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

Deletion Map of *Triticum aestivum* cv. Chinese Spring (Chromosome 2A)*

*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.

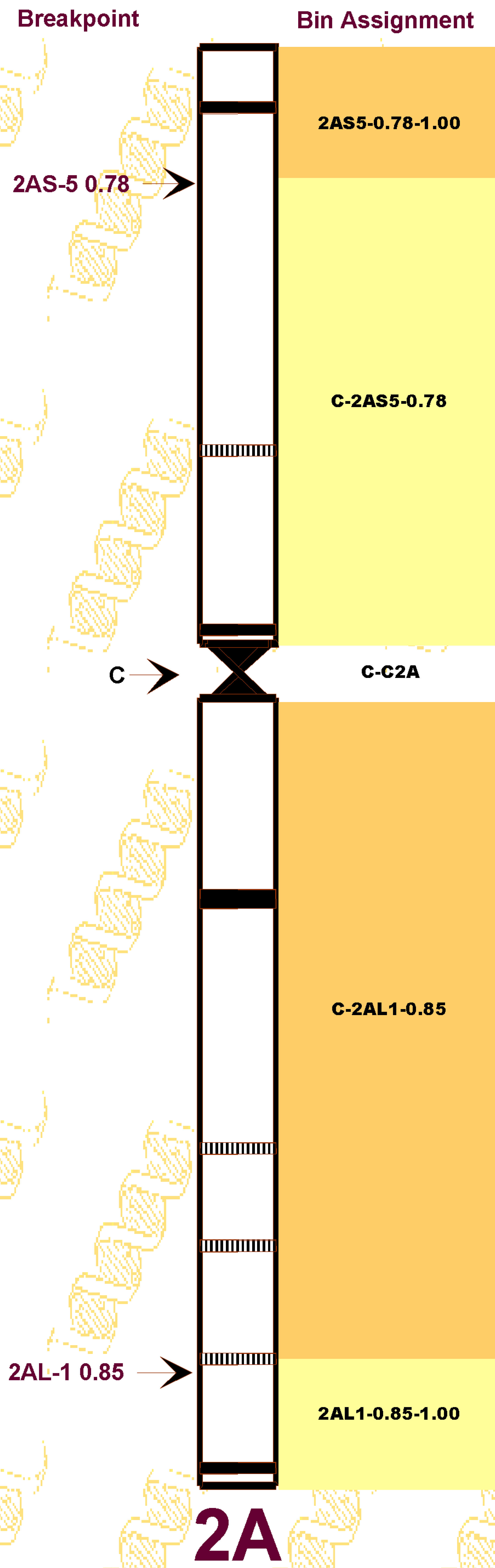
How to Interpret This Image:

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



2AS5-0.78-1.00

CNL001BE426431-2	1.1	Homo sapiens chromosome 21 clone PAC 198E8, map 21q	7.0e-19	F-ACTIN CAPPING PROTEIN ALPHA SUBUNIT (CAPZ-ALPHA) t
CNL014BE406474-1	2.0e-44	Rice mRNA for 40S subunit ribosomal protein, complete cc	7.0e-26	40S RIBOSOMAL PROTEIN S21
CNL031BF201315-1	2.0e-15	Arabidopsis thaliana AT3g58680 (AT3g58680\T20N10_30) m	1.0e-46	(AC006931) unknown protein [Arabidopsis thaliana]
CSU046BE443026-2	1.0e-04	Arabidopsis thaliana DNA chromosome 3, BAC clone T27I1	2.0e-44	hypothetical protein T4C21.320 - Arabidopsis thaliana
CSU059BG262864-2	6.0e-05	Colletotrichum gloeosporioides f. sp. malvae pectate lyas	6.0e-39	(AB019228) receptor-like protein kinase [Arabidopsis thali
KSU001BE403860-7	3.0e-10	Oryza sativa microsatellite MRG5838 containing (TCT)X14,	7.0e-30	(AF198054) NAC1 [Arabidopsis thaliana]
KSU001BE406616-6	7.0e-19	Zea mays seven transmembrane protein Mlo4 mRNA, com	1.0e-23	(AY029315) seven transmembrane protein Mlo4 [Zea mays
KSU001BE442903-2	0.38	Human chromosome 14 DNA sequence BAC R-817G13 of lil	4.0e-09	(AB007727) gene_id:MXC9.20~unknown protein [Arabidops
KSU001BE443747-3,4	1.5	Sorghum bicolor ADP-glucose pyrophosphorylase subuni	5.0e-25	(AB025632) dihydroflavonol 4-reductase-like [Arabidopsis
KSU001BE444297-3,4	0.17	Ensis minor (clone 1\6) nuclear protein mRNA, complete c	0.003	hypothetical protein T20B5.15 - Arabidopsis thaliana protei
KSU002BE426431-2	1.1	Homo sapiens chromosome 21 clone PAC 198E8, map 21q	7.0e-19	F-ACTIN CAPPING PROTEIN ALPHA SUBUNIT (CAPZ-ALPHA) t
KSU012BE406474-1	2.0e-44	Rice mRNA for 40S subunit ribosomal protein, complete cc	7.0e-26	40S RIBOSOMAL PROTEIN S21
KSU019BE488780-2	0	Triticum aestivum thiol protease mRNA, complete cds	3.0e-97	benzothiadiazole-induced protein (clone WCI-4) - wheat
KSU019BE494262-3	4.0e-09	Arabidopsis thaliana DNA chromosome 4, contig fragment	3.0e-38	GTP-binding protein F23K16.150 - Arabidopsis thaliana
KSU019BE494450-9	7.0e-40	Avena maroccana clone Ma7 ribulose-1,5-bisphosphate ca	3.0e-15	(AB042068) ribulose-1,5-bisphosphate carboxylase\oxyger
KSU019BE518306-1	8.0e-36	Hordeum vulgare nicotianamine synthase 2 (nashor2) mRNA, complete cds		
KSU019BF201235-2	e-166	Wheat mRNA for Rubisco subunit binding-protein alpha su	2.0e-48	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECUF
KSU024BE499478-3	1.0e-16	Arabidopsis thaliana chromosome II section 105 of 255 of	4.0e-86	hypothetical protein T13L16.5 - Arabidopsis thaliana
KSU027BE517877-3	7.0e-98	Zea mays ribosomal protein S6 RPS6-1 (rps6-1) mRNA, con	3.0e-53	(AJ277533) S6 ribosomal protein [Asparagus officinalis]
KSU030BE606438-2	5.0e-09	Arabidopsis thaliana CBL-interacting protein kinase 2 (CIP	3.0e-59	serine\threonine protein kinase-like protein - Arabidopsis
KSU038BE444512-1	6.0e-15	Arabidopsis thaliana putative protein translocation comple	4.0e-16	PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT
NDS018BE404835-1	e-120	Zea mays strain W64A x A182E putative cytosolic 6-phosph	2.0e-80	phosphogluconate dehydrogenase (decarboxylating) (EC 1
NDS034BE470890-3	0	H.vulgare mRNA for lipid transfer protein 7a2b	2.0e-48	lipid transfer protein 7a2b - barley
NDS034BE606438-2	5.0e-09	Arabidopsis thaliana CBL-interacting protein kinase 2 (CIP	3.0e-59	serine\threonine protein kinase-like protein - Arabidopsis
NDS043BF293115-5	0.062	Homo sapiens chromosome 10 clone CIT987SK-1144G6 ma	4.0e-16	(AB017063) gene_id:K3K7.22~pir||T31651~similar to unknow
NDS043BG274878-2	0.34	Oryza sativa genomic DNA, chromosome 1, PAC clone:P05	2.0e-83	(AC027034) unknown protein\; 9920-11896 [Arabidopsis tha
TTU025BE406474-1	2.0e-44	Rice mRNA for 40S subunit ribosomal protein, complete cc	7.0e-26	40S RIBOSOMAL PROTEIN S21
TTU047BE405597-2	7.0e-27	Arabidopsis thaliana DNA chromosome 4, contig fragment	1.0e-73	hypothetical protein T14P8.7 - Arabidopsis thaliana activite
TTU047BE444659-2	0.095	Deinococcus radiodurans R1 section 146 of 229 of the com	1.0e-33	(U80185) pyruvate dehydrogenase E1 alpha subunit [Arabic
TTU047BE494209-2	0.42	Mesorhizobium loti, complete genome	7.0e-28	(AB023037) MtN3-like protein [Arabidopsis thaliana]
UCD001BE443449-3	0.92	Homo sapiens solute carrier family 2 (facilitated glucose t	6.0e-28	(AC007592) F12K11.6 [Arabidopsis thaliana]
UCD001BE443747-3,4	1.5	Sorghum bicolor ADP-glucose pyrophosphorylase subuni	5.0e-25	(AB025632) dihydroflavonol 4-reductase-like [Arabidopsis
UCD017BE488865-2	5.0e-06	Hordeum vulgare genomic DNA fragment\; clone MWG0874	6.8	(AC084831) putative polyprotein [Oryza sativa]
UCD037BE488719-5,6	4.0e-29	Cicer arietinum mRNA for glyoxalase I	1.0e-76	LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALD
UCD037BE606912-1	1.1	Human DNA sequence from clone RP5-1060K6 on chromos	1.0e-13	(X17302) trypsin inhibitor cme precursor [Hordeum vulgar
UCW016BE518306-1	8.0e-36	Hordeum vulgare nicotianamine synthase 2 (nashor2) mRNA, complete cds		
UCW026BE498730-2	5.0e-74	Oryza sativa 10 kDa chaperonin mRNA, complete cds	6.0e-41	probable chaperonin 10 - rice
UMC032BE471323-2	0	Hordeum vulgare photosystem I protein (PSI-L) mRNA, coi	4.0e-87	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR
UMC040BG262345-8	e-138	Oryza sativa pyruvate decarboxylase 2 (Pdc2) mRNA, comp	4.0e-80	PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC)
UMN013BE443006-4,11	4.0e-07	Salmonella typhimurium strain 3027 cold shock protein C	3.0e-27	COLD SHOCK-LIKE PROTEIN CSPC (CSP-C)
UMN013BE444541-2	3.0e-51	Arabidopsis thaliana arginase mRNA, complete cds	5.0e-99	ARGINASE PF00491, Score=419.6, E=3.7e-142 N=1)
UNL001BE444297-3,4	0.17	Ensis minor (clone 1\6) nuclear protein mRNA, complete c	0.003	hypothetical protein T20B5.15 - Arabidopsis thaliana protei
UNL002BE499523-2	e-157	Triticum ventricosum Vrga1 (Vrga1) gene, complete cds	7.0e-79	(AF158634) Vrga1 [Aegilops ventricosa]
UNL044BG314234-1	2.0e-33	Daucus carota mRNA for 181, partial cds	1.0e-94	embryogenic callus protein 181 - carrot (fragment)
UNL048BE445628-2	0.3	Mus musculus AKR voltage-gated potassium-channel (KCl	4.0e-13	(AB007727) contains similarity to unknown protein~gene_i
UNL048BE591555-2	1.0e-39	Brassica oleracea ATP-sulfurylase precursor (ASBo) gene	4.0e-57	sulfate adenylyltransferase (EC 2.7.7.4) ASBo precursor - v

C-2AS5-0.78

CNL001BE425962-1	0.026	Musa acuminata sucrose synthase mRNA, partial cds	1.0e-68	(AB017068) sucrose synthase [Arabidopsis thaliana]
CNL023BE405331-3	7.0e-55	Arabidopsis thaliana mRNA for AtClpC, complete cds	1.0e-77	(AB017063) ATP-dependent Clp protease, ATP-binding sub
CSU046BE444144-2	1.1	Arabidopsis thaliana DNA chromosome 3, BAC clone T15B	3.0e-22	(AC005278) F15K9.14 [Arabidopsis thaliana]
CSU046BE445242-2	4.0e-07	Arabidopsis thaliana transcription factor APFI mRNA, comp	3.0e-78	(AC079677) unknown protein\; 6976-8939 [Arabidopsis thali
KSU002BE425962-1	0.026	Musa acuminata sucrose synthase mRNA, partial cds	1.0e-68	(AB017068) sucrose synthase [Arabidopsis thaliana]
KSU002BE426158-2	6.0e-43	Oryza sativa putative tyrosine phosphatase mRNA, partial	4.0e-26	(AC005223) 55585 [Arabidopsis thaliana]
KSU012BE404385-6	e-170	Zea mays golgi associated protein se-wap41 mRNA, comp	e-108	(AF294725) reversibly glycosylated polypeptide [Oryza sati
KSU012BE406808-2	7.0e-16	Oryza sativa reversibly glycosylated polypeptide mRNA, cc	3.0e-11	(Y18626) reversibly glycosylated polypeptide [Triticum aes
KSU012BE442655-1	6.0e-06	Arabidopsis thaliana chromosome II section 205 of 255 of	1.0e-52	(AF221857) unknown [Euphorbia esula]
KSU012BE442876-4	2.0e-49	Oryza sativa clone riceipp2 isopentenyl pyrophosphate:dir	1.0e-75	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) 1 - C
KSU019BE443112-1	3.0e-75	O.sativa mRNA for calcium dependent protein kinase 2	2.0e-33	CALCIUM-DEPENDENT PROTEIN KINASE 2 (CDPK 2)
KSU024BE498252-1	1.0e-68	H.vulgare (pMaW20) pseudo mRNA for beta-ketoacyl-ACP synthase (partial)		
KSU024BE498388-1	e-154	Triticum aestivum beta-tubulin 1 (tubb1) mRNA, complete	1.0e-67	tubulin beta-2 chain - garden pea (fragment)
KSU024BE499648-1	7.0e-81	Rice mRNA for ferredoxin-NADP+ reductase, complete cds	8.0e-44	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR
KSU027BE406676-12	3.0e-96	Triticum aestivum germin protein precursor, mRNA, comp	2.0e-40	GERMIN GF-2.8 PRECURSOR
KSU030BE636802-2	5.0e-28	Arabidopsis thaliana glucose 6 phosphate\/phosphate trar	1.0e-44	probable glucose-6-phosphate\/phosphate-translocator pr
KSU035BE403404-1	9.0e-22	Catharanthus roseus PAPS-reductase-like protein (par2ne	8.0e-42	(U63784) PAPS-reductase-like protein [Catharanthus roseu
KSU035BE406923-1,5	2.0e-11	Amaranthus hypochondriacus C4 photosynthetic NAD-dep	2.0e-57	NAD-DEPENDENT MALIC ENZYME 65 KDA ISOFORM, MITOCHO
KSU035BE496863-3	e-165	H.vulgare mRNA for sucrose synthase	3.0e-63	(AJ001117) sucrose synthase type I [Triticum aestivum]
KSU035BE496900-1	0	Triticum aestivum heat shock protein HSP26 (hsp26.6) mR	1.0e-32	(AF097659) heat shock protein HSP26 [Triticum aestivum]
KSU035BE496951-5,8,11	0	Triticum aestivum rbcS gene for ribulose-1,5-bisphosphat	7.0e-82	ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chai
KSU035BE497171-1,3	1.4	Homo sapiens guanosine monophosphate reductase (GM	6.0e-15	(AF227619) Tic20-like protein [Euphorbia esula]
KSU035BE497393-1	4.0e-21	Rice mRNA for 3-deoxy-D-arabino-heptulosonate 7-phosph	2.0e-53	2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15
KSU035BE497590-3	2.0e-37	Zea mays translation initiation factor 5A (TIF5A) mRNA, cor	5.0e-19	INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
KSU035BE497622-1	1.0e-08	Petroselinum crispum plastidic 3-deoxy-D-arabino-heptulc	4.0e-40	(Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate sy
KSU038BE444638-1	0.34	Human DNA sequence from clone RP11-300B2 on chromos	3.0e-23	POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE 2
NDS018BE404835-6	e-120	Zea mays strain W64A x A182E putative cytosolic 6-phosph	2.0e-80	phosphogluconate dehydrogenase (decarboxylating) (EC 1
NDS034BE470848-3	0	Triticum aestivum mRNA for triosephosphat-isomerase (t	3.0e-90	(AJ278243) triosephosphat-isomerase [Triticum aestivum]
NDS043BG274976-1	6.0e-18	Arabidopsis thaliana WRKY DNA-binding protein 4 (WRKY4)	8.0e-45	DNA-binding protein WRKY2 - parsley (fragment)
TTU047BE494321-2	3.0e-38	Daucus carota mRNA for P40-like protein, complete cds	7.0e-38	40S RIBOSOMAL PROTEIN SA (P40)
UCD017BE488732-3	2.0e-08	Brassica napus proplastid omega-6 desaturase mRNA, coi	9.0e-29	OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECUF
UCD037BF473259-3,4	0.26	Human DNA sequence from clone RP11-534I8 on chromoso	2.0e-24	(AB013390) contains similarity to NADH dehydrogenase cha
UCW001BE444378-3	6.0e-09	Arabidopsis thaliana genomic DNA, chromosome 3, TAC cl	1.0e-53	hypothetical protein T24A18.30 - Arabidopsis thaliana
UCW020BE404332-3	0	Hordeum vulgare ribosomal protein S12 (rps12) mRNA, coi	4.0e-65	40S RIBOSOMAL PROTEIN S12
UCW026BG263377-2	0.12	Mus musculus RIKEN cDNA 0710008N11 gene (0710008N11Ri	2.9	glycine-rich protein - carrot (fragment)
UCW039BE496162-2	9.0e-08	Arabidopsis thaliana mRNA for nitrilase associated proteir	8.0e-13	(AC013427) Contains similarity to PIR7A protein from Oryza
UNL044BG263521-1	e-104	Oryza sativa mitogen activated protein kinase kinase (MEK	6.0e-87	probable mitogen activated protein kinase - rice

C-2AL1-0.85

CNL001BE425566-2	1.0e-47	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	9.0e-70	(AP002843) putative UTP-glucose glucosyltransferase [Ory
CNL023BE638034-3	3.0e-99	Zea mays chlorophyll a\/b-binding apoprotein CP24 (Lhcb6	4.0e-54	CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
CNL023BG263263-1',1,4	2.0e-17	Arabidopsis thaliana UVB-resistance protein UVR8 (UVR8)	7.0e-75	UVB-resistance protein UVR8 [imported] - Arabidopsis tha
CNL031BF201315-5	2.0e-15	Arabidopsis thaliana AT3g58680 (AT3g58680\T20N10_30) m	1.0e-46	(AC006931) unknown protein [Arabidopsis thaliana]
CNL031BF291891-7,8	9.0e-11	Arabidopsis thaliana AT3g04520 (AT3g04520\T27C4_17) mF	4.0e-72	L-allo-threonine aldolase homolog F22O13.11 - Arabidopsis
CNL031BF428799-7	e-142	Oryza sativa GAD mRNA for glutamate decarboxylase, com	e-108	(AF020425) glutamate decarboxylase isozyme 1 [Nicotiana
CSU001BE403217-1	0.24	Arabidopsis thaliana chromosome II section 191 of 255 of	3.0e-23	multidrug-resistance protein homolog T29F13.13 - Arabido
CSU001BE425207-5	8.0e-08	Nicotiana tabacum (clone: L24-2) chloroplast ribosomal prc	3.0e-36	(AB016879) 50S ribosomal protein L24, chloroplast precurs
CSU001BE425566-2	1.0e-47	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	9.0e-70	(AP002843) putative UTP-glucose glucosyltransferase [Ory
CSU001BE442858-4	1.3	Homo sapiens chromosome 19, cosmid R27216 (LLNLR-23	4.0e-05	(X98316) peroxidase [Arabidopsis thaliana]
CSU001BE443735-4	3.0e-57	Aegilops tauschii starch synthase I gene, complete cds	0.63	(AB046670) includes endonuclease domain and reverse tra
CSU046BE442794-1,3	0.083	Arabidopsis thaliana chromosome 1 BAC F28P5 genomic s	2.0e-20	(AC069273) unknown protein [Arabidopsis thaliana]
CSU046BE442981-2,5	3.0e-17	Oryza sativa genomic DNA, chromosome 4, BAC clone: H08	7.0e-34	(AP000381) gb|AAF57656.1~gene_id:K17E12.13~similar to un
CSU046BE444599-3	2.0e-40	Oryza sativa indica(GLA4) genomic DNA, chromosome 4, B	3.0e-73	(AL117264) zwh13.1 [Oryza sativa]
CSU046BE445250-1	0.36	Homo sapiens BAC clone RP11-95A10 from 7, complete se	5.0e-31	(AC007211) unknown protein [Arabidopsis thaliana]
CSU046BE445431-4	0.42	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	8.0e-52	(AB025634) gene_id:MSD21.18~unknown protein [Arabidop
CSU057BE403352-1	2.0e-05	Theobroma cacao microsatellite DNA, clone mTcCIR57	3.0e-41	(AF239836) Glu-tRNA(Gln) amidotransferase subunit B [Ara
CSU058BG262381-3	1.0e-06	Arabidopsis thaliana chromosome 1 BAC F23O10 genomic	6.0e-56	(AC009755) putative protein kinase [Arabidopsis thaliana]
KSU001BE442858-2	1.3	Homo sapiens chromosome 19, cosmid R27216 (LLNLR-23	4.0e-05	(X98316) peroxidase [Arabidopsis thaliana]
KSU001BE442884-2	0.057	Camptotheca acuminata isopentenyl diphosphate isomera	0.98	(AB008267) gene_id:MMG4.18~unknown protein [Arabidop
KSU001BE443706-5	2.0e-06	Secale cereale mRNA for catalase	0.19	CATALASE ISOZYME 2
KSU002BE403217-4	0.24	Arabidopsis thaliana chromosome II section 191 of 255 of	3.0e-23	multidrug-resistance protein homolog T29F13.13 - Arabido
KSU002BE405234-1,12	2.0e-67	Oryza sativa COX6b2 mRNA for cytochrome c oxidase subu	2.0e-35	(AB047923) cytochrome c oxidase subunit 6b [Oryza sativa]
KSU002BE425566-3	1.0e-47	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	9.0e-70	(AP002843) putative UTP-glucose glucosyltransferase [Ory
KSU012BE403167-4	4.0e-32	Arabidopsis thaliana fumarase (FUM1) mRNA, complete cd	1.0e-73	fumarate hydratase (EC 4.2.1.2) - Arabidopsis thaliana
KSU012BE403506-3	1.2	Homo sapiens clone RP11-159N20, complete sequence	5.0e-16	(AB010075) 2-oxoglutarate dehydrogenase, E1 component
KSU012BE403516-1	3.0e-60	Zea mays ribosomal protein L25 mRNA, partial cds	3.0e-42	(AL442115) putative 60s Ribosomal protein L25 [Oryza sativ
KSU012BE403556-1	6.0e-15	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	5.0e-24	(AB006700) contains similarity to RAV2-like DNA-binding pr
KSU012BE403597-2	0	Sporobolus stapfianus small GTP binding protein Rab2 mF	e-106	RAS-RELATED PROTEIN RAB-2-B
KSU012BE403867-8	2.0e-71	Sorghum bicolor pathogenesis-related protein (PR-10) mR	2.0e-51	pathogenesis-related protein - sorghum
KSU012BE442608-3	e-126	Oryza sativa casein kinase mRNA, partial cds	4.0e-71	(Y11526) casein kinase II alpha subunit [Zea mays]
KSU012BE443423-11	1.0e-19	Oryza sativa chromosome 3 BAC OSJNBa0091J19 genomic	4.2	(AL117195) Y57A10A.1 [Caenorhabditis elegans]
KSU012BE490735-3	e-128	H.vulgare mRNA for coproporphyrinogen oxidase	4.0e-36	COPROPORPHYRINOGEN III OXIDASE, CHLOROPLAST PRECUR
KSU019BE445233-1	1.0e-13	Oryza sativa chromosome 10 BAC OSJNBa0055P24 genomi	0.006	(AC037425) hypothetical protein [Oryza sativa]
KSU019BE494381-6	2.0e-95	Oryza sativa genomic DNA, chromosome 4, BAC clone: B08	1.0e-67	(AF236369) prohibitin [Zea mays]
KSU019BE498620-4,6	0	Hordeum vulgare mRNA for MADS-box protein 8 (m8 gene)	7.0e-75	(AJ249146) MADS-box protein 8 [Hordeum vulgare]
KSU024BE498038-1	0	Triticum aestivum p34cdc2 (cdc2TaA) mRNA, complete cds	e-125	(U23409) p34cdc2 [Triticum aestivum]
KSU024BE606324-1	5.0e-34	Oryza sativa microsatellite MRG6585 containing (TCTT)X6,	8.0e-23	(AC013483) unknown protein [Arabidopsis thaliana]
KSU024BE606476-2	0.34	Homo sapiens BAC clone RP11-251G23 from 7, complete s	0.28	MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MAR
KSU027BE426364-2,6	7.0e-43	Maize pseudo-Gpa1 pseudogene for glyceraldehyde-3-phe	1.0e-85	(AB024023) contains similarity to serine protease~gene_id
KSU027BE495560-3	7.0e-33	Oryza sativa chromosome 3 BAC OSJNBa0026A15 genomic	3.0e-59	(AC084404) unknown protein [Oryza sativa]
KSU027BE517627-1	2.0e-95	Oryza sativa mRNA for translation initiation factor eIF-5A	4.0e-78	(AF094773) translation initiation factor 5A [Oryza sativa]
KSU030BE493826-2,4	0.025	Mus musculus adult male testis cDNA, RIKEN full-length er	2.0e-05	hypothetical protein T24P15.17 - Arabidopsis thaliana
KSU030BF473744-2,5	1.0e-06	Cymodocea nodosa CCA5 gene for P-type ATPase	1.0e-51	(AB023042) Ca2+-transporting ATPase-like protein [Arabid
KSU030BF482280-3	0	A.fatua mRNA for tetraubiquitin	e-101	polyubiquitin - tomato
KSU030BG263884-1	1.2	Thielavia heterothallica cellobiose dehydrogenase (cdh) m	4.0e-08	(AC007357) F3F19.15 [Arabidopsis thaliana]
KSU035BE403397-3	4.0e-87	Zea mays tonoplast membrane integral protein ZmTIP2-3	6.0e-70	(AJ307662) putative aquaporin [Oryza sativa]
KSU035BE403768-2	5.0e-72	Oryza sativa aminotransferase-like protein mRNA, comple	7.0e-81	(AF351125) gamma-aminobutyrate transaminase subunit p
KSU035BE404384-4,5	0.02	Arabidopsis thaliana chromosome II section 234 of 255 of	2.0e-51	(AC004450) putative carboxyphosphonoenolpyruvate muta
KSU035BE404630-2,4	3.0e-50	Oryza sativa thioredoxin h mRNA, complete cds	4.0e-45	THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KDA PROTEIN
KSU035BE404740-5,13	0.024	Homo sapiens chromosome 5, BAC clone 45m2 (LBNL H14	6.0e-61	(AB016893) 26S proteasome p55 protein-like [Arabidopsis
KSU038BE443094-1	5.0e-13	Arabidopsis thaliana chromosome 1 BAC F12B7 genomic s	e-105	(AC011020) putative protein kinase [Arabidopsis thaliana]
KSU038BE443159-1,4	3.0e-05	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	7.0e-69	(AC024594) putative phosphate translocator [Oryza sativa]
KSU038BE443294-2	0.34	Homo sapiens BAC clone RP11-154O23 from 2, complete s	4.0e-34	(AC009273) Contains similarity to acyl-CoA thioesterase fr
KSU038BE443711-5	1.4	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	3.0e-23	(AP002543) glycolate oxidase subunit D-like\; D-lactate deh
KSU038BE444851-3	0.002	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 conti	6.0e-75	(Z99708) actin interacting protein [Arabidopsis thaliana]
KSU038BE489323-5	0.086	Arabidopsis thaliana DNA chromosome 3, BAC clone F1P2	9.0e-15	(AF247646) transposase [Zea mays]
NDS018BE404821-2	4.0e-19	Oryza sativa genomic DNA fragment, chromosome 2	1.0e-57	(AJ307662) putative protein [Oryza sativa]
NDS018BE404932-3	e-148	Hordeum vulgare mRNA for expressed sequence tag	1.0e-81	(AF324991) AT4g13930 [Arabidopsis thaliana]
NDS018BE405045-1	0.34	Homo sapiens clone RP11-182J23 from 7p14-15, complete	3.0e-47	(AB010069) gb|AAC80624.1~gene_id:MAC9.17~strong simila
NDS021BG313179-2	0.45	Brucella abortus cyclic beta 1-2 glucan synthetase (cgs) ge	1.0e-43	(AP000600) gene_id:MAG2.4~unknown protein [Arabidopsi
NDS043BF292245-3	0.37	Human DNA sequence from clone RP3-522J7 on chromoso	9.0e-31	(AP001305) gene_id:MHC9.8~unknown protein [Arabidopsi
TTU025BE490735-3	e-128	H.vulgare mRNA for coproporphyrinogen oxidase	4.0e-36	COPROPORPHYRINOGEN III OXIDASE, CHLOROPLAST PRECUR
UCD001BE406509-2	0.39	Homo sapiens chromosome 5 clone CTD-2071N17, comple	2.0e-10	(AC007519) Contains 3 PF gb|T20424 comes from this gene
UCD001BE443703-5	0.005	Human DNA sequence from clone RP11-330C15 on chromo	1.4	(AE003826) CG7741 gene product [Drosophila melanogaste
UCD017BE488220-2	9.0e-08	Arabidopsis thaliana BAC F5O24	2.0e-16	(AE003512) CG14199 gene product [Drosophila melanogast
UCD028BF201830-1,5	8.0e-79	Oryza sativa elicitor-responsive gene-3 (ERG3) mRNA, com	2.0e-52	elicitor-responsive gene 3 [imported] - rice
UCD029BE404371-1,3	8.0e-20	Asparagus officinalis mRNA for NADH glutamate dehydrog	5.0e-51	(AJ011006) NADH glutamate dehydrogenase [Asparagus of
UCD029BE471201-2,3	e-141	Avena fatua Af10-protein mRNA, complete cds	7.0e-58	(U80041) Af10-protein [Avena fatua]
UCD029BE497623-5	0.2	Nicotiana tabacum centrin (CEN2) mRNA, complete cds	2.4	(Y13797) phytochrome [Platycerium angolense]
UCD029BG314395-2	1.0e-04	Arabidopsis thaliana mRNA for AKIN gamma	2.0e-22	hypothetical protein T8P19.40 - Arabidopsis thaliana
UCD037BE443207-4	1.0e-38	Rice mRNA EN312, partial sequence	8.0e-84	(AC009526) Putative histidine decarboxylase [Arabidopsis
UCD037BE443420-2	1.4	Homo sapiens non-coding RNA DD3 gene, exons 2, 3, and 4	4.0e-16	PROBABLE PROTEASE INHIBITOR P322 PRECURSOR
UCD037BE489517-4	1.6	Human DNA sequence from clone RP11-136B8 on chromos	3.0e-40	(AC005275) putative protein phosphatase regulatory subu
UCD037BE498441-5,6	0.41	Homo sapiens hexose-6-phosphate dehydrogenase (gluc	2.0e-42	(AF019248) RNA polymerase I, II and III 24.3 kDa subunit [Ar
UCD037BE498533-1	0	Triticum aestivum starch branching enzyme IIa variant mR	3.0e-75	(AF338432) starch branching enzyme IIa variant [Triticum a
UCD037BE498566-1,3	0	Zea mays protein kinase CK2 catalytic subunit CK2 alpha-3	e-118	(Y11526) casein kinase II alpha subunit [Zea mays]
UCD037BE498599-4	1.0e-81	Rice mRNA stearyl-ACP desaturase, complete cds	5.0e-54	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (
UCW016BE517946-2	e-108	Rice mRNA for serine carboxypeptidase-like protein	2.0e-88	SERINE CARBOXYPEPTIDASE III PRECURSOR
UCW039BE495991-3	0	Hordeum vulgare chloroplast photosystem I PSK-I subunit	3.0e-59	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (
UMC040BE591089-4	2.0e-21	O.sativa mRNA for Ca+2-binding EF hand protein	6.0e-66	abscisic acid-induced protein - rice
UMN013BE442608-1	e-126	Oryza sativa casein kinase mRNA, partial cds	4.0e-71	(Y11526) casein kinase II alpha subunit [Zea mays]
UMN013BE443016-3	1.0e-07	Arabidopsis thaliana DNA chromosome 3, BAC clone T10K	2.0e-92	hypothetical protein T10K17.100 - Arabidopsis thaliana
UMN013BE443651-3	9.0e-33	Oryza sativa genomic DNA, chromosome4, BAC clone: H04	3.0e-88	(AF082031) senescence-associated protein 6 [Hemerocallis
UNL002BE446789-3	1.0e-06	Arabidopsis thaliana chromosome II section 131 of 255 of	6.0e-32	(AC004401) unknown protein [Arabidopsis thaliana]
UNL002BF201372-2	1.0e-06	Arabidopsis thaliana chromosome II section 131 of 255 of	4.0e-32	(AC004401) unknown protein [Arabidopsis thaliana]
UNL036BE496834-2	e-145	T.aestivum mRNA for peptidylprolyl isomerase	2.0e-52	probable peptidylprolyl isomerase (EC 5.2.1.8) FKBP77 - wh
UNL036BF200528-1	7.0e-05	Mesorhizobium loti, complete genome	8.0e-52	(AC004809) Strong simialrity to the disulfide isomerase pr
UNL044BF483853-1	0.72	Homo sapiens BAC clone RP11-511G7 from 5, complete se	1.0e-38	hypothetical protein - Arabidopsis thaliana

2AL1-0.85-1.00

CNL031BE498892-4	3.0e-54	Lilium longiflorum cytosolic pyruvate kinase mRNA, comp	7.0e-84	pyruvate kinase (EC 2.7.1.40), cytosolic - potato
CSU046BE445437-2	3.0e-20	Oryza sativa chromosome 10 BAC OSJNBa0076F20 genomi	e-101	(AC025296) unknown protein [Oryza sativa]
CSU057BE426620-2,3	2.0e-08	Arabidopsis thaliana Glu-tRNA(Gln) amidotransferase subu	1.0e-59	(AF224745) Glu-tRNA(Gln) amidotransferase subunit A [Ara
KSU001BE444178-3,7	4.6	Homo sapiens ret proto-oncogene (multiple endocrine ne	3.0e-17	(AC006053) putative protein phosphatase 2C [Arabidopsis
KSU001BE444596-1	0.086	Human DNA sequence from clone RP11-569G13 on chromo	1.0e-06	(AL590346) putative protein [Arabidopsis thaliana]
KSU027BE490384-4,5	0	Triticum aestivum manganese superoxide dismutase (SO	e-101	superoxide dismutase (EC 1.15.1.1) (Mn) precursor - whea
KSU030BG274214-1	5.0e-15	Arabidopsis thaliana AT5g40780\K1B16_3 mRNA, complete	8.0e-46	(AB011477) amino acid permease [Arabidopsis thaliana]
KSU038BE444894-1	1.0e-68	Rice mRNA for oryzain beta (EC 3.4.22)	2.0e-52	ORYZAIN BETA CHAIN PRECURSOR
NDS001BE443747-2	1.5	Sorghum bicolor ADP-glucose pyrophosphorylase subuni	5.0e-25	(AB025632) dihydroflavonol 4-reductase-like [Arabidopsis
NDS034BE426818-4	0	Secale cereale beta-glucosidase mRNA, complete cds	e-113	(AF293849) beta-glucosidase [Secale cereale]
UCD017BE488358-5	3.0e-47	A.thaliana mRNA for hypothetical 3-isopropylmalate dehyd	3.0e-68	(AB007650) 3-isopropylmalate dehydrogenase [Arabidopsi
UCD028BE499251-4	1.0e-68	Zea mays unknown mRNA	2.0e-47	(AF152601) unknown [Zea mays]
UCD029BE426097-5	2.0e-61	Arabidopsis thaliana AT5g08290\F8L15_20 gene, complete	9.0e-78	(AL392174) putative protein [Arabidopsis thaliana] thaliana]
UCD029BE426818-5	0	Secale cereale beta-glucosidase mRNA, complete cds	e-113	(AF293849) beta-glucosidase [Secale cereale]
UCD029BE490384-4	0	Triticum aestivum manganese superoxide dismutase (SO	e-101	superoxide dismutase (EC 1.15.1.1) (Mn) precursor - whea
UCD037BG263038-3,7	0.27	Human DNA sequence from clone RP11-30E16 on chromos	8.0e-13	(AF283536) cystatin-like protein [Citrus x paradisi]
UCW001BE399113-1	0.46	Human DNA sequence from clone RP11-147C23 on chromosome 1, complete sequence [Homo sapiens]		
UCW039BE591353-6	0.061	Pseudacrobeles variabilis large subunit ribosomal RNA ge	3.0e-31	(AC007196) putative snRNP splicing factor [Arabidopsis tha
UMC040BF474210-5	1.0e-38	Zea mays ribosomal protein L30 (rpl30) mRNA, complete c	2.0e-46	60S RIBOSOMAL PROTEIN L30
UMN013BE443006-10	4.0e-07	Salmonella typhimurium strain 3027 cold shock protein C	3.0e-27	COLD SHOCK-LIKE PROTEIN CSPC (CSP-C)
UNL001BE444178-1,6	4.6	Homo sapiens ret proto-oncogene (multiple endocrine ne	3.0e-17	(AC006053) putative protein phosphatase 2C [Arabidopsis
UNL001BE444596-1	0.086	Human DNA sequence from clone RP11-569G13 on chromo	1.0e-06	(AL590346) putative protein [Arabidopsis thaliana]
UNL044BG312758-2	1.0e-19	Hordeum vulgare mRNA for gamma tubulin (gtub gene)		
UNL053BG313738-2	1.0e-09	Arabidopsis thaliana putative diacylglycerol kinase (F5H14	8.0e-61	(AF360300) putative diacylglycerol kinase [Arabidopsis thal

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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