

Cloning Maize Homologs/Orthologs of Known Apex-Specific Genes

1. Identify possible family members in Arabidopsis
2. Identify conserved domains
3. Identify smaller conserved motifs that may distinguish closely related family members

use standard sequence analysis software or BLAST analysis

YABBY genes contain 2 highly conserved domains

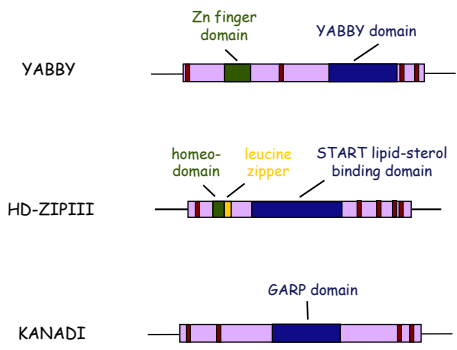
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FIL MNSNSNSPFS SAVCSDFPFS FSDQLCTVQC FQTLAVNV FYSLSFKVTV VRCQGCNILL SVN--MSTV
YAB3 MNSNSNSPFS AVAFPPDFPFS FSDQLCTVQC FQTLAVNV FYSLSFKVTV VRCQGCNILL SVTYSVHALL
YAB2 MNSVDFP --SEVYCVVRC FQTLAVNV FYSLSFKVTV VRCQGCNILL SVN--I--GVSS
YAB5 MANSVM MFDQCTVQC FQTLAVNV FYSLSFKVTV VRCQGCNILL SVN--MNAAL
INO NTKLPMY TLYNHLFDFP --SQICVQC FQTLAVNV FYSLSFKVTV VRCQGCNILL SVN--LMSAF
CRC MNLEKRP TMTASASFP --AEHLTVQC IONTLAVG FLSKMLDVTV VRCQGCNILL SVL--TTPFL

FIL LPAS-NQLQL QLPQHYVFP Q----- DILEHLSDAP ENNHNNMNOQ HPTMNDIP-- -----EFK
YAB3 LQVY-ENLGR FLPQPPFPFP PP----- NLLEEMDGG QNINNNMMS HGAHAKHPE SLVWATNNGR
YAB2 LQVYRAPPF QLPQHYVFP TS----- -LVYEDCK SEHRTNLS IN -----
YAB5 QSLRPNFQA NYTA----- -VPEYDSE RHTLPIRI ST -----
INO FLRLGLLALSL LLNTEKREY AATDQVHERA WFNWLEHNS FTLVLSIDM ID -----
CRC QDQVETLQM QPFS----- -QETVKG SSSSSSIFR IQ-----

FIL DLQQLQELDK -APVNNRPF KRQVPSAYN SFIKERQI KAGNFOISR EAFSAALKM ADFPHH-FO
YAB3 SVDELKEMPR -PPFANRPF KRQVPSAYN SFIKERQI KAGNFOISR EAFSAALKM ADFPHH-FO
YAB2 --IDLEADR -MFI--RPF KRQVPSAYN SFIKERQI KAGNFOISR EAFSAALKM ADFPHH-FO
YAB5 --RITTSQR ---LTV--RPF KRQVPSAYN SFIKERQI KAGNFOISR EAFSAALKM ADFPHH-FO
INO ----LUVSR VQVNNRPF KRQVPSAYN SFIKERQI KAGNFOISR EAFSAALKM HFFPAHNERA
CRC ----LPPFS -PPVVRPF KRQVPSAYN SFIKERQI KAGNFOISR EAFSAALKM AKTIPNS-PT

FIL LVPQNGVKK TNPQGGED NM---VMEK FVAPAAA--- NVGVVFP
YAB3 LMKHPFEEK ANVQGGED QE---MSEK FVGA--- NVGVVAM
YAB2 LKLD--GNKK QKQLQ--- -SVAGQSNQ YI
YAB5 LML--ENKQ AKTA
INO ANKIQPQEE DONALPCNV FEDREKSNQ FFERKAQHS INKSLPFE
CRC SITGQ-GRHM INGLQFQEK
    
```



3. Identify possible rice and maize homologs using Gramene

tblastn of Arabidopsis protein using:
 -Gramene BLAST search select database <http://www.gramene.org/>
 Rice genome
 Rice indica clusters (non-GenBank ESTs)
 Rice TIGR GI clusters (GenBank ESTs) or Rice dbEST
 Corn unigenes clusters or Maize consensus (public ESTs and Dupond data)
 Use the Gramene rice genome browser to obtain predicted cDNA sequences for rice and other monocots
 TC# (tentative consensus)
 Access sequence info via the TIGR plant gene indexes <http://www.tigr.org/db/tp/tpplant.shtml>

†BLASTn result with KANADI

Sequence	Description	Details	High Score	P _N	N
AP005430.003	-2	Alignment	249	4.1e-29	4
AP005904.003	+2	Alignment	242	1.3e-27	3
AP005868.001	-3	Alignment	186	2.6e-17	3
AP005859.002	+2	Alignment	186	3.6e-17	3
AP005734.001	+3	Alignment	189	5.1e-15	5
AP004635.001	+1	Alignment	167	8.5e-14	4
AC092780.003	+2	Alignment	134	1.4e-12	4
AP003885.001	-1	Alignment	189	3.8e-11	1
AL954829.001	-2	Alignment	142	5.0e-11	3
AP004463.001	+1	Alignment	189	8.8e-11	2

Access Rice Genome Browser Coordinates on the BAC

Customising 'ContigView Detailed Window'

Also include:
Sorghum GI
Wheat GI
Barley GI

Feature	Colour	Depth
DNA(contigs)		
primary		
Sequence		
Amino acids		
BLAST hits	red	2
SSAHA hits	red	2
Markers	magenta	3
Igenesprediction trans.		
Submitted Genes		
Rice_est	green1	2
Rice_01	green1	2
Rice_ind_est	green1	2
Rice_ind_cluster	green1	2
Rice_CDS	green1	2
Rice_hg	green1	2
Rice_jac_cDNA_KDME	green1	2
Maize_mashers	green1	2
Maize_Mu_insert	green1	2
Maize_est	green1	2
Maize_consensus	green1	2
Maize_01	green1	2
Maize_hg	green1	2
Maize_N_cdf	green1	2
Maize_mash_01_N_cdf_cluster	green1	2
Arabidopsis_transcript	red	2
Start/Stop	purple1	2
Repeats	gray50	2
Restr. Enzymes		
Length	black	2
%GC	gray50	2
Gene legend		
road		
info		

Chromosome fragment R9_AP005430 clone info

Overview

Detailed View

Jump to: [R9_AP0054] bp [103000] to [105000] Refresh

Zoom: 2 Mb, 1 Mb, 500 kb, 250 kb, 100 kb, 50 kb, 25 kb, 10 kb, 5 kb, 2 kb, 1 kb, 500 bp, 250 bp, 100 bp, 50 bp, 25 bp, 10 bp, 5 bp, 2 bp, 1 bp

enter gene coordinates

The tracks shown below are only a fraction of what is available. To see more, choose the Advanced option under Features.

Features: Repeats, Decorations, Export, Jump to, Image size

Help

Length

DNA(contigs)

Igenesprediction trans.

Wheat_01

Gene legend

Chromosome fragment R9_AP005430 clone info

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Detailed View

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Zoom: 2 Mb, 1 Mb, 500 kb, 250 kb, 100 kb, 50 kb, 25 kb, 10 kb, 5 kb, 2 kb, 1 kb, 500 bp, 250 bp, 100 bp, 50 bp, 25 bp, 10 bp, 5 bp, 2 bp, 1 bp

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Help

Length

DNA(contigs)

Igenesprediction trans.

Wheat_01

Gene legend

Other databases that can be used for BLAST analysis to identify possible rice and/or maize homologs

- ZmDB
- MaizeGDB (includes public and Dupond EST data?)
- GenBank via NCBI (daily updated, includes GSS and other genomic sequences and full length rice EST data; does not include Dupond or indica ESTs)

4. Identify possible rice and maize homologs using NCBI

<http://www.ncbi.nlm.nih.gov/BLAST/>

Nucleotide	<ul style="list-style-type: none"> * Discontiguous megablast * Megablast * Nucleotide-nucleotide BLAST (blastn) * Search for short, nearly exact matches 	Select database: gss (genomic) est_other
Protein	<ul style="list-style-type: none"> * Protein-protein BLAST (blastp) * PHI- and PSI-BLAST * Search for short, nearly exact matches * Search the conserved domain database (rpsblast) * Search by domain architecture (cdart) 	
Translated	<ul style="list-style-type: none"> * Translated query vs. protein database (blastx) * Protein query vs. translated database (tblastn) * Translated query vs. translated database (tblastx) 	
Genomes	<ul style="list-style-type: none"> * Human, mouse, rat * Fugu rubripes, zebrafish * Flies, nematodes, plants, yeasts, malaria * Microbial genomes, other eukaryotic genomes 	Select database: rice maize

NCBI formatting BLAST

Nucleotide Protein Translations Retrieve results for an RIG

Your request has been successfully submitted and put into the Blast Queue.

Query = (403 letters)

The request ID is [900205487560279137] BLAST[Q]

Format

Show: Detailed Overview Linkout Sequence Retrieval NCBI Alignment in HTML Format

Number of:

Alignment type:

Link results by: or select from [20] maps [RIG]

Export table:

