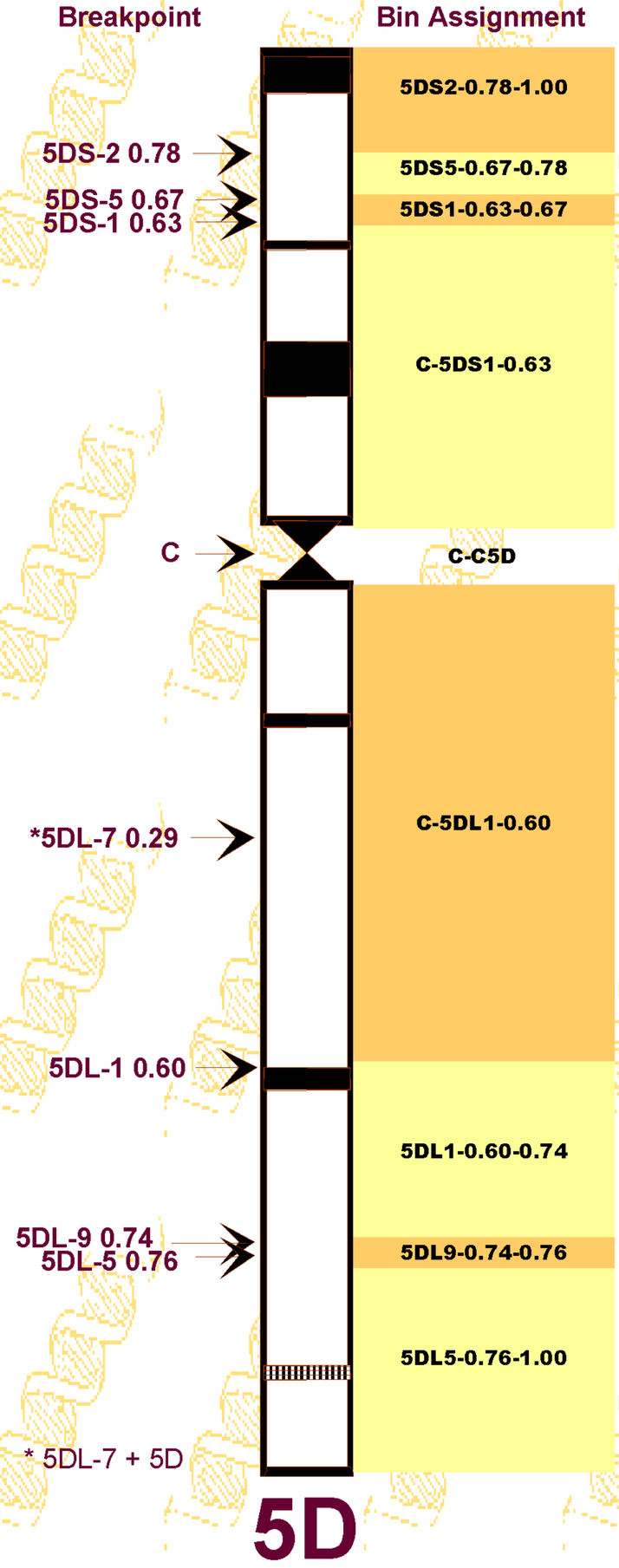
The Structure and Function of the Expressed Portion of the Wheat Genomes

Deletion Map of *Triticum aestivum* cv. Chinese Spring (Chromosome 5D)*

*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

5DS2-0.78-1.00

CNL014BE444113-2	0.029	Caenorhabditis elegans cosmid C52A11, complete sequer	6.5	probable lipR protein - Mycobacterium tuberculosis (strai
CNL031BE405667-3	0	Triticum aestivum sucrose-6F-phosphate phosphohydrol	4.0e-81	(AY029159) sucrose-6F-phosphate phosphohydrolase SPP
CSU001BE399994-7	0.16	Smilax rotundifolia phytochrome C (PHYC) gene, partial cds		
CSU057BE403785-3,5	0	Hordeum vulgare mRNA for sucrose transporter 2 (sut2 g	6.0e-71	(AJ272308) sucrose transporter 2 [Hordeum vulgare]
KSU001BE443751-3	0.087	Cicer arietinum nodulin-35 gene	5.0e-05	(AF145657) BcDNA.GH10120 [Drosophila melanogaster]
KSU012BE498728-1	0	Hordeum vulgare methyljasmonate-inducible lipoxygenas	3.0e-94	lipoxygenase (EC 1.13.11.12) 2 - barley
KSU024BE484620-4	5.0e-71	Solanum tuberosum methionine synthase (MS) mRNA, cor	1.0e-61	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYS
KSU035BE404480-3	2.0e-37	Oryza sativa subsp. japonica clone C63266_1A putative glu	7.0e-68	(AP002914) putative glutathione S-transferase [Oryza sativ
NDS001BE443751-5	0.087	Cicer arietinum nodulin-35 gene	5.0e-05	(AF145657) BcDNA.GH10120 [Drosophila melanogaster]
NDS018BE404462-1	0.33	Drosophila melanogaster genomic scaffold 1420000133868	3.0e-55	(AB006784) contains similarity to unknown protein-gene_i
UCD001BE443751-3	0.087	Cicer arietinum nodulin-35 gene	5.0e-05	(AF145657) BcDNA.GH10120 [Drosophila melanogaster]
UCD028BE404135-4	7.0e-46	Zea mays glutathione S-transferase GST 8 mRNA, complet	6.0e-82	(AP002914) putative glutathione S-transferase [Oryza sativ
UCD029BE497470-1	0.017	Oryza sativa chromosome 10 BAC OSJNBa0006L06 genomi	2.0e-15	(AB024029) gene_id:K21L19.11~ref|NP_036243.1~similar to u
UCD037BE499835-3	3.0e-26	Lycopersicon esculentum mRNA for beta-alanine synthas	1.0e-79	(Y19104) beta-alanine synthase [Lycopersicon esculentum
UCW002BE399993-3	9.0e-74	T.aestivum GSP-1b mRNA for grain softness protein	1.0e-06	grain softness protein 1b, 15K - wheat
UCW026BE636954-3	e-144	Oryza sativa plasma membrane proton-ATPase gene OSA	2.0e-94	(D18207) H-ATPase [Oryza sativa]
UMC040BE637485-3	0	Ha=GSP-1a [Triticum=wheat, cv. Timgalen, endosperm, mR	5.0e-70	grain softness protein 1a, 15K (clone TSF69) - wheat Timg
UMN013BE444854-1,3	0	Triticum aestivum sucrose-6F-phosphate phosphohydrol	2.0e-99	(AF321556) sucrose-6F-phosphate phosphohydrolase SPP
UNL036BF201102-4	2.0e-23	C.roseus MetE mRNA for methionine synthase	8.0e-43	(Z49158) cobalamine-independent methionine synthase [S

5DS5-0.67-0.78

CNL014BE490728-2	0	Hordeum vulgare methyljasmonate-inducible lipoxygenas	3.0e-94	lipoxygenase (EC 1.13.11.12) 2 - barley

5DS1-0.63-0.67

KSU035BE403373-1	0	Triticum aestivum oxalate oxidase mRNA, partial cds	1.0e-72	(AF005084) oxalate oxidase [Triticum aestivum]
KSU035BE403471-1	5.0e-15	Oryza sativa microsatellite MRG2437 containing (CT)X18, g	6.0e-57	(AF370443) Ran binding protein-1 [Lycopersicon esculentu
KSU035BE496903-3	2.0e-05	Arabidopsis thaliana At1g09340 (At1g09340/T31J12_6) mRN	2.0e-47	(Y15382) putative RHA binding protein [Arabidopsis thalian
KSU038BE444720-2	5.0e-19	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-62	(AF123588) Nt-iaa28 deduced protein [Nicotiana tabacum]
TTU047BE405636-5	8.0e-15	Arabidopsis thaliana chromosome II section 19 of 255 of t	5.0e-85	hypothetical protein T8K22.14 - Arabidopsis thaliana
UCD028BF146193-6	0.005	Rhodobacter sphaeroides strain 2.4.1T quinol oxidase sub	5.0e-42	hypothetical protein F9D16.100 - Arabidopsis thaliana
UMN013BE444030-2	e-101	Hordeum vulgare L41 ribosomal protein		

C-5DS1-0.63

CSU001BE403221-1	3.0e-32	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	7.0e-69	hypothetical protein F4H1.8 - Arabidopsis thaliana
CSU001BE406368-1	0.9	Pseudomonas aeruginosa PA01, section 33 of 529 of the complete genome		
KSU001BE406368-1	0.9	Pseudomonas aeruginosa PA01, section 33 of 529 of the complete genome		
KSU012BE352603-2	1.0e-43	Arabidopsis thaliana calcineurin B-like protein 3 (CBL3) mF	1.0e-77	calcineurin B-like protein 3 T15N24.20 [imported] - Arabido
KSU019BE443334-3	0	Barley acyl carrier protein I (ACP I) mRNA, complete cds	1.0e-72	ACYL CARRIER PROTEIN I PRECURSOR (ACP I)
KSU024BE498878-4	3.0e-08	Musa acuminata mRNA for unknown ripening-related prot	2.0e-08	(AB007644) contains similarity to enolase-phosphatase-ge
KSU024BE500291-1	1.0e-31	Z.mays (Black Mexican Sweet) mRNA for 1-acyl-glycerol-3-	5.0e-60	probable 1-acyl-glycerol-3-phosphate acyltransferase - ma
KSU027BE404894-1	4.0e-19	Glycine max plasma membrane Ca2+-ATPase (SCA2) mRN	9.0e-75	(AF195029) plasma membrane Ca2+-ATPase [Glycine max]
KSU035BE403618-3	e-173	Oryza sativa mRNA for adenylate kinase-a, complete cds	6.0e-90	(AB041773) adenylate kinase [Oryza sativa]
KSU035BE496951-10	0	Triticum aestivum rbcS gene for ribulose-1,5-bisphosphat	7.0e-82	ribulose-bisphosphate carboxylase (EC 4.1.1.39) small cha
TTU047BE444644-2	0.023	Homo sapiens PAC clone RP5-1132H15 from 7, complete se	4.0e-26	(AB007727) gene_id:MXC9.13~pir||T09989~similar to unkno
UCW026BE636795-2	6.0e-64	Oryza sativa small zinc finger-like protein (TIM9) mRNA, co	2.0e-43	MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE
UNL002BE415688-1	0.22	Homo sapiens PAC clone RP4-741M6 from 7p21-p15.3, com	7.0e-04	(AF158635) V6 [Aegilops ventricosa]
UNL002BE429766-1	0.006	Arabidopsis thaliana DNA chromosome 5, BAC clone T1E3	2.0e-57	disease resistance-like protein - Arabidopsis thaliana pro
UNL002BE517827-2	e-106	Oryza sativa mRNA for protein phosphatase 2A regulatory	2.0e-59	(AJ243828) phosphatase 2A regulatory A subunit [Oryza sa
UNL036BF200703-2	7.0e-04	Streptomyces sp. QM-B814 (ATCC 11238) bgl3 gene for bet	2.0e-21	(X94986) beta glucosidase [Manihot esculenta]
UNL048BE446646-3,4	6.0e-44	Oryza sativa OsPAE1 mRNA for alpha 5 subunit of 20S prote	8.0e-33	(AF043525) 20S proteasome subunit PAE2 [Arabidopsis tha

C-5DL1-0.60

CNL023BG274156-9	2.0e-22	Petunia x hybrida ribosomal protein L15 mRNA, complete c	1.0e-27	60S RIBOSOMAL PROTEIN L15
CSU001BE406612-1	2.0e-22	Oryza sativa chromosome 5 clone P0574H01, complete seq	2.0e-08	cysteine proteinase (EC 3.4.22..) F23E12.90 - Arabidopsis th
CSU001BE425296-2	5.0e-52	Triticum aestivum rbcS gene for ribulose-1,5-bisphosphat	2.0e-10	(AB042066) ribulose-1,5-bisphosphate carboxylase\/oxyger
CSU046BE443954-3	7.0e-09	Arabidopsis thaliana AT5g24420/K16H17_13 mRNA, comple	3.0e-58	(AB016884) 6-phosphogluconolactonase-like protein [Arab
CSU058BE496864-1	4.0e-47	O.sativa mRNA for chilling-inducible protein	1.0e-62	(AF133708) PP2A regulatory subunit [Arabidopsis thaliana]
KSU001BE406494-3	5.0e-51	Hordeum vulgare partial mRNA for putative acid phosphat	1.0e-40	(AJ250282) putative acid phosphatase [Hordeum vulgare]
KSU001BE443692-6,7	0.31	Human DNA sequence from cosmid U56D2, between mark	6.0e-19	(AC016041) F27J15.15 [Arabidopsis thaliana]
KSU002BE403221-7	3.0e-32	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	7.0e-69	hypothetical protein F4H1.8 - Arabidopsis thaliana
KSU002BE403518-3	1.0e-65	Oryza sativa Ca2+ sensitive 3'(2'),5'-diphosphonucleoside	2.0e-70	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHO
KSU002BE406545-4	1.0e-44	Setaria italica actin mRNA, complete cds	1.0e-27	ACTIN 2
KSU012BE403556-3	6.0e-15	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	5.0e-24	(AB006700) contains similarity to RAV2-like DNA-binding pr
KSU012BE403761-2	1.0e-72	Hordeum vulgare mRNA for alpha-keto acid dehydrogenas	e-102	(AL391712) branched-chain alpha keto-acid dehydrogenas
KSU012BE404462-1	0.33	Drosophila melanogaster genomic scaffold 1420000133868	3.0e-55	(AB006784) contains similarity to unknown protein-gene_i
KSU019BE442680-4	6.0e-12	P.sativum PHSP1 mRNA for HSP70	3.0e-70	HEAT SHOCK 70 KD PROTEIN, MITOCHONDRIAL PRECURSOR
KSU012BE442676-2	5.0e-19	Vigna aconitifolia 5'-phosphoribosyl-4-(N-succinocarboxar	7.0e-89	PHOSPHORIBOSYLAMIDOIMIDAZOLE-SUCCINOCARBOXAMID
KSU012BE442892-1	6.0e-12	M.sativa mRNA for annexin-like protein	1.0e-08	(Y11348) annexin-like protein [Medicago sativa]
KSU012BE443430-4	2.0e-05	Arabidopsis thaliana RNA polymerase II 13.6 kDa subunit (I	1.0e-47	DNA-DIRECTED RNA POLYMERASE II 13.6 KDA POLYPEPTIDE /
KSU019BE403648-3,5	5.0e-25	Chicken 78-kD glucose-regulated protein, complete cds	9.0e-73	HEAT SHOCK 70 KD PROTEIN, MITOCHONDRIAL PRECURSOR
KSU019BE404234-1	3.0e-41	S.tuberosum mRNA for NADH dehydrogenase, NADH-bindi	1.0e-82	(AB006697) NADH dehydrogenase [Arabidopsis thaliana]
KSU019BE494450-11	7.0e-40	Avena maroccana clone Ma7 ribulose-1,5-bisphosphate ca	3.0e-15	(AB042068) ribulose-1,5-bisphosphate carboxylase\/oxyger
KSU024BE405060-3	3.0e-85	Oryza sativa protein kinase mRNA, complete cds	1.0e-58	protein kinase homolog - rice
KSU024BE495790-5,6	0.004	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K	3.0e-40	(AF120494) phosphoglucose isomerase precursor [Arabid
KSU024BE499599-2	5.0e-13	Vigna unguiculata phosphatidic acid phosphatase alpha m	8.0e-88	(AC007591) Contains similarity to gb acid phosphatase alpl
KSU024BE499843-2,4	e-122	Zea mays variety B73 hypersensitive-induced response pr	2.0e-81	(AF236375) hypersensitive-induced response protein [Zea
KSU030BE590997-4	0	Hordeum vulgare chlorophyll a\/b-binding protein precurs	e-110	(AF287276) chlorophyll a\/b-binding protein precursor [Hor
KSU035BE404454-2	0.3	Thermobifida fusca SbpA (sbpA) gene, partial cds; BglA (t	3.0e-38	(AJ005950) beta-glucosidase [Cicer arietinum]
KSU035BE406996-2	8.0e-11	Rice mRNA, sequence homologous to ADP-ribosylation fac	6.0e-12	ADP-RIBOSYLATION FACTOR 1
TTU047BE446873-1,5	0.89	C.freundii araC gene encoding an araBAD operon regulato	7.0e-19	(AC006264) unknown protein [Arabidopsis thaliana]
TTU047BE494817-1,3	6.0e-06	Arabidopsis thaliana glutathione dependent dehydroasco	1.0e-36	waline -tRNA ligase-like protein - Arabidopsis thaliana
TTU047BE495277-3	0.021	Arabidopsis thaliana DNA chromosome 5, BAC clone T22P2	3.0e-50	hypothetical protein T22P22.70 - Arabidopsis thaliana
UCD028BE426080-1,7	e-132	Zea mays cultivar TX-5855 acetoacetyl CoA thiolase mRNA,	2.0e-81	(AF113522) acetoacetyl CoA thiolase [Zea mays]
UCD028BE605231-3	e-100	Zea mays pyruvate dehydrogenase E1 beta subunit isofor	5.0e-59	(AF069910) pyruvate dehydrogenase E1 beta subunit isofo
UCD029BE497820-2	1.0e-07	A.thaliana mRNA for chloroplast thylakoidal processing pe	9.0e-71	(U93215) putative signal peptidase I [Arabidopsis thaliana]
UCD029BF483378-3	e-110	Oryza sativa OsPAG1 mRNA for alpha 7 subunit of 20S prot	3.0e-87	PROTEASOME SUBUNIT ALPHA TYPE 3 (20S PROTEASOME AL
UCD029BG314435-3,4	8.0e-52	Arabidopsis thaliana mRNA for arginine methyltransferase	e-103	protein-arginine N-methyltransferase (EC 2.1.1.23) - Arabid
UCW016BE403761-2	1.0e-72	Hordeum vulgare mRNA for alpha-keto acid dehydrogenas	e-102	(AL391712) branched-chain alpha keto-acid dehydrogenas
UCW039BE445696-2	0.022	S.latifolia mRNA, clone CCLS 29	2.0e-46	(AC060755) unknown protein [Oryza sativa]
UMC055BF483513-4	7.0e-18	A.thaliana protein phosphatase mRNA	3.0e-42	SERINE\/THREONINE PROTEIN PHOSPHATASE PP-X ISOZYME 2
UNL002BE493858-1	0.091	Hordeum vulgare homeodomain protein JUBEL2 (JuBel2) c	2.0e-20	(AB020745) gene_id:MJE7.2~pir||C71412~similar to unknow
UNL002BF473933-3,4	0.44	Rat cytomegalovirus Maastricht, complete genome	4.0e-47	(Z39707) putative protein [Arabidopsis thaliana]
UNL002BF482744-1	1.0e-07	Oryza sativa NBS-LRR type resistance protein (r10) gene, p	2.0e-48	NBS-LRR type resistance protein - rice (fragment)

5DL1-0.60-0.74

CNL014BE423288-3	0.006	Oryza sativa genomic DNA, chromosome 6, BAC clone:OSJ	1.0e-19	(AP002869) Similar to Prunus armeniaca ethylene-forming,
CNL018BE446282-3	0.09	Homo sapiens 12 BAC RP11-340M11 (Roswell Park Cancer	5.0e-60	(AC024174) Contains similarity to glyoxalase II isozyme fro
CNL018BE445424-3	1.0e-21	Oryza sativa mRNA for C-type cyclin, complete cds	5.0e-27	G1\/S-SPECIFIC CYCLIN C-TYPE
CSU102BE406609-1	2.8	Human DNA sequence from clone RP4-586J11 on chromos	1.0e-16	comes from this gene. [Arabidopsis thaliana]
KSU012BE352633-2	3.0e-32	Elaeis guineensis oleoyl-ACP thioesterase mRNA, partial c	5.0e-91	(AF213478) acyl-ACP thioesterase [Iris germanica]
KSU012BE443439-2	1.0e-04	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	1.0e-70	(AB010872) gb|AAC64874.1~gene_id:MEE6.19~strong simila
KSU019BE494426-3	7.0e-24	P.ciliare (Hagins) apospory associated mRNA, 876bp	2.0e-53	(AF352797) ankyrin-repeat protein HBP1 [Nicotiana tabacur
KSU027BE403482-1	2.0e-28	Iris germanica acyl-ACP thioesterase (FatA) mRNA, compl	5.0e-28	(AF213478) acyl-ACP thioesterase [Iris germanica]
KSU030BF478964-2	8.0e-15	Arabidopsis thaliana mRNA for ERD1 protein, complete cds	4.0e-91	ERD1 PROTEIN PRECURSOR
KSU035BE407068-2	e-126	Zea mays LON1 protease (LON1) mRNA, complete cds	1.0e-72	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR -
KSU038BE443616-2	1.0e-07	Arabidopsis thaliana DNA chromosome 5, BAC clone T6G2	4.0e-72	(AL589883) mannosyltransferase-like protein [Arabidopsis
NDS043BE352575-2	0.083	Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57),	5.0e-23	(AC007060) Strong similarity to F19J3.8 gi UDP-galactose-4-e
NDS043BE471131-2,4	9.0e-24	Vicia faba immunophilin precursor (FKBP15) mRNA, compl	3.0e-59	probable peptidylprolyl isomerase (EC 5.2.1.8) FKBP15-1 - A
NDS043BF291915-3	0.42	Streptomyces coelicolor cosmid H69	2.0e-43	(AC013483) unknown protein [Arabidopsis thaliana]
UCD001BE406463-3	2.0e-97	Saccharum hybrid cultivar H65-7052 membrane protein mR	5.0e-43	(L13655) membrane protein [Saccharum hybrid cultivar H6
UCD029BE490552-3,5	0	Triticum aestivum cultivar Mironovska 808 cold-responsiv	2.0e-60	(AF207545) cold-responsive protein COR14a [Triticum aest
UCD029BF483378-6	e-110	Oryza sativa OsPAG1 mRNA for alpha 7 subunit of 20S prot	3.0e-87	PROTEASOME SUBUNIT ALPHA TYPE 3 (20S PROTEASOME AL
UCW039BE446342-2	1.6	Homo sapiens chromosome 18, clone RP11-583B12, compl	6.0e-43	(AB008268) beta-ureidopropionase [Arabidopsis thaliana]
UMC032BE426712-3	4.0e-22	Z.mays mRNA for cysteine proteinase	7.0e-15	cysteine proteinase (EC 3.4.22..), glucose starvation-induc
UMC040BF474257-3	0.1	S.pombe chromosome II cosmid c646	4.0e-13	probable serine\/threonine-specific protein kinase T20F6.6
UMN013DE442763-6	1.0e-16	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	2.0e-73	(AB010069) gb|AAC80624.1~gene_id:MAC9.17~strong simila
UMN013BE444081-1	0.006	Oryza sativa genomic DNA, chromosome 1, BAC clone:OSJNBa0010K01		
UMN013BE444562-1	5.0e-06	Arabidopsis thaliana transcription factor TFIIB mRNA, com	3.0e-14	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB)
UNL036BE590970-6	0.31	Homo sapiens BAC clone RP11-339F13 from 7, complete se	9.0e-41	(AB036735) allyl alcohol dehydrogenase [Nicotiana tabacur

C-5DL5-0.76-1.00

CNL014BE445094-2	3.0e-18	Hordeum vulgare beta-D-glucan exohydrolase isoenzyme	3.7	(AC074110) hypothetical protein [Arabidopsis thaliana]
CNL031BF428799-13	e-142	Oryza sativa GAD mRNA for glutamate decarboxylase, com	e-108	(AF020425) glutamate decarboxylase isozyme 1 [Nicotiana t
CSU046BE443002-1	3.0e-14	Oryza sativa genomic DNA, chromosome 6, PAC clone:P08	6.0e-81	(AC008016) Similar to gb from Homo sapiens. ESTs gb|H76
CSU102BE406609-6	2.8	Human DNA sequence from clone RP4-586J11 on chromos	1.0e-16	comes from this gene. [Arabidopsis thaliana]
KSU001BE399281-4	0.035	Homo sapiens genomic DNA, chromosome 11q, clone:RP1	1.2	(U81849) ORF2 [Trypanosoma brucei]
KSU001BE444339-5	1.4	Drosophila melanogaster genomic scaffold 1420000133868	3.5	(AF264768) cAMP-dependent protein kinase [Neurospora c
KSU012BE403211-2	2.0e-05	N.tabacum mRNA for PRT1 protein	9.0e-62	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9
KSU012BE443423-7	1.0e-19	Oryza sativa chromosome 3 BAC OSJNBa0091J19 genomic	4.2	(AL117195) Y57A10A.1 [Caenorhabditis elegans]
KSU019BE494320-3	1.0e-62	Zea mays calreticulin (CRT) mRNA, complete cds	1.0e-51	CALRETICULIN PRECURSOR
KSU024BE500310-4	4.0e-59	Oryza sativa chromosome 10 BAC OSJNBa0003O19 genomi	2.0e-57	(AC068755) unknown protein [Oryza sativa]
KSU030BE403710-3	0.001	Arabidopsis thaliana AT3g62110 (AT3g62110/T17J13_70) m	3.0e-53	(AF324992) AT3g62110 [Arabidopsis thaliana]
KSU030BE498241-1	0.007	Petromyzon marinus Spi transcription factor mRNA, comp	2.0e-29	(AB022215) hydroxyproline-rich glycoprotein [Arabidopsis
KSU030BE498573-3	e-107	Zea mays protein kinase AKINbetagamma-1 mRNA, compl	4.0e-81	(AF276086) protein kinase AKINbetagamma-2 [Zea mays]
KSU030BE500513-6	e-100	Hordeum vulgare ECA1 protein mRNA, complete cds	7.0e-41	(AF109193) ECA1 protein [Hordeum vulgare]
KSU030BF474029-1	1.0e-59	Atriplex nummularia homologous sequence (AHJ1) mRNA	7.0e-81	DNAJ PROTEIN HOMOLOG 2
KSU030BF474862-2	2.0e-76	Oryza sativa OSKgamma mRNA for shaggy-related protein	1.0e-95	(AP001278) ESTs C22403(C50132),C22404(C50132) corresp
KSU030BG314423-3,6	1.1	Bifidobacterium longum Ha=\/H+ antiporter (nhaB), cytosin	0.001	(AF049820) PGPS\/D4 [Petunia x hybrida]
KSU035BE403256-4,7	4.0e-04	Arabidopsis thaliana galactose kinase (GAL1) mRNA, comp	2.0e-67	GALACTOKINASE (GALACTOSE KINASE)
KSU035BE403395-2	5.0e-96	N.tabacum mRNA for elongation factor 2	e-103	ELONGATION FACTOR 2 (EF-2)
KSU035BE404437-1	6.0e-34	Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, compl	5.0e-70	DNAJ PROTEIN HOMOLOG (DNAJ-1)
KSU035BE497238-3	e-102	Zea mays variety BMS prohibitin (PHB4) mRNA, complete c	2.0e-59	(AF236368) prohibitin [Zea mays]
KSU038BE443191-14	e-115	Triticum aestivum 70 kDa heat shock protein (TaHSP70d) r	2.0e-62	dnaK-type molecular chaperone hsp70 - rice (fragment)
KSU038BE445268-5,6	1.0e-34	Arabidopsis thaliana AT5g66760/MSN2_16 gene, complete	e-99	succinate dehydrogenase (EC 1.3.99.1) flavoprotein alpha c
NDS018BE405176-3	3.0e-63	Oryza sativa FNR gene for ferredoxin-NADP+ reductase, co	1.0e-31	FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOF
NDS021BE500260-1,5	0.001	Arabidopsis thaliana scarecrow-like 21 (SCL21) mRNA, cor	2.0e-58	(AF153443) phytochrome A signal transduction 1 protein [A
NDS021BF473953-1	0	Secale cereale ribosomal protein S7 mRNA, complete cds	1.0e-97	(AF118149) ribosomal protein S7 [Secale cereale]
NDS034BE403710-3	0.001	Arabidopsis thaliana AT3g62110 (AT3g62110/T17J13_70) m	3.0e-53	(AF324992) AT3g62110 [Arabidopsis thaliana]
NDS034BE406557-4	6.0e-37	Hordeum vulgare low temperature-responsive RNA-bindir	2.0e-29	glycine-rich RNA-binding protein, low-temperature-respor
NDS034BE406569-4	2.0e-63	Rice mRNA for ribosomal protein L44 (L44 gene), partial se	6.0e-24	60S RIBOSOMAL PROTEIN L44
NDS034BE471188-1	5.0e-05	Elaeis guineensis calmodulin mRNA, complete cds	6.3	(X69926) HRPII [Plasmodium falciparum]
NDS034BE498573-2,7,8	e-107	Zea mays protein kinase AKINbetagamma-1 mRNA, compl	4.0e-81	(AF276086) protein kinase AKINbetagamma-2 [Zea mays]
NDS034BF474029-1	1.0e-59	Atriplex nummularia homologous sequence (AHJ1) mRNA	7.0e-81	DNAJ PROTEIN HOMOLOG 2
NDS043BF292161-1	1.2	Homo sapiens chromosome 17, clone hE_2_C4, complete c	2.0e-39	hypothetical protein FLJ25110 - Arabidopsis thaliana
TTU047BE494680-3	9.0e-05	Arabidopsis thaliana AT4g37830\/T28H19_110 mRNA, compl	2.0e-24	hypothetical protein T28H19.110 - Arabidopsis thaliana
UCD001BE406335-1	0.87	Homo sapiens sema domain, immunoglobulin domain (Ig)	2.0e-41	(AC079279) unknown protein [Arabidopsis thaliana]
UCD001BE444339-6	1.4	Drosophila melanogaster genomic scaffold 1420000133868	3.5	(AF264768) cAMP-dependent protein kinase [Neurospora c
UCD017BE494102-2	3.0e-20	H.chilense x T.turgidum conv. durum (Tritordeum) mRNA f	4.0e-57	(AJ251899) S-adenosylmethionine decarboxylase 2 [Oryza
UCD028BG274017-12	1.0e-04	Arabidopsis thaliana galactose kinase (GAL1) mRNA, comp	3.0e-96	GALACTOKINASE (GALACTOSE KINASE)
UCD037BE498609-5,10	0.1	Hordeum vulgare homeodomain protein JUBEL1 (JuBel1) c	7.0e-67	fructokinase (EC 2.7.1.4) - Arabidopsis thaliana kinases (PF
UCD037BE500170-1,2	0.1	Oryza sativa microsatellite MRG5263 containing (CTC)X9, cl	1.0e-33	zinc-finger protein Lsd1 - Arabidopsis thaliana
UCW001BE399900-3	0.004	Streptomyces seoulensis dihydrolipoamide dehydrogena	0.21	hypothetical protein F22O13.28 - Arabidopsis thaliana
UCW016BE590622-4	0	T.aestivum mRNA for serpin WZS3	2.0e-65	serpin homolog WZS3 - wheat
UCW020BE499789-6	0	Oryza sativa mRNA for EF-1 alpha, complete cds	1.0e-97	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) aestivum]
UCW039BE444569-2	1.4	Caenorhabditis elegans cosmid M04B2, complete sequen	1.0e-42	(AB016885) protein kinase-like protein [Arabidopsis thalia
UCW039BE494906-2	0.007	Streptomyces coelicolor cosmid 8G12	2.0e-23	(AC069471) lipid transfer protein, putative [Arabidopsis tha
UMC032BE426008-2,4	1.7	Oryza sativa subsp. japonica acidic PR-1 type pathogenesi	3.0e-56	polyphosphoinositide binding protein Ssh2 - soybean
UMC032BE426032-3	1.0e-12	Cicer arietinum mRNA for putative cytidine or deoxycytidyl	3.0e-57	(AJ006764) putative deoxycytidylate deaminase [Cicer arie
UMC032BE426127-8	0	Barley elongation factor 1 alpha, (EF-1A) mRNA sequence	2.0e-90	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
UMC032BE637097-2	1.0e-30	Arabidopsis thaliana chaperone protein (atj) mRNA, compl	2.0e-47	(AF169022) seed maturation protein PM37 [Glycine max]
UMC040BE591042-5	e-163	Hordeum vulgare plasma membrane associated protein (j	1.0e-65	(AF218627) plasma membrane associated protein [Hordeu
UMC040BE637463-6	0	H.vulgare BLT63 mRNA, complete CDS	2.0e-88	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) vulgare]
UMC055BF484028-2	2.0e-17	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	2.0e-63	(AB022223) kinase-like protein [Arabidopsis thaliana]
UMN013BE443423-6	1.0e-19	Oryza sativa chromosome 3 BAC OSJNBa0091J19 genomic	4.2	(AL117195) Y57A10A.1 [Caenorhabditis elegans]
UMN013BE443893-4	9.0e-36	Oryza sativa genomic DNA, chromosome 1, clone:P0702F0	2.0e-84	(AP002481) ESTs C97518(C60304),C28188(C60304) corresp
UNL002BE498327-3,4	0.084	Caulobacter crescentus section 11 of 359 of the complete	5.0e-07	(AJ302292) MLA6 protein [Hordeum vulgare]
UNL036BE496891-2	5.0e-43	Hordeum vulgare photosystem-I PSI-F subunit precursor	0.006	(AF093634) photosystem-I F subunit precursor [Oryza sati
UNL044BG263544-1	4.0e-04	Cruznema tripartitum large subunit RNA polymerase II mR	1.0e-47	DNA-directed RNA polymerase I 190K chain homolog F15B8

5DL9-0.74-0.76

KSU030BF483487-3	1.0e-46	Glycine max seed maturation protein PM37 (PM37) mRNA,	2.0e-40	DnaJ protein homolog ZMDJ1 - maize
NDS021BF472974-1	0	Triticum aestivum Sec61p (sec61) mRNA, complete cds	e-109	(AF161718) Sec61p [Triticum aestivum]
UMC015BE606573-4	6.0e-22	Aerides japonica 3-hydroxy-3-methylglutaryl-CoA-synthas	9.0e-92	(AF148847) HMG-CoA synthase [Brassica juncea]
UNL044BG263643-1	2.0e-08	Zea mays putative methyl-binding domain protein MBD105	1.0e-22	(AY029558) putative methyl-binding domain protein MBD10

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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