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

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

*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.

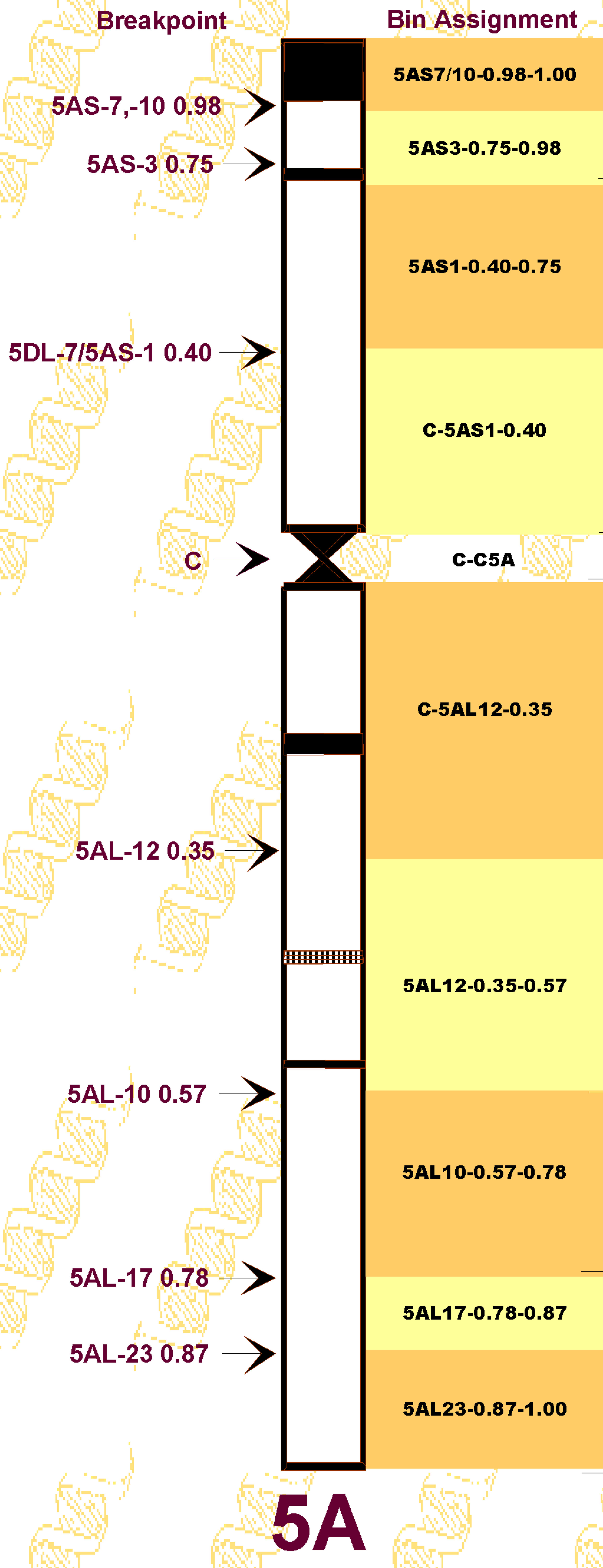
How to Interpret This Image:

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



5AS7/10-0.98-1.00

TTU047BE405630-2	*8.0e-15*	Arabidopsis thaliana chromosome II section 10 of 255 of th	*5.0e-85*	hypothetical protein T8K22.14 - Arabidopsis thaliana
UCD001BE405224-6	*0.44*	Human chromosome 14 DNA sequence BAC R-757K12 of lib	*2.0e-16*	(AC009465) unknown protein\; 32997-32284 [Arabidopsis th
UCW026BE636954-1	*e-144*	Oryza sativa plasma membrane proton-ATPase gene OSA	*2.0e-94*	(D10207) H-ATPase [Oryza sativa]
UCW026BE636954-2	*e-144*	Oryza sativa plasma membrane proton-ATPase gene OSA	*2.0e-94*	(D10207) H-ATPase [Oryza sativa]
UMC001BE399975-8	*3.0e-27*	Barley ubiquitin (mub2) gene, complete cds	*0.57*	40S RIBOSOMAL PROTEIN S27A

5AS3-0.75-0.98

CSU001BE399994-6	*0.16*	Smilax rotundifolia phytochrome C (PHYC) gene, partial cds		
KSU001BE399088-3	*2.0e-08*	Arabidopsis thaliana DNA chromosome 5, BAC clone T20K	*1.0e-61*	(AC008261) unknown protein [Arabidopsis thaliana]
KSU001BE443751-2	*0.087*	Cicer arietinum nodulin-35 gene	*5.0e-05*	(AF145657) BcDNA.GH10120 [Drosophila melanogaster]
KSU012BE490728-3	*0*	Hordeum vulgare methyljasmonate-inducible lipoxygenas	*3.0e-94*	lipoxygenase (EC 1.13.11.12) 2 - barley
KSU027BE404894-2	*4.0e-19*	Glycine max plasma membrane Ca2+-ATPase (SCA2) mRN	*9.0e-75*	(AF195029) plasma membrane Ca2+-ATPase [Glycine max]
KSU035BE403373-2	*0*	Triticum aestivum oxalate oxidase mRNA, partial cds	*1.0e-72*	(AF005084) oxalate oxidase [Triticum aestivum]
KSU035BE403471-2	*5.0e-15*	Oryza sativa microsatellite MRG2437 containing (CT)X18, g	*6.0e-57*	(AF370443) Ran binding protein-1 [Lycopersicon esculentu
KSU035BE404480-4	*2.0e-37*	Oryza sativa subsp. japonica clone C63266_1A putative glut	*7.0e-68*	(AP002914) putative glutathione S-transferase [Oryza sativ
KSU035BE406937-5	*1.2*	S.pombe chromosome II cosmid c3B8	*3.0e-22*	(AF096247) ethylene-responsive elongation factor EF-Ts pr
KSU035BE496903-1,5	*2.0e-05*	Arabidopsis thaliana At1g09340 (At1g09340\T31J12_6) mRN	*2.0e-47*	(Y15382) putative RNA binding protein [Arabidopsis thalian
KSU038BE444720-3	*5.0e-19*	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	*1.0e-62*	(AF123508) Nt-iaa28 deduced protein [Nicotiana tabacum]
NDS001BE443751-4	*0.087*	Cicer arietinum nodulin-35 gene	*5.0e-05*	(AF145657) BcDNA.GH10120 [Drosophila melanogaster]
NDS021BE591003-2,3	*0.002*	Glycine max seed maturation protein PM23 (PM23) mRNA,	*2.0e-42*	(AF116752) seed maturation protein PM23 [Glycine max]
TTU025BE490728-1	*0*	Hordeum vulgare methyljasmonate-inducible lipoxygenas	*3.0e-94*	lipoxygenase (EC 1.13.11.12) 2 - barley
UCD001BE443751-2	*0.087*	Cicer arietinum nodulin-35 gene	*5.0e-05*	(AF145657) BcDNA.GH10120 [Drosophila melanogaster]
UCD028BE404135-3,6	*7.0e-46*	Zea mays glutathione S-transferase GST 8 mRNA, complet	*6.0e-82*	(AP002914) putative glutathione S-transferase [Oryza sativ
UCD028BF484536-7	*1.1*	Methylococcus capsulatus putative nonaheme c-cytochro	*0.43*	(AF277399) cat eye syndrome critical region 6 [Mus muscu
UCD029BE497470-2	*0.017*	Oryza sativa chromosome 10 BAC OSJNBa0006L06 genomi	*2.0e-15*	(AB024029) gene_id:K21L19.11~ref|NP_036243.1~similar to u
UCD037BE499835-2	*3.0e-26*	Lycopersicon esculentum mRNA for beta-alanine synthas	*1.0e-79*	(Y19104) beta-alanine synthase [Lycopersicon esculentum
UCD037BF473571-4	*0*	Oryza sativa enolase mRNA, complete cds	*3.0e-98*	ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2) (2-PHO
UCW001BE399088-2	*2.0e-08*	Arabidopsis thaliana DNA chromosome 5, BAC clone T20K	*1.0e-61*	(AC008261) unknown protein [Arabidopsis thaliana]
UCW002BE399993-2	*9.0e-74*	T.aestivum GSP-1b mRNA for grain softness protein	*1.0e-06*	grain softness protein 1b, 15K - wheat
UMC032BF483595-4	*2.0e-08*	Triticum aestivum PST19 (Pst19), LRR19 (Lrr19), TAK19-1 (Tak19-1), and LRK19 (Lrk19) genes, complete cds		
UMC040BE637485-2	*0*	Ha=GSP-1a [Triticum=wheat, cv. Timgalen, endosperm, mR	*5.0e-70*	grain softness protein 1a, 15K (clone TSF69) - wheat Timga
UMN013BE444854-4,5	*0*	Triticum aestivum sucrose-6F-phosphate phosphohydrola	*2.0e-99*	(AF321556) sucrose-6F-phosphate phosphohydrolase SPP
UNL036BF201102-1	*2.0e-23*	C.roseus MetE mRNA for methionine synthase	*8.0e-43*	(Z49150) cobalamine-independent methionine synthase [S

5AS1-0.40-0.75

CNL001BE406368-3,4	*0.9*	Pseudomonas aeruginosa PA01, section 33 of 529 of the complete genome		
CSU001BE403221-3	*3.0e-32*	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	*7.0e-69*	hypothetical protein F4I1.8 - Arabidopsis thaliana
CSU046BE444377-2	*0.3*	Pyrococcus abyssi complete genome\; segment 5\6	*2.0e-25*	(AC004557) F17L21.12 [Arabidopsis thaliana]
KSU001BE406368-3,4	*0.9*	Pseudomonas aeruginosa PA01, section 33 of 529 of the complete genome		
KSU001BE443755-11	*0.007*	Dictyostelium discoideum nucleoside diphosphate kinase	*6*	(AF202730) Niemann-Pick type C1 disease protein [Oryctola
KSU001BE443968-2	*5.9*	Caenorhabditis elegans cosmid Y81G3A, complete sequen	*5.0e-14*	(AB025613) receptor protein kinase-like [Arabidopsis thali
KSU019BE443334-1	*0*	Barley acyl carrier protein I (ACP I) mRNA, complete cds	*1.0e-72*	ACYL CARRIER PROTEIN I PRECURSOR (ACP I)
KSU024BE498878-3,5	*3.0e-08*	Musa acuminata mRNA for unknown ripening-related prot	*2.0e-08*	(AB007644) contains similarity to enolase-phosphatase~ge
KSU024BE500291-2,3	*1.0e-31*	Z.mays (Black Mexican Sweet) mRNA for 1-acyl-glycerol-3-	*8.0e-60*	probable 1-acyl-glycerol-3-phosphate acyltransferase - ma
TTU047BE444644-1	*0.023*	Homo sapiens PAC clone RP5-1132H15 from 7, complete se	*4.0e-26*	(AB007727) gene_id:MXC9.13~pir||T09909~similar to unknov
UCD028BF146193-7	*0.005*	Rhodobacter sphaeroides strain 2.4.1T quinol oxidase sub	*5.0e-42*	hypothetical protein F9D16.100 - Arabidopsis thaliana
UCD037BE444434-4,6	*0.39*	Arabidopsis thaliana unknown protein (T11H3_70\AT5g250	*2.0e-08*	pectate lyase-like protein - Arabidopsis thaliana
UCW026BE636795-1	*6.0e-64*	Oryza sativa small zinc finger-like protein (TIM9) mRNA, co	*2.0e-43*	MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE

C-5AS3-0.75

CSU001BE406368-2,3	*0.9*	Pseudomonas aeruginosa PA01, section 33 of 529 of the complete genome		

C-5AS1-0.40

KSU002BE403518-2	*1.0e-65*	Oryza sativa Ca2+ sensitive 3'(2'),5-diphosphonucleoside 3	*2.0e-70*	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHO
KSU012BE352603-3	*1.0e-43*	Arabidopsis thaliana calcineurin B-like protein 3 (CBL3) mR	*1.0e-77*	calcineurin B-like protein 3 T15N24.20 [imported] - Arabido
KSU012BE403761-1	*1.0e-72*	Hordeum vulgare mRNA for alpha-keto acid dehydrogenas	*e-102*	(AL391712) branched-chain alpha keto-acid dehydrogenase
KSU030BF485004-4	*1.0e-18*	Lycopersicon esculentum transaldolase (TAL) mRNA, com	*4.0e-34*	transaldolase-like protein - Arabidopsis thaliana
KSU035BE497510-6	*e-139*	Avena sativa vacuolar H+-ATPase 16 kDa proteolipid subun	*3.0e-42*	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT oat
UCD001BE403518-2	*1.0e-65*	Oryza sativa Ca2+ sensitive 3'(2'),5-diphosphonucleoside 3	*2.0e-70*	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHO
UCD001BE443755-13	*0.007*	Dictyostelium discoideum nucleoside diphosphate kinase	*6*	(AF202730) Niemann-Pick type C1 disease protein [Oryctola
UCD017BE488825-6	*e-101*	Oryza sativa aldolase mRNA, complete cds	*3.0e-56*	fructose-bisphosphate aldolase (EC 4.1.2.13) - rice
UCW016BE517956-4	*4.0e-16*	Oryza sativa hypothetical protein mRNA, partial cds	*8.0e-62*	(AB013395) trehalose-6-phosphate phosphatase [Arabidop
UNL036BF200703-4	*7.0e-04*	Streptomyces sp. QM-B814 (ATCC 11238) bgl3 gene for bet	*2.0e-21*	(X94986) beta glucosidase [Manihot esculenta]
UNL048BE446646-2	*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-5AL12-0.35

CNL014BE445436-2	*e-174*	Triticum aestivum poly(A)-binding protein (wheatpab) mR	*7.0e-40*	polyadenylate-binding protein - wheat
CNL031BE403624-6,7	*0*	Hordeum vulgare germin F (GerF) gene, complete cds	*e-118*	(AF250935) germin F [Hordeum vulgare]
KSU012BE403556-6	*6.0e-15*	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	*5.0e-24*	(AB006700) contains similarity to RAV2-like DNA-binding pr
KSU012BE442892-3	*6.0e-12*	M.sativa mRNA for annexin-like protein	*1.0e-08*	(Y11348) annexin-like protein [Medicago sativa]
KSU024BE405060-5	*3.0e-85*	Oryza sativa protein kinase mRNA, complete cds	*1.0e-58*	protein kinase homolog - rice
KSU035BE403618-4,5	*e-178*	Oryza sativa mRNA for adenylate kinase-a, complete cds	*6.0e-90*	(AB041773) adenylate kinase [Oryza sativa]
KSU035BE406996-3	*8.0e-11*	Rice mRNA, sequence homologous to ADP-ribosylation fac	*6.0e-12*	ADP-RIBOSYLATION FACTOR 1
KSU038BE445803-1	*6.0e-40*	Oryza sativa mRNA for NADH dependent Glutamate Synthas	*2.0e-28*	(AB008845) NADH dependent Glutamate Synthase [Oryza sa
UCD017BE495133-2	*1.0e-16*	Dunaliella salina partial mRNA for heat shock protein (hsp7	*8.0e-63*	(AF217459) heat shock protein 70 [Arabidopsis thaliana]
UCD028BE426080-2	*e-132*	Zea mays cultivar TX-5855 acetoacetyl CoA thiolase mRNA,	*2.0e-81*	(AF113522) acetoacetyl CoA thiolase [Zea mays]
UCD028BE605231-1	*e-100*	Zea mays pyruvate dehydrogenase E1 beta subunit isofor	*5.0e-59*	(AF069910) pyruvate dehydrogenase E1 beta subunit isofor
UCD028BF201976-1,2	*0.068*	Homo sapiens similar to solute carrier family 16 (monocarboxylic acid transporters), member 3 (H. sapiens) (LOC65816), mRN		
UCD028BG263656-3,9	*0.019*	Chlamydomonas reinhardtii apospory-associated protein	*3.0e-38*	(AB013389) apospory-associated protein C-like [Arabidops
UCD029BE490552-1,4	*0*	Triticum aestivum cultivar Mironovska 808 cold-responsiv	*2.0e-60*	(AF207545) cold-responsive protein COR14a [Triticum aest
UCD029BE497368-2,4	*8.0e-07*	Arabidopsis thaliana putative PHD finger transcription fact	*1.0e-49*	receptor like protein - Arabidopsis thaliana (fragment)
UCD029BE497820-1	*1.0e-07*	A.thaliana mRNA for chloroplast thylakoidal processing pe	*9.0e-71*	(U93215) putative signal peptidase I [Arabidopsis thaliana]
UCD029BF293395-2	*2.0e-70*	Vicia faba vfPP2Ac-3 mRNA for type 2A protein phosphatas	*1.0e-92*	SERINE\THREONINE PROTEIN PHOSPHATASE PP2A-2 CATALY
UCD029BF483378-2	*e-110*	Oryza sativa OsPAG1 mRNA for alpha 7 subunit of 20S prot	*3.0e-87*	PROTEASOME SUBUNIT ALPHA TYPE 3 (20S PROTEASOME AL
UCD037BE443280-3	*2.0e-36*	Arabidopsis thaliana DNA chromosome 3, BAC clone T14D	*7.0e-35*	(AB023032) ubiquitin-like protein [Arabidopsis thaliana]
UCD037BE488542-4	*0.38*	Mesorhizobium loti, complete genome	*1.0e-23*	(AC011437) ankyrin-like protein [Arabidopsis thaliana]
UCD037BE489028-1	*4.0e-23*	Rice mRNA, partial homologous to ribosomal protein S19 g	*3.0e-07*	40S RIBOSOMAL PROTEIN S19
UCD037BE498147-3	*0.1*	Gallus gallus GIRK1 mRNA, complete cds	*2.0e-29*	(AJ251087) ABI3-interacting protein 2, AIP2 [Arabidopsis th
UCD037BE499592-1	*0.079*	Mouse LLRep3 protein pseudogene from a repetitive eler	*4.0e-37*	(AC069472) serine carboxypeptidase, putative\; 23596-2121
UCW020BE404341-3	*e-115*	Zea mays phytochelatin synthetase-like protein (CISEZmG	*e-102*	(AF160475) phytochelatin synthetase-like protein [Zea may
UMC040BE590865-2	*0.022*	Homo sapiens mRNA for KIAA1320 protein, partial cds	*1.0e-81*	(AF127565) ubiquitin-protein ligase 2 [Arabidopsis thaliana
UMC040BF474342-3	*0.41*	Arabidopsis thaliana eIF3e mRNA, complete cds	*1.0e-85*	(AF285832) eukaryotic initiation factor 3E subunit [Arabidop
UNL002BE493050-3	*0.091*	Hordeum vulgare homeodomain protein JUBEL2 (JuBel2) g	*2.0e-20*	(AB020745) gene_id:MJE7.2~pir||C71412~similar to unknow
UNL002BF473933-2	*0.44*	Rat cytomegalovirus Maastricht, complete genome	*4.0e-47*	(Z99707) putative protein [Arabidopsis thaliana]

C-5AL10-0.57

CSU058BE496864-3	*4.0e-47*	O.sativa mRNA for chilling-inducible protein	*1.0e-62*	(AF133708) PP2A regulatory subunit [Arabidopsis thaliana]
UCD029BG314435-1	*8.0e-52*	Arabidopsis thaliana mRNA for arginine methyltransferase	*e-103*	protein-arginine N-methyltransferase (EC 2.1.1.23) - Arabid
UCW039BE446342-3	*1.6*	Homo sapiens chromosome 18, clone RP11-583B12, compl	*6.0e-43*	(AB008268) beta-ureidopropionase [Arabidopsis thaliana]
UMN013BE443423-2	*1.0e-19*	Oryza sativa chromosome 3 BAC OSJNBa0091J19 genomic	*4.2*	(AL117195) Y57A10A.1 [Caenorhabditis elegans]
UMN013BE443430-5,6	*2.0e-05*	Arabidopsis thaliana RNA polymerase II 13.6 kDa subunit (	*1.0e-47*	DNA-DIRECTED RNA POLYMERASE II 13.6 KDA POLYPEPTIDE

5AL12-0.35-0.57

CNL001BE406506-1	*1.2*	Drosophila melanogaster, chromosome 3R, region 97E-98	*0.004*	(AC002337) unknown protein [Arabidopsis thaliana]
CNL014BE423288-4,6	*0.006*	Oryza sativa genomic DNA, chromosome 6, BAC clone:OSJ	*1.0e-19*	(AP002069) Similar to Prunus armeniaca ethylene-forming-
CNL014BE604574-2	*4.0e-10*	Arabidopsis thaliana DNA chromosome 5, BAC clone F12B	*8.0e-61*	(AB013395) poly(A)-binding protein II-like [Arabidopsis thal
CNL023BE405358-3	*0.002*	Thermobifida fusca SbpA (sbpA) gene, partial cds\; BglA (	*2.0e-39*	(AJ005950) beta-glucosidase [Cicer arietinum]
CSU001BE406612-2	*2.0e-22*	Oryza sativa chromosome 5 clone P0574H01, complete seq	*2.0e-08*	cysteine proteinase (EC 3.4.22.-) F23E12.90 - Arabidopsis th
CSU001BE425296-1	*5.0e-52*	Triticum aestivum rbcS gene for ribulose-1,5-bisphosphat	*2.0e-10*	(AB042066) ribulose-1,5-bisphosphate carboxylase\oxygen
KSU001BE406494-1,2	*5.0e-51*	Hordeum vulgare partial mRNA for putative acid phosphata	*1.0e-40*	(AJ250282) putative acid phosphatase [Hordeum vulgare]
KSU001BE443692-5	*0.31*	Human DNA sequence from cosmid U56D2, between mark	*6.0e-19*	(AC016041) F27J15.15 [Arabidopsis thaliana]
KSU002BE403221-8	*3.0e-32*	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	*7.0e-69*	hypothetical protein F4I1.8 - Arabidopsis thaliana
KSU002BE406380-5	*0.23*	Homo sapiens 12 BAC RP11-173C20 (Roswell Park Cancer I	*2.9*	nidogen 2\; nidogen 2 (osteonidogen) [Homo sapiens]
KSU002BE406545-1	*1.0e-44*	Setaria italica actin mRNA, complete cds	*1.0e-27*	ACTIN 2
KSU002BE425207-1	*8.0e-08*	Nicotiana tabacum (clone: L24-2) chloroplast ribosomal pro	*3.0e-36*	(AB016879) 50S ribosomal protein L24, chloroplast precurs
KSU012BE352633-5,6	*3.0e-32*	Elaeis guineensis oleoyl-ACP thioesterase mRNA, partial c	*5.0e-91*	(AF213478) acyl-ACP thioesterase [Iris germanica]
KSU012BE404462-2	*0.33*	Drosophila melanogaster genomic scaffold 1420000133860	*3.0e-55*	(AB006704) contains similarity to unknown protein~gene_i
KSU012BE442600-3	*6.0e-12*	P.sativum PHSP1 mRNA for HSP70	*3.0e-70*	HEAT SHOCK 70 KD PROTEIN, MITOCHONDRIAL PRECURSOR
KSU012BE442676-3	*5.0e-19*	Vigna aconitifolia 5'-phosphoribosyl-4-(N-succinocarboxar	*3.0e-89*	PHOSPHORIBOSYLAMIDOIMIDAZOLE-SUCCINOCARBOXAMIDI
KSU012BE442918-2	*2.0e-05*	Cicer arietinum mRNA for NADPH oxidoreductase homolog	*4.0e-64*	(AB027757) NADPH oxidoreductase homolog [Cicer arietinu
KSU012BE443423-2	*1.0e-19*	Oryza sativa chromosome 3 BAC OSJNBa0091J19 genomic	*4.2*	(AL117195) Y57A10A.1 [Caenorhabditis elegans]
KSU012BE443430-6,7	*2.0e-05*	Arabidopsis thaliana RNA polymerase II 13.6 kDa subunit (	*1.0e-47*	DNA-DIRECTED RNA POLYMERASE II 13.6 KDA POLYPEPTIDE
KSU012BE443439-7	*1.0e-04*	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	*1.0e-70*	(AB010072) gb|AAC64874.1~gene_id:MEE6.19~strong similar
KSU019BE403649-4	*5.0e-25*	Chicken 78-kD glucose-regulated protein, complete cds	*9.0e-73*	HEAT SHOCK 70 KD PROTEIN, MITOCHONDRIAL PRECURSOR
KSU019BE494426-1	*7.0e-24*	P.ciliare (Higgins) apospory associated mRNA, 876bp	*2.0e-53*	(AF352797) ankyrin-repeat protein HBP1 [Nicotiana tabacum
KSU024BE495790-4	*0.004*	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K	*3.0e-40*	(AF120494) phosphoglucose isomerase precursor [Arabid
KSU024BE499599-3	*5.0e-13*	Vigna unguiculata phosphatidic acid phosphatase alpha m	*8.0e-88*	(AC007591) Contains similarity to gb acid phosphatase alp
KSU024BE499843-1,6	*e-122*	Zea mays variety B73 hypersensitive-induced response pr	*2.0e-81*	(AF236375) hypersensitive-induced response protein [Zea
KSU027BE403482-4	*2.0e-28*	Iris germanica acyl-ACP thioesterase (FatA) mRNA, comple	*5.0e-28*	(AF213478) acyl-ACP thioesterase [Iris germanica]
KSU030BE590997-2	*0*	Hordeum vulgare chlorophyll a\b-binding protein precurso	*e-110*	(AF287276) chlorophyll a\b-binding protein precursor [Hor
KSU035BE403679-1	*e-135*	Oryza sativa aldehyde dehydrogenase (ALDH) mRNA, comp	*1.0e-77*	(AF323586) aldehyde dehydrogenase [Oryza sativa]
KSU035BE403768-1	*5.0e-72*	Oryza sativa aminotransferase-like protein mRNA, comple	*7.0e-81*	(AF351125) gamma-aminobutyrate transaminase subunit p
KSU035BE404437-2	*6.0e-34*	Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, compl	*5.0e-70*	DNAJ PROTEIN HOMOLOG (DNAJ-1)
KSU035BE404454-3	*0.3*	Thermobifida fusca SbpA (sbpA) gene, partial cds\; BglA (	*3.0e-38*	(AJ005950) beta-glucosidase [Cicer arietinum]
TTU047BE494680-6	*9.0e-05*	Arabidopsis thaliana AT4g37830\T28I19_110 mRNA, comple	*2.0e-24*	hypothetical protein T28I19.110 - Arabidopsis thaliana
TTU047BE495277-1	*0.021*	Arabidopsis thaliana DNA chromosome 5, BAC clone T22P	*3.0e-50*	hypothetical protein T22P22.70 - Arabidopsis thaliana
UCD001BE352592-2	*0*	Hordeum vulgare arabinoxylan arabinofuranohydrolase is	*2.0e-91*	(AF320325) arabinoxylan arabinofuranohydrolase isoenzym
UCD001BE405224-8	*0.44*	Human chromosome 14 DNA sequence BAC R-757K12 of lib	*2.0e-16*	(AC009465) unknown protein\; 32997-32284 [Arabidopsis th
UCD001BE406324-2	*3.0e-15*	Zea mays seven transmembrane protein Mlo7 mRNA, com	*1.0e-06*	MLO PROTEIN HOMOLOG 1 (ATMLO-H1)
UCD001BE406380-4	*0.23*	Homo sapiens 12 BAC RP11-173C20 (Roswell Park Cancer I	*2.9*	nidogen 2\; nidogen 2 (osteonidogen) [Homo sapiens]
UCD001BE406506-2	*1.2*	Drosophila melanogaster, chromosome 3R, region 97E-98	*0.004*	(AC002337) unknown protein [Arabidopsis thaliana]
UCD001BE406545-1	*1.0e-44*	Setaria italica actin mRNA, complete cds	*1.0e-27*	ACTIN 2
UCD001BE443755-4	*0.007*	Dictyostelium discoideum nucleoside diphosphate kinase	*6*	(AF202730) Niemann-Pick type C1 disease protein [Oryctola
UCD017BE494102-3	*3.0e-20*	H.chilense x T.turgidum conv. durum (Tritordeum) mRNA f	*4.0e-57*	(AJ251899) S-adenosylmethionine decarboxylase 2 [Oryza
UCW016BE403761-1	*1.0e-72*	Hordeum vulgare mRNA for alpha-keto acid dehydrogenas	*e-102*	(AL391712) branched-chain alpha keto-acid dehydrogenase
UMC032BE471323-1	*0*	Hordeum vulgare photosystem I protein (PSI-L) mRNA, co	*4.0e-87*	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR
UMC040BG262290-2,3	*e-141*	Oryza sativa subsp. indica embryo-specific protein (Ose73	*4.0e-57*	(AF049892) unknown [Oryza sativa]
UMC055BF483513-2	*7.0e-18*	A.thaliana protein phosphatase mRNA	*3.0e-42*	SERINE\THREONINE PROTEIN PHOSPHATASE PP-X ISOZYME 2
UMC055BF484913-4	*6.0e-09*	Arabidopsis thaliana chromosome 1 BAC F2P9 genomic se	*2.0e-87*	(AC016662) putative enolase\; 31277-33713 [Arabidopsis tha
UMN013BE443538-3	*0*	Zea mays LIM transcription factor homolog (lim1) mRNA, c	*3.0e-98*	(AF135591) LIM transcription factor homolog [Zea mays]
UMN013BE443745-4	*7.0e-28*	Hordeum vulgare partial mRNA\; clone cMWG0784	*3.0e-97*	hypothetical protein F15B8.20 - Arabidopsis thaliana
UMN013BE444201-2	*0.001*	Homo sapiens hypothetical protein MGC10500 (MGC10500)	*2.0e-30*	hypothetical protein T29A15.230 - Arabidopsis thaliana
UNL036BE590970-2	*0.31*	Homo sapiens BAC clone RP11-339F13 from 7, complete se	*9.0e-41*	(AB036735) allyl alcohol dehydrogenase [Nicotiana tabacum
UNL048BE493886-3	*0.007*	Streptomyces coelicolor cosmid D16A	*3.0e-12*	(AC012328) unknown protein [Arabidopsis thaliana]

5AL10-0.57-0.78

CNL014BE445204-4	*3.0e-18*	Hordeum vulgare beta-D-glucan exohydrolase isoenzyme	*3.7*	(AC074110) hypothetical protein [Arabidopsis thaliana]
KSU001BE399281-3	*0.035*	Homo sapiens genomic DNA, chromosome 11q, clone:RP1	*1.2*	(U01849) ORF2 [Trypanosoma brucei]
KSU002BE426715-1	*0.1*	Homo sapiens BAC clone RP11-493I5 from 2, complete seq	*2.2*	transcription initiation factor IID-associated protein, 80K - f
KSU024BE498038-3	*0*	Triticum aestivum p34cdc2 (cdc2TaA) mRNA, complete cds	*e-125*	(U23409) p34cdc2 [Triticum aestivum]
KSU030BE500513-3	*e-100*	Hordeum vulgare ECA1 protein mRNA, complete cds	*7.0e-41*	(AF109193) ECA1 protein [Hordeum vulgare]
KSU030BF474029-2	*1.0e-59*	Atriplex nummularia homologous sequence (ANJ1) mRNA	*7.0e-81*	DNAJ PROTEIN HOMOLOG 2
KSU030BF483487-4,5	*1.0e-46*	Glycine max seed maturation protein PM37 (PM37) mRNA,	*2.0e-40*	DnaJ protein homolog ZMDJ1 - maize
KSU035BE407068-1	*e-126*	Zea mays LON1 protease (LON1) mRNA, complete cds	*1.0e-72*	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR -
KSU038BE443610-1	*1.0e-07*	Arabidopsis thaliana DNA chromosome 5, BAC clone T6G2	*4.0e-72*	(AL589883) mannosyltransferase-like protein [Arabidopsis
KSU038BE445260-1,4	*1.0e-84*	Arabidopsis thaliana AT5g66760\MSN2_16 gene, complete	*e-99*	succinate dehydrogenase (EC 1.3.99.1) flavoprotein alpha c
NDS034BE406569-2	*2.0e-63*	Rice mRNA for ribosomal protein L41 (340 gene), partial se	*6.0e-24*	60S RIBOSOMAL PROTEIN L44
NDS034BE471188-3	*5.0e-05*	Elaeis guineensis calmodulin mRNA, complete cds	*6.3*	(X69926) HRPII [Plasmodium falciparum]
NDS034BF474029-2	*1.0e-59*	Atriplex nummularia homologous sequence (ANJ1) mRNA	*7.0e-81*	DNAJ PROTEIN HOMOLOG 2
NDS043BF292161-3	*1.2*	Homo sapiens chromosome 17, clone 84_E_24, complete s	*2.0e-39*	hypothetical protein F17I5.110 - Arabidopsis thaliana
TTU047BE445873-4,6	*0.89*	C.freundii araC gene encoding an araBAD operon regulato	*7.0e-19*	(AC006264) unknown protein [Arabidopsis thaliana]
UCD001BE406463-1	*2.0e-97*	Saccharum hybrid cultivar H65-7052 membrane protein mR	*5.0e-43*	(L13655) membrane protein [Saccharum hybrid cultivar H6
UCD037BE500170-3,5	*0.1*	Oryza sativa microsatellite MRG5263 containing (CTC)X9, cl	*1.0e-33*	zinc-finger protein Lsd1 - Arabidopsis thaliana
UCW016BE590622-3	*0*	T.aestivum mRNA for serpin WZS3	*2.0e-65*	serpin homolog WZS3 - wheat
UCW020BE499738-2	*e-115*	Eleusine indica alpha tubulin 1 (TUA1) mRNA, complete cds	*3.0e-77*	TUBULIN ALPHA-1 CHAIN
UMC032BE426712-2	*4.0e-22*	Z.mays mRNA for cysteine proteinase	*7.0e-15*	cysteine proteinase (EC 3.4.22.-), glucose starvation-induc
UMC055BF484028-3	*2.0e-17*	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	*2.0e-63*	(AB022223) kinase-like protein [Arabidopsis thaliana]
UMN013BE444081-2	*0.006*	Oryza sativa genomic DNA, chromosome 1, BAC clone:OSJNBa0010K01		
UMN013BE444562-2	*5.0e-06*	Arabidopsis thaliana transcription factor TFIIB mRNA, com	*3.0e-14*	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB)
UNL002BF484437-1	*1.5*	Homo sapiens BAC clone RP11-210M15 from 15, complete	*1.0e-19*	(AP001168) Similar to gene for Pib (AB013448) [Oryza sativa
UNL036BE496891-3	*5.0e-43*	Hordeum vulgare photosystem-I PSI-F subunit precursor	*0.006*	(AF093634) photosystem-1 F subunit precursor [Oryza sati
UNL044BF484831-2	*2.0e-05*	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence	*1.0e-46*	(AC004809) ESTs gb|N65605, gb|N38087, gb|T20485, gb|T137
UNL044BG263643-2	*2.0e-08*	Zea mays putative methyl-binding domain protein MBD105	*1.0e-22*	(AY029558) putative methyl-binding domain protein MBD10

5AL17-0.78-0.87

CSU046BE443002-3	*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
CSU102BE406609-4,5	*2.8*	Human DNA sequence from clone RP4-586J11 on chromos	*1.0e-16*	comes from this gene. [Arabidopsis thaliana]
KSU030BE498241-3	*0.007*	Petromyzon marinus Spi transcription factor mRNA, comp	*2.0e-29*	(AB022215) hydroxyproline-rich glycoprotein [Arabidopsis
NDS021BF473953-2	*0*	Secale cereale ribosomal protein S7 mRNA, complete cds	*1.0e-97*	(AF118149) ribosomal protein S7 [Secale cereale]
NDS034BE498241-2	*0.007*	Petromyzon marinus Spi transcription factor mRNA, comp	*2.0e-29*	(AB022215) hydroxyproline-rich glycoprotein [Arabidopsis
UMN013BE443893-1	*9.0e-36*	Oryza sativa genomic DNA, chromosome 1, clone:P0702F0	*2.0e-84*	(AP002481) ESTs C97518(C60304),C28188(C60304) correspo

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CNL014BE444334-1	*e-125*	Triticum aestivum delta-24-sterol methyltransferase (TA-I	*9.0e-24*	(U60755) delta-24-sterol methyltransferase [Triticum aesti
CNL014BE444820-13	*1.0e-07*	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	*5.0e-52*	(AB005243) contains similarity to unknown protein~emb|C
CNL023BF291638-3	*8.0e-39*	Oryza sativa genomic DNA, chromosome 1, PAC clone:P05	*6.0e-53*	respiratory burst oxidase protein D [imported] - Arabidop
CNL031BF291891-10	*9.0e-11*	Arabidopsis thaliana AT3g04520 (AT3g04520\T27C4_17) mR	*4.0e-72*	L-allo-threonine aldolase homolog F22O13.11 - Arabidopsis
CSU001BE442582-1	*0.42*	Microtus arvalis smc4 gene for SMC4 protein, exons 1-19	*6.0e-26*	(AC004135) T17H7.16 [Arabidopsis thaliana]
KSU001BE444334-2	*e-125*	Triticum aestivum delta-24-sterol methyltransferase (TA-I	*9.0e-24*	(U60755) delta-24-sterol methyltransferase [Triticum aesti
KSU001BE444421-3,8,9	*0.09*	Homo sapiens chromosome 5 clone RP11-138C1, complete sequence		
KSU001BE444473-5,9,11	*0.016*	Drosophila melanogaster genomic scaffold 1420000133860	*2.0e-23*	(AC084763) hypothetical protein [Oryza sativa]
KSU012BE403305-3	*5.0e-19*	Oryza sativa chromosome 10 BAC OSJNBa0001O14 genomi	*6.0e-74*	(AC025783) putative protein phosphatase 2C [Oryza sativa]
KSU024BE498921-3	*e-113*	Hordeum vulgare mRNA for putative kinetochore protein (	*6.0e-50*	(AJ277096) putative kinetochore protein [Hordeum vulgare
KSU024BE499840-1	*3.0e-94*	Hordeum vulgare partial sucrose-phosphate synthase 1 (	*6.0e-71*	(AF322116) sucrose-phosphate synthase [Medicago sativa
KSU024BE499927-1,3,4,5,7	*7.0e-05*	Sequence of BAC F5D14 from Arabidopsis thaliana chromo	*2.0e-60*	(AC007767) Strong similarity to an unknown pre-mRNA spl
KSU027BF482595-2,3	*0*	Oryza sativa rCOP11 protein (rCOP11) mRNA, complete cds	*e-105*	(AF160800) constitutive photomorphogenic 11 [Oryza sativ
KSU030BF482216-1	*8.0e-24*	Arabidopsis thaliana CAF protein (CAF) mRNA, complete c	*2.0e-77*	(AF292940) short integuments 1 [Arabidopsis thaliana]
KSU035BE403378-2	*0.081*	Homo sapiens BAC clone GS1-286B23 from 7q21.1-q21.3, c	*5.0e-38*	(AC069300) putative transcription regulatory protein [Oryz
KSU035BE404665-4	*0.006*	Homo sapiens suppressor of Ty (S.cerevisiae) 5 homolog	*2.0e-25*	(AL161577) signal recognition particle receptor-like protei
KSU038BE444566-2	*0.006*	Arabidopsis thaliana putative DNA-binding protein (T20K12	*2.0e-13*	(AF123265) remorin 1 [Lycopersicon esculentum]
KSU038BE444681-3	*2.0e-61*	Oryza sativa GTP-binding protein mRNA, complete cds	*1.0e-56*	RAS-RELATED PROTEIN RAB2BV
NDS034BE406557-2	*6.0e-87*	Hordeum vulgare low temperature-responsive RNA-bindir	*2.0e-29*	glycine-rich RNA-binding protein, low-temperature-respor
TTU047BE405064-5	*1.3*	Pseudomonas aeruginosa PA01, section 328 of 529 of the	*3.0e-49*	(AC007767) Strong similarity to an unknown protein F19D1
UCD001BE442582-4	*0.42*	Microtus arvalis smc4 gene for SMC4 protein, exons 1-19	*6.0e-26*	(AC004135) T17H7.16 [Arabidopsis thaliana]
UCD017BE490291-2	*0*	Triticum aestivum cold acclimation protein WCOR615 (Wco	*8.0e-85*	cold acclimation protein WCOR615 - wheat
UCD017BE494988-2	*7.0e-19*	Oryza sativa genomic DNA, chromosome 6, PAC clone:P06	*6.0e-30*	(AP001129) ESTs AU029388(E30287),D49277(S16474) corresp
UCD028BE498551-21	*2.0e-36*	Oryza sativa poly(A)-binding protein gene, partial cds	*5.0e-35*	(AF153689) poly(A)-binding protein [Oryza sativa]
UCD037BE489538-5	*e-109*	Triticum aestivum clone CYP73-TA cytochrome P450 mRNA	*6.0e-29*	(AF123608) cytochrome P450 [Triticum aestivum]
UCD037BE498609-3,6,7,16	*0.1*	Hordeum vulgare homeodomain protein JUBEL1 (JuBel1) g	*7.0e-67*	fructokinase (EC 2.7.1.4) - Arabidopsis thaliana kinases (Pf
UCW016BE517624-1	*e-152*	Oryza sativa hypersensitive-induced response protein (RI	*1.0e-89*	(AJ292360) putative membrane protein [Zea mays]
UMC040BF474251-5	*0*	Triticum aestivum mRNA for PR-1.1 protein	*7.0e-57*	(AJ007348) pathogenisis-related protein 1.1 [Triticum aesti
UMN013BE443205-2	*7.0e-30*	Citrus limon aconitase-iron regulated protein 1 (IRP1) mR	*1.0e-70*	(AC007170) cytoplasmic aconitate hydratase [Arabidopsis
UNL001BE444421-6,7	*0.09*	Homo sapiens chromosome 5 clone RP11-138C1, complete sequence		
UNL001BE444473-6,8	*0.016*	Drosophila melanogaster genomic scaffold 1420000133860	*2.0e-23*	(AC084763) hypothetical protein [Oryza sativa]
UNL002BE444616-1	*0.006*	Human DNA sequence from clone RP1-211D12 on chromos	*7.0e-32*	(AC051633) putative ubiquitin protein [Oryza sativa]
UNL036BF200656-1	*0.61*	Homo sapiens, Similar to thiosulfate sulfurtransferase (rh	*2.0e-06*	(AF156782) nod factor binding lectin-nucleotide phosphohy
UNL044BG263172-4	*9.0e-11*	Arabidopsis thaliana chromosome II section 141 of 255 of t	*1.0e-73*	clpB heat shock protein-like - Arabidopsis thaliana
UNL044BG312582-3	*e-100*	Hordeum vulgare DNA for chromosome 4H	*6.0e-53*	ribophorin I homolog - barley (fragment)

5AL17-0.78-1.00

NDS043BF291915-1	*0.42*	Streptomyces coelicolor cosmid H69	*2.0e-43*	(AC013483) unknown protein [Arabidopsis thaliana]

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

http://wheat.pw.usda.gov/wEST