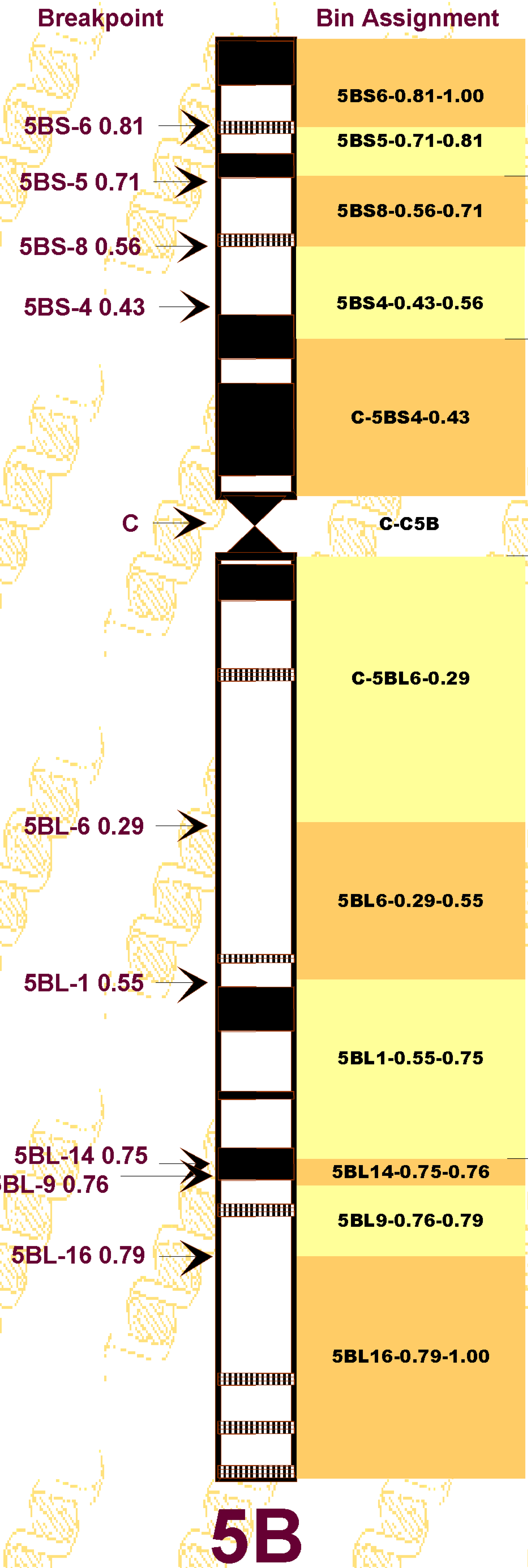
The Structure and Function of the Expressed Portion of the Wheat Genomes

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

*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.



5BS6-0.81-1.00

CSU001BE399994-5	0.16	Smilax rotundifolia phytochrome C (PHYC) gene, partial cds		
KSU001BE443751-1	0.087	Cicer arietinum nodulin-35 gene	5.0e-05	(AF145657) BcDNA.GH10120 [Drosophila melanogaster]
KSU012BE490728-10	0	Hordeum vulgare methyljasmonate-inducible lipoxygenas	3.0e-94	lipoxygenase (EC 1.13.11.12) 2 - barley
KSU035BE404480-1,5	2.0e-37	Oryza sativa subsp. japonica clone C63266_1A putative glut	7.0e-68	(AP002914) putative glutathione S-transferase [Oryza sativ
KSU035BE496903-2,4	2.0e-05	Arabidopsis thaliana At1g09340 (At1g09340\T31J12_6) mRN	2.0e-47	(Y15382) putative RNA binding protein [Arabidopsis thalian
UCD001BE443751-1	0.087	Cicer arietinum nodulin-35 gene	5.0e-05	(AF145657) BcDNA.GH10120 [Drosophila melanogaster]
UCD028BE404135-2,7,8	7.0e-46	Zea mays glutathione S-transferase GST 8 mRNA, complet	6.0e-82	(AP002914) putative glutathione S-transferase [Oryza sativ
UCD037BE499835-1	3.0e-26	Lycopersicon esculentum mRNA for beta-alanine synthas	1.0e-79	(Y19104) beta-alanine synthase [Lycopersicon esculentum
UCD037BF473571-3	0	Oryza sativa enolase mRNA, complete cds	3.0e-98	ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2) (2-PHC
UCW002BE399993-1	9.0e-74	T.aestivum GSP-1b mRNA for grain softness protein	1.0e-06	grain softness protein 1b, 15K - wheat
UCW026BE636954-4	e-144	Oryza sativa plasma membrane proton-ATPase gene OSA	2.0e-94	(D10207) H-ATPase [Oryza sativa]
UMC040BE637485-1	0	Ha=GSP-1a [Triticum=wheat, cv. Timgalen, endosperm, mR	5.0e-70	grain softness protein 1a, 15K (clone TSF69) - wheat Timga
UMN013BE444854-2,6	0	Triticum aestivum sucrose-6F-phosphate phosphohydrol	2.0e-99	(AF321556) sucrose-6F-phosphate phosphohydrolase SPP
UNL036BF201102-2	2.0e-23	C.roseus MetE mRNA for methionine synthase	8.0e-43	(Z49150) cobalamine-independent methionine synthase [S

5BS5-0.71-0.81

KSU035BE403373-4	0	Triticum aestivum oxalate oxidase mRNA, partial cds	1.0e-72	(AF005084) oxalate oxidase [Triticum aestivum]
KSU035BE403471-4	5.0e-15	Oryza sativa microsatellite MRG2437 containing (CT)X18, g	6.0e-57	(AF370443) Ran binding protein-1 [Lycopersicon esculentu
KSU038BE444720-1	5.0e-19	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-62	(AF123508) Nt-iaa28 deduced protein [Nicotiana tabacum]
NDS001BE443751-3	0.087	Cicer arietinum nodulin-35 gene	5.0e-05	(AF145657) BcDNA.GH10120 [Drosophila melanogaster]
TTU047BE405630-3	8.0e-15	Arabidopsis thaliana chromosome II section 10 of 255 of th	5.0e-85	hypothetical protein T8K22.14 - Arabidopsis thaliana
UMC032BF146083-3	1.0e-05	Arabidopsis thaliana At1g09340 (At1g09340\T31J12_6) mRN	6.0e-25	(Y15382) putative RNA binding protein [Arabidopsis thalian

5BS8-0.56-0.71

KSU001BE399088-4	2.0e-08	Arabidopsis thaliana DNA chromosome 5, BAC clone T20K	1.0e-61	(AC008261) unknown protein [Arabidopsis thaliana]
KSU002BE405200-2	1.5	Homo sapiens chromosome 5 clone CTB-70H11, complete	8.1	testis expressed sequence 14 [Homo sapiens]
KSU012BE352603-1	1.0e-43	Arabidopsis thaliana calcineurin B-like protein 3 (CBL3) mR	1.0e-77	calcineurin B-like protein 3 T15N24.20 [imported] - Arabido
KSU027BE404894-3	4.0e-19	Glycine max plasma membrane Ca2+-ATPase (SCA2) mRN	9.0e-75	(AF195029) plasma membrane Ca2+-ATPase [Glycine max]
UCD001BE405200-3	1.5	Homo sapiens chromosome 5 clone CTB-70H11, complete	8.1	testis expressed sequence 14 [Homo sapiens]
UCD001BE443755-15	0.007	Dictyostelium discoideum nucleoside diphosphate kinase	6	(AF202730) Niemann-Pick type C1 disease protein [Oryctola
UCD037BE444434-5	0.39	Arabidopsis thaliana unknown protein (T11H3_70\AT5g250	2.0e-08	pectate lyase-like protein - Arabidopsis thaliana
UCW001BE399088-3	2.0e-08	Arabidopsis thaliana DNA chromosome 5, BAC clone T20K	1.0e-61	(AC008261) unknown protein [Arabidopsis thaliana]
UNL002BE406845-2	1.1	Homo sapiens chromosome 3 clone RP11-593J10 map 3p,	6.0e-24	hypothetical protein F17M5.60 - Arabidopsis thaliana
UNL002BE415680-2	0.22	Homo sapiens PAC clone RP4-741M6 from 7p21-p15.3, com	7.0e-04	(AF158635) V6 [Aegilops ventricosa]
UNL002BE429766-2	0.006	Arabidopsis thaliana DNA chromosome 5, BAC clone T1E3	2.0e-57	disease resistance-like protein - Arabidopsis thaliana prot
UNL002BE445244-1,3	0.1	Lycopersicon esculentum disease resistance protein I2 (I	1.0e-18	NBS-LRR type resistance protein - rice (fragment)
UNL036BE606874-1	0	Triticum aestivum granule-bound starch synthase I (Wx-Dl	1.0e-58	(AB019624) starch synthase (GBSSI) [Triticum aestivum] ta

5BS4-0.43-0.71

UMC001BE399088-4	2.0e-08	Arabidopsis thaliana DNA chromosome 5, BAC clone T20K	1.0e-61	(AC008261) unknown protein [Arabidopsis thaliana]

5BS4-0.43-0.56

CSU001BE403221-2	3.0e-32	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	7.0e-69	hypothetical protein F4I1.8 - Arabidopsis thaliana
CSU001BE406368-4	0.9	Pseudomonas aeruginosa PA01, section 33 of 529 of the complete genome		
KSU001BE406368-5	0.9	Pseudomonas aeruginosa PA01, section 33 of 529 of the complete genome		
KSU001BE442924-4,6	0.007	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K6M13		
KSU001BE443968-1	5.9	Caenorhabditis elegans cosmid Y81G3A, complete sequer	5.0e-14	(AB025613) receptor protein kinase-like [Arabidopsis thali
KSU019BE443334-2	0	Barley acyl carrier protein I (ACP I) mRNA, complete cds	1.0e-72	ACYL CARRIER PROTEIN I PRECURSOR (ACP I)
KSU024BE498878-1	3.0e-08	Musa acuminata mRNA for unknown ripening-related prot	2.0e-08	(AB007644) contains similarity to enolase-phosphatase~ge
KSU024BE500291-4	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
KSU035BE403618-1	e-178	Oryza sativa mRNA for adenylate kinase-a, complete cds	6.0e-90	(AB041773) adenylate kinase [Oryza sativa]
NDS021BE591003-4	0.002	Glycine max seed maturation protein PM23 (PM23) mRNA,	2.0e-42	(AF116752) seed maturation protein PM23 [Glycine max]
TTU047BE444644-3	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
UCD037BE488542-7	0.38	Mesorhizobium loti, complete genome	1.0e-23	(AC011437) ankyrin-like protein [Arabidopsis thaliana]
UCW026BE636795-3,4	6.0e-64	Oryza sativa small zinc finger-like protein (TIM9) mRNA, co	2.0e-43	MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE
UMN013BE443538-2	0	Zea mays LIM transcription factor homolog (lim1) mRNA, c	3.0e-98	(AF135591) LIM transcription factor homolog [Zea mays]

C-5BS4-0.43

UCD017BE488825-1	e-101	Oryza sativa aldolase mRNA, complete cds	3.0e-56	fructose-bisphosphate aldolase (EC 4.1.2.13) - rice
UCW001BE400002-2	0.15	Homo sapiens chromosome 5 clone CTC-540O12, complet	0.97	venom protein, 33K - braconid wasp (Chelonus sp.)
UNL002BE517827-3	e-106	Oryza sativa mRNA for protein phosphatase 2A regulatory	2.0e-59	(AJ243828) phosphatase 2A regulatory A subunit [Oryza sa
UNL036BF200703-1	7.0e-04	Streptomyces sp. QM-B814 (ATCC 11238) bgl3 gene for be	2.0e-21	(X94986) beta glucosidase [Manihot esculenta]
UNL036BF200825-2	0.12	Oryza sativa chromosome 3 BAC OSJNBb0072E24 genomic	1.0e-17	(AB005243) GDSL-motif lipase\hydrolase-like protein [Arab
UNL048BE446646-1	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-5BL6-0.29

CNL001BE403518-6	1.0e-65	Oryza sativa Ca2+ sensitive 3'(2'),5-diphosphonucleoside 3	2.0e-70	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHC
CNL001BE406545-2	1.0e-44	Setaria italica actin mRNA, complete cds	1.0e-27	ACTIN 2
KSU002BE403518-5	1.0e-65	Oryza sativa Ca2+ sensitive 3'(2'),5-diphosphonucleoside 3	2.0e-70	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHC
KSU002BE406545-2	1.0e-44	Setaria italica actin mRNA, complete cds	1.0e-27	ACTIN 2
KSU012BE403761-4	1.0e-72	Hordeum vulgare mRNA for alpha-keto acid dehydrogenas	e-102	(AL391712) branched-chain alpha keto-acid dehydrogenase
KSU012BE442892-2	6.0e-12	M.sativa mRNA for annexin-like protein	1.0e-08	(Y11348) annexin-like protein [Medicago sativa]
KSU019BE404234-2	3.0e-41	S.tuberosum mRNA for NADH dehydrogenase, NADH-bindi	1.0e-82	(AB006697) NADH dehydrogenase [Arabidopsis thaliana]
KSU035BE406996-1	8.0e-11	Rice mRNA, sequence homologous to ADP-ribosylation fac	6.0e-12	ADP-RIBOSYLATION FACTOR 1
KSU035BE497510-5	e-139	Avena sativa vacuolar H+-ATPase 16 kDa proteolipid subun	3.0e-42	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT oat
KSU038BE445803-3	6.0e-40	Oryza sativa mRNA for NADH dependent Glutamate Synthas	2.0e-28	(AB008845) NADH dependent Glutamate Synthase [Oryza sa
NDS043BF291915-2	0.42	Streptomyces coelicolor cosmid H69	2.0e-43	(AC013483) unknown protein [Arabidopsis thaliana]
UCD001BE403518-7	1.0e-65	Oryza sativa Ca2+ sensitive 3'(2'),5-diphosphonucleoside 3	2.0e-70	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHC
UCD001BE406545-2	1.0e-44	Setaria italica actin mRNA, complete cds	1.0e-27	ACTIN 2
UCD028BE426080-5	e-132	Zea mays cultivar TX-5855 acetoacetyl CoA thiolase mRNA,	2.0e-81	(AF113522) acetoacetyl CoA thiolase [Zea mays]
UCD028BE590485-1	0	T.durum mRNA for lipid transfer protein	6.0e-50	lipid transfer protein - wheat Protein Complexed With Two
UCD028BE605231-2	e-100	Zea mays pyruvate dehydrogenase E1 beta subunit isofor	5.0e-59	(AF069910) pyruvate dehydrogenase E1 beta subunit isofo
UCD028BG263656-4,6	0.019	Chlamydomonas reinhardtii apospory-associated protein	3.0e-38	(AB013389) apospory-associated protein C-like [Arabidops
UCD029BE490552-6	0	Triticum aestivum cultivar Mironovska 808 cold-responsiv	2.0e-60	(AF207545) cold-responsive protein COR14a [Triticum aest
UCD029BE497368-1,6	8.0e-07	Arabidopsis thaliana putative PHD finger transcription fact	1.0e-49	receptor like protein - Arabidopsis thaliana (fragment)
UCD029BE497820-3	1.0e-07	A.thaliana mRNA for chloroplast thylakoidal processing pe	9.0e-71	(U93215) putative signal peptidase I [Arabidopsis thaliana]
UCD029BF293395-5	2.0e-70	Vicia faba vfPP2Ac-3 mRNA for type 2A protein phosphatas	1.0e-92	SERINE\THREONINE PROTEIN PHOSPHATASE PP2A-2 CATALY
UCD029BF483378-5	e-110	Oryza sativa OsPAG1 mRNA for alpha 7 subunit of 20S prot	3.0e-87	PROTEASOME SUBUNIT ALPHA TYPE 3 (20S PROTEASOME AL
UCD037BE443280-4	2.0e-36	Arabidopsis thaliana DNA chromosome 3, BAC clone T14D3	7.0e-35	(AB023032) ubiquitin-like protein [Arabidopsis thaliana]
UCW016BE403761-4	1.0e-72	Hordeum vulgare mRNA for alpha-keto acid dehydrogenas	e-102	(AL391712) branched-chain alpha keto-acid dehydrogenase
UMN013BE442918-6	2.0e-05	Cicer arietinum mRNA for NADPH oxidoreductase homolog	4.0e-64	(AB027757) NADPH oxidoreductase homolog [Cicer arietinu
UMN013BE444081-4	0.006	Oryza sativa genomic DNA, chromosome 1, BAC clone:OSJNBa0010K01		
UNL002BF473933-1,5	0.44	Rat cytomegalovirus Maastricht, complete genome	4.0e-47	(Z99707) putative protein [Arabidopsis thaliana]

5BL6-0.29-0.55

CNL014BE423964-1	e-151	Rice mRNA for ribosomal protein L3, complete cds	1.0e-83	60S RIBOSOMAL PROTEIN L3
KSU001BE443692-1	0.31	Human DNA sequence from cosmid U56D2, between mark	6.0e-19	(AC016041) F27J15.15 [Arabidopsis thaliana]
KSU001BE443755-9	0.007	Dictyostelium discoideum nucleoside diphosphate kinase	6	(AF202730) Niemann-Pick type C1 disease protein [Oryctola
KSU002BE403221-3	3.0e-32	Oryza sativa genomic DNA, chromosome 1, PAC clone:P00	7.0e-69	hypothetical protein F4I1.8 - Arabidopsis thaliana
KSU012BE403556-4	6.0e-15	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	5.0e-24	(AB006700) contains similarity to RAV2-like DNA-binding pr
KSU012BE404462-3	0.33	Drosophila melanogaster genomic scaffold 1420000133860	3.0e-55	(AB006704) contains similarity to unknown protein~gene_i
KSU012BE442918-3,5	2.0e-05	Cicer arietinum mRNA for NADPH oxidoreductase homolog	4.0e-64	(AB027757) NADPH oxidoreductase homolog [Cicer arietinu
KSU024BE405060-6	3.0e-85	Oryza sativa protein kinase mRNA, complete cds	1.0e-58	protein kinase homolog - rice
KSU024BE495790-1	0.004	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K	3.0e-40	(AF120494) phosphoglucose isomerase precursor [Arabid
KSU024BE499599-4,5	5.0e-13	Vigna unguiculata phosphatidic acid phosphatase alpha m	8.0e-88	(AC007591) Contains similarity to gb acid phosphatase alpl
KSU024BE499843-3,5,7	e-122	Zea mays variety B73 hypersensitive-induced response p	2.0e-81	(AF236375) hypersensitive-induced response protein [Zea
KSU030BE590997-1	0	Hordeum vulgare chlorophyll a\b-binding protein precurs	e-110	(AF287276) chlorophyll a\b-binding protein precursor [Hor
UMN013BE442600-1	6.0e-12	P.sativum PHSP1 mRNA for HSP70	3.0e-70	HEAT SHOCK 70 KD PROTEIN, MITOCHONDRIAL PRECURSOR
UMN013BE443745-1	7.0e-28	Hordeum vulgare partial mRNA\; clone cMWG0784	3.0e-97	hypothetical protein F15B8.20 - Arabidopsis thaliana
UNL002BE493050-2	0.091	Hordeum vulgare homeodomain protein JUBEL2 (JuBel2) g	2.0e-20	(AB020745) gene_id:MJE7.2~pir||C71412~similar to unknow
UNL048BE493886-2	0.007	Streptomyces coelicolor cosmid D16A	3.0e-12	(AC012328) unknown protein [Arabidopsis thaliana]
UNL048BE591308-5	1.0e-06	Chlamydia trachomatis section 12 of 87 of the complete ge	6.0e-67	ERD1 PROTEIN PRECURSOR

C-5BL14-0.75

CSU058BE496864-2	4.0e-47	O.sativa mRNA for chilling-inducible protein	1.0e-62	(AF133708) PP2A regulatory subunit [Arabidopsis thaliana]
UCD001BE403518-6	1.0e-65	Oryza sativa Ca2+ sensitive 3'(2'),5-diphosphonucleoside 3	2.0e-70	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHC

5BL1-0.55-0.75

CNL001BE406368-5	0.9	Pseudomonas aeruginosa PA01, section 33 of 529 of the complete genome		
CNL001BE406506-2	1.2	Drosophila melanogaster, chromosome 3R, region 97E-98	0.004	(AC002337) unknown protein [Arabidopsis thaliana]
CNL014BE444736-8	2.0e-08	Arabidopsis thaliana chromosome 1 BAC T1F15 sequence	4.0e-54	hypothetical protein T1F15.13 - Arabidopsis thaliana (fragn
CNL014BE445248-5,7	8.0e-36	Arabidopsis thaliana chromosome 1 BAC T19D16 genomic	8.0e-54	(U95973) endomembrane protein EMP70 precusor isolog\;
CNL014BE445282-2	0.09	Homo sapiens 12 BAC RP11-340M11 (Roswell Park Cancer	5.0e-60	(AC024174) Contains similarity to glyoxalase II isozyme fro
CNL014BE445424-2	1.0e-21	Oryza sativa mRNA for C-type cyclin, complete cds	5.0e-27	G1\S-SPECIFIC CYCLIN C-TYPE
CNL014BE604419-3	e-140	Hordeum vulgare thaumatin-like protein TLP7 mRNA, com	1.0e-55	(AF355457) thaumatin-like protein TLP7 [Hordeum vulgare]
CNL014BE604574-1	4.0e-10	Arabidopsis thaliana DNA chromosome 5, BAC clone F12B1	8.0e-61	(AB013395) poly(A)-binding protein II-like [Arabidopsis thal
CNL023BG274279-4	2.0e-21	Oryza sativa chromosome 3 BAC OSJNBb0033N16 genomic	1.0e-62	probable DNA-binding protein F22O6.60 - Arabidopsis thalia
CSU001BE403512-1	2.0e-48	Oryza sativa chromosome 7 clone OSJNBb0024A20, compl	2.0e-36	(AC079038) Putative nucleic acid binding protein [Oryza sat
CSU001BE425296-3	5.0e-52	Triticum aestivum rbcS gene for ribulose-1,5-bisphosphat	2.0e-10	(AB042066) ribulose-1,5-bisphosphate carboxylase\oxyger
CSU001BE443735-2	3.0e-57	Aegilops tauschii starch synthase I gene, complete cds	0.63	(AB046670) includes endonuclease domain and reverse tr
CSU046BE443954-1	7.0e-09	Arabidopsis thaliana AT5g24420\K16H17_13 mRNA, comple	3.0e-58	(AB016884) 6-phosphogluconolactonase-like protein [Arab
KSU001BE406494-4,5	5.0e-51	Hordeum vulgare partial mRNA for putative acid phosphat	1.0e-40	(AJ250282) putative acid phosphatase [Hordeum vulgare]
KSU002BE406380-7	0.23	Homo sapiens 12 BAC RP11-173C20 (Roswell Park Cancer I	2.9	nidogen 2\; nidogen 2 (osteonidogen) [Homo sapiens]
KSU012BE352633-4	3.0e-32	Elaeis guineensis oleoyl-ACP thioesterase mRNA, partial c	5.0e-91	(AF213478) acyl-ACP thioesterase [Iris germanica]
KSU012BE442600-1	6.0e-12	P.sativum PHSP1 mRNA for HSP70	3.0e-70	HEAT SHOCK 70 KD PROTEIN, MITOCHONDRIAL PRECURSOR
KSU012BE442676-1	5.0e-19	Vigna aconitifolia 5'-phosphoribosyl-4-(N-succinocarboxar	7.0e-89	PHOSPHORIBOSYLAMIDOIMIDAZOLE-SUCCINOCARBOXAMID
KSU012BE443430-1	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
KSU019BE403649-1,2	5.0e-25	Chicken 78-kD glucose-regulated protein, complete cds	9.0e-73	HEAT SHOCK 70 KD PROTEIN, MITOCHONDRIAL PRECURSOR b
KSU019BE494426-2,4	7.0e-24	P.ciliare (Higgins) apospory associated mRNA, 876bp	2.0e-53	(AF352797) ankyrin-repeat protein HBP1 [Nicotiana tabacum
KSU027BE403482-3	2.0e-28	Iris germanica acyl-ACP thioesterase (FatA) mRNA, compl	5.0e-28	(AF213478) acyl-ACP thioesterase [Iris germanica]
KSU030BF478964-1	8.0e-15	Arabidopsis thaliana mRNA for ERD1 protein, complete cds	4.0e-91	ERD1 PROTEIN PRECURSOR
KSU035BE404454-1	0.3	Thermobifida fusca SbpA (sbpA) gene, partial cds\; BglA (t	3.0e-38	(AJ005950) beta-glucosidase [Cicer arietinum]
KSU035BE407068-3	e-126	Zea mays LON1 protease (LON1) mRNA, complete cds	1.0e-72	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR -
NDS021BF472974-2	0	Triticum aestivum Sec61p (sec61) mRNA, complete cds	e-109	(AF161718) Sec61p [Triticum aestivum]
NDS034BE406569-3	2.0e-63	Rice mRNA for ribosomal protein L41 (340 gene), partial se	6.0e-24	60S RIBOSOMAL PROTEIN L44
TTU047BE495277-2	0.021	Arabidopsis thaliana DNA chromosome 5, BAC clone T22P	3.0e-50	hypothetical protein T22P22.70 - Arabidopsis thaliana
UCD001BE352592-1	0	Hordeum vulgare arabinoxylan arabinofuranohydrolase iso	2.0e-91	(AF320325) arabinoxylan arabinofuranohydrolase isoenzym
UCD001BE405224-3	0.44	Human chromosome 14 DNA sequence BAC R-757K12 of lib	2.0e-16	(AC009465) unknown protein\; 32997-32284 [Arabidopsis th
UCD001BE406324-3	3.0e-15	Zea mays seven transmembrane protein Mlo7 mRNA, com	1.0e-06	MLO PROTEIN HOMOLOG 1 (ATMLO-H1)
UCD001BE406380-5	0.23	Homo sapiens 12 BAC RP11-173C20 (Roswell Park Cancer I	2.9	nidogen 2\; nidogen 2 (osteonidogen) [Homo sapiens]
UCD001BE406463-4	2.0e-97	Saccharum hybrid cultivar H65-7052 membrane protein mR	5.0e-43	(L13655) membrane protein [Saccharum hybrid cultivar H6
UCD001BE406506-3	1.2	Drosophila melanogaster, chromosome 3R, region 97E-98	0.004	(AC002337) unknown protein [Arabidopsis thaliana]
UCD017BE494102-1	3.0e-20	H.chilense x T.turgidum conv. durum (Tritordeum) mRNA f	4.0e-57	(AJ251899) S-adenosylmethionine decarboxylase 2 [Oryza
UMC015BE426279-3	3.5	Homo sapiens Xp BAC RP11-86G5 (Roswell Park Cancer Ins	8.5	(AC009525) Similar to beta-glucosidases [Arabidopsis thal
UMC015BE606474-4	5.0e-62	Glycine max clathrin heavy chain mRNA, complete cds	2.0e-95	(AC074395) clathrin heavy chain, putative [Arabidopsis thal
UMC032BE426712-1	4.0e-22	Z.mays mRNA for cysteine proteinase	7.0e-15	cysteine proteinase (EC 3.4.22.-), glucose starvation-induc
UMC032BF483595-2	2.0e-08	Triticum aestivum PST19 (Pst19), LRR19 (Lrr19), TAK19-1 (Tak19-1), and LRK19 (Lrk19) genes, complete cds		
UMC040BF474334-4	e-178	Oryza sativa vacuolar H+-ATPase (vatp-P1) mRNA, complete	8.0e-61	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT oat
UMC040BF474342-2	0.41	Arabidopsis thaliana eIF3e mRNA, complete cds	1.0e-85	(AF285832) eukaryotic initiation factor 3E subunit [Arabidop
UMC040BF474508-10	e-138	H.vulgare blt14.1 gene	1.0e-04	acclimation protein - rye
UMC040BF474511-2	1.0e-04	Arabidopsis thaliana IAA2 (MXC7.6) mRNA, complete cds	2.0e-21	(AF123509) Nt-iaa4.1 deduced protein [Nicotiana tabacum]
UMC040BG262290-1	e-141	Oryza sativa subsp. indica embryo-specific protein (Ose73	4.0e-57	(AF049892) unknown [Oryza sativa]
UMC055BF483513-3	7.0e-18	A.thaliana protein phosphatase mRNA	3.0e-42	SERINE\THREONINE PROTEIN PHOSPHATASE PP-X ISOZYME 2
UMN013BE442763-4	1.0e-16	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clo	2.0e-73	(AB010069) gb|AAC80624.1~gene_id:MAC9.17~strong simil
UMN013BE443937-3	3.0e-17	Lotus japonicus rac GTPase activating protein 2 mRNA, pa	1.0e-65	(AF064787) rac GTPase activating protein 1 [Lotus japonicu
UMN013BE444562-3	5.0e-06	Arabidopsis thaliana transcription factor TFIIB mRNA, com	3.0e-14	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB)
UNL001BE443978-1	1.1	Drosophila melanogaster, chromosome 2R, region 57F-58	3	probable MFS transporter PA0241 [imported] - Pseudomon
UNL002BF482744-2	1.0e-07	Oryza sativa NBS-LRR type resistance protein (r10) gene, p	2.0e-48	NBS-LRR type resistance protein - rice (fragment)
UNL036BE590970-4,5	0.31	Homo sapiens BAC clone RP11-339F13 from 7, complete se	9.0e-41	(AB036735) allyl alcohol dehydrogenase [Nicotiana tabacum

5BL14-0.75-0.76

CNL001BE403217-4	0.24	Arabidopsis thaliana chromosome II section 191 of 255 of t	3.0e-23	multidrug-resistance protein homolog T29F13.13 - Arabido
CSU001BE442858-2	1.3	Homo sapiens chromosome 19, cosmid R27216 (LLNLR-23	4.0e-05	(X98316) peroxidase [Arabidopsis thaliana]
CSU101BE403968-2	0.014	Drosophila melanogaster genomic scaffold 142000013386047 section 24 of 52, complete sequence		
KSU002BE403217-2	0.24	Arabidopsis thaliana chromosome II section 191 of 255 of t	3.0e-23	multidrug-resistance protein homolog T29F13.13 - Arabido
KSU035BE404740-14	0.024	Homo sapiens chromosome 5, BAC clone 45m2 (LBNL H14	6.0e-61	(AB016893) 26S proteasome p55 protein-like [Arabidopsis
NDS034BE471131-1	9.0e-24	Vicia faba immunophilin precursor (FKBP15) mRNA, compl	3.0e-59	probable peptidylprolyl isomerase (EC 5.2.1.8) FKBP15-1 - A
NDS043BF291915-5	0.42	Streptomyces coelicolor cosmid H69	2.0e-43	(AC013483) unknown protein [Arabidopsis thaliana]
UCD017BE495133-1	1.0e-16	Dunaliella salina partial mRNA for heat shock protein (hsp7	8.0e-63	(AF217459) heat shock protein 70 [Arabidopsis thaliana]
UCW020BE499738-1	e-115	Eleusine indica alpha tubulin 1 (TUA1) mRNA, complete cds	3.0e-77	TUBULIN ALPHA-1 CHAIN
UMC040BE590499-4	0.26	Tupaia herpesvirus strain 2, complete genome	5.0e-23	GAMMA-2 PUROTHIONIN
UNL002BF484437-3,5	1.5	Homo sapiens BAC clone RP11-210M15 from 15, complete	1.0e-19	(AP001168) Similar to gene for Pib (AB013448) [Oryza sativa

5BL9-0.76-0.79

CNL001BE425993-1	e-154	Oryza sativa chromosome 3 BAC OSJNBa0040E01 genomic	1.0e-68	(AC079887) putative UDP-glucose dehydrogenase [Oryza s
CNL014BE604920-3	2.0e-51	Hordeum vulgare lipoxygenase 2 (LoxC) mRNA, complete	4.0e-22	lipoxygenase (EC 1.13.11.12) 2 - barley
CSU046BE443002-2	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
CSU057BE403785-4	0	Hordeum vulgare mRNA for sucrose transporter 2 (sut2 g	6.0e-71	(AJ272308) sucrose transporter 2 [Hordeum vulgare]
KSU001BE399281-2	0.035	Homo sapiens genomic DNA, chromosome 11q, clone:RP1	1.2	(U01849) ORF2 [Trypanosoma brucei]
KSU002BE425993-3	e-154	Oryza sativa chromosome 3 BAC OSJNBa0040E01 genomic	1.0e-68	(AC079887) putative UDP-glucose dehydrogenase [Oryza s
KSU030BF483487-1,2	1.0e-46	Glycine max seed maturation protein PM37 (PM37) mRNA,	2.0e-40	DnaJ protein homolog ZMDJ1 - maize
KSU038BE443610-3	1.0e-07	Arabidopsis thaliana DNA chromosome 5, BAC clone T6G2	4.0e-72	(AL589883) mannosyltransferase-like protein [Arabidopsis
KSU038BE445260-2,3	1.0e-84	Arabidopsis thaliana AT5g66760\MSN2_16 gene, complete	e-99	succinate dehydrogenase (EC 1.3.99.1) flavoprotein alpha c
NDS018BE405176-1	3.0e-63	Oryza sativa FNR gene for ferredoxin-NADP+ reductase, co	1.0e-31	FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR
NDS021BE500260-2,3	0.001	Arabidopsis thaliana scarecrow-like 21 (SCL21) mRNA, cor	2.0e-58	(AF153443) phytochrome A signal transduction 1 protein [A
NDS034BE403710-1,4	0.001	Arabidopsis thaliana AT3g62110 (AT3g62110\T17J13_70) m	3.0e-53	(AF324992) AT3g62110 [Arabidopsis thaliana]
NDS034BE406557-3	6.0e-87	Hordeum vulgare low temperature-responsive RNA-bindir	2.0e-29	glycine-rich RNA-binding protein, low-temperature-respor
NDS034BE498241-1	0.007	Petromyzon marinus Spi transcription factor mRNA, comp	2.0e-29	(AB022215) hydroxyproline-rich glycoprotein [Arabidopsis
NDS034BF474029-3	1.0e-59	Atriplex nummularia homologous sequence (ANJ1) mRNA	7.0e-81	DNAJ PROTEIN HOMOLOG 2
TTU047BE445873-2,3	0.89	C.freundii araC gene encoding an araBAD operon regulato	7.0e-19	(AC006264) unknown protein [Arabidopsis thaliana]
TTU047BE494680-2	9.0e-05	Arabidopsis thaliana AT4g37830\T28I19_110 mRNA, comple	2.0e-24	hypothetical protein T28I19.110 - Arabidopsis thaliana
UCD037BE500170-4	0.1	Oryza sativa microsatellite MRG5263 containing (CTC)X9, cl	1.0e-33	zinc-finger protein Lsd1 - Arabidopsis thaliana
UCW001BE399900-2	0.004	Streptomyces seoulensis dihydrolipoamide dehydrogena	0.21	hypothetical protein F22O13.28 - Arabidopsis thaliana
UCW001BE400000-1	e-176	T.aestivum TthV gene for wheat type V thionin	6.0e-09	TYPE V THIONIN PRECURSOR
UMC015BE426274-3	3.0e-75	Hordeum vulgare mRNA for hypothetical protein, partial, cl	1.0e-50	(AB007627) homeobox gene [Oryza sativa]
UMC015BE426680-5	0	Avena fatua ras-like small monomeric GTP-binding protei	7.0e-79	(AF084005) ras-like small monomeric GTP-binding protein
UMC015BE590667-1	9.0e-05	Oryza sativa globulin-like protein mRNA, clone Ose709, par	2.0e-22	globulin-2 precursor - maize
UMC032BE426127-10	0	Barley elongation factor 1 alpha, (EF-1A) mRNA sequence	2.0e-90	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
UMC055BF484028-4	2.0e-17	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	2.0e-63	(AB022223) kinase-like protein [Arabidopsis thaliana]
UMN013BE443423-1	1.0e-19	Oryza sativa chromosome 3 BAC OSJNBa0091J19 genomic	4.2	(AL117195) Y57A10A.1 [Caenorhabditis elegans]
UMN013BE443893-2	9.0e-36	Oryza sativa genomic DNA, chromosome 1, clone:P0702F03	2.0e-84	(AP002481) ESTs C97518(C60304),C28188(C60304) correspo
UMN013BE444030-1	e-101	Hordeum vulgare L41 ribosomal protein		

5BL16-0.79-1.00

CNL031BF428799-14	e-142	Oryza sativa GAD mRNA for glutamate decarboxylase, com	e-108	(AF020425) glutamate decarboxylase isozyme 1 [Nicotiana t
CSU102BE406499-2	6.0e-04	Saccharomyces cerevisiae chromosome XV, complete chromosome sequence		
CSU102BE406609-2,3	2.8	Human DNA sequence from clone RP4-586J11 on chromos	1.0e-16	comes from this gene. [Arabidopsis thaliana]
KSU012BE443423-6,10	1.0e-19	Oryza sativa chromosome 3 BAC OSJNBa0091J19 genomic	4.2	(AL117195) Y57A10A.1 [Caenorhabditis elegans]
KSU019BE490584-6	0	Triticum aestivum chlorophyll a\b-binding protein WCAB p	2.0e-77	(U73218) chlorophyll a\b-binding protein WCAB precursor [
KSU019BE494320-1,2	1.0e-62	Zea mays calreticulin (CRT) mRNA, complete cds	1.0e-51	CALRETICULIN PRECURSOR
KSU030BE403710-1,4	0.001	Arabidopsis thaliana AT3g62110 (AT3g62110\T17J13_70) m	3.0e-53	(AF324992) AT3g62110 [Arabidopsis thaliana]
KSU030BE498241-2	0.007	Petromyzon marinus Spi transcription factor mRNA, comp	2.0e-29	(AB022215) hydroxyproline-rich glycoprotein [Arabidopsis
KSU030BE498573-2	e-107	Zea mays protein kinase AKINbetagamma-1 mRNA, comple	4.0e-81	(AF276086) protein kinase AKINbetagamma-2 [Zea mays]
KSU030BE500513-7	e-100	Hordeum vulgare ECA1 protein mRNA, complete cds	7.0e-41	(AF109193) ECA1 protein [Hordeum vulgare]
KSU030BF474029-3	1.0e-59	Atriplex nummularia homologous sequence (ANJ1) mRNA	7.0e-81	DNAJ PROTEIN HOMOLOG 2
KSU030BF474862-3	2.0e-76	Oryza sativa OSKgamma mRNA for shaggy-related protein	1.0e-95	(AP001278) ESTs C22403(C50132),C22404(C50132) correspo
KSU030BG314423-2	1.1	Bifidobacterium longum Na+\H+ antiporter (nhaB), cytosine	0.001	(AF049920) PGPS\D4 [Petunia x hybrida]
KSU035BE403256-2	4.0e-04	Arabidopsis thaliana galactose kinase (GAL1) mRNA, comp	2.0e-67	GALACTOKINASE (GALACTOSE KINASE)
KSU035BE404437-3	6.0e-34	Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, compl	5.0e-70	DNAJ PROTEIN HOMOLOG (DNAJ-1)
KSU035BE497238-1	e-102	Zea mays variety BMS prohibitin (PHB4) mRNA, complete c	2.0e-59	(AF236368) prohibitin [Zea mays]
NDS018BE426655-1,2	e-153	Oryza sativa genomic DNA, chromosome 1, PAC clone:P04	1.0e-57	(AP002913) putative ribosomal protein L26 [Oryza sativa]
NDS021BF201678-1	9.0e-57	Rice (O.sativa) G11A protein, partial cds	2.0e-77	protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana
NDS034BE471188-2	5.0e-05	Elaeis guineensis calmodulin mRNA, complete cds	6.3	(X69926) HRPII [Plasmodium falciparum]
NDS043BF292161-2	1.2	Homo sapiens chromosome 17, clone 84_E_24, complete s	2.0e-39	hypothetical protein F17I5.110 - Arabidopsis thaliana
UCD001BE406335-3	0.87	Homo sapiens sema domain, immunoglobulin domain (Ig)	2.0e-41	(AC079279) unknown protein [Arabidopsis thaliana]
UCD028BG274817-5	1.0e-04	Arabidopsis thaliana galactose kinase (GAL1) mRNA, comp	3.0e-96	GALACTOKINASE (GALACTOSE KINASE)
UCD029BG263563-1	3.0e-08	Nicotiana tabacum anther ethylene-upregulated protein ER	4.0e-52	(AF096260) ER66 protein [Lycopersicon esculentum]
UCD037BE498609-4,8,15	0.1	Hordeum vulgare homeodomain protein JUBEL1 (JuBel1) g	7.0e-67	fructokinase (EC 2.7.1.4) - Arabidopsis thaliana kinases (Pf
UCW016BE590622-1,2	0	T.aestivum mRNA for serpin WZS3	2.0e-65	serpin homolog WZS3 - wheat
UCW020BE499799-9	0	Oryza sativa mRNA for EF-1 alpha, complete cds	1.0e-97	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) aestivum]
UMC040BE637463-8	0	H.vulgare BLT63 mRNA, complete CDS	2.0e-88	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) vulgare]
UMC040BF474210-3	1.0e-38	Zea mays ribosomal protein L30 (rpl30) mRNA, complete c	2.0e-46	60S RIBOSOMAL PROTEIN L30
UMC055BF483884-4,5	1.0e-09	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clo	2.0e-69	(AC011698) putative casein kinase [Arabidopsis thaliana]
UNL002BE498327-2	0.084	Caulobacter crescentus section 11 of 359 of the complete	5.0e-07	(AJ302292) MLA6 protein [Hordeum vulgare]
UNL036BE496891-1	5.0e-43	Hordeum vulgare photosystem-I PSI-F subunit precursor	0.006	(AF093634) photosystem-1 F subunit precursor [Oryza sati
UNL053BF293281-2	0	Triticum aestivum (1,4)-beta-xylan endohydrolase (WxI1) g	e-117	(AF156977) (1,4)-beta-xylan endohydrolase [Triticum aestiv

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

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