0e-28	trypsin inhibitor CMx precursor - wheat
UNL044BG312734-2	2.0e-18	Oryza sativa chromosome 10 BAC OSJNBa0027P10 genomi	2.0e-49	(AC084763) putative arm repeat protein [Oryza sativa]
UNL044BG605592-3	2.0e-04	Homo sapiens ariadne (Drosophila) homolog, ubiquitin-conjugating enzyme E2-binding protein, 1 (ARIH1), mRNA		

4DL13-0.56-1.00

CNL014BE424255-3	6.0e-09	Genomic sequence for Arabidopsis thaliana BAC T25N20 fr	2.0e-65	probable transport protein - Arabidopsis thaliana
CNL014BE591000-2	3.0e-04	Arabidopsis thaliana chromosome II section 130 of 255 of	9.0e-61	HYPOTHETICAL GTP-BINDING PROTEIN AT2G22870 thaliana]
CNL014BE591172-3	e-132	Oryza sativa phytoene desaturase precursor (Pds) mRNA,	4.0e-77	PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATU
UCW020BF473204-1	6.0e-06	Arabidopsis thaliana transcription factor CRC mRNA, comp	2.0e-22	(AF132606) transcription factor CRC [Arabidopsis thaliana]
UMN013BE443205-3	7.0e-30	Citrus limon aconitase-iron regulated protein 1 (IRP1) mR	1.0e-70	(AC007170) cytoplasmic aconitate hydratase [Arabidopsis
UNL002BE425301-2	6.0e-74	Avena fatua 40S ribosomal protein S3A mRNA, partial cds	7.0e-46	40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
UNL002BE444616-3	0.006	Human DNA sequence from clone RP1-211D12 on chromos	7.0e-32	(AC051633) putative ubiquitin protein [Oryza sativa]
UNL036BE518255-1	e-106	Z.mays CPNA gene encoding mitochondrial chaperonin-60	1.0e-80	CHAPERONIN CPN60-1, MITOCHONDRIAL PRECURSOR (HSP60
UNL036BE637560-3	0	T.aestivum ltrl-1 mRNA for CMx	3.0e-52	trypsin inhibitor CMx precursor (clones pCMx1 and pCMx3
UNL036BF200656-3	0.61	Homo sapiens, Similar to thiosulfate sulfurtransferase (rh	2.0e-06	(AF156782) nod factor binding lectin-nucleotide phosphohy
UNI036BF200656-4	0.61	Homo sapiens, Similar to thiosulfate sulfurtransferase (rh	2.0e-06	(AF156782) nod factor binding lectin-nucleotide phosphohy

4DL12-0.71-1.00

CNL014BE444334-2	e-125	Triticum aestivum delta-24-sterol methyltransferase (TA-I	9.0e-24	(U60755) delta-24-sterol methyltransferase [Triticum aesti
CNL014BE444820-11	1.0e-07	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	5.0e-52	(AB005243) contains similarity to unknown protein~emb|C
CNL031BF291891-5	9.0e-11	Arabidopsis thaliana AT3g04520 (AT3g04520\/T27C4_17) mR	4.0e-72	L-allo-threonine aldolase homolog F22O13.11 - Arabidopsis
CSU001BE442582-2	0.42	Microtus arvalis smc4 gene for SMC4 protein, exons 1-19	6.0e-26	(AC004135) T17H7.16 [Arabidopsis thaliana]
CSU001BE444616-3	0.006	Human DNA sequence from clone RP1-211D12 on chromos	7.0e-32	(AC051633) putative ubiquitin protein [Oryza sativa]
KSU001BE444334-3	e-125	Triticum aestivum delta-24-sterol methyltransferase (TA-I	9.0e-24	(U60755) delta-24-sterol methyltransferase [Triticum aesti
KSU012BE403305-2	5.0e-19	Oryza sativa chromosome 10 BAC OSJNBa0001O14 genomi	6.0e-74	(AC025783) putative protein phosphatase 2C [Oryza sativa]
KSU024BE498921-5	e-113	Hordeum vulgare mRNA for putative kinetochore protein (	6.0e-50	(AJ277096) putative kinetochore protein [Hordeum vulgare
KSU024BE499546-2	7.0e-06	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G	0.99	aspartate kinase - fission yeast (Schizosaccharomyces po
KSU024BE499685-5	1.0e-04	Prunus armeniaca putative auxin-repressed protein mRNA	4.0e-07	(U93273) putative auxin-repressed protein [Prunus armeni
KSU024BE638039-1	2.0e-11	Arabidopsis thaliana At1g69340\/F10D13.28 mRNA, complete	6.0e-61	(AC073178) unknown protein [Arabidopsis thaliana]
KSU027BF484401-2	7.0e-64	Genomic Sequence for Oryza sativa, Nipponbare strain, cl	5.0e-15	(AB016893) emb|CAB61744.1~gene_id:MYH9.17~similar to u
KSU030BE499019-3	2.0e-67	Arabidopsis thaliana Ser\/Thr protein phosphatase mRNA,	6.0e-84	SERINE\/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALY
KSU035BE497160-1	e-133	Oryza sativa ribulose-5-phosphate-3-epimerase (RPE) mR	4.0e-63	RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR (PENTOSE-
NDS001BE442582-3	0.42	Microtus arvalis smc4 gene for SMC4 protein, exons 1-19	6.0e-26	(AC004135) T17H7.16 [Arabidopsis thaliana]
NDS001BE444334-3	e-125	Triticum aestivum delta-24-sterol methyltransferase (TA-I	9.0e-24	(U60755) delta-24-sterol methyltransferase [Triticum aesti
NDS021BF473020-6	0	Oryza sativa MAP kinase kinase 1 mRNA, complete cds	1.0e-98	protein kinase MEK1 (EC 2.7.1.-) - maize
NDS034BE403814-3,4	0.34	Oryza sativa chromosome 10 BAC OSJNBa0010C11 genomi	6.0e-48	(AC069300) putative dioxygenase [Oryza sativa]
NDS034BE403881-1	0.11	Glycine max putative purple acid phosphatase precursor (	1.0e-79	(AF236109) putative purple acid phosphatase precursor [P
NDS034BE499019-2	2.0e-67	Arabidopsis thaliana Ser\/Thr protein phosphatase mRNA,	6.0e-84	SERINE\/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALY
NDS043BF293366-3,4	1.2	Genomic Sequence for Oryza sativa, Nipponbare strain, cl	7.0e-11	(AF245482) OSE3 [Oryza sativa]
TTU047BE405064-4	1.3	Pseudomonas aeruginosa PA01, section 328 of 529 of the	3.0e-49	(AC007767) Strong similarity to an unknown protein F19D1
UCD001BE442582-5	0.42	Microtus arvalis smc4 gene for SMC4 protein, exons 1-19	6.0e-26	(AC004135) T17H7.16 [Arabidopsis thaliana]
UCD017BE490291-3	0	Triticum aestivum cold acclimation protein WCOR615 (Wco	8.0e-85	cold acclimation protein WCOR615 - wheat
UCD029BG263563-4	3.0e-08	Nicotiana tabacum anther ethylene-upregulated protein ER	4.0e-52	(AF096260) ER66 protein [Lycopersicon esculentum]
UCW016BE424208-2	0	T.aestivum mRNA for CM 17 protein	6.0e-71	alpha-amylase inhibitor, tetrameric, chain CM17 precursor
UCW020BF200716-3	9.0e-81	Oryza sativa OsPAA1 mRNA for alpha 1 subunit of 20S prot	7.0e-34	PROTEASOME SUBUNIT ALPHA TYPE 6 (20S PROTEASOME AL
UMC040BF474251-3	0	Triticum aestivum mRNA for PR-1.1 protein	7.0e-57	(AJ007348) pathogenisis-related protein 1.1 [Triticum aesti
UMC040BF474257-1,4	0.1	S.pombe chromosome II cosmid c646	4.0e-13	probable serine\/threonine-specific protein kinase T20F6.6
UNL044BG263172-1	9.0e-11	Arabidopsis thaliana chromosome II section 141 of 255 of	1.0e-73	clpB heat shock protein-like - Arabidopsis thaliana
UNL044BG312582-4,5	e-100	Hordeum vulgare DNA for chromosome 4H	6.0e-53	ribophorin I homolog - barley (fragment)

These mapping data are being made public in a preliminary, unverified state because of their potential value to the research community. These data are in the process of validation and are therefore subject to change. Users may not publish or redistribute the data or derivatives thereof without the written consent of the Project's mapping coordinator, Bikram Gill (bsg@ksu.edu). **NSF Project #DBI-9975989**

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