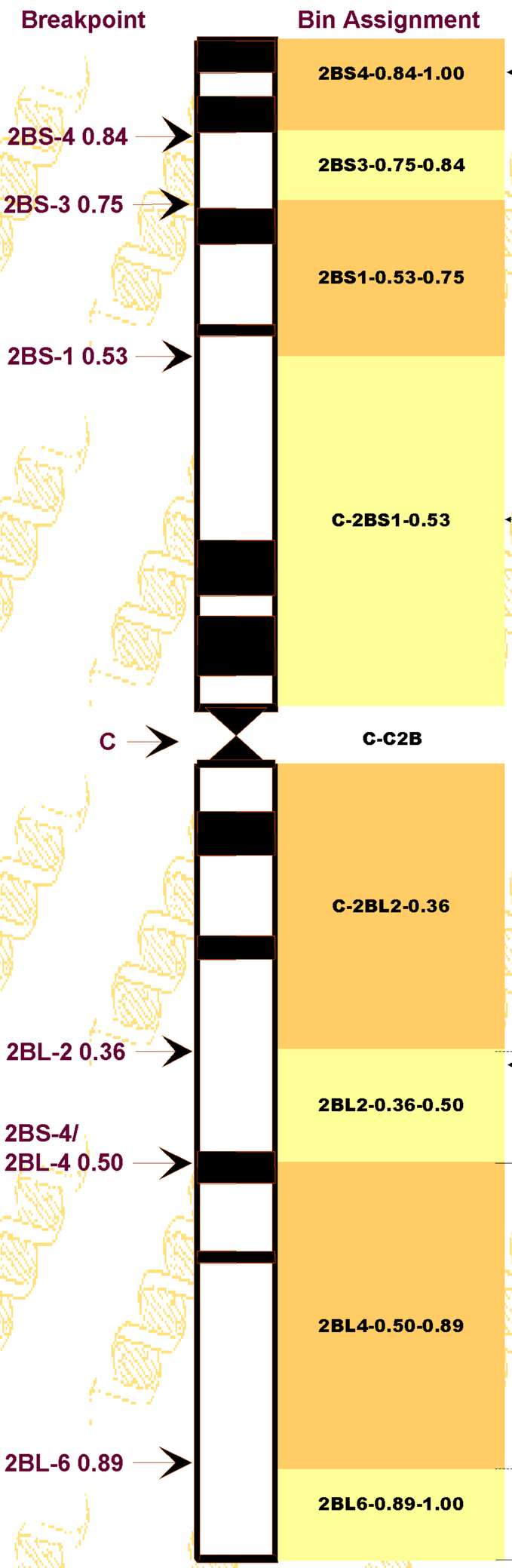
The Structure and Function of the Expressed Portion of the Wheat Genomes

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



2BS4-0.84-1.00

CNL014BE-490444-10	0.012	Homo sapiens MLL septin-like fusion (MSF), mRNA	4.4 (AB013286) MTG16 [Homo sapiens]
CSU046BE-443885-2	0.002	Arabidopsis thaliana DNA chromosome 5, BAC clone F2K1	3.0e-49 (AC018363) unknown protein [Arabidopsis thaliana]
KSU001BE-443747-1	1.5	Sorghum bicolor ADP-glucose pyrophosphorylase subunit	5.0e-25 (AB025632) dihydroflavonol 4-reductase-like [Arabidopsis t
KSU012BE-443439-1,3	1.0e-04	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	1.0e-70 (AB010872) gb|AAC64874.1~gene_id:MEE5.19~strong simila
KSU012BE-490444-2,4,13,14	0.012	Homo sapiens MLL septin-like fusion (MSF), mRNA	4.4 (AB013286) MTG16 [Homo sapiens]
KSU019BE-494450-10	7.0e-40	Avena maroccana clone Ma7 ribulose-1,5-bisphosphate ca	3.0e-15 (AB042068) ribulose-1,5-bisphosphate carboxylase\oxyger
KSU019BF-201235-1	e-166	Wheat mRNA for Rubisco subunit binding-protein alpha su	2.0e-43 RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECUR
KSU024BE-500008-1	1.0e-07	Arabidopsis thaliana genomic DNA, chromosome 5, BAC cl	2.0e-71 (AP002829) N-glyceraldehyde-2-phosphotransferase-like [
KSU024BF-484829-1	1.0e-06	Arabidopsis thaliana ZW18 mRNA, partial cds	1.0e-50 (AB025640) ZW18-like protein [Arabidopsis thaliana]
KSU027BE-517877-5	7.0e-98	Zea mays ribosomal protein S6 RPS6-1 (rps6-1) mRNA, con	3.0e-53 (AJ277533) S6 ribosomal protein [Asparagus officinalis]
KSU035BE-496951-1,6,7,9	0	Triticum aestivum rbcS gene for ribulose-1,5-bisphosphat	7.0e-82 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small cha
KSU038BE-442681-5	0.026	Arabidopsis thaliana chromosome II section 127 of 255 of	5.0e-54 (AJ011892) cyclin D2.1 protein [Nicotiana tabacum]
NDS001BE-442903-1	0.38	Human chromosome 14 DNA sequence BAC R-817G13 of lil	4.0e-09 (AB008727) gene_id:MXC9.20~unknown protein [Arabidops
NDS018BE-426229-1,4	2.0e-09	Zea mays O-methyltransferase (OMT) gene, complete cds	9.0e-63 (AF033540) caffeic acid O-methyltransferase\ LPOMT3 [LoI
NDS034BE-470848-2	0	Triticum aestivum mRNA for triosephosphat-isomerase (t	3.0e-90 (AJ278243) triosephosphat-isomerase [Triticum aestivum
NDS034BE-637473-4	e-115	Triticum aestivum secretory protein (WAS-2) mRNA, comp	1.0e-42 (AF079526) secretory protein [Triticum aestivum]
NDS043BF-293115-6	0.062	Homo sapiens chromosome 10 clone CIT987SK-1144G6 ma	4.0e-16 (AB017063) gene_id:K3K7.22~pir||T31651~similar to unknow
NDS043BG-274878-6	0.34	Oryza sativa genomic DNA, chromosome 1, PAC clone:P85	2.0e-83 (AC027034) unknown protein\ 9928-11896 [Arabidopsis tha
TTU047BE-444658-1	0.095	Deinococcus radiodurans R1 section 146 of 229 of the com	1.0e-33 (I88185) pyruvate dehydrogenase E1 alpha subunit [Arabic
UCD001BE-443449-2	0.92	Homo sapiens solute carrier family 2 (facilitated glucose t	6.0e-28 (AC007592) F12K11.6 [Arabidopsis thaliana]
UCD028BF-484320-1,2,3,5,6,8,9,11	0.76	Trichoplusia ni inhibitor of apoptosis protein (IAP1) mRNA,	5.0e-08 (AB011474) contains similarity to unknown protein~gb|AAF
UCD037BE-488719-3,4	4.0e-29	Cicer arietinum mRNA for glyoxalase I	1.0e-76 LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALI
UCD037BE606912-2,3	1.1	Human DNA sequence from clone RP5-1060K6 on chromos	1.0e-13 (X17382) trypsin inhibitor cme precursor [Hordeum vulgar
UMC001BE-444171-3	0.73	Oryza sativa genomic DNA, chromosome 1, clone:P0708G8	6.0e-73 (AP001539) Similar to Arabidopsis thaliana chromosome 4
UMC015BE-426229-2	2.0e-09	Zea mays O-methyltransferase (OMT) gene, complete cds	9.0e-63 (AF033540) caffeic acid O-methyltransferase\ LPOMT3 [LoI
UMC032BF-483595-6	2.0e-08	Triticum aestivum PST19 (Pst19), LRR19 (Lrr19), TAK19-1 (Tak19-1), and LRK19 (Lrk19) genes, complete cds	
UMN013BE-443737-4	e-109	Hordeum vulgare putative 32.7 kDa jasmonate-induced prc	8.0e-78 jacalin homolog - barley
UMN013BE-444541-1	3.0e-51	Arabidopsis thaliana arginase mRNA, complete cds	5.0e-99 ARGINASE PF00491, Score=419.6, E=3.7e-142 N=1)
UNL002BE-497251-3	0.1	Human DNA sequence from clone RP11-458H11 on chromosc	4.0e-13 (AY009938) Mla1 [Hordeum vulgare]
UNL002BE-499523-1	e-157	Triticum ventricosum Vrga1 (Vrga1) gene, complete cds	7.0e-79 (AF158634) Vrga1 [Aegilops ventricosa]
UNL002BF-484266-1	8.0e-05	Hordeum vulgare genomic sequence, clone BAC 88H14, is	2.0e-29 (AJ302292) MLA6 protein [Hordeum vulgare]
UNL036BE-590970-1,3	0.31	Homo sapiens BAC clone RP11-339F13 from 7, complete se	9.0e-41 (AB036735) allyl alcohol dehydrogenase [Nicotiana tabacur
UNL036BF-474028-1	0.1	Human DNA sequence from PAC 204E5 on chromosome 12	1.0e-22 tumor antigen SLP-8p [Homo sapiens]
UNL036BF-474397-1	0	T.aestivum ACCase mRNA, 3' CDS	9.0e-92 acetyl-CoA carboxylase (EC 6.4.1.2) - wheat (fragment)
UNL044BG-263366-3	5.0e-08	Hordeum vulgare glucan endo-1,3-beta-glucosidase isoen	4.0e-17 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, ACIDIC ISOFORM PR

2BS3-0.75-0.84

NDS021BE-500240-2	e-110	Porteresia coarctata translational initiation factor eIF1 mR	2.0e-40 PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PRO
NDS034BE-606438-4	5.0e-09	Arabidopsis thaliana CBL-interacting protein kinase 2 (CIP	3.0e-59 serine\threonine protein kinase-like protein - Arabidopsi
UCW016BE-518306-3	8.0e-36	Hordeum vulgare nicotianamine synthase 2 (nashor2) mRNA, complete cds	
UNL048BE-591555-1	1.0e-39	Brassica oleracea ATP-sulfurylase precursor (ASBo) gene	4.0e-57 sulfate adenylyltransferase (EC 2.7.7.4) ASBo precursor - v

2BS1-0.53-0.75

CNL001BE-426431-1	1.1	Homo sapiens chromosome 21 clone PAC 198E8, map 21q	7.0e-19 F-ACTIN CAPPING PROTEIN ALPHA SUBUNIT (CAPZ-ALPHA) t
CNL014BE-406474-4	2.0e-44	Rice mRNA for 40S subunit ribosomal protein, complete cc	7.0e-26 40S RIBOSOMAL PROTEIN S21
CNL031BF-428792-4	4.0e-04	Pisum sativum apyrase 2 (apy2) mRNA, complete cds	2.0e-58 (AF385783) apyrase 2 [Pisum sativum]
CSU046BE-443026-3	1.0e-04	Arabidopsis thaliana DNA chromosome 3, BAC clone T27H	2.0e-44 hypothetical protein T4C21.320 - Arabidopsis thaliana
CSU059BG-262864-1	6.0e-05	Colletotrichum gloeosporioides f. sp. malvae pectate lyas	6.0e-39 (AB019228) receptor-like protein kinase [Arabidopsis thali
KSU001BE-406616-1	7.0e-19	Zea mays seven transmembrane protein Mlo4 mRNA, cor	1.0e-23 (AY029315) seven transmembrane protein Mlo4 [Zea mays
KSU001BE-442903-3	0.38	Human chromosome 14 DNA sequence BAC R-817G13 of lil	4.0e-09 (AB007727) gene_id:MXC9.20~unknown protein [Arabidops
KSU001BE-444297-2	0.17	Ensis minor (clone 1\6) nuclear protein mRNA, complete c	0.003 hypothetical protein T20B5.15 - Arabidopsis thaliana protei
KSU002BE-426431-1	1.1	Homo sapiens chromosome 21 clone PAC 198E8, map 21q	7.0e-19 F-ACTIN CAPPING PROTEIN ALPHA SUBUNIT (CAPZ-ALPHA) t
KSU012BE-406474-3	2.0e-44	Rice mRNA for 40S subunit ribosomal protein, complete cc	7.0e-26 40S RIBOSOMAL PROTEIN S21
KSU019BE-494262-1	4.0e-09	Arabidopsis thaliana DNA chromosome 4, contig fragment	3.0e-38 GTP-binding protein F23K16.150 - Arabidopsis thaliana
KSU019BE-518306-3	8.0e-36	Hordeum vulgare nicotianamine synthase 2 (nashor2) mRNA, complete cds	
KSU019BE-637878-6	7.0e-14	Oryza sativa chromosome 3 BAC OSJNBa0013M12 genomic	1.0e-08 (AP002070) Similar to Arabidopsis thaliana low temperatur
KSU024BE-499478-2,4	1.0e-16	Arabidopsis thaliana chromosome II section 185 of 255 of	4.0e-86 hypothetical protein T13L16.5 - Arabidopsis thaliana
KSU027BF-201733-3	e-165	H.vulgare mRNA for xyloglucan endotransglycosylase-like	2.0e-53 xyloglucan endo-1,4-beta-D-glucanase (EC 3.2.1.-) - barley
KSU030BE-590566-5	1.0e-09	Thuja plicata clone 1 pinoresinol-lariciresinol reductase m	8.0e-62 ISOFLAVONE REDUCTASE HOMOLOG lupine
KSU030BE-606438-3,4	5.0e-09	Arabidopsis thaliana CBL-interacting protein kinase 2 (CIP	3.0e-59 serine\threonine protein kinase-like protein - Arabidopsi
NDS034BE-470890-4,6	0	H.vulgare mRNA for lipid transfer protein 7a2b	2.0e-48 lipid transfer protein 7a2b - barley
NDS034BE-606438-3	5.0e-09	Arabidopsis thaliana CBL-interacting protein kinase 2 (CIP	3.0e-59 serine\threonine protein kinase-like protein - Arabidopsi
TTU025BE-406474-4	2.0e-44	Rice mRNA for 40S subunit ribosomal protein, complete cc	7.0e-26 40S RIBOSOMAL PROTEIN S21
TTU047BE-405597-1	7.0e-27	Arabidopsis thaliana DNA chromosome 4, contig fragment	1.0e-73 hypothetical protein T14P8.7 - Arabidopsis thaliana activite
TTU047BE-494209-1	0.42	Mesorhizobium loti, complete genome	7.0e-28 (AB023037) MNH3-like protein [Arabidopsis thaliana]
UCD017BE-888865-1	5.0e-06	Hordeum vulgare genomic DNA fragment; clone MWG0874	6.8 (AC084831) putative polyprotein [Oryza sativa]
UCD037BE-499194-3	0.2	Human DNA sequence from clone RP3-429O6 on chromosc	4.0e-06 DNA BINDING PROTEIN S1FA
UCW026BE-498730-1	5.0e-74	Oryza sativa 70 kDa chaperonin mRNA, complete cds	6.0e-41 probable chaperonin 10 - rice
UMC015BE-606357-10	1.0e-15	Sorghum bicolor BAC clone 25.M18, complete sequence	3.0e-52 (AF141471) hypothetical protein [Sorghum bicolor]
UMC040BF-474508-6	e-138	H.vulgare blt14.1 gene	1.0e-04 acclimation protein - rye
UMN013BE-443006-8,9	4.0e-07	Salmonella typhimurium strain 3027 cold shock protein C	3.0e-27 COLD SHOCK-LIKE PROTEIN CSPC (CSP-C)
UNL001BE-444297-2	0.17	Ensis minor (clone 1\6) nuclear protein mRNA, complete c	0.003 hypothetical protein T20B5.15 - Arabidopsis thaliana protei
UNL036BE-517987-2	0	Hordeum vulgare aleurone ribonuclease mRNA, partial cds	2.0e-93 aleurone ribonuclease (EC 3.1.--) - barley (fragment)
UNL044BG-314234-2	2.0e-33	Daucus carota mRNA for 191, partial cds	1.0e-94 embryogenic callus protein 191 - carrot (fragment)
UNL048BE-445628-1	0.3	Mus musculus AKR voltage-gated potassium-channel (KC	4.0e-13 (AB007727) contains similarity to unknown protein~gene_i
UNL053BG-274905-3	1	Canis familiaris TCTA gene, AMT gene, DAG1 gene and BS	4.0e-14 (U64925) NTGP4 [Nicotiana tabacum]

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

C-2BS1-0.53

CNL001BE-425962-3	0.026	Musa acuminata sucrose synthase mRNA, partial cds	1.0e-68 (AB017068) sucrose synthase [Arabidopsis thaliana]
CNL001BE-426158-5	6.0e-43	Oryza sativa putative tyrosine phosphatase mRNA, partial	4.0e-26 (AC005223) 55585 [Arabidopsis thaliana]
CSU001BE-425962-3	0.026	Musa acuminata sucrose synthase mRNA, partial cds	1.0e-68 (AB017068) sucrose synthase [Arabidopsis thaliana]
CSU046BE-444144-3	1.1	Arabidopsis thaliana DNA chromosome 3, BAC clone T15B	3.0e-22 (AC005278) F15K9.14 [Arabidopsis thaliana]
KSU002BE-425962-3	0.026	Musa acuminata sucrose synthase mRNA, partial cds	1.0e-68 (AB017068) sucrose synthase [Arabidopsis thaliana]
KSU002BE-426158-1,5	6.0e-43	Oryza sativa putative tyrosine phosphatase mRNA, partial	4.0e-26 (AC005223) 55585 [Arabidopsis thaliana]
KSU012BE-406808-1	7.0e-16	Oryza sativa reversibly glycosylated polypeptide mRNA, cc	3.0e-11 (Y18526) reversibly glycosylated polypeptide [Triticum aes
KSU012BE-442655-4	6.0e-06	Arabidopsis thaliana chromosome II section 205 of 255 of	1.0e-52 (AF221857) unknown [Euphorbia esula]
KSU012BE-442876-6	2.0e-49	Oryza sativa clone riceipp2 isopentenyl pyrophosphatedir	1.0e-75 isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) 1 - C
KSU019BE-443112-2	3.0e-75	O.sativa mRNA for calcium dependent protein kinase 2	2.0e-33 CALCIUM-DEPENDENT PROTEIN KINASE 2 (CDPK 2)
KSU024BE-498252-3	1.0e-68	H.vulgare (pMaW20) pseudo mRNA for beta-ketoacyl-ACP synthase (partial)	
KSU024BE-498388-4	e-154	Triticum aestivum beta-tubulin 1 (tub1) mRNA, complete	1.0e-67 tubulin beta-2 chain - garden pea (fragment)
KSU024BE-499648-3	7.0e-81	Rice mRNA for ferredoxin-NADP+ reductase, complete cds	8.0e-44 FERREDOXIN-NADP REDUCTASE, LEAF ISOZYME PRECURSOR
KSU027BE-517877-2	7.0e-98	Zea mays ribosomal protein S6 RPS6-1 (rps6-1) mRNA, con	3.0e-53 (AJ277533) S6 ribosomal protein [Asparagus officinalis]
KSU030BE-636802-1	5.0e-28	Arabidopsis thaliana glucose 6 phosphate\phosphate tran	1.0e-44 probable glucose-6-phosphate\phosphate-translocator pr
KSU035BE-403404-3	9.0e-22	Catharanthus roseus PAPS-reductase-like protein (par2ne	8.0e-42 (U63784) PAPS-reductase-like protein [Catharanthus rosee
KSU035BE-404630-1	3.0e-50	Oryza sativa thioredoxin h mRNA, complete cds	4.0e-45 THIOREDOXIN H-TYPE (TOX-H) (PHLOEM SAP 13 KDA PROTEIN
KSU035BE-406923-4,6	2.0e-11	Amaranthus hypochondriacus C4 photosynthetic NAD-dep	2.0e-57 NAD-DEPENDENT MALIC ENZYME 65 KDA ISOFORM, MITOCHO
KSU035BE-406943-3	5.0e-45	Oryza sativa mRNA for elongation factor 1B gamma, compl	8.0e-35 ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA) (EEF-1B GAI
KSU035BE-496863-2	e-165	H.vulgare mRNA for sucrose synthase	3.0e-63 (AJ001117) sucrose synthase type I [Triticum aestivum]
KSU035BE-496900-3	0	Triticum aestivum heat shock protein HSP26 (hsp26.6) mR	1.0e-32 (AF097659) heat shock protein HSP26 [Triticum aestivum]
KSU035BE-497171-2	1.4	Homo sapiens guanosine monophosphate reductase (GM	6.0e-75 (AF227619) Tic20-like protein [Euphorbia esula]
KSU035BE-497590-2	2.0e-37	Zea mays translation initiation factor 5A (TIF5A) mRNA, cor	5.0e-19 INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
KSU038BE-446243-2	e-110	Rice mRNA for ribosomal protein L41 (340 gene), partial se	3.0e-40 60S RIBOSOMAL PROTEIN L44
NDS021BE-500725-2	7.0e-13	Picea mariana probable 60s ribosomal protein L13a (Sb16)	3.0e-26 60S RIBOSOMAL PROTEIN L13A
NDS034BE-403166-3,4	8.0e-08	Nicotiana plumbaginifolia partial mRNA for RNA Binding Pro	2.0e-53 (AC084319) putative RNA binding protein [Oryza sativa]
NDS043BF-293115-1,4	0.062	Homo sapiens chromosome 10 clone CIT987SK-1144G6 ma	4.0e-16 (AB017063) gene_id:K3K7.22~pir||T31651~similar to unknow
NDS043BG-274844-2	5.0e-22	T.aestivum (clone pTAU2.3) U2 snRNA	2 purple acid phosphatase-like protein - Arabidopsis thalian
NDS043BG-274878-7	0.34	Oryza sativa genomic DNA, chromosome 1, PAC clone:P85	2.0e-83 (AC027034) unknown protein\ 9928-11896 [Arabidopsis tha
NDS043BG-274976-2	6.0e-18	Arabidopsis thaliana WRKY DNA-binding protein 4 (WRKY4)	8.0e-45 DNA-binding protein WRKY2 - parsley (fragment)
UCD001BE-443747-1	1.5	Sorghum bicolor ADP-glucose pyrophosphorylase subunit	5.0e-25 (AB025632) dihydroflavonol 4-reductase-like [Arabidopsis t
UCD037BE-443010-8	3.0e-82	Oryza sativa mRNA for adenylate kinase-a, complete cds	1.0e-53 ADENYLATE KINASE A (ATP-AMP TRANSPHOSPHORYLASE)
UCD037BF-473259-5,6	0.26	Human DNA sequence from clone RP11-53J8B on chromosc	2.0e-24 (AB013390) contains similarity to NADH dehydrogenase chi
UCW001BE-444378-1,4	6.0e-09	Arabidopsis thaliana genomic DNA, chromosome 3, TAC cl	1.0e-53 hypothetical protein T24A18.30 - Arabidopsis thaliana
UCW020BE-404332-1	0	Hordeum vulgare ribosomal protein S12 (rps12) mRNA, co	4.0e-65 40S RIBOSOMAL PROTEIN S12
UCW026BG-263377-3,4	0.12	Mus musculus RIKEN cDNA 0710008H11 gene (0710008H11R	2.9 glycine-rich protein - carrot (fragment)
UCW039BE-496162-3	9.0e-08	Arabidopsis thaliana mRNA for nitrilase associated protei	8.0e-13 (AC013427) Contains similarity to PIR7A protein from Oryz
UMC015BE-444378-1	6.0e-09	Arabidopsis thaliana genomic DNA, chromosome 3, TAC cl	1.0e-53 hypothetical protein T24A18.30 - Arabidopsis thaliana
UMN013BE-443771-1	6.0e-87	T.aestivum histone H2A gene	3.7 (AF147227) ASAPETALA1 [Madia nutans]
UNL002BE-401939-2	4.0e-29	Panax ginseng mRNA for 60S ribosomal protein L27a, com	5.0e-53 (AF088913) ribosomal protein L27a [Petunia x hybrida]
UNL002BE-591764-1,2	0.29	Human DNA sequence from clone 659F15 on chromosome	4.0e-18 NADPH HC toxin reductase hm1 - maize
UNL002BF-483292-1	1.0e-09	Triticum aestivum NBS-LRR type protein pseudogene, con	2.0e-42 (AF325198) LRR14 [Triticum aestivum]
UNL036BE-518419-4	2.0e-05	Arabidopsis thaliana mRNA for nitrilase associated protei	9.0e-13 (AC013427) Contains similarity to PIR7A protein from Oryz
UNL044BG-263521-4	e-104	Oryza sativa mitogen activated protein kinase kinase (MEK	6.0e-87 probable mitogen activated protein kinase - rice

C-2BL2-0.36

CSU046BE-442981-1	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
CSU058BG-262381-4	1.0e-06	Arabidopsis thaliana chromosome 1 BAC F23O10 genomic	6.0e-56 (AC009755) putative protein kinase [Arabidopsis thaliana]
KSU001BE-442884-1	0.057	Camptotheca acuminata isopentenyl diphosphate isomer	0.98 (AB008267) gene_id:MMG4.18~unknown protein [Arabidop
KSU001BE-442924-5	0.007	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K6M13	
KSU001BE-443755-17	0.007	Dictyostelium discoideum nucleoside diphosphate kinase	6 (AF202730) Niemann-Pick type C1 disease protein [Oryctola
KSU002BE-426715-2	0.1	Homo sapiens BAC clone RP11-493I5 from 2, complete seq	2.2 transcription initiation factor IID-associated protein, 80K - f
KSU012BE-442608-4	e-126	Oryza sativa casein kinase mRNA, partial cds	4.0e-71 (Y11526) casein kinase II alpha subunit [Zea mays]
KSU019BE-498620-2,3	0	Hordeum vulgare mRNA for MADS-box protein 8 (m8 gene	7.0e-75 (AJ249146) MADS-box protein 8 [Hordeum vulgare]
KSU024BE-606324-4	5.0e-34	Oryza sativa microsatellite MRG6585 containing (TCTT)X6,	8.0e-23 (AC013483) unknown protein [Arabidopsis thaliana]
KSU027BE-495560-2	7.0e-33	Oryza sativa chromosome 3 BAC OSJNBa0026A15 genomic	3.0e-59 (AC084404) unknown protein [Oryza sativa]
KSU027BE-517627-2	2.0e-95	Oryza sativa mRNA for translation initiation factor eIF-5A	4.0e-78 (AF094773) translation initiation factor 5A [Oryza sativa]
KSU030BF-474781-1	7.0e-77	Sorghum bicolor 22 kDa kafirin cluster	4.0e-88 (AF061282) patatin-like protein [Sorghum bicolor]
KSU038BE-443711-3	1.4	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	3.0e-23 (AP002543) glycolate oxidase subunit D-like; D-lactate deh
KSU038BE-444638-2,4	0.34	Human DNA sequence from clone RP11-300B2 on chromos	3.0e-23 POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE 2
UCD001BE-406625-6,7	1.9	Homo sapiens epididymis-specific, whey-acidic protein ty	2.0e-04 (AP001168) Similar to gene for Pib (AB013448) [Oryza sativa
UCD017BE-488220-1	9.0e-08	Arabidopsis thaliana BAC F5O24	2.0e-16 (AE003512) CG14199 gene product [Drosophila melanogast
UCD029BE-497623-3	0.2	Nicotiana tabacum centrin (CEN2) mRNA, complete cds	2.4 (Y13797) phytochrome [Platycerium angolense]
UCD037BE-498599-3	1.0e-31	Rice mRNA stearyl-ACP desaturase, complete cds	5.0e-54 ACYL [ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (
UCW039BE-495991-2	0	Hordeum vulgare chloroplast photosystem I PSK-I subunit	3.0e-59 PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (
UMN013BE-442655-4	6.0e-06	Arabidopsis thaliana chromosome II section 205 of 255 of	1.0e-52 (AF221857) unknown [Euphorbia esula]
UMN013BE-444081-3	0.006	Oryza sativa genomic DNA, chromosome 1, BAC clone:OSJNBa0010K01	
UNL002BE-446789-1	1.0e-06	Arabidopsis thaliana chromosome II section 131 of 255 of	6.0e-32 (AC004401) unknown protein [Arabidopsis thaliana]
UNL002BF-201372-1	1.0e-06	Arabidopsis thaliana chromosome II section 131 of 255 of	4.0e-32 (AC004401) unknown protein [Arabidopsis thaliana]

2BL2-0.36-0.50

CNL001BE-425566-1	1.0e-47	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	9.0e-70 (AP002843) putative UTP-glucose glucosyltransferase [Ory
CNL014BE-604170-4	0	Triticum aestivum heat shock protein 70 (HSP70) mRNA, H	4.0e-38 (AF074969) heat shock protein 70 [Triticum aestivum]
CNL023BE-538034-4	3.0e-99	Zea mays chlorophyll a/b-binding apoprotein CP24 (Lhcb6	4.0e-54 CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
CNL023BG-263263-5	2.0e-17	Arabidopsis thaliana UVB-resistance protein UVR8 (UVR8)	1.0e-75 UVB-resistance protein UVR8 [imported] - Arabidopsis tha
CSU001BE-425566-1	1.0e-47	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	9.0e-70 (AP002843) putative UTP-glucose glucosyltransferase [Ory
CSU046BE-442794-4	0.083	Arabidopsis thaliana chromosome 1 BAC F28P5 genomic s	2.0e-20 (AC069273) unknown protein [Arabidopsis thaliana]
CSU046BE-445250-3	5.0e-31	Homo sapiens BAC clone RP11-95A10 from 7, complete se	3.0e-27 (AC007211) unknown protein [Arabidopsis thaliana]
KSU002BE-405234-5	2.0e-67	Oryza sativa COX6b2 mRNA for cytochrome c oxidase subu	2.0e-35 (AB047923) cytochrome c oxidase subunit 6b [Oryza sativa]
KSU002BE-425566-2	1.0e-47	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	9.0e-70 (AP002843) putative UTP-glucose glucosyltransferase [Ory
KSU012BE-403167-3	4.0e-32	Arabidopsis thaliana fumarase (FUM1) mRNA, complete cd	1.0e-73 fumarate hydratase (EC 4.2.1.2) - Arabidopsis thaliana
KSU012BE-403506-2	1.2	Homo sapiens clone RP11-159N20, complete sequence	5.0e-16 (AB010075) 2-oxoglutarate dehydrogenase, E1 component
KSU012BE-403516-2,3	3.0e-62	Zea mays ribosomal protein L25 mRNA, partial cds	3.0e-42 (AL342115) putative 60s Ribosomal protein L25 [Oryza sativ
KSU012BE-403597-3	0	Sporobolus stapfianus small GTP binding protein Rab2 mR	e-106 RAS-RELATED PROTEIN RAB-2-B
KSU012BE-443423-5	1.0e-19	Oryza sativa chromosome 3 BAC OSJNBa0091J19 genomic	4.2 (AL117195) Y57A10A.1 [Caenorhabditis elegans]
KSU019BE-445233-2	1.0e-13	Oryza sativa chromosome 10 BAC OSJNBa0055P24 genomi	0.006 (AC037425) hypothetical protein [Oryza sativa]
KSU019BE-494381-7	2.0e-95	Oryza sativa genomic DNA, chromosome 4, BAC clone: B86	1.0e-67 (AF236369) prohibitin [Zea mays]
KSU024BE-606502-7	0.11	Human DNA sequence from clone RP1-138E4 on chromoso	0.83 pleckstrin homology domain-containing, family A (phosph
KSU027BE-426364-3,5	7.0e-43	Maize pseudo-Gpa1 pseudogene for glyceraldehyde-3-ph	1.0e-85 (AB024023) contains similarity to serine protease~gene_id
KSU030BE-493826-3	0.025	Mus musculus adult male testis cDNA, RIKEN full-length er	2.0e-05 hypothetical protein T24P15.17 - Arabidopsis thaliana
KSU030BF-482280-2	0	A.fatua mRNA for tetraubiquitin - tomato	e-101 polyubiquitin - tomato
KSU030BG-263384-3	1.2	Thielavia heterothallica cellobiose dehydrogenase (cdh) m	4.0e-08 (AC007357) F3F19.15 [Arabidopsis thaliana]
KSU035BE-404384-1,6	0.02	Arabidopsis thaliana chromosome II section 234 of 255 of	2.0e-51 (AC004450) putative carboxyphosphoenolpyruvate muta
KSU035BE-404740-8,10	0.024	Homo sapiens chromosome 5, BAC clone 45m2 (LBNL H14	6.0e-61 (AB016893) 26S proteasome p55 protein-like [Arabidopsis
KSU035BE-405790-2	0.094	Caulobacter crescentus section 248 of 359 of the complet	6.0e-47 (AB026651) aluminum-induced protein-like [Arabidopsis th
KSU038BE-443191-7	e-115	Triticum aestivum 70 kDa heat shock protein (TaHSP70d) m	2.0e-62 dnaK-type molecular chaperone hsp70 - rice (fragment)
NDS018BE-404886-2	1.0e-10	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	5.0e-68 DNA-binding protein GT-1a - common tobacco
NDS043BF-292219-2	e-161	T.aestivum dihydrodipicolinate synthase (DHDPS) mRNA, c	5.0e-39 DIHYDRODIPICOLINATE SYNTHASE 2 PRECURSOR (DHDPS) [wa
NDS043BF-292245-2	0.37	Human DNA sequence from clone RP3-522J7 on chromoso	9.0e-31 (AP001305) gene_id:MHC9.8~unknown protein [Arabidopsi
UCD001BE-405197-6	1.0e-31	Zea mays ZmHP2 mRNA for histidine-containing phosphot	3.0e-27 (AB024292) histidine-containing phosphotransfer protein [
UCD001BE-405234-6	2.0e-67	Oryza sativa COX6b2 mRNA for cytochrome c oxidase subu	2.0e-35 (AB047923) cytochrome c oxidase subunit 6b [Oryza sativa
UCD001BE-406589-3	0.39	Homo sapiens chromosome 5 clone CTD-2071H17, comple	2.0e-10 (AC007519) Contains 3 PF gb|T29424 comes from this gene
UCD001BE-443773-5	0.081	Danio rerio alternatively spliced brn-1.1 protein variant (bri	7.0e-54 (AC006921) unknown protein [Arabidopsis thaliana]
UCD001BE-444339-2	1.4	Drosophila melanogaster genomic scaffold 142000013386O	3.5 (AF264760) cAMP-dependent protein kinase [Neurospora c
UCD028BF-201830-4,6	8.0e-79	Oryza sativa elicitor-responsive gene-3 (ERG3) mRNA, com	2.0e-52 elicitor-responsive gene 3 [imported] - rice
UCD029BE-404371-2,6	5.0e-51	Asparagus officinalis mRNA for NADH glutamate dehydrog	5.0e-51 (AJ011006) NADH glutamate dehydrogenase [Asparagus of
UCD029BG-314395-3	1.0e-04	Arabidopsis thaliana mRNA for AKIH gamma	2.0e-22 hypothetical protein T8P19.40 - Arabidopsis thaliana
UCD037