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

Deletion Map of *Triticum aestivum* cv. Chinese Spring (Chromosome 1A)*

*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.

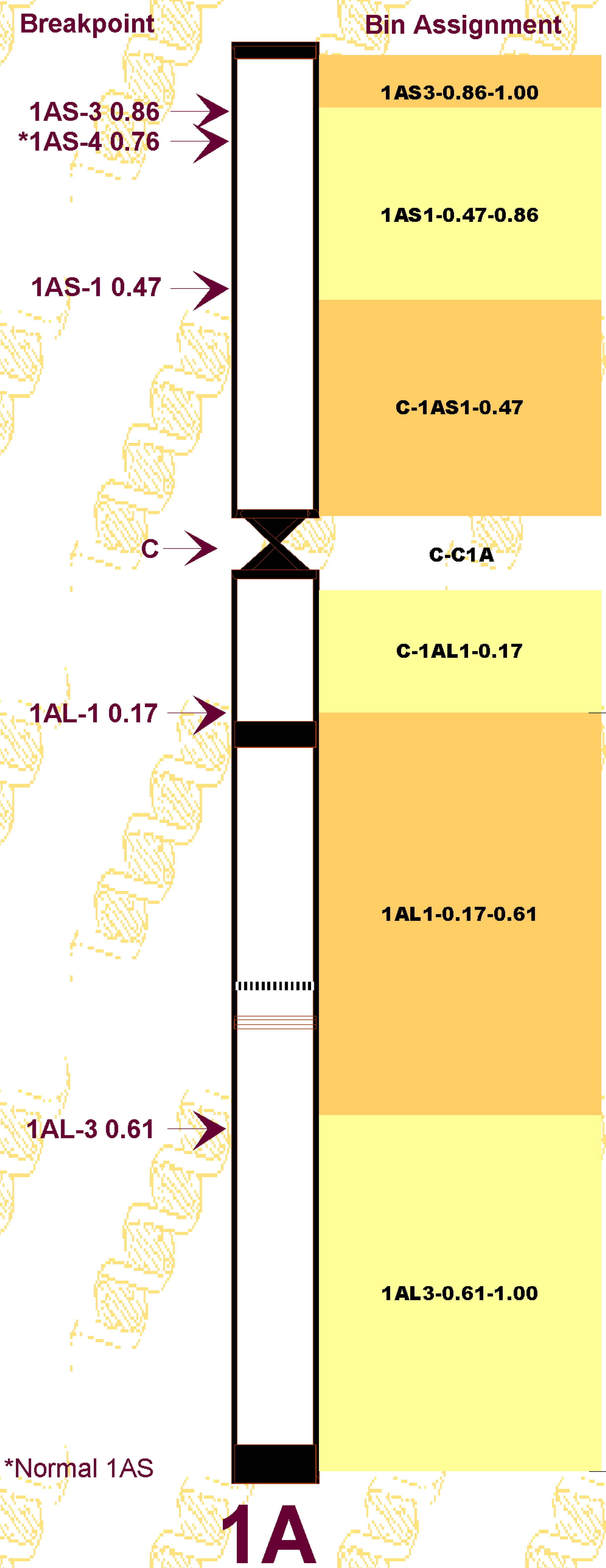
How to Interpret This Image:

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



1AS3-0.86-1.00

CNL014BE406450-3,5	3.0e-07	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-51	(U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsi
CNL031BE637310-4	0	Lolium perenne nucleoside diphosphate kinase (NDPK) m	4.0e-80	(AF271362) nucleoside diphosphate kinase [Lolium perenn
CNL031BE637568-3	7.0e-08	A.sativa seed storage protein gene, complete cds	9.0e-21	avenin precursor - oat
CSU001BE425993-3	e-154	Oryza sativa chromosome 3 BAC OSJNBa0040E01 genomic	1.0e-68	(AC079887) putative UDP-glucose dehydrogenase [Oryza s
CSU046BE443002-5	3.0e-14	Oryza sativa genomic DNA, chromosome 6, PAC clone:P00	6.0e-81	(AC008016) Similar to gb from Homo sapiens. ESTs gb|H76
KSU001BE399288-1	0.078	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIG10		
KSU002BE406387-1	9.0e-26	Oryza sativa aldehyde dehydrogenase (Aldh) mRNA, comp	6.0e-13	(AB044537) aldehyde dehydrogenase ALDH2b [Oryza sativa
KSU002BE426715-6	0.1	Homo sapiens BAC clone RP11-493I5 from 2, complete seq	2.2	transcription initiation factor IID-associated protein, 80K - f
KSU012BE406438-4,6	2.0e-07	Arabidopsis thaliana chromosome II section 86 of 255 of th	8.0e-14	(AF116752) seed maturation protein PM23 [Glycine max]
KSU012BE406450-4,6	3.0e-07	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-51	(U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsi
KSU012BE442682-1	1.0e-28	H.vulgare chymotryposin inhibitor-2 gene		
KSU012BE443401-3	4.0e-63	Hordeum vulgare mRNA for hypothetical protein, clone RG	3.0e-84	(AC003672) putative heme A: farnesyltransferase [Arabido
KSU024BE499711-1	0.083	Homo sapiens clone RP11-355K7, complete sequence	3.0e-56	(AF367323) AT5g27410\F21A20_120 [Arabidopsis thaliana]
KSU024BE500104-1	0.1	Drosophila melanogaster genomic scaffold 1420000133860	2.0e-08	(D21813) ORF [Lilium longiflorum]
KSU027BE490041-3	0.006	Petunia x hybrida PHAP2A protein (Ap2A) mRNA, complete	1.0e-32	(AF134116) APETALA2 protein homolog HAP2 [Hyacinthus o
KSU027BE590674-4	0	T.aestivum Glu-B3 gene	5.0e-31	glutenin low molecular weight - wheat (fragment)
KSU027BF482663-7	5.0e-12	Oryza sativa lipoxygenase (CM-LOX1) mRNA, partial cds	5.0e-30	probable lipoxygenase (EC 1.13.11.12) (clone H1) - potato
KSU030BE606926-2	0.49	Homo sapiens unconventional myosin (MYO15) gene, part	1.0e-19	(AC013483) putative GTPase activator protein [Arabidopsis
KSU030BG313350-3	3.0e-17	A.thaliana mRNA for CaLB protein	9.0e-91	CaLB protein - Arabidopsis thaliana
KSU035BE405834-2	1.0e-22	Zea mays inorganic pyrophosphatase (IPP) mRNA, comple	3.0e-66	inorganic pyrophosphatase-like protein - Arabidopsis thal
KSU038BE444890-3,5	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
TTU025BE406438-4,6,7	2.0e-07	Arabidopsis thaliana chromosome II section 86 of 255 of th	8.0e-14	(AF116752) seed maturation protein PM23 [Glycine max]
TTU025BE406450-4,6,7	3.0e-07	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-51	(U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsi
UCD037BE443103-2	1.8	Arabidopsis thaliana DNA chromosome 4, BAC clone F20B	2.0e-23	DNA-BINDING PROTEIN HEXBP (HEXAMER-BINDING PROTEIN)
UCW001BE399288-1	0.078	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIG10		
UMC015BE426301-4	4.0e-65	Oryza sativa chromosome 4 BAC I1332 genomic sequence	1.0e-80	(AL117264) zwh21.1 [Oryza sativa]
UMC015BE489841-6	8.0e-30	Arabidopsis thaliana At2g27860\F15K20.4 gene, complete c	8.0e-95	(AC011438) T23G18.6 [Arabidopsis thaliana]
UMC040BE591042-6	e-163	Hordeum vulgare plasma membrane associated protein (g	1.0e-65	(AF218627) plasma membrane associated protein [Hordeu
UNL002BE405778-2	e-120	Hordeum vulgare genomic sequence, clone BAC 711N16, is	2.0e-65	(AY009938) Mla1 [Hordeum vulgare]
UNL002BE499561-3	0.36	Human DNA sequence from clone RP5-1126B2 on chromos	2.0e-13	(AC007980) Very similar to disease resistance proteins [A
UNL002BE518223-3	3.0e-63	Hordeum vulgare NBS-LRR type resistance protein (b6) ge	2.0e-46	(AB019240) RPR1h [Oryza sativa]
UNL002BF474204-1	3.0e-05	Triticum aestivum cyst nematode resistance gene candid	5.0e-37	probable cyst nematode resistance gene - wheat (fragme
UNL002BF475048-1	3.0e-09	Oryza sativa mRNA for RPR1h, complete cds	3.0e-34	(AB019186) RPR1 [Oryza sativa]
UNL048BF428925-3	4.0e-07	Arabidopsis thaliana chromosome III P1 MGH6 genomic se	3.0e-67	ELONGATION FACTOR 2 (EF-2)

1AS1-0.47-0.86

CNL001BE426257-1	7.0e-27	Oryza sativa chromosome 5 clone P0001A07, complete se	1.0e-85	(AC084218) similar to Pisum sativum methylenetetrahydro
UCW003BE590695-2	2.0e-91	H.vulgare gene encoding serine carboxypeptidase II, CP-M	3.0e-85	Chain B, Structural Basis For Light Acitvation Of A Chloropl
CNL014BE591757-2,3	8.0e-04	Oryza sativa genomic DNA, chromosome 1, BAC clone:B10	1.0e-14	(AP002804) EST D48432(S14625) corresponds to a region of
CSU001BE426257-1	7.0e-27	Oryza sativa chromosome 5 clone P0001A07, complete se	1.0e-85	(AC084218) similar to Pisum sativum methylenetetrahydro
CSU001BE426488-1	5.0e-16	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7	7.0e-95	argininosuccinate synthase (EC 6.3.4.5) - Arabidopsis thali
CSU046BE443071-3	9.0e-27	Oryza sativa chromosome 5 clone P0431G05, complete se	2.0e-87	hypothetical protein F26K9.30 - Arabidopsis thaliana
CSU046BE444846-1	2.0e-18	Oryza sativa chromosome 5 clone P0001A07, complete se	3.0e-53	(AC084218) similar to Arabidopsis thaliana putative stress
CSU057BE489895-2	3.0e-11	Arabidopsis thaliana putative serine protease (F17A22.33\	1.0e-90	(AC005309) putative serine protease [Arabidopsis thaliana
KSU001BE443735-1	3.0e-57	Aegilops tauschii starch synthase I gene, complete cds	0.63	(AB046670) includes endonuclease domain and reverse tra
KSU002BE425354-3	1.1	Arabidopsis thaliana DNA chromosome 3, BAC clone T6L1	1.0e-42	hypothetical protein T11I11.70 - Arabidopsis thaliana
KSU002BE426257-1	7.0e-27	Oryza sativa chromosome 5 clone P0001A07, complete se	1.0e-85	(AC084218) similar to Pisum sativum methylenetetrahydro
KSU012BE403153-2,4	e-148	Avena fatua mRNA for VIP2 protein (vip2 gene)	4.0e-61	(AJ251051) VIP2 protein [Avena fatua]
KSU012BE403553-4	7.0e-39	Oryza sativa chromosome 4 BAC q3037-207F1 complete ge	6.0e-50	(AJ245900) CAA303716.1 protein [Oryza sativa]
KSU019BE406901-2,4	1.0e-15	Oryza sativa genomic DNA, chromosome 1, PAC clone:P05	1.0e-31	(AP002869) putative lipase homolog [Oryza sativa]
KSU019BE426701-2	2.0e-20	Oryza sativa OsIF1-1 mRNA for F1F0-ATPase inhibitor prote	8.0e-13	(AB029059) F1F0-ATPase inhibitor protein [Oryza sativa]
KSU024BE500081-2	1.0e-07	Arabidopsis thaliana genomic DNA, chromosome 5, BAC cl	2.0e-71	(AP002029) N-glyceraldehyde-2-phosphotransferase-like [
KSU035BE406998-9	2.0e-35	ric1=ras-related GTP binding protein possessing GTPase	3.0e-43	(AP002524) putative GTP-binding protein [Oryza sativa]
KSU035BE497372-3,4	1.0e-05	Hordeum vulgare mRNA for expressed sequence tag	4.0e-45	(AC011620) putative serine\threonine protein phosphatas
KSU038BE489323-9	0.086	Arabidopsis thaliana DNA chromosome 3, BAC clone F1P2	9.0e-15	(AF247646) transposase [Zea mays]
TTU047BE405648-2	e-114	Zea mays mus1 gene, exons 1-13	e-102	DNA MISMATCH REPAIR PROTEIN MSH2 (MUS1)
UCD001BE406516-3	2.0e-26	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	2.0e-64	(AP003244) casein kinase-like protein [Oryza sativa]
UCD037BE606302-4	0.063	Plasmodium falciparum MAL4P2, complete sequence	2.0e-36	(AB026632) contains similarity to senescence-associated p
UCD037BG263028-4	e-105	Rice mRNA for aspartic proteinase, complete cds	3.0e-85	ASPARTIC PROTEINASE PRECURSOR
UCW001BE399975-9	3.0e-27	Barley ubiquitin (mub2) gene, complete cds	0.57	40S RIBOSOMAL PROTEIN S27A
UCW003BE590760-3	2.0e-85	Hordeum vulgare glucose and ribitol dehydrogenase hom	4.0e-21	glucose and ribitol dehydrogenase homolog - barley
UCW016BE590695-2	2.0e-91	H.vulgare gene encoding serine carboxypeptidase II, CP-M	3.0e-85	Chain B, Structural Basis For Light Acitvation Of A Chloropl
UCW016BE590760-3	2.0e-85	Hordeum vulgare glucose and ribitol dehydrogenase hom	4.0e-21	glucose and ribitol dehydrogenase homolog - barley
UCW020BE403749-3	e-177	Zea mays ribosomal protein S4 (rps4) mRNA, complete cds	2.0e-89	40S RIBOSOMAL PROTEIN S4
UCW026BE498820-2	0	Oryza sativa mRNA for importin alpha 1b, complete cds	e-102	(AB024311) importin alpha 1b [Oryza sativa]
UCW026BG262247-1	5.0e-62	Oryza sativa 2-oxoglutarate\malate translocator mRNA, pa	e-102	2-oxoglutarate\malate translocator (clones OMT134 and O
UCW039BE443797-1	8.0e-52	Oryza sativa genomic DNA, chromosome 1, PAC clone:P05	2.0e-34	(AB012245) 26S proteasome subunit-like protein [Arabidop
UMN013BE443531-2	4.0e-38	S.tuberosum LAP mRNA for leucine aminopeptidase	4.0e-81	leucyl aminopeptidase (EC 3.4.11.1) - parsley (fragment)
UNL044BG263172-3	9.0e-11	Arabidopsis thaliana chromosome II section 141 of 255 of	1.0e-73	clpB heat shock protein-like - Arabidopsis thaliana
UNL048BF429033-2	1.0e-06	Arabidopsis thaliana transcription factor (AGL5) mRNA, co	1.0e-14	floral homeotic protein ZAG1 - maize

C-1AS1-0.47

KSU012BE443430-5	2.0e-05	Arabidopsis thaliana RNA polymerase II 13.6 kDa subunit (A	1.0e-47	DNA-DIRECTED RNA POLYMERASE II 13.6 KDA POLYPEPTIDE A
KSU027BF202643-3	1.0e-28	Oryza sativa chromosome 10 clone nbxb0045B21, complet	1.0e-46	(AB026644) prolyl 4-hydroxylase alpha subunit-like protein
NDS001BE442851-2	0.11	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-639F2 of library RPCI-11 from chromosome 14 of Homo sapi		
TTU047BE494680-1	9.0e-05	Arabidopsis thaliana AT4g37830\T28I19_110 mRNA, comple	2.0e-24	hypothetical protein T28I19.110 - Arabidopsis thaliana

C-1AL1-0.17

KSU035BE403420-1	8.0e-30	Oryza sativa chromosome 10 BAC OSJNBb0011A08 genomi	3.0e-62	(AC034258) putative thiolase [Oryza sativa]
KSU035BE497107-2,3,4	5.0e-47	Oryza sativa chromsome 9 clone PAC0645D04, complete s	7.0e-84	RAS-RELATED PROTEIN RAB11D
KSU035BE497584-3	e-123	Z.mays CPNB gene encoding mitochondrial chaperonin-60	2.0e-52	CHAPERONIN CPN60-2, MITOCHONDRIAL PRECURSOR (HSP60
KSU038BE444094-2	0.09	Human DNA sequence from clone 1045J21 on chromosom	3.0e-61	(AJ238212) glutamine synthetase I [Medicago truncatula]
KSU038BE446010-3,5	2.0e-52	Oryza sativa chromosome 10 BAC OSJNBa0079L16 genomi	2.0e-62	(AB004568) cyanase [Arabidopsis thaliana]
UNL036BE518393-8	e-119	Oryza sativa chromosome 10 BAC OSJNBa0006L06 genomi	7.0e-71	(AF334838) ribosomal protein L17 [Castanea sativa]

1AL1-0.17-0.61

CNL001BE403217-8	0.24	Arabidopsis thaliana chromosome II section 191 of 255 of	3.0e-23	multidrug-resistance protein homolog T29F13.13 - Arabido
CNL001BE405581-4	2.0e-06	Arabidopsis thaliana chromosome II section 201 of 255 of	7.0e-23	(AC006922) unknown protein [Arabidopsis thaliana]
CNL023BG274294-2,4	0.021	Triticum aestivum high-affinity phosphate transporter PT1	1.0e-68	(AC021666) unknown protein\; 24499-21911 [Arabidopsis th
CNL031BE405692-6	7.0e-49	Zea mays glutathione S-transferase GST 42 mRNA, partial	2.0e-54	(AF244707) glutathione S-transferase GST 42 [Zea mays]
CSU001BE405581-3	2.0e-06	Arabidopsis thaliana chromosome II section 201 of 255 of	7.0e-23	(AC006922) unknown protein [Arabidopsis thaliana]
CSU001BE444191-1	0.004	Homo sapiens potassium voltage-gated channel, shaker-r	1.0e-13	(AC005917) putative recA protein [Arabidopsis thaliana]
CSU046BE444527-1	0.094	Pestivirus type 1 cytopathic genomic RNA, complete genom	1.0e-41	hypothetical protein T27E13.16 - Arabidopsis thaliana thalia
KSU001BE443706-9	2.0e-06	Secale cereale mRNA for catalase	0.19	CATALASE ISOZYME 2
KSU001BE443755-15	0.007	Dictyostelium discoideum nucleoside diphosphate kinase	6	(AF202730) Niemann-Pick type C1 disease protein [Oryctola
KSU001BE444339-6,8	1.4	Drosophila melanogaster genomic scaffold 1420000133860	3.5	(AF264760) cAMP-dependent protein kinase [Neurospora c
KSU002BE405581-4,6	2.0e-06	Arabidopsis thaliana chromosome II section 201 of 255 of	7.0e-23	(AC006922) unknown protein [Arabidopsis thaliana]
KSU002BE406605-2	0.15	Drosophila melanogaster, chromosome 3R, region 98A-98	0.2	HYPOTHETICAL 113.1 KD PROTEIN T28D9.7 IN CHROMOSOME
KSU002BE426488-3	5.0e-16	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7	7.0e-95	argininosuccinate synthase (EC 6.3.4.5) - Arabidopsis thali
KSU012BE352628-3	2.0e-37	Oryza sativa chromosome 10 BAC OSJNBb0089A17 genomi	2.0e-85	(AC079890) unknown protein [Oryza sativa]
KSU012BE403956-3	2.0e-79	Zea mays beta-expansin 8 (expB8) mRNA, complete cds	2.0e-65	(AF261272) beta-expansin [Oryza sativa]
KSU012BE442716-2	e-108	A.sativa (Pewi) ASTCP-K19 mRNA for t complex polypeptid	4.0e-92	T complex protein [Cucumis sativus]
KSU012BE442818-5	4.0e-10	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	4.0e-71	(AP000604) contains similarity to unknown protein~gb|AAF
KSU019BE405414-3	1.0e-09	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	8.0e-60	(AC009853) unknown protein [Arabidopsis thaliana]
KSU024BE500310-1	4.0e-59	Oryza sativa chromosome 10 BAC OSJNBa0003O19 genomi	2.0e-57	(AC060755) unknown protein [Oryza sativa]
KSU024BF202735-2	2.0e-07	Oryza sativa protein phosphatase 2A 55 kDa B regulatory subunit gene, complete cds		
KSU027BE495028-2	e-147	Oryza sativa calmodulin (CaM2) mRNA, complete cds	5.0e-72	(X65016) calmodulin [Oryza sativa]
KSU030BE637473-1	e-115	Triticum aestivum secretory protein (WAS-2) mRNA, comp	1.0e-42	(AF079526) secretory protein [Triticum aestivum]
KSU035BE403404-5	9.0e-22	Catharanthus roseus PAPS-reductase-like protein (par2ne	8.0e-42	(U63784) PAPS-reductase-like protein [Catharanthus roseu
KSU035BE406977-3,5	e-117	H.vulgare ids-1 mRNA	1.0e-17	(D50641) plant metallothionein-like protein [Hordeum vulga
KSU035BE407013-2	0.28	Caulobacter crescentus section 121 of 359 of the complet	4.0e-44	(AB012239) autophagocytosis protein AUT1-like [Arabidops
KSU035BE496824-2	0.021	Caenorhabditis elegans cosmid B0496, complete sequenc	1.0e-36	(AB023036) contains similarity to endo-1,3-1,4-beta-D-gluca
KSU035BE497600-2	0.045	Nicotiana tabacum mRNA for ethylene responsive element	4.0e-17	transcription factor DREB2A, drought induced [validated] - .
KSU038BE443930-1,4	3.0e-72	Saccharum officinarum pyruvate orthophosphate dikinase	5.0e-40	(M58656) pyruvate,orthophosphate dikinase [Zea mays]
KSU038BE444757-8	4.0e-65	Oryza sativa chromosome 10 clone nbxb0046P18, complet	2.0e-76	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CON
KSU038BE445834-1	0.85	Arabidopsis thaliana BAC F7K24	3.0e-13	(AB017067) TMV resistance protein-like [Arabidopsis thalia
NDS001BE405594-2	0.12	Homo sapiens chromosome 5 clone CTB-2J5, complete se	2.2	probable regulatory protein - Streptomyces coelicolor A3(
NDS001BE443789-2	0.23	Homo sapiens spindlin (SPIN), mRNA		
NDS018BE404880-5	3.0e-05	N.crassa mRNA for mitochondrial 12 kD subunit of NADH:ub	1.0e-30	probable acyl carrier protein T8F5.6 - Arabidopsis thaliana
NDS034BE403158-1	4.0e-87	H.vulgare Bsi1 gene for putative protease inhibitor	5.0e-36	wheat aluminum induced protein wali 5 - wheat
NDS034BE490430-1,3	6.0e-23	Oryza sativa chromosome 10 BAC OSJNBa0027P10 genomi	1.0e-10	(AC084763) putative casein kinase II beta subunit [Oryza sa
NDS043BF291369-2	0.002	Oryza sativa microsatellite MRG5514 containing (GCG)X8, c	1.0e-09	(AL022198) hypothetical protein [Arabidopsis thaliana]
UCD001BE405594-2	0.12	Homo sapiens chromosome 5 clone CTB-2J5, complete se	2.2	probable regulatory protein - Streptomyces coelicolor A3(
UCD001BE406605-5	0.15	Drosophila melanogaster, chromosome 3R, region 98A-98	0.2	HYPOTHETICAL 113.1 KD PROTEIN T28D9.7 IN CHROMOSOME
UCD001BE444339-7,9	1.4	Drosophila melanogaster genomic scaffold 1420000133860	3.5	(AF264760) cAMP-dependent protein kinase [Neurospora c
UCD017BE494376-1	2.0e-39	Rice mRNA for Cytochrome b5	1.0e-57	(AC025296) putative cytochrome [Oryza sativa]
UCD017BE494527-1	0.24	Caenorhabditis elegans cosmid C38H2, complete sequenc	5.0e-10	(AC079676) phosphoethanolamine N-methyltransferase, pu
UCD017BE494853-4	5.0e-09	Oryza sativa putative lipid transfer protein (Ltp-2) gene, co	2.0e-22	probable lipid transfer protein - rice
UCD028BE490596-2	0	T.aestivum atp-2 mRNA for ATP synthase beta subunit	2.0e-96	H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mito
UCD028BF146193-5	0.005	Rhodobacter sphaeroides strain 2.4.1T quinol oxidase sub	5.0e-42	hypothetical protein F9D16.100 - Arabidopsis thaliana
UCD028BF202674-2	1.0e-10	Oryza sativa chromosome 10 BAC OSJNBa0010C11 genomi	5.0e-13	(AC055769) zinc-finger protein, putative\; 7043-7771 [Arabid
UCD029BE426097-2	2.0e-61	Arabidopsis thaliana AT5g08290\F8L15_20 gene, complete	9.0e-78	(AL392174) putative protein [Arabidopsis thaliana] thaliana
UCD029BE517991-1	1.0e-04	A.thaliana rpl1 gene	2.0e-29	(X90855) L1 protein [Arabidopsis thaliana]
UCD029BF483378-7	e-110	Oryza sativa OsPAG1 mRNA for alpha 7 subunit of 20S prot	3.0e-87	PROTEASOME SUBUNIT ALPHA TYPE 3 (20S PROTEASOME AL
UCD029BF483456-4	2.0e-80	Arabidopsis thaliana AT3g62830\F26K9_260 gene, complet	e-109	dTDP-glucose 4-6-dehydratase homolog T30B22.4 - Arabid
UCD037BE443332-2	5.0e-10	Arabidopsis thaliana unknown protein (AT4g21860) mRNA,	6.0e-45	(AF360341) unknown protein [Arabidopsis thaliana]
UCD037BE488529-1,3	1.4	Homo sapiens chromosome 5 clone CTD-2213L16, comple	5.0e-55	(AC006434) F10A5.27 [Arabidopsis thaliana] subunit [Arabic
UCW020BE404660-1	e-170	Zea mays ubiquitin conjugating enzyme (UBC) mRNA, com	6.0e-85	(AF034946) ubiquitin conjugating enzyme [Zea mays]
UMC040BE590637-5	0.084	Cicer arietinum mRNA for cytochrome P450 (cyp93C3 gene	2.0e-30	(AJ296346) cytochrome P450 [Solanum tuberosum]
UMC040BE606632-5	1.0e-98	Hordeum vulgare cv. Haisa mRNA for MCB1 protein	3.0e-31	(AJ303354) MCB1 protein [Hordeum vulgare]
UMC040BF474284-4	0	T.aestivum VDAC2 mRNA for voltage dependent anion cha	3.0e-61	porin VDAC2 - wheat (fragment)
UMC040BF474511-7	1.0e-04	Arabidopsis thaliana IAA2 (MXC7.6) mRNA, complete cds	2.0e-21	(AF123509) Nt-iaa4.1 deduced protein [Nicotiana tabacum]
UMC055BF483683-3	1.0e-06	Nicotiana plumbaginifolia mRNA for acetolactate synthase	3.0e-57	(AJ234901) acetolactate synthase small subunit [Nicotiana
UMC055BG263233-3	e-147	Oryza sativa OsFEN-1 mRNA for FEN-1, complete cds	8.0e-86	(AB021666) FEN-1 [Oryza sativa]
UMN013BE442876-3	2.0e-49	Oryza sativa clone riceipp2 isopentenyl pyrophosphate:dir	1.0e-75	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) 1 - C
UMN013BE443570-4	1.0e-04	Arabidopsis thaliana BAC F2P16, complete sequence	9.0e-46	(AC000132) Identical to A. thaliana AtK-1 (gb|X79279). [Arabi
UMN013BE443722-5	1.0e-06	Hordeum vulgare (cv. Bomi) B12D mRNA	9.0e-30	hypothetical protein T24C20.20 - Arabidopsis thaliana
UMN013BE444505-3	0.38	Human DNA sequence from clone RP11-473L1 on chromos	9.0e-25	(AC051629) Unknown protein [Arabidopsis thaliana]
UNL002BE426789-1	0.007	Cricetulus griseus mRNA for RNA polymerase II largest su	4.0e-41	(AF158634) Vrga1 [Aegilops ventricosa]
UNL002BE426790-1	0.39	Bos taurus blue cone pigment protein mRNA, complete cd	1.0e-09	(AF114171) disease resistance protein RPM1 homolog [Sor
UNL036BE590719-2	1.0e-37	Triticum aestivum cold-responsive LEA\RAB-related COR	2.0e-51	LEA protein - rice
UNL044BF482786-5	0.32	Caenorhabditis elegans transmembrane cell adhesion rec	5.0e-32	(AC009519) F1N19.9 [Arabidopsis thaliana]

1AL1-0.17-1.00

KSU001BE443720-2	0.024	Homo sapiens BAC clone RP11-235I1 from Y, complete sec	9.0e-18	(AC010926) protein phosphatase 2C (AtP2C-HA)\; 19519-176
KSU001BE443789-2	0.23	Homo sapiens spindlin (SPIN), mRNA		
KSU001BE444305-2	0.026	Staphylococcus aureus serine protease spl operon, comp	4.0e-15	(AJ276270) hypothetical protein [Cicer arietinum]
KSU001BE444359-2	2.0e-06	Arabidopsis thaliana chromosome III BAC F3E22 genomic s	3.0e-37	(AC023912) unknown protein [Arabidopsis thaliana]
UCW039BE405167-3	2.0e-64	Zea mays ubiquitin-conjugating enzyme mRNA, partial cds	3.0e-73	E2 ubiquitin-conjugating-like enzyme Ahus5 - Arabidopsis

1AL3-0.61-1.00

CNL014BE490592-2,3	2.0e-42	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	9.0e-76	(AP003053) putative malate dehydrogenase [Oryza sativa]
CSU102BE406562-2	0.96	Sus scrofa large white\landrace cross myosin heavy chain mRNA, partial cds		
KSU001BE398611-6	0.096	Drosophila melanogaster maroon-like protein (mal) gene,	0.35	(AE003708) ldlCp gene product [Drosophila melanogaster]
KSU012BE403322-3	0.66	Homo sapiens excision repair cross-complementing rode	4.0e-07	(AB016886) emb|CAB71043.1~gene_id:MCA23.10~strong sir
KSU012BE442876-3	2.0e-49	Oryza sativa clone riceipp2 isopentenyl pyrophosphate:dir	1.0e-75	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) 1 - C
KSU012BE490592-2,3	2.0e-42	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	9.0e-76	(AP003053) putative malate dehydrogenase [Oryza sativa]
KSU019BE444620-1	e-142	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	5.0e-84	(AP002522) hypothetical protein [Oryza sativa]
KSU019BE490584-9	0	Triticum aestivum chlorophyll a\b-binding protein WCAB g	2.0e-77	(U73218) chlorophyll a\b-binding protein WCAB precursor [
KSU019BE495150-1,3	1.0e-99	Zea mays cytochrome b5 reductase (NFR) mRNA, complet	2.0e-73	(AF077372) cytochrome b5 reductase [Zea mays]
KSU019BE500394-2,4	2.0e-21	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	3.0e-51	(AP002744) putative late embryogenesis abundant protein
KSU019BE518339-1,2	4.0e-18	Zea mays O-methyltransferase (OMT) gene, complete cds	1.0e-32	(AF033540) caffeic acid O-methyltransferase\; LPOMT3 [Lol
KSU024BE497808-9	0	Wheat histone H4 gene	9.0e-40	histone H4 [Triticum aestivum]
KSU027BE590822-3	2.0e-24	Citrus sinensis mRNA for ACC synthase (acs-1 gene)	2.0e-59	peptidylprolyl isomerase (EC 5.2.1.8) F23F1.12 - Arabidopsi
KSU030BF200980-3,5	3.0e-57	Zea mays translation initiation factor GOS2 (TIF) mRNA, cor	4.0e-54	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PRO
KSU035BE403428-4	1.4	Oryctolagus cuniculus heat shock protein 47 mRNA, partia	1.0e-35	(AC069300) putative dioxygenase [Oryza sativa]
KSU035BE406918-2	2.0e-11	Oryza sativa subsp. indica putative aldehyde dehydrogena	5.0e-45	(AC074228) aldehyde dehydrogenase, putative [Arabidopsi
KSU038BE442681-3	0.026	Arabidopsis thaliana chromosome II section 127 of 255 of	5.0e-54	(AJ011892) cyclin D2.1 protein [Nicotiana tabacum]
KSU038BE443905-1	0.43	Drosophila melanogaster, chromosome 2L, region 37D, BA	4.0e-26	pit2 protein (clone pAL141), Pi starvation induced - commo
KSU038BE445134-3	0.017	Caenorhabditis elegans cosmid F21H11, complete sequen	4.0e-37	(AC008030) Similar to apoptosis related protein 19 [Arabid
KSU038BE446240-1	e-157	Oryza sativa GDP dissociation inhibitor protein OsGDI2 (Os	2.0e-87	GDP dissociation inhibitor protein - rice
KSU038BE446672-1	0.28	Vigna mungo yellow mosaic virus B component DNA, com	6.0e-50	(AP000836) ESTs AU068544(C30430),C98487(E0325),D23445(C
NDS018BE404147-3	1.0e-15	Pisum sativum nucleoside diphosphate kinase (ndpk) mR	2.0e-21	hypothetical protein T32A16.70 - Arabidopsis thaliana
NDS034BE470696-6	0.005	Arabidopsis thaliana mRNA for 2-oxoglutarate dehydrogen	3.0e-25	(AB010071) 2-oxoglutarate dehydrogenase E2 subunit [Aral
NDS034BF200980-3,5	3.0e-57	Zea mays translation initiation factor GOS2 (TIF) mRNA, cor	4.0e-54	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PRO
NDS043BF292349-2	0.016	Zea mays clone tac_919.27 Ac insertion site sequence	1.0e-33	(AC012654) Strong similarity to the putative GDSL-motif co
NDS043BG274939-4	2.0e-14	Z.mays Zmhox1a mRNA for homeobox protein	2.0e-19	HOMEOBOX PROTEIN HOX1A
TTU025BE490592-2	2.0e-42	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	9.0e-76	(AP003053) putative malate dehydrogenase [Oryza sativa]
TTU047BE495913-9	0.011	Mus musculus 1 BAC RP23-337F12 (Roswell Park Cancer In	1.0e-11	hypothetical protein - garden asparagus
UCW026BG263358-1	5.0e-40	Hordeum vulgare var. distichum soluble inorganic pyroph	1.0e-73	(AC007323) T25K16.5 [Arabidopsis thaliana]
UCW039BE446525-3	0.005	Lycopersicon esculentum ER6 protein mRNA, partial cds	1.0e-21	(AF096262) ER6 protein [Lycopersicon esculentum]
UMC001BE399975-10	3.0e-27	Barley ubiquitin (mub2) gene, complete cds	0.57	40S RIBOSOMAL PROTEIN S27A
UMC015BE426279-4	3.5	Homo sapiens Xp BAC RP11-86G5 (Roswell Park Cancer Ins	8.5	(AC009525) Similar to beta-glucosidases [Arabidopsis thal
UMC015BE426304-3	e-148	Z.mays mRNA for calmodulin	5.0e-72	(X65016) calmodulin [Oryza sativa]
UMC015BE426661-1	5.0e-07	Hordeum vulgare genomic DNA fragment\; clone MWG0952	3.0e-91	(AP002897) putative CTP synthase [Oryza sativa]
UMC015BE426686-4	0.27	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	2.0e-06	(AB007649) emb|CAB62355.1~gene_id:MLE2.13~similar to u
UNL002BE605005-2	1.1	Homo sapiens Chromosome 11q12.2 PAC clone pDJ52b24	8.0e-09	(AB013451) NBS-LRR type resistance gene [Oryza sativa]
UNL002BF473313-3	1.0e-06	Hordeum vulgare NBS-LRR type resistance protein (b7) ge	3.0e-39	NBS-LRR type resistance protein - barley (fragment)
UNL036BE517729-2	1.0e-04	Arabidopsis thaliana proline iminopeptidase mRNA, compl	6.0e-92	PROLINE IMINOPEPTIDASE (PIP) (PROLYL AMINOPEPTIDASE)
UNL036BE517992-2	2.0e-15	C.reinhardtii chloroplast ATP synthase gamma subunit ml	2.0e-80	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
UNL036BE518048-2	9.0e-33	Cicer arietinum partial mRNA for MAP kinase protein	6.0e-96	(AC006931) putative MAP kinase [Arabidopsis thaliana]
UNL036BE518221-2	1	Homo sapiens 12q BAC RP11-848D3 (Roswell Park Cancer I	1.0e-29	(AB022330) nClpP5 [Arabidopsis thaliana] gb|AB022330 and
UNL036BE590634-2	e-117	Zea mays farnesyl pyrophosphate synthetase (fps) mRNA	8.0e-89	FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASI
UNL036BF200636-4	0.01	Andira aubletii clone CwB12-II microsatellite sequence	3.0e-08	peptidylprolyl isomerase (EC 5.2.1.8), microsomal - maize
UNL036BF473773-2	1.0e-04	sucrose-phosphate synthase [Spinacia oleracea, leaves, r	5.0e-73	SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE
UNL044BF483820-3	2.0e-17	Rice gene for ferredoxin, complete cds	1.0e-14	ferredoxin [2Fe-2S], root - rice
UNL044BG312759-3	7.0e-07	Homo sapiens chromosome 19 clone CTC-539A10, comple	3.0e-15	snRNP core Sm protein homolog Sm-X5 from Mus muscul
UNL048BE445579-2	1.2	Streptomyces antibioticus putative 3-ketoreductase (oleW	1.0e-53	(AF002109) unknown protein [Arabidopsis thaliana]
UNL048BE605158-3	0	T.aestivum mRNA for alpha1-thionin	3.0e-73	ALPHA-2-PUROTHIONIN PRECURSOR
UNL053BF293953-1	3.0e-20	Selaginella lepidophylla trehalose-6-phosphate synthase r	3.0e-77	(Y08568) trehalose-6-phosphate synthase [Arabidopsis tha

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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