

Additional Data File 3. ClustalW alignment of the two rice duplicated genes and their orthologous gene from Arabidopsis (bottom one). The phases of introns (0,1,2) are highlighted. The intron loss and intron gain are highlighted in red and green respectively. The “~” indicates missing of intron at that position.

CLUSTAL W (1.83) Multiple Sequence Alignments

```

Sequence format is Pearson
Sequence 1: LOC_0s01g13130.1      256 aa
Sequence 2: LOC_0s05g14240.1      251 aa
Sequence 3: At2g25810.1           249 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 60
Sequences (1:3) Aligned. Score: 53
Sequences (2:3) Aligned. Score: 56
Guide tree      file created:  [/tmp/3MLr1SjSp3/6kTga9wjJ5.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences:  2      Score:4325
Group 2: Sequences:  3      Score:4113
Alignment Score 2629
GCG-Alignment file created  [/tmp/3MLr1SjSp3/P5W730m2jT]

```

MPLLPMTKLELGHRGEAWEPGCLRAVAGELLFTFLVFVIGVASTITA**1**G--KAAGGAGEA
----MAKEVDPCDHGEVVDAGCVRAVLAEVLTFVFVTGVAATMAA**1**GVPEVAGAAMP
-----MKKIELGHHSAAKPDCIKALIVEFITTLFVFAGVGSAMAT**1**D--SLVG--NTL
. . . . * . . . * . . . * . . . * . . . * . . . * . . . *

AAVTAAAMAQALVAVLATAGFHVSGGHLNPAVTLSLAVGGHITLFRSALYVAAQLAGSS
AALAGVAIATALAAGVLVTAGFHVSGGHLNPAVTVALLARGHITAFRSALYVAAQLLASS
VGLFAVAVAHAFVVAVMISAG-HISGGHLNPAVTLGLLLGGHISVFRAFLYWIDQLLASS

. . . * . * . . . * . . ** * . ***** . * *** . : . : ** ** *

LACLLLRCLTGGAAATPVLHALADGVGPVQGVAAAEAVFTFTLLLVCATILDPRRAAPPGT
LACILLRYLTGGMCAATPVHTLGSGIGPMQGLVMEIILTFSLLFVVYATILDP-SSVPGF
AACFLLSYLTGMMCGTPVHTLASGSYTQGIIWEIILTFSLLFTVYATIVDPPKKSLDGF

..* *.*.* *.*.*.* *.*.* * .*.*****.*****.* *

GPLLTGLLVGANTVAGGALTGASMNPARSFGPALATGEWAHHVWYWGPLAGGPLAVVAY
 GPLLTGLIVGANTIAGGNFSGASMNPARSFGPALATGVWTHHWIYWLGPLIGGPLAGLVY
 GPLLTGFFVGANILAGGAFSGASMNPARSFGPALVSGNWDTHWVWYWGPLIGGGLAGFIY
 ***** . . ***** . *** . . ***** . . * * . . ***** ** ** *

ELLFMDVEDA--GGAHQPLPQE--
ESLFLVKR-----THEPLLDNSF
ENVLIDRPHVPVADDEQPLLN---
* ::: ::** ;

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: LOC_0s01g61080.1 555 aa


```

NHDVPAARGSAALYRATPPQASNAGMMPTTAQPSSYLQGGGGVLPAGGYGASYGGAP
NHDVPAARG--SGYATNRAPQDSSSVPIRPAIAGHSNYTTSSQAPYTLQMLHNNNTNTG
*****  :. . :* :: . . . . .

PFGGVVGGSSFGGFSG-FDDARG--SYMSQHQQQRQNDAMH-ASRAKEEPGDD--MFF
TTTQPANGGGFAALSGRFDDDATGASYSYTSQQQQQPNDAVYYASRAKDEPRDDGIMSFF
PFGYAMNNN-----NNNSNLQTQQNFVGGGFSRAKEEPNEE--TSFF
.      ...      : * : * .      *****: ** :: **

QNSLY-
EQPLLF
DSFMP-
:. :

```

CLUSTAL W (1.83) Multiple Sequence Alignments

```

Sequence format is Pearson
Sequence 1: LOC_0s01g62490.1      577 aa
Sequence 2: LOC_0s05g38420.1      574 aa
Sequence 3: At5g60020.1           577 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 79
Sequences (1:3) Aligned. Score: 69
Sequences (2:3) Aligned. Score: 69
Guide tree      file created:  [/tmp/3MLr1SjSp3/bAG0qqcFug.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences:  2      Score:11378
Group 2: Sequences:  3      Score:10714
Alignment Score 8267
GCG-Alignment file created      [/tmp/3MLr1SjSp3/P5W730m2jT]

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```

MAISYLLRSSILAVAALLFSVNLAKGDIREYQFD0VKTTNVTRLCSSKSIVTVNGQFPG
MAAASSVLRCLLVAALMTLSAMGAEAITRQYLF0VQTTSVTRLCSTKSIVTVNGQYPG
-----MALQLLLAVFSCVLLLPQAFGITRHYTLE0IKMQNVTRLCSTKSLVSVNGQFPG
      * * : : :      * . *. * :: :: .***** :*:*:*:*:*:*:

```

```

PTVFAREGLVIRVINHSPYNMSIH2WHGIRQLRSGWADGPAYITQCPIQPGGSYVYKY
PTLFAREGDHVEVTVVNHSPYNMSIH2WHGIRQLLSGWADGPSYITQCPIQPGGSYVYRF
PKLIAREGDQVLKVVNQVPNNISLH2WHGIRQLRSGWADGPAYITQCPIQTGQSYVYNY
*.:*:***** * : *:*: * *:*: * ***** *****:*****.* *****.:

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```

TITGQRGTLWWHAHISWLRATVYGPIIILPKAGVPYPFPAPDKEVPVVF1GEWWKADTEA
TITGQRGTLWWHAHISWLRATVHGPMVILPPAGVGYPFPAPHEEVPIMF~GEWWNNDTEA
TIVGQRGTLWYHAHISWLRSTVYGPIIILPKRGVPYPFAKPHKEVPMIF1GEWFNADTEA
**.******:*****:*:*:*:** * * * *. *:*****: * *****: *

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```

VISQATQTGGGPNVSDAFTINGLPGLYNCSAK1DTFKLKVEAGKTYMLRLINAALNDEL
VISQALQTGGGPNISDAYTLNGLPGLYNCSAQ1DTFKLKVKPGKTYMLRLINAALNDEL
IIRQATQTGGGPNVSDAYTINGLPGLYNCSAK1DTFRLRVKPGKTYLLRLINAALNDEL
:* ** *****:*****:*****:*****:*****:*****:*****:

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```

FFSIAGHTLTVVDVDAVYVKPFTVDTLLITPGQTTNVLLTTKPSYPGATFYMLAAPYSTA
FFSIANHTLTVVDVDALYVKPFTVDTLIIAPGQTSNVLLTAKPTYPGASYMLARPYTTT

```


SFLFHKDDAACPARGFYTYASFVRAATRFRFAATGCADARKREVA AFLAQISHETTGGW
SLFIHKDDAACPARNFYTYAAFLRAADQYPSPFGGAGGRDTRRREVA AFLAQVSHETTGGW
KIFIHKNTACPANGFYTYESFVQATRRFRPGSVGSPVTQRLEVA AFLAQISHETTGGW

. . * . * . : . * . * . : : : * * . . : : : * . * . * : : : * . * . * . * : : : *

ATAPDGPYAWGLCYKEEINPQSSYCD-ATDKQWPCYPGKSYHGRGPIQIS2WNFNYPGAG
ATAPDGPYTWGLCFKEELKPASNYCDAVAARWPCFPGKSYHGRGPIQLS2WNFNYPGAG
ATAPDGPYAWGLCFKEEVSPQSTYCD-SSDTQWPCFPNKTYQGRGPIQLS2WNFNYPGAG
*****:*****:*****: * *.*** : :*****:*.***:*****: * **:*

QALGFDGLRNPEIVANCSDIAFQTALWFWMTTPR-DTKP-SCHQVMVGEYRPGPADVAANR
EAVGFDGLREPEVVAGDAVFAFKTALWFWMTTPRPPSKPYSCHDVMGTGRYRPSRADAAANR
RALGFDGLRNPETVSNNSVIAFQTALWFWMTTPQ-SPKP-SCHDVMIGKYRPTAADLAANR
.***:*****:*** *:. : :***:*****: : ** ***:*** * .*** ** *

TAG-FGLVTNIVNGGLECN--RAGDARVNNRIGFYRRYCQVLGVDVGNLDCHEHQPF-
TAAGFGLTTNIINGGLECNRTGGDPRVEDRIGFFRRYCGALGVDVGNLDCAHQLPYS
TGG-FGLTTNIINGGLECG--IPGDGRVNDRIGFFQRYTGLFKVATGPNLDCENQRPYA
*.. ***.***:*****. ** **::*****:*** : * . * *** : * *:

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: LOC_0s01g55240.1 327 aa
Sequence 2: LOC_0s05g48700.1 353 aa
Sequence 3: At1g30040.1 341 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 59
Sequences (1:3) Aligned. Score: 50
Sequences (2:3) Aligned. Score: 46
Guide tree file created: [/tmp/3MLr1SjSp3/99yTDExg5u.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:5528
Group 2: Sequences: 3 Score:5272
Alignment Score 3115
GCG-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

MVVLGPPAVD-HIPLLRSPD--PGDVFSGVVVDLGSPGAARAVVDACERYGFFKVVNH
MVAITAPSSIE-HIPLVRCPKANAGPQAVIPCIDLSAPGAAAADACRTLGFFKATNH
MVVLPQPVTLDNHISLIPTYKVPVLTSHSIPVNLADPEAKTRIVKACEEFGFFKVVNH
.. * ::: **.* : * ::* . * * :.. . *****

GVATDTMDKAESEAVRFFSQTQPKD-DRSGPAYPFGYGSKRIGFNGDMGWLEYLLALD-
GVPAGLADALESSAMAFFALPHQEKLDMGPARPLGYGSKSIGSNVDVGWLEYLLSAG-
GVRPELMTRLEQEAIGFFGLPQSLK-NRAGPPEPYGYGNKRIGPNGDVGWIEYLLNANP
** . *..*: ** . : * : :*** . * *** . * * ***:***:***** .

--DASLADACTVPSCAVF2RAALNEYISGVRKVAVRVMEAMSEGLGIAQAD---ALSAL
--AASSGGAALP---AAL2RAAVEAYTGAVRGVGRVMELMAEGLGLGASEEGRCVLRM
QLSSPKTSAVFRQTPQIF2RESVEEYMKIEKVSYKVLEMVAEELGIEPRD---TL SKM
:. . * : * ::: * :: * . :*: * :* ** : : . * :

VT-AEGSDQVFRVNHYPPCRALQGLG--CSVTGFGHTDPQLVSVLRNNGTSGLQIALR
VVGCEGSDEMLRVNHYPCLLPGRDRDECGVTGFGHTDPQIIISVLRNCTAGLQILLR
LR-DEKSDSCLRLNHYPAAEEEAEMK---VKVGFGHTDPQIIISVLRNNTAGLQICVK
: * ** . :*:*****. *****:***** *:***** ::

```

-----DGQWVSPSDRDSFFVNVGDSLQ0VLTNGRFKSVKHRVVAN-SLKSRVSFIYFGG
GDYSSPARWVPVPPDPDSFFVNVGDSLQ0VLTNGRFRSVKHRVLAPEGEESRLSVIYFGG
-----DGSWVAVPPDHSSFFINVGDALQ0VMTNGRFKSVKHRVLAD-TRRSRISMIYFGG
      .  **.*.*.*  .***:****:*  *:*****:*****:*  .***:*****

```

```

PPLAQRIAPLPQLLGEQSLYKEFTWDEYKKAAYKSRLGDNRLAQFEK-----
PAASQRIAPLEQVMREGEQSLYREFTWGEYKKAAYKTRLGDNRLGPYELQHAAANDEAAT
PPLSQKIAPLPCLVPEQDDWLYKEFTWSQYKSSAYKSKLGDYRLGLFEKQPLLNHKTLV-
*  .  *:*****  ::  *  ::  **:******:***:*****:***  **  .  *:  :

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KK
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CLUSTAL W (1.83) Multiple Sequence Alignments

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Sequence format is Pearson
Sequence 1: LOC_0s10g39810.1      301 aa
Sequence 2: LOC_0s03g01820.1      300 aa
Sequence 3: At4g12110.1          298 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 65
Sequences (1:3) Aligned. Score: 64
Sequences (2:3) Aligned. Score: 54
Guide tree      file created:  [/tmp/3MLr1SjSp3/gszx61aBcw.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences:  2      Score:5546
Group 2: Sequences:  3      Score:5307
Alignment Score 3822
GCG-Alignment file created      [/tmp/3MLr1SjSp3/P5W730m2jT]

```

```

MLPYATAAEAEAAALGRAMTAAESLWFRYSAGIPDYVLFWHNILFLFVVFTLAPLPVALLE
MLPYATAAEAEAAVGRGLTWAEAAWFRYSAAIPDYCLYCHNVPILLVYTLAPLPLALLE
MIPYATVEEASIALGRNLTRLETLWFDYSATKSDYYLYCHNIFLFLVFSLVPLPLVFVE
*:****.  **.  *:***  :*  *:  **  ***  .**  *:  **:  :*:*:*:*.****:***

```

```

LRA--PAAVGPFKLQPKVRLSREEFFRCYRDVMRLFFLVIGPLQLVSYPTVK0MVGIIHTG
LRR--HLPL-PHKLQPGVRHPPAAFLRCYAATARVLLAVGPPVQLASFPAVR~AVGIRTG
LARSASGLFNRYKIQPKVNYSLSDMFKCYKDVMTMFILVVGPLQLVSYPYSIQ0MIEIRSG
*      .  .*:**  *  .  :*:**  .  :*:*:*:*:*.***:***  :  *:**

```

```

LPLPSLGEMAAQLLVYFLVEDYLNWIHRLHGEWGYEKIHRVHHEFTAPIGFAAPYAHW
LPLPSAGETAAQVAVYLLVEDYLGWIHRLHPTWAYHHIHRVHHEFTAPMGYAAPYAHW
LPLPTITEMLSQLVYFLIEDYTNYWVHRFFHSKWGYDKIHRVHHEFTAPIGYAAPYAHW
****:  *  :*:  **:*:*****  .***:***:***  *.*:*****:***:***:*****

```

```

AEVLILGIPSFVGPALAPGHMITFWLWIVLRQMEAIETHS2GFDFPFNLTKYIPFYGGAE
AEILILGFPAFAGPAIVPCHMTTFWLWVLRHLEAIIHS2GFKLPDPTKYIPLYGGVE
AEVLLLGIPTFMGPAPAGHMITFWLWIALRQMEAIETHS2GYDFPWSPTKYIPFYGGAE
**:*:*:*:*:*  ***:  *  **  *****:***:***.  **  *:***:  *****:***.

```

```

YHDYHHYVGRQSQSNFASVFTYCDYLYGTDK0GYRYHKAYQAK0MKALGQTEGEKADSNG
YHDYHHFVGGSQSNFSSVFTFCDYIYGTDROGYRYHKASLSK0LKEMAGNHVEKGDENG

```


QEIASPAVLS-----
QGHEPSAVITSNPMDDYYV
KNYELMIH-----
:

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: LOC_0s02g52830.1 482 aa

Sequence 2: LOC_0s06g10850.1 489 aa

Sequence 3: At5g67050.1 477 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 61

Sequences (1:3) Aligned. Score: 45

Sequences (2:3) Aligned. Score: 41

Guide tree file created: [/tmp/3MLr1SjSp3/RMLx7X2LxF.dnd]

Start of Multiple Alignment

There are 2 groups

Aligning...

Group 1: Sequences: 2 Score:8388

Group 2: Sequences: 3 Score:7254

Alignment Score 4404

CGC-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

-MAGAGEYGGGGGGGGGGGGFGGDFMVLRPDKGGIGDLFHLLWSCKVAENAAVDCP-IGTEIA
-MDDDDDCRRRD---VTLGDEFMVLQPENGGARSLADLLLCKVGENKAVRCGRPGAeva
MMNSDDDDDEPRG-----YLILRPEELRPWELVRLLFSGDIEKPRSDSS--ETEEH
* . . . : : : : : * * * * . : : : * . : *

ERRRRWALFVSLVAQMLLLWTKKPMALLGGGTEYWMNLLNENGGSVFMLITNALQ1GKVK
LPWHRWIIAVSLLAQMLRLSKGVMAKVGRAVEYWMNLVSEND-NVLGLIRNALH1GKVK
SFRHRWLIFVSLVLLKLLRFFSKLLALVGSALFSLNFLSNNS----FSGFLFLR1GEV
: ** : ***: * * . : * : * . * : : * : : * . : : * : * : *

MPDKSSINRSCIGLLDTRIDLDEKIKPED-RNYHAALSIMAAKLAYENELVVRTVQNH
TPDRNSPNYRSFIGLLDTRIDLDEKIKPGD-SNYHAALCIMAACLAYENELVIKDAVEKN
MPQRTSENYQSFIGHLDTRVSLDMTLNREDGEKYAALSIMASKIAYENAARIKHVVENH
* : : * * : * * * * : : * : * : * : * : * : * : * : * : * : *

WQ0MNFVGFYNCWN1EFQEDYTTQAFMVSDKAE-----DASLAVVAFCGTKPFDTEQWC
WK0MTFLEFFNCWN1DFQNDYTTQAFMFADKPE-----DAELVVVAFRGTPFDMEQWS
WN~MKYLGLVDYWN1EYQEKETTQAFIMSTDETTTRSNGQETTvvvAFRGTELFNSDWC
* : * : : : * * : : : * * : : : * * : : : * * : : : * * : : *

ADVDFSWYEIPGVGKVHGGFMKALGLQRNGG-----WPEQPTGAGDDGGSDK-KPFAYY
TDVDISWYEIPGVGKVHGGFMKALGLQNNAAAGKKPSWPAEIAPPSAAKNSEKTKSFAYY
SDFDITWFELPNIGNIHGGFMKALGLQNNCS-----WPKEPLS-----NPDRKSPLAYY
: * : : : : * : : : : * : : : : * : : : : * : : : : * : : : *

VIRERLRAFLAENPRARFVAGHSLGGALAILFPTVLALHG--EEDMLARLHGvyTfGQ
AIRARLRAFLAANPRARLVVTHSLGGALAALFPVVLALHGGEADAAALGRLDGVYTYGQ
SIRDSLKTLIAQNKNTKFVLTGHSLGGALAILFTAVLVIHH--ETELLERIQGVYTYGQ
* * * : : : * * : : : * : : : * : : : * : : : * : : : * : : : *

PRVGDEGLCRFMDGHLATPVSRYFRFVYCNDIVPRVPYDDTALLFKHFGTCLYFDSFYKG


```

SHKLFEILPVLRYLIYTP2TYHSLHHQEMGTNFCFLMPLFDVLGDTQNPNSWELQKKIRL
* : * : . * . * * * * * * : * * * * : * : * * * * * : * * * : * : * : *
1--~GKNDQAPDFVFLAHVVDIMASMHVPFVLRSCSSTPFANHFVLLPFWPVAFGFMLLM
1--~GKNHRVPDFVFLVHVVDVSSMHVPFAFRACSSLPFATHLVLLPLWPIAFGFMLLQ
~SA1GERKRVPEFVFLAHGVDVMSAMHAPFVFRSFASMPYTTTRIFLLPMWPFTFCVMLGM
* : . . . : * : * * * . * * * : : : * * . * : : : * * : : : . * * : * : * . * *
WCCSKTFLVSSYRLRGNLHQMWTVPYRGFQ0YFIPAACKGINEQIELAILRADRMGVKVL
WFCSKTFTVSFYKLRGFLHQTWSVPRYGFQ0YFIPSAKKGINEMIELAILRADKMGVKVL
WAWSKTFLFSFYTLRNNLCQTWGVPRFGFQ0YFLPFATKGINDQIEAAILRADKIGVKVI
* * * * . * * * . * * * * * : * * * * * : * * * * : * * * * * : * * * * : * * * * :
SLAALNK0NEALNGGGTLFVNKHPDLRVRVVGNTLTAAVILNEIPSNVKDVFLTGTASK
SLAALNK0NEALNGGGTLFVRKHPDLRVRVVGNTLTAAVILNEIPGDVAEVFLTGTASK
SLAALNK0NEALNGGGTLFVNKHPDLRVRVVGNTLTAAVILYEIPKDVNEVFLTGTASK
* * * * * * * * * * * * * * . * * : * * * * * * * * * * * * * * * * * : * : * * * * * * *
LGRAIALYLCRKKIRVL0MLTLSSERFLKIQREAPAEFQQYLVQVTKYQPAQNCK0TWLV
LGRAIALYLCRKKIRVL0MLTLSTERFMNIQREAPAEFQQYLVQVTKYQAAQNCK0TWIV
LGRAIALYLCRRGVRVL0MLTSMERFQKIQKEAPVEFQNNLVQVTKYNAAQHCK0TWIV
* * * * * * * * * : : * * * * * * * * * : * * : * * * . * * : * * * * * : * * * * : * * : * * * * : *
GKWLSPREQRWAPAGTHFHQFVVPPIIGFRRDCTYGKLAAMRLPKDVQGLGYCE0YTMER
GKWLSPREQRWAPAGTHFHQFVVPPIIGFRRDCTYGKLAAMRLPEDVEGLGTCE~YTMRG
GKWLTPREQSWAPAGTHFHQFVVPPIILKFRNCTYGDLAAMKLPKDVEGLGTCE0YTMER
* * * * . * * * * * * * * * * * * * * : * * : * * * . * * * : * * : * * * * * * * * * * * * * * * *
GVVHACHAGGVVHFLEGWEHVEVGAIDVDRIDVVWKAALKHGLTPA-----
GVVHACHAGGVVHFLEGWDHHEVGAIDVDRIDAVWNAALRHGLTPA-----
GVVHACHAGGVVHMLEGWKHVEVGAIDVDRIDLWEAAMKYGLSAVSSLTN
* * * * * * * * * : * * * . * * * * * * * * * * * * * * : * * : * * : * * : . .

```

CLUSTAL W (1.83) Multiple Sequence Alignments

```

Sequence format is Pearson
Sequence 1: LOC_0s02g14430.1      327 aa
Sequence 2: LOC_0s06g35480.1      318 aa
Sequence 3: At5g58400.1          325 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 60
Sequences (1:3) Aligned. Score: 58
Sequences (2:3) Aligned. Score: 52
Guide tree      file created:  [/tmp/3MLr1SjSp3/9QckQp43uH.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences:  2      Score:5595
Group 2: Sequences:  3      Score:5362
Alignment Score 3362
GCG-Alignment file created      [/tmp/3MLr1SjSp3/P5W730m2jT]

```

```

MASR-SSWHCCLLAFFLLSSAAGAAYGQQLSTTFYAASCPTLQVVVRATVLGALLAERRM
MAT--QWVLVVVAVMAVLFAGGAAGG-QLSTRYYDGKCPNVQSIVRAGMAQAVAAEPRM
MECYEQSRQRAAFVLLFIVMLGSQAQAQLRTDFYSDSCPSLLPTVRRVVQREVAKERRI

```

LVTKGSTGVGFATSTAGKGN - -VIYGLVQCRGDVSTSDCQACLASAA NQILTSCNYQSD
LVPRASA- GYYATATAGRGGDSAIWGLAQCRG DIPAPDCALCASAAARQLAGACRGRAD
LVSKTPS-KGFKTTTSSSYNNKEKVYGLAQCRGDISNTDCSTCIQDAAKKIREVCQNQSD
** . : . * . * . : . : ** * * * * . ** * ** : . * : *

SRI2WYDYCFMRFENENFFGQADTDNGVIMENVQAMDN - -AKAFQKAVGKVMASKATAQVS
ARV~WYDYCFARYDDADFGVLPDTGYALILLNTQNATD - -PEAFEKAQRKVMARVAADAG
SRI~LYDFCFRLYSQENFIGKLDTGAGLIYFNVANVTEIDPKKFDNELGALFDKIRSEAV
*: **:*** *: : :*. * ** . : * * : : * : : : : : :

QAGSGGLGRVKDQYTPFINIYGFAQCTRDLSPLTCAQCLSTAVSRFDQYCGAQQGCRILY
DAGGGGLARETARFKDGVTIYGLGWCTRDITAADCGLCVAQAVAEMPNYCRFRRGCRVLY
LPKNKGLGKGKTKLTPFVTLNGLVQCTRDLSLDCAQCFATAVGSFMTTCHNKKGCRVLY
. . ** : . : . : : * : ***** : * . * : ** . : * : : : : : *

SSCMVRYEIYPFYFPLAT - - -SSTATDMTKYTKTIVHH
SSCMARYETYPFFFLDGGQSADASASAAGDYDRVVLNP
SSCYVRYEFYPFYFPLDP - - -AKTGPS-VGRISSVHLSP
*** . *** ** : *** : : : : : . :

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: LOC_0s03g21820.1 259 aa
Sequence 2: LOC_0s05g39990.1 246 aa
Sequence 3: At2g40610.1 253 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 75
Sequences (1:3) Aligned. Score: 64
Sequences (2:3) Aligned. Score: 71
Guide tree file created: [/tmp/3MLr1SjSp3/gg0HAWZdw5.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:4764
Group 2: Sequences: 3 Score:4623
Alignment Score 3486
GCG-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

MAPP--LLLLLASLLLVAARRALGLGLGQWQPGHATFYGGGDASGTM1GGACGYGNLYSQ
-----MAIAGVLFLLFLARQASAAGYGGWQSAHATFYGGGDASGTM1GGACGYGNLYSQ
MYTPSYLKYSIISIISVLFLLQGTGDDGGWQGGHATFYGGEDASGTM1GGACGYGNLYGQ
: : : . : . . * ** .***** ***** ***** *

GYGTSTAALSTALFNRGLSCGSCYELRCAGDHRRSCLPGGATVTVTATNFCPPNYALPSD
GYGTNTAALSTALFNDGAACGSCYELRCD-NAGSSCLPG - -SITVTATNFCPPNYGLPSD
GYGTNTAALSTALFNGLTCGACYEMKCN-DDPRWCLGS - -TITVTATNFCPPNPGLSND
****.***** * : **:*** : : ** . : :***** * . . *

GGGWCNPPRRHFDLAEPAFLRIARHAAGIVPVSFR~RVACARKGGVRFTVNGHAYFNLVL
DGGWCNPPRPHFDMAEPAFLHIAQYRAGIVPVSFR2RVPCVKKGGVRFTVNGHSYFNLVL
NGGWCNPLQHFDLAEPAFLQIAQYRAGIVPVSFR2RVPCMKKGGIRFTINGHSYFNLVL
.***** **:***** : : : ***** * . * : : : : : : : *

VTNVGGAGDVRS LAVKSGSGSRVGGRWQPM SRNWQNWQSNAYLDGKALSFRVTAGDGR
VTNVAGAGDVRSVSIKGSRTG - - - -WQPM SRNWQNWQSN AFLDGQSLSFQVTASDGR
ISNVGGAGDVHAVSIKGSKTQS - - - -WQAM SRNWQNWQSN SYMNDQSLSFQVTTSDGR
: : * .***** : : : : : ** .***** : : : : : : : : : : *

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: LOC_0s03g55420.1 324 aa
Sequence 2: LOC_0s07g02440.1 330 aa
Sequence 3: At4g37520.1 329 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 73
Sequences (1:3) Aligned. Score: 60
Sequences (2:3) Aligned. Score: 62
Guide tree file created: [/tmp/3MLr1SjSp3/nQGP0Eh4wP.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:6132
Group 2: Sequences: 3 Score:5751
Alignment Score 4043
GCG-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

-MGAGIR-----ILVVMLAVAAAGSGVVAQLRRDYYASVCPDVETIVRDAVTKKVQETS
MMVVMMRRRMAAAAMLVLVAMAGGATVCAAQLRRNYYAGVCPNVESIVRGAVARKVQETF
-MVVVNKTN----LLLLLLSLCLTLDLSSAQLRRNFYAGSCPVEQIVRNAVQKKVQQTF
* . : ::::: *****:*. **:** ***.** :***:*

VAVGATVRLFFHDCFVE0GCDASVIVVSSGNNTAEKDHPNNLSLAGDGFDTVIKARAAVD
ATVGATVRLFFHDCFVD0GCDASVVVASAGNNTAEKDHPNNLSLAGDGFDTVIKAKAAVD
TTIPATLRLRYFHDCFVN0GCDASVMIASTNNNKAEKDHEENLSLAGDGFDTVIKAKEALD
.:. **:***:*****: *****:*.**:** ***** :*****:*****: **:

AVPQCTNQVSCADILVMATRDVIAL0AGGPSYAVELGRLDGLSSTASSVDGKLPPPSFNL
AVPGCRDRVSCADILAMATRDAL0AGGPSYAVELGRLDGLRSTASSVNGRLPPPTFNL
AVPNCRNKVSCADILTMATRDVVNL0AGGPQYDVELGRLDGLSSTAASVGGKLPHPTDDV
*** * :*****.*****.: * *****.***** ***:**.*:*** *: ::

DQLTSLFAANNLSQTDMIALS1AAHTVGFAHCGTFASRIQ---PSAVDPTMDAGYASQL
DQLTALFAANGLSQADMIALS1AGHTVGFAHCNTFLGRIR---GSSVDPTMSPRYAAQL
NKLTSLFAKNGLSLNDMIALS1GAHTLGFAHCTKVFNRITYTFNKTTKVDPTVNKDYVTEL
:***:*** *.** ***** ..**:* ***** ..** : *****: *.:**:

QAACPAGVDPNIALELDPVTPRAFDNQYFVNLQKGMGLFTSDQVLYSDDRSRPTVDAWAA
QRSCPPNVDPRIAVTMDPVTTPRAFDNQYFKNLQNGMGLLGSDQVLYSDPRSRPIVDSWAQ
KASCPRNIDPRVAINMDPTTPRQFDNVYYKNLQQGKGLFTSDQVLFDDRSPKPTVDLWAN
: :** ..**.:**.:**.***.***.*: ***:**.***.:*****:*.**:* **.***

NSSDFELAFVAAMTNLGRVGKTDPSQGNIRRDCAMLI
SSAAFNQAFVTAMTKLGRVGKGTG-SQGNIRRNCAVLN
NGQLFNQAFINSMIKLGRVGKGTG-SNGNIRRDCAFN
.. *: **.:**.:**.:*****. *:*****:*. :

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: LOC_0s03g60080.1 316 aa
Sequence 2: LOC_0s07g12340.1 276 aa
Sequence 3: At5g08790.1 283 aa

Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 63
Sequences (1:3) Aligned. Score: 45
Sequences (2:3) Aligned. Score: 43
Guide tree file created: [/tmp/3MLr1SjSp3/mrU8SdWzr0.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:4970
Group 2: Sequences: 3 Score:4221
Alignment Score 2711
GCG-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

MGMGMRRRERDAEALNLPFGFRFHPTDDELVEHYLCRKAAGQRLPVPIIAEVDLYKFDPW
MAAAKRRVRDAEADLNLPFGFRFHPTDEELVAHYLCPRAGRAAPVPIIAELDLYRHDPW
-----MKSELNLPAGFRFHPTDEELVKFYLCRKCASEQISAPVIAEIDLYKFNPW
:::****.*****:***.***:.*.. ..*:****:***:.*

DLP~ERALFGAREWYFFTPDRKYPNGSRPNRAAGNGYWKATGADKPVAPRGRTLGIKKA
DLP~HRALFGRREWYFFTPDRKYPNGSRPNRAAASGYWKATGADKPV LHNGRTAGIKKA
ELP1EMSLYGEKEWYFFSPDRKYPNGSRPNRAAGTGYWKATGADKPIG-KPKTLGIKKA
:* . :*: :*****:*****.*****: . :* *****

LVFYAGKAPRGVKTDWIMHEYRLADAGRAAAGAKKGSRLR~LDDWVLCRLYNKKNEWEKMQ
LVFYHGKPPRGVKTEWIMHEYRLAKKGGAAAAAGAGALR~LDDWVLCRLYNKKNEWEKMQ
LVFYAGKAPKGIKTWIMHEYRLANVDRSASVNKKNNLR~LDDWVLCRIYNKKGTMEKYF
**** *.*:*:*****. . :*: . ** *****:****. **

QGKEVKEEASDMVTSQSHSTHSWGETRTPSEIVDNDPPELDSFPAFQPAPPPATAMM
SRK---EEEEAMAAQs-----WGETRTPSEIVDSDAFPEMD----YSLPAASFDDAL
PAD---EKPRTTTMAEQSSSPFDTSSTYPTLQEDDSSSSGGHG----HVVSPDVLEVQS
. *: . :*. :*: * : *... . .

VPKKEsMDDATAAAAAAATIPRNSSLFVDLSYDDIQGMYSGLDMLPPGDDFYSSLFASP
LPKEEARDDD-----WLMGMSLDDLQGLGS----LLQADDL--SMLAPP
EPKWGELEDALEAFDT-----SMFGSSMELLQPDFAVPQFLYQSDYF--TSFQDP
** :* :.. * :*: * .*: : : *

RVKGTTPRAGAGMGMVPF-
PAAKTEP-----LGAPFF-
PEQKPFLN---WSFAPQG
. .

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: LOC_0s03g18140.1 558 aa
Sequence 2: LOC_0s07g49280.1 605 aa
Sequence 3: At3g55990.1 487 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 54
Sequences (1:3) Aligned. Score: 55
Sequences (2:3) Aligned. Score: 48
Guide tree file created: [/tmp/3MLr1SjSp3/JKoVtWUlcR.dnd]

Start of Multiple Alignment

There are 2 groups

Aligning...

Group 1: Sequences: 2 Score:8369

Group 2: Sequences: 3 Score:8112

Alignment Score 4945

CGC-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

MQQRRKSVFASA-----PFAMKQAALGAGVAAR-RNGAPLSLAAVVFALFVF---AT
MKKKKNGMGAAADRGRLLALAHDKLNPTKPSEAQR RFKPSILLLLGSSLPRLVPPLPSS
MQPWRR-----KFPLFETGVTMKQRKNSNLSIFVVVFSVFLF---GI
*: :. * .. : : : * : .. :.

FLYNEDIKSIADFPFGAGALRAKSPDLHVLQETVGAH LAAGSIAKRGEIVIRVLD---
FLPVVIKQTEFHQRWLVGDLNPPPPCHLLPIQGQGMQMQRKPPPAAPVAAKQPS
FMYNEDVKSIAEFPFST----SKPHDVH-----
*: :. :. :. : *

--APASTAMAAAAGSSSNSTIEVAKANANANANAADAGVKVDEGQERERDVTLP SVKEG
RRTPGPLSFAGALLSLLVATFLYINDHGNMMPPHASPDPLRL LQEAHQKVNSILLR
-----DEATPITEITTLPVQESIKNSDP-IQESIKNADSVQDSVKDVAEP-----
.: : * . . . * : : .

GADEARRREDEEAAEKES-----SAKAAAATAALRTVVSVPDT-----
HAPAPPPRTNTNTSSSDQHLRLINIPMSSDLDELGGNSTSSSGVEIQFEQQQQEENL
-----VQEEVSKTEEVK-----KIELFAATEDEEDVELPPEE-----
: : . :. . : : . *

--CDLYRGNWVYDEVN--APVYKESQCEFLTEQVTCMRNGRRDDSYQKWRWQPTDCDLP2
RGCELYKGRWVYDAAGREAPLYRESECGFLTEQVTCMRNGRRDDSYQKWRWQPEGCDLP~
--CDLFTGEWVFDNET--HPLYKEDQCEFLTAQVTCMRNGRRDSLYQKWRWQPRDCSLP2
*: : * : * : * : * : * : * : * : * : * : * : * : * : *

RFDARLLLERLRNKRMLFVGDSLNRNQWESMVCLVQSVIPKGKKT LTKFVNGGNSNIFYA
SFDARALLERLRNKRMMFVGDSLNRNQWESMVCLVQSAIPYGQKT LTKFVNNGSLNVFRA
KFKAKLLLEKLNRNKRMMFVGDSLNRNQWESMVCLVQSVVPPGRKSLN--KTGSLSVFRV
* : * : * : * : * : * : * : * : * : * : * : * : * : *

H0EYNATVEFYWAPFLVESNSDNPQVHVSVPDRVIQWHSIAKHAHNWLGVDYLIFNTYIWW
H0EYNATVEFYWAPFLVQSNSDDPQVHVSVRDRVIAWRSIAKHAANWKGVHYLVFNTYIWW
E0DYNATVEFYWAPFLVESNSDDPNMHSILNRIIMPESIEKHGVNWKGVDFLVFNTYIWW
. : * : * : * : * : * : * : * : * : * : * : * : * : *

LNTLDMKV2LKG--SFDQG--ATEYVEVDRPVAYKEVLKTWAKWVDRNIDPNRTTVFF
LNNFQIKV2LKSRGAPFAGSGGWSSRYALVDRAIAYREVLKTWAKWVDRRIDPNKTHVFF
MNTFAMKV2LRG--SFDKG--DTEYEEIERPVAYRRVMRTWGDWVERNIDPLRTTVFF
: : : * :. * : : * : : * : : * : : * : : * : *

MSMSPNHI2TPEAWG-NYGGIKCAMETLPITNRTTS-LDVGTDWRLYAGAQEVLTQFRRV
MAMSPNHF2MPEAWGGSAGAVKCAMETQPIVNRTSGGLDIGTDWRLHGVARGVLRSMRRV
ASMSPLHI2KSLDWE-NPDGIKCALETPILNMSMP-FSVGTDYRLFSAENVTHSLN-V
: * * : . * . : : * : * : * : * : : : * : * : * : * : *

PVHLVDITALSELRKDAHTSVHTLRQGKLLTPEQQSDPKTYADCIHWCLPGLPDTWNQFL
GVRFVDITALSELRKDAHTSVHTLRQGKLLTPEQQADPRTYADCIHWCLPGLPDTWNHFL
PVYFLNITKLSEYRKDAHTSVHTIRQGKMLTPEQQADPNTYADCIHWCLPGLPDTWNEFL
* : : * : * : * : * : * : * : * : * : * : * : * : *

YARIASAPWSSDQ
YAHIVAHAA----
YTRIISRS-----
:: : .

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: LOC_0s03g18690.1 450 aa
Sequence 2: LOC_0s07g49150.1 448 aa
Sequence 3: At4g29040.1 443 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 98
Sequences (1:3) Aligned. Score: 91
Sequences (2:3) Aligned. Score: 92
Guide tree file created: [/tmp/3MLr1SjSp3/pNSWckggam.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:9562
Group 2: Sequences: 3 Score:9237
Alignment Score 7656
GCG-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

MGQGTTPGGMGKQGGPLPGDRKPGDGGAGDKKDRKFEPAPSRVGRKQRKQKGPEAAARLP
MGQGTTPGGMGKQGGAPGDRKPG--GDGDKKDRKFEPAPSRVGRKQRKQKGPEAAARLP
MGQGSPGGLNRQG----DRKPD---GGDKKEKKFEPAPPARVGRKQRKQKGPEAAARLP
****.:.:.*:****.*****:.*:*****

AVAPLSKCRLLRLKLERVKDYLLMEEEFVVSQERLRPSEDKTEEDRSKVDDL RGT PMSVG
NVAPLSKCRLLRLKLERVKDYLLMEEEFVAAQERLRPTEDKTEEDRSKVDDL RGT PMSVG
TVTPSTKCKLRLKLERIKDYLLMEEEFVANQERLKPQEEKAEEDRSKVDDL RGT PMSVG
:.:.*:*****:*****.*****:.*:*****

SLEEIIDESHAIVSSSVGPEYYVGILSFVDKDQLEPGCAILMHNK0VLSVVGILQDEVDP
SLEEIIDESHAIVSSSVGPEYYVGILSFVDKDQLEPGCSILMHNK0VLSVVGILQDEVDP
NLEELIDENHAIVSSSVGPEYYVGILSFVDKDQLEPGCSILMHNK0VLSVVGILQDEVDP
.***:***.*****:*****:*****

MVSVMKVEKAPLESYADIGGLDAQIQEIKEAVELPLTHPELYEDIGIRPPKGVILYGE
MVSVMKVEKAPLESYADIGGLDAQIQEIKEAVELPLTHPELYEDIGIRPPKGVILYGE
MVSVMKVEKAPLESYADIGGLEAQIQEIKEAVELPLTHPELYEDIGIKPPKGVILYGE
*****:*****:*****

TGKTLLAK0AVANSTSATFLRVVGSELIQKYLGDGPKLVRELFVADDLSPSIVFIDEID
TGKTLLAK0AVANSTSATFLRVVGSELIQKYLGDGPKLVRELFVADLSPSIVFIDEID
TGKTLLAK0AVANSTSATFLRVVGSELIQKYLGDGPKLVRELFVADDLSPSIVFIDEID
***** *****:*****

AVGTK2RYDAHSGGEREIQRTMLELLNQLDGFDSRGDVKVILATNRIESLDPALLRPGRI
AVGTKRYDAHSGGEREIQRTMLELLNQLDGFDSRGDVKVILATNRIESLDPALLRPGRI
AVGTK2RYDAHSGGEREIQRTMLELLNQLDGFDSRGDVKVILATNRIESLDPALLRPGRI

DRKIEFPLPDIKTRRRIFQ0IHTSKMTLADDVNLEEFVMTKDEFSGADIKAICTEAGLLA
DRKIEFPLPDIKTRRRIFQ0IHTSKMTLADDVNLEEFVMTKDEFSGADIKAICTEAGLLA
DRKIEFPLPDIKTRRRIFQ0IHTSKMTLSEDEVNLEEFVMTKDEFSGADIKAICTEAGLLA
*****:*****

LRERRMK0VTHADFKKAKEKVMFKKKEGVPEGLYM
LRERRMK0VTHADFKKAKEKVMFKKKEGVPEGLYM
LRERRMK0VTHPDFKKAKEKVMFKKKEGVPEGLYM

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: LOC_0s03g19200.1 668 aa
Sequence 2: LOC_0s07g49000.1 603 aa
Sequence 3: At4g02100.1 546 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 70
Sequences (1:3) Aligned. Score: 49
Sequences (2:3) Aligned. Score: 49
Guide tree file created: [/tmp/3MLr1SjSp3/R8JVidYg6w.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:10978
Group 2: Sequences: 3 Score:8827
Alignment Score 5936
GCG-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

MAVSSPTSAPEKKRKWLLSNRK0-VIDKYLREARAILATAPEA-----GG--GDVAALG
MAVSS----PDRRRNWLGRHK0QIIGDYLAEARAALAAAAAPLDGEGGEHSAATAALG
MAVYG-----EKKHWWLRNKK0-IVDKYMKEAKSLIASQDPN-----DVKSALN
*** . :*: :*: :*: :*: :*: :*:

LVDAALELSPRMESAELRGRALLSLRRYRDVAEMLRDYIPSCAKTCSGDDTLSSSTSSS
LVEAVLEMSPRMEAELRARSLLALRRYRAVADMLRDYIPCTKPCSADDTSSSSSSSS
LLESALSVPYELALELKARSLLYLRRYKDVADMLQDYIPSLKLAGGSGIGSSSELS
:

LSSSGSGDLGTISRAKLLS--PDRHRSDAAEPGA AVARSFRCFDISELKRRVLASLSKN
SCSSAS-----RTDLLS--PARDRSDAAS---AASRFLCCFDISDLKHRVLAGFSKN
FTHSSR-----ESVKLLNDLPSHHHHHDSS-----FKCFSVSDLKKKVMAGLTKN
* . :*: :*: :*: :*: :*: :*: :*: :*: :*: :*: :*: :*: :*

PNTDTQW2RYLVLGQACFHLGLIEDAMVLLQTGRRLASAAFRRESVCLSEDSFS-SSSPA
TSADTQW~RYLVLGQACFHLGLMEDAAALLQTGRRLASAAFRRESVCWSEDSFSPSNLTA
CDEQGQW2RYLVLGQACCHLGLMEDAMVLLQTGKRLATAAFRRQICWSDDSFILFSSD
. : * * * * * : * * * * * : * * * * * : * * * * * : * * * * *

AAVAPIPSGNTTKSGSAFIIPAMESEAVSQLLAHVKLLLRRTAAMAALDAGLPAEAVRH
NAISAPASRRASKG---AAGSEAESVSQLLAHVKLLLRRAAVALDADLPAEAVRH
GGSSPPSSVVVTSAS-----QPRSEIAHVLSHIKLLLRRAAALAALDAGLYTESIRH
. : . * : * * : * * : * * : * * : * * : * * : * * : * * : *

FSKILEARRGVLPHPFAAACLVGRAAAFQAGGRPADAIA DCNRALALDPAYIPALRARAD

FSKVL DARRGVLPHPFATA CLVGRAEALRSSGRAADAIADCNRALALDPAFIPALRSRAD
FSKILDSRRG-APQGF LAQCFMHRASAYRSAGRIAESIADCNKTLALDP SCLQALETRAA
::*** * : * : ***: ** * :.*** *:*****:*****: : **.:**

LLQSVGALADCLRDLDHLKLLYDAALRDGKLP GPRWRPQGGVRYREIAG AHRKLTARIQQ
LLESVGALSDCLRDLEHLKLLYDAALRDGKLP GPTWRPQGGVRFSEIAG AHRALTPRIQQ
LLESVRCFPDSLHDLEHLKLLYNSILRDRKLP GPVWKRHN-VRYREIPGKLCVLT TTKIQQ
: .:.*.**:*:*:*:*:*:*:*: ** * ** * :. ** : **.* **.:**

LRSRVAAGEACNIDYYALLGVRRGCTRSELERAHLLLT LKLPDRAVVFGERLELVDEHR
LRGRVAGGEACSV DYYALLGVRRGCTRSELERAHLLLT LKLRPDR CASFAERLELVDEHR
LKQKIANGEIGNVDYYALMGIRRDCSRSELD RAYLLLNLKHKPERSMSFIDRFELTDDEE
* : : * ** .:*****:*:*:*:*:*:*:*:*:*:* ** :*: * :*:***.*:..

DLEAVRDQARMSALLLYRMLQKGYSFIMSAVIDEEAERQ RAREAAAAAAAAAAAAAAAAA
DLEAVRDQARMSALSLYRMLQKGYSFIMSVVQDEEAERQ RAKDAAAAT---AAAAAAA
ELDSVKDRARMSTLLLYRLIQKGYSVVT SNIA---AVEKQRK-----AI
:***:***:***:* ***:*****.: * : * .*:** *

AAALAVKQEATKQELAAPPMPEKPRQTESAPCAKRSMA SKAKPKAKPAATVP SMMSRKAA
AAALAREQEET-----AAVPEKAR-----ISSVSPSTN-----
AAAVATESHRS-----
***:* :.. :

TTTTTAKAAMSKAAVTAPKAAAATAVAATAVAAAATAASTSTAAPVYQGVFCRDM AVVGT
-----VQVQVTQAAAMPTAAMAAAAAMGSPVFQGVFCRDM AVVGT
-----NIIETPIRAVAVAVNSNNNTNVVKGVFCRDLTVVGS
:..:.* *. : : * :*****:***:

LLSRGGFVDRAMPVKCEAMSC
LLSRGGF-DRPIPVKCEAMSC
LIARTGF-NQPIPVKYEALSC
: ** :..:*** **:**

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: LOC_0s08g39370.1 548 aa
Sequence 2: LOC_0s09g31130.1 543 aa
Sequence 3: At5g47560.1 540 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 76
Sequences (1:3) Aligned. Score: 60
Sequences (2:3) Aligned. Score: 63
Guide tree file created: [/tmp/3MLr1SjSp3/MwHzm6VzGx.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:10402
Group 2: Sequences: 3 Score:9516
Alignment Score 6826
GCG-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

MDKNGSSYGESSSDVEAPLLLPAARGGTMAKGDRRRP ASSAAAAWVRALLAHKYP AIAA
MDPR-RSHWESSSEDVTRPLLPLHDDG--AAGRR-----SCAALRSLLANKYLAVAS

--MNGGDVTVAGSDDLKSPLLPVVHNDEPFERQTVG-----QQLRTIFTPKNCYIAL
.:*:*:* : * : * : * : *

GPAACAAVCAAVDLGD-GHGEARNMLGVLAWVFLWVVTGAVPLAVASMAPLFLFPALGIS
GPVACALICGLVDLG--GHRAARNMLGVLAWVFLWVITDAVPLAVASMAPLFLFPVFGIS
GPLLCVVCLCVDLGGDETTARNMLGVLVWVFAWWL TEAVPMPITSMTPLFLFPFLFGIS
** * : * : * : * : * : * : * : * : * : * : * : * : *

SSDDVARAYMGDVISLVLSFILALAVDHHRIHRRALN VLSLFCGDPVRPSLLLLLGV
SSDAVAKAYMDDVISLVLSFILALAEHYNIHRRALN ITS LFCGDPVKPPLLLLIGIC
AADDVANSYMDDVISLVLSFILALAVEHYNIHRRALN ITLVFCVEPLNAPLLLIGIC
: : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

GTTALVSMWIIHNTACTVMMMPVATGILQRFPRGD-----IDGGGQEVRRFSKAVVLGV
GTTMFISMWIIHNTCTVMMMPVATGILQRFPRVDGASSASSAADAREVQRFSAVVLGV
ATTAFFVSMWVHNVAAMVMMMPVATGILQRLPSSS-----STTEVVHPAVGKFSRAVVLGV
.* : : * : * : * : * : * : * : * : * : * : * : * : * : * : *

VYASAIGGMATLTGTGVNIIILVGMWSSYFPEQRPITFSSWMSFGLPMAIILFLALWLTLC
VYASAIGGMATLTGTGVNIIILVGMWSTYFPEQPPITFSSWMSFGLPLALVLFVALWATLC
IYSAAVGGMSTLTGTGVNIIILVGMWKSIFPEADPISFSQWFFFGFPLALCIFVVLWCVLC
: : : : * : * : * : * : * : * : * : * : * : * : * : * : *

LMYCSNNTAKALSAYLDRSHLRRELSLL 1GPMFAFAEKMVLAVFG 0GLVVLWMSRNITDNI
VLYCSKNTGRALSAYLDRSHLRRELSLL 1GPMFAFAEKMVLAVFG 0GLIVLWMTSLTDDI
VMYCPKGAGQALSPYLHKSHLRRELDLL ~GPMNFAEKMVLAVFG ~GLVVLWMTRNITDDI
: : * : * : * : * : * : * : * : * : * : * : * : * : * : *

PGWGVLFHNKVGDTVT 0IMMATLLFIIPSGKREGEKLMWKNCKKIQWNIILLGAGFA
PGWGS LFHGEVGDGTVT 0IMMATLLFIIPSGKNDGEKLMWKGCRRLQWNIILLGAGFA
PGWGRIFAGRAGDGTVS ~VMMATLLFIIPSNIKKGEKLMWKNCKKLPWNIVLLGAGFA
**** : * : * : * : * : * : * : * : * : * : * : * : *

IADGFKTSGLTDILSNGLRFLKGAPTLVIVPVACVFSGIMTEFTSDDSTTTLVLPFAEL
IADGFRASGLTDILSEGLGFLRGAPALAIAPVACVFSGAITEFTSDDATATLVPLLAEL
IADGVRTSGLAEVLSKGLVFLETAPYWAIAPTCLIAATITEFTSNNATTTLVPLLIEI
**** : : * : * : * : * : * : * : * : * : * : * : * : *

AKSIEVHPALLMVSGAIGAQLSYLLPTGSPSNVVGFTSGYITIKDLVATGLPLKIVAI
GKSIGVHPLLLMVPGAIGAQLSYLLPTGSPGNVVGFTSGYISIKDMVIAGTPLKIVGAA
AKNMGIIHPLLLMVPGAIGAQAFLPTGTSPSNVVGFTTGHIKDMIKTGLPLKIAGTIF
. * : : * : * : * : * : * : * : * : * : * : * : *

LTVLLPTL 1GSTIFGMDIKS
LTILLPTL 1GSVVFMDQKL
LSILMPTL 1GAYVFASMGV
* : : * : * : * : *

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: LOC_0s08g41730.1 219 aa
Sequence 2: LOC_0s09g32800.1 221 aa
Sequence 3: At3g60820.1 223 aa
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score: 86
Sequences (1:3) Aligned. Score: 73
Sequences (2:3) Aligned. Score: 75
Guide tree file created: [/tmp/3MLr1SjSp3/dw2JJkNhWY.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:4481
Group 2: Sequences: 3 Score:4231
Alignment Score 3240
GCG-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

```
MAR---FEVYENNG~GTCVAVAGADYCVVAADTRLSVGYSILSRDSSKIAH2LADKCVL
MSRR--GDWVYENNG2GTCVAIAGADYCVVAADTRLSVGYNILTRDHSKICE2LADKCAL
MTKQHANSWPYDNNG2GTCVAIAGSDYCVIAADTRMSTGYSILSRDYSKIHK2LADRAVL
*::          *:***  *****:***:*****:*****:*.**.**:**  ***  .  ***:..*
```

```
ASSGFQGDVKALQRNLTAKEL0LYEHNHNKKMSCPAMAQLLSNTLYYKRFFPYAFNVLG
ASSGFQGDIKALHKNLAAREL0LYQHQNKRMSCPAMAQLLSNTLYYKRFFPYAFNVLG
SSSGFQADVKAQKVLKSRHL0IYQHQNKMSPAMAQLLSNTLYFKRFFPYAFNVLG
:*****.*:***:: * ::.* :*:*:*****:*****:*****:*****:*****
```

```
GLDSE1GKGCVFITYDAVGSYERTGYSAQGTGAALMMPVLNQLKSPSPLLLPAR0DAVTP
GLDSE1GKGCVFITYDAVGSYERTGYSAQGTGSALIMPVLNQLKSPSPLLLPAR0DAVTP
GLDEE1GKGCVFITYDAVGSYERVGGAQGSSTLIMPFLNQLKSPSPLLLPKQ0DSNTP
***.* *****.***.***:***:***.*****:*****:*****:*****:*****
```

```
LSQSDAVDLVKDVFASATERDIYT0GDKLEIVVINSAGSHREFIELRKD
LSETEAVDLVKDVFASATERDIYT0GDKLEIVVINKAGTKREYIDLRKD
LSEAEAVDLVKTVFASATERDIYT0GDKLEIMILKADGIKTELMDLRKD
**:::***** ***** *****:***: * : * :*****
```

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: LOC_0s08g41880.1 623 aa
Sequence 2: LOC_0s09g32840.1 630 aa
Sequence 3: At5g50400.1 611 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 69
Sequences (1:3) Aligned. Score: 64
Sequences (2:3) Aligned. Score: 64
Guide tree file created: [/tmp/3MLr1SjSp3/UZsZ6RdDIh.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:11695
Group 2: Sequences: 3 Score:11250
Alignment Score 8366
GCG-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

```
MVSRKRGGGGGVAMAVAMLLAAASA-----SRPSSSLEGFQPLSKIHAVHKAT
MAMP----LGGILLFLVLLAAAAAGGGGGVWAFSSSSSSSSYSRIGEQPLSLIGIHRAT
MARN-----FLLVLLWFIVQVSS-----SHENGRGDQALSQIDIYAIN
*.          . : . :.. :::          . .  * *.** * : : .
```


Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 64
Sequences (1:3) Aligned. Score: 42
Sequences (2:3) Aligned. Score: 42
Guide tree file created: [/tmp/3MLr1SjSp3/TC2FU2P9Ws.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:11029
Group 2: Sequences: 3 Score:9035
Alignment Score 5606
GCG-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

MSTTFSDFDPIERRHVERQRRRRVMVAAGAASVILIIIVMGGAAYN--ASFGDG
MSSAFGDFGPLTERRRAEKARQRRRIMIALGTVSIIIIILIVMGAAITYSGKKSEDEG
--MAFQDFDKIQERVNANRKRKFRKRIIVGTVSLLVVVAAIVGGAFAYVAYEKRNEQQQQ
:* ** . : ** . . . : * : * : * : . : : : ** * . * . . :

GSSSSSGSAS-----GGGAQPSLHGVS-----KIIKAMCAQTDY
GSKGSSKGGKSKGGGGGDDDEGGGGGGKADLRAVS-----KSIKMMCAQTD
QQQAKNHKSGSGNNVVKDSKKSPSPPTPSQKAPVSAAQSVKPGQGDKIIQTLCSSTLY
. * . . . : * * : : * : * :

KDTCEKSLAKAAANASASSSSSPKDVVRASVAVIGDAIEKAFDKSSVIVSDDPRVKA
ADSCATSIGKAAN----ASVSSPKDIIRTAVDVIGGAVDQAFDRADLIMSNDPRVKA
MQICEKTLKNRTDKG--FALDNPTTFLKSAIEAVNEDLDLVLEKVLSTKTENQDDKDAI
: * . . . : : : . . * . . : . . : : : : : : * * :

ADCKEIIYENAKDDLDRTLAGIDAGGVDGLTKGGYQLRVWLSAVIAHQETCIDGFPDGLK
ADCKELFDDAKDDLNLCTLKGD--GKDGLKQG-FQLRVWLSAVIANMETCIDGFPDGEFR
EQCKLLVEDAKEETVASLNKINVTEVNSFEKVVPDLESWLSAVMSYQETCLDGFEENLK
:* : : : * : : * : : : : : * . * : : : : : * : : : * : : :

DKMRDAMESGKELTSNALALIGKASSFLAALHLPASSAASHRRLLSFAFDEDVTKQPEVN
DKVKESFNNGREFTSNALALIEKASSFLSALK-----GSQRRL-----
SEVKTSVNSSQVLTSNLAALIKTFTENLSPVMK-----VVERHLLD-----
. . . : . . . : * : * : . . : * : : . : * : *

RSSGNSLRRLLSFAFDEDATKQPEVNRSSGNSLRRLLSFAFDENAPKQPKGNDDDLVWV
-----AGEEDN-----GGGAADPHLALAEDG-----IPEWV
-----DIPSWV
: **

NRQERRLLKAK-FQNKLPNVVAKDGSQKFTINDALAAMPKKTG2RYVIYVKEGVYE
PDGDRRLKGGGFKNNLTPNVIVAKDGSQKFTINEALAAMPKTYSG-RYVIYVKEGVYA
SNDDRRMLRAVDVK-ALKPNATVAKDGSQFTTINDALRAMPEKYEG2RYIIYVKQGIYD
: * : : . : * . * . * : * : * : * : * : * : * : * : * : * : *

EYVTITKKMANVTMYGDGAKKTIITGNRNFVDGLTTYKTATF1NAQGDGFMGVALGFRNT
EYVTITKKMASVTMYGDGSRKSIVTGSKNFADGLTTFKTATF1AAQGDGFMAIGMGFQNT
EYVTVDKKANLTMVGDGSQKTIVTGNKSHAKKIRTFATF1VAQGEFGMAQSMGFRNT
* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

ARAAKHQAVALLVQSDKSIFLNCRMEGHQDTLYAHSKAQFYRNCVISGTVDFIFGDAAAV
AGAAKHQAVALLVQSDKSVFLNCWMDGFQDTLYAHSKAQFYRNCVITGTIDFVFGDAAAV
AGPEGHQAVAIRVQSDRSIFLNCRFEGYQDTLYAYTHRQYRSCVIVGTIDFIFGDAAAI

FQNCVIVLRRPLDNQNIATAQGRADRREATGFVLQHYRFAAESALGDASRPVRSYLAR
FQNCVLTLRRPMDNQNIATAQGRADGREATGFVLQKCEFNAEPALTDAKLPPIRNYLGR
FQNCNIFIRKGLPGQKNTVTAQGRVDKFQTTGFVVHNCIAANEDLKPVK-EEYKSYLGR
**** : . : * : : * : * : * : * : * : * : * : * : * : * : *

PWREYSRTLIMNSDIPAFVDKAGYLPWSG-DFGLKTLWYA EYGNGKGAGAATAGRVS WPGY
PWREFSRTVMESDIPAIDKAGYMPWNG-EFALKTLYA EYANKGPGADTAGRVA WPGY
PWKNYSRTIIMESKIENVDPVGLRWQETDFAIDTLYA EYNNGSSGD TTSRVKWPGF

:::*:*:*:* * :.* *:*: * .*:**::*** **::*:**::*

KKVISKKEATKFTVQNFLHAEPWIKPTGTPVKYGMWA-
KKVISKADATKFTVDNFLHAKPWIDPTGTPVKYDFFT-
K-VINKEEALNYTVGPFLQGD-WISASGSPVKLGLYDA
* * * * : * : : * * * * : * * * : * * * * : : :

```

Sequence format is Pearson
Sequence 1: LOC_0s02g51600.1      566 aa
Sequence 2: LOC_0s06g11920.1      533 aa
Sequence 3: At5g65090.1           529 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 58
Sequences (1:3) Aligned. Score: 55
Sequences (2:3) Aligned. Score: 51
Guide tree      file created:  [/tmp/3MLr1SjSp3/mpEDgHxD23.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences:  2      Score:9051
Group 2: Sequences:  3      Score:8511
Alignment Score 5492
GCG-Alignment file created  [/tmp/3MLr1SjSp3/P5W730m2jT]

```

MSNHNSPCDIPKPAVDFVKGKKKKQSFMSIFR~KKGRSGT~GSSDKLLSRRDIVF
MS-----~--SNMFG~KKGWDSN1G-----
MNN-----RGNDDL~DHHYGVFN1DFERRMT~SRK-----
* . *

1GLDEKCDRSELLDSSPAVRKSFS1DR---HCATKIESLTLSCLDSPHR-QFDTREY2R
 ~-----MDTSGSVCRSSS1DINYINQARLRKSASLNCVGSPPRKNNNATQY2R
 ~-----KSVLDNTSPMIWKTVS1ER---KSSPGIEGLNLSSFDRMPAPTTEIREL2R
 : : * : : : * : : : : : * : : : : : * : : *

VFVGTWNVAGKPPNSSLNLEDFLQIEGLPDIYVL2GFQEIVPLNAGNVLVIEDNEPAAKW
MFVATWNVGGRTPNKRLNLQDFLQVEESPDYIYVL2GFQEIVPLTAGNVLVLEDNEPAAKW
VFLATWNVGGRTPNNDLNLEDFLLVEGTADLYIC2GFQEIVPLSAGNVLVVEDNEPAAKW
. * . * * * * . * . * * * . * * . * * * . * * * * * * * * * * * * * * * . *

LGLIYQALNKPQDQSSGDE---LSP-----ETSDSRQGGSRSRDSIPKSSSGMLFFQ
LALI HQALNP QEPADGD E P S L T P P P S S T T T S E S N G A R T R R R D A V S R S A S G - N L F F H
L A I S Q A L N K P K Q E S V Y S N -----A A Y S A S R T T C S S S C G S E E S R A P S S - L S F F Q

* * * * : . :
 : * : . : . : . : * ** :

MGSSSLPRAAVLAVALLLLLLADSGEAFDLSIFRPRSDSDYFP--FDGSPGQAKRKPK-
 --MKASTRVIWTISVLMIAVSEAIFFLPFLPFLPGFNNG-----FRDNEAVKVAKPQ-
 * : : : : : * *

GGLRREQQELGAAGPGGSGLSKAPPRSAPSKVALDSLKL PVDTSAGFAGGWNLVSENSGV
 ---IEQEEDGAAPATATGLTKVPPLGAPSKAALDTIVLPVDDSGHAGSWTIVSENSGV
 -----PAGAVGGKAARRQGGGLDAQTTWGGKWELFLENSGV
 * : * : . * * : . *****

SAMHLVVMQHG-KAIMFDTCTTGRSLMRLPPGRCRPDPRSKQPGAMDCWAHAVEFDYNTG
 SAMHLAVMRHG-KAIMFDTSTTGRSLMRLPMNNCRADPRAKREGTMDCWAHAVEFDYSTG
 SGMHAILMPVINKVQYYDATIWRISKIKLPFG-VPCHVDAKTNKVDCWAHSILMDVNTG
 * . . . : * . . : : * : : * . . : . : ***** : : * . . *

ALRSLK0IVTDTWCSSGAFDADGNMVQTGGFFEGDKSVRYLSACGTCDWKEFPKSLADGR
 ALRSLK~TATDTWCSSGAFDADGNLIQTGGYFEGDKAVRRLDACDTCDWREYPNSFAEGR
 ALKPLG0LSTDTWCSSGGLTVNGTLVSTGGYGGGANTARYLSSCENCKWEEYPQALAAKR
 * . . . * : : * : : * : * : * . . *

2WYGTQLVLPDGSFIVIGGRRAFSYEFVPAAGRANARATPLRLLRDTTDDVENNLYPFVN
 ~WYATQQVLPDGRFIVFGGRRAFSYEFVPQPGMTNGQSIKFLLRETTDDVENNLYPFVN
 ~WYSTQATLPDGKFFVIGGRDALNYEYIPEEGQNNRKLFDLRLRQTDDPEENNLYPFVW
 * * : * . . : * *

LLPDGTLFIFANDRSIVFNRYTGQVVRELPILPGGSRNYPASAMSTLLPLDLR--KGAG
 LLPDGNLFVVFANDRSVVFDRHTGKVVRELPKLAGGGRNHPASAMSAMLPLDLRNLTRGAD
 LNTDGNLFIFANNRSILLSPKTNQVIKEFPQLPGGARNYPGSGSSALLPIQLYVK-NPKV
 * : * . . : : * : * *

LSAEVIICGGATKNAFKLGETSTFPPALRDCARINPSKPGARWALDQMPSGRVMGDVLIL
 PEPEVIVCGGALKTAFLRGENNTYQPTLRDCARINLGKIDAVWAVEAMPVGRVMGDLLVL
 IPAENVLCGGSKQDAYYKAGKKIYEPALQDCARIRINSAKPRWKTEMMPTPRIMSDTVIL
 . * . : : * . : . . : * . : * * : * * * . . . : *

PTGDLMLNGAAKGCSGWGFRQALLSPVLYSPYLRRGKRFRVLNPSNIPRMYHSTSALL
 PTGDLMLNGAAKGSSGWGFARQPILSPILYSPRHPEGSFRPLAASVARMYHSTSALL
 PNGDILLVNGAKRGCSGWGYGKDPAPAFLLYKPHAARGKRFRQLKPTTIPRMYHSSAIIIL
 * : * : : * * : : *

PDATVLVAGSNTNSAYNFSGVDFPTEVRVERFTPPYLSPQLSPNRPAIDAASVPGDGMR
 PDATVLVAGGNTNAAYNFSGVDFPTEVRVERFAPPYLSRELGNRAVIDVASVPAGGMRY
 PDGKVLVGGSNNDGYKYN-VEFPTLRVEKFSPPYLDPALANIRPKIVTTGTP-KQVKY
 * * : * : * : * *

GARFTFRFTTPAQGVGQDFKVTMYAPPFTTHGYSMNQRLILPVTAFAAQGQRHTVTVD
 GTKFTFRFHTPVAAVEWGDVRVTMYAPPFTTHGYSMNQRLVLPVAGFSAQGQMYELTVD
 GQFFNVKVDLKEKGATKGNLKVTLAPAFTHSISMNMRMLILGVNNVKPAGAGYDIQAV
 * : * . . : : * * : * . . : : *

APPKPELAPPGYYMVVYVAKGVPSKAAWVKMHK
 TPRKPELAPPGYYLVVYVSKDVPSEAAWVKIQ-
 APPNGNIAPPGYYLIFAIYKGPSTGEWIQVV-
 : * : : : * : * *

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: LOC_0s04g59540.1 1381 aa
Sequence 2: LOC_0s08g01390.1 1610 aa
Sequence 3: At3g14270.1 1791 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 57
Sequences (1:3) Aligned. Score: 33
Sequences (2:3) Aligned. Score: 32
Guide tree file created: [/tmp/3MLr1SjSp3/rvKkMRRs7R.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:23443
Group 2: Sequences: 3 Score:15923
Alignment Score 9820
GCG-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

MGTRDSNNRTFSEIVGLIKSWLPWRSEPATVSRDFWMPDQSCRVCYECDCQFTLINRRHH

CRHCGRVFCGKCTANSIPFAPSDLRTPREDWERIRVCNYCFRQWEQGDGGPHVSNITELS

TSPSETSLSSKTSTTANSSSFALGSMPGLIGLNQRVHHGSDVSLHGVSSMETS SVTKQGK

---- -MSCAQQDMDPPT2RDALS~EALDGNRSDHS----- -VYDAEHSG
ETSRSSFIATDVEDPS~RFALN2SIRSDDEYDEYGAYQTDIETSHSPRANEYYGPMEYN

--- -MNSVVEIMAI SYP PEDGRYYCS----- -SVAAGDDSPA AHHTN-
QNGIGDTKKRTSSSDLSTDDNFSSALQSKHEHMNRDALSIDDRSVKSGDESDGAESTSG
GMGIDDVPCKHLGGETADQKSLSGSPLIHQCLESLIREGSEQFQKKSEHDGRDECEASSP
: : * . * . . .

----- -AHDDWDW----- -DWVPPPPAD----- -AAAAAADD DDDDDGDPTPAGSPGS
KSGSIDSTCTENDS----- -IWIPPEAADKEYEADSVSGKIAYADDDDDYSDGIKWGRSSF
ADISDDQVVEPVDFENGLLWVPEPENEEDERE - -SALFDEEDNEGDASGEWGYLRPST
 . * * : * : : : . : . * : : *

RGEDEEEEERQR----- -AQMV SAMNGQLNMLASRFLASAGV----- -EEEWLEVVTAL
PATNEEQEVSHNTRDERESAMLDAMNGQLKILVSRFLASAGISFSKGESGESWLDILTSL
SFGSGEYRGEDRTTEEHKKAMKNVVDGHRALLAQLLQVENISVSDEEGKESWLEIITSL
 . * . . . * . : : : * : : * . : . * . * : : : * *

SWEAALLIQTHACTAGNDMDPASHVKIKCVASGRRRQ SQVVRGLVFRKNAAHKHMPTKC
SWEAALLIKPDAS -KGKEMDPGSIKVKCIASGTRRQ2SEVIKGLVFKKNAAHKHMPTSC
SWEAANLLKPDMS -KSGGMDPGGYVKVKCLASGFRHD2SMVVKG VVCKKNVVNRRMSTKI
***** * : : . . . * : : : : : * : : * * : : : * : * : : : * : *

HRPTLLLLHGALGLDSHLG-FSSFDSMEQ~D~KLILRASISHIIHTCSPNVVMVEKTVSR
HNPRLLLKGVLG-HSDVG-LSSFNSMDQ~E~KDHLEAISKMMEICSPNVILVEKTVSR
EKARLLILGGGLEQYRVSNQLSSFDTLQ~Q~EKDHLKMAVAKIHAERPNIILLVEKSVSR
... **: * * * . . :****: : * : : : . . ****:****:***

DIQELLLHHGVTLLLDMLHRLQRIARCSGAPLLSFSQLLHDCPNHLKHCDYFHIDKFFE
DIQELLLKEGVTLIFDMKLNRLERARCTGSPIIISFSEVLDPK--KLKRCDSFHIEKFIE
FAQEYLLAKDISLVLNRIKRPLLDRIARCTGAQIIPSVDLSSQ--KLGYCENFRVDTYPE
* * * * . . :****: : * : * * * * : : . . : * . : * : * : * : * : *

DHNTTTTTTSAALNKPSKTLMFLEGFSNPLGCT~ILLRGASTQELKKIKQVLHYTIFAAY
EHN---SASDGGKRLSKTLMFLEGFPKPLGCT~ILLRGANSEELKKVKQVMHYTVFAAY
EHG---STGQVGKKVVKTLMYFEHCPKPLGFT~ILLRGANEDELKKVKHVQYGVFAAY
:* . : : . : : ****: : * . : * * * * * . : * * * * : * : * * *

HLVVETSFEDQRVFLNDTNVDGTPQITHQT-----SIVSNRSLPTD-----Y
HLILETSFFEDQRIFLNDQNASRENSVTAMAGPSANGYDPSVLCASDFPSRDDSPALRLY
HLALETSLADEGASPELPLNSPITVALPDK-----STSIERSISTVP-----
* * : * * * : * : : . . * . . : :

DVTCTSRGSLLEYHDGDHKATVPFTNKPDSYTDQEGTAIHCEAPP--SENLLSSVSGSL
HATSNGYTDVKKSLSSSTKVDAPSSITNSSSSVGEDASIRYDSKPPLHSQRLPSPVPGTL
GFTVSTYEKSPTMLSCAEPQRANSVPVSELLSTTTNLSIQKDIPPIPYGSGWQAREINPS
* : . : * : . . : . .

RRFIDIFRYQNIYLPVTSSQDTTGHQNEQDTETSQETASD-----TLTKDHSC
RKYVGMLSHQNIYLPVTSLQETSATQIEGEVESGKEIVSNGFHVGSKVEEPAVSTANVDC
FVFSRHNISLNLPRVIESRNSDLSGRSVPVDTPADKSNP-----IVVADETTNN
: * : * . : : . . : :

EYMDQLND-LQEQVFAKTNQKMSQDPDPFGTEKHQQNVEQYRAGENINSDTDEADDVMDSQ
SQDHQRQERIQDIMPTNSTHDKREESPMVEDGEQHSTIDIISKEKTTNEDQADDALDTH
SLHLSGQGFVRKSSQIGTSIMVENQDNGSELTIAQQQNNNEKPKETQSQKEEFPSPSPDHQ
. . : : . . : . * : : . . : . . * :

SILILLSSQCVTKQVCEESHLYRINYGNFVSLGRYLQDILQ----NQ~NLSCSSCG
SILILMSSQCITKQVICEQSHLSRIKYYGNFVSLGRYLQDILQNPVLQNQ~KLSCSSCG
SILVSLSSRSVWKGTVCERSHLFRIKYYGSFDKPLGRFLRDHLF----DQ~SYRCRSC
***: **: : * . : * * * * * : * * * * * : * * * * * : * * *

EPPDAHMYSYTHRNGLTINVRLLPQHHLPGESEGKIWMWTRCLRCHEHERGISKSSRRV
EFPESHLYSYTHRNGLTVRVKHLAPQHHLPGESEGKIWMWTRCLRCENEHGMSKSTPRV
MPSEAHVHCYTHRQGLTISVKKLQ-DYLLPGEKEGKIWMWHRCLRCPRNLNGFPATLRV
. : * : . * * * : * * : : * * * * * * * * * * . . * : : *

LISTEARNLSFGKFLELSFSSSHAARRLSVCGHLVNRDCLRYF~2GLGSKVAKFYSSVEI
LISSEARSLSFGKFLELSFSSSHAARRLSICGHLVNRDCLRFF~2GLGSKVAMFRYSSVEI
VMSDAAWGLSFGKFLELSFSNHAASRVACCGHSLHRDCLRYF~2GFGNMVACFRYATIDV
: * * . * * * * * * * * * * : * * : * * : * * * * : * * . * * * : * * :

YTACKPQRTLEFHNPDMREWFQEGRN~VLARGVKLFYEVSSLIQHMK--IFSEVAINCG
YTTCKPQTTLQFDNPCRQDWKEERRY~VLARGIKLFSEVASMLQPLKDQLLDVTTTNTCT
HSVYLPPSILSFN-YENQDWIQRETDE~VIERAELLFSEVLNAISQIAEKGFRRRIG--
: : . * * * . : * : * : * * * * . : : : :

DSLVPKEVSQLEEMLIEEKAQFV~DSLKVAVDESGMSSSSVNEILGVNCLYQDLLIRLYV

GSLPVKDFSELEELLIKEKAFFE0DSLEKTINQENLSASVHELVDINWSYQDLLLELYL
-----ELEEVQLQKEKAFFE0ENMQKILHREVNEGQPLVDILELYRIHRQLLFQSYM
:***:* :*** * :.: * :... . .: :.: : : : :***: *:

WDRRFHQIVECKSGRMANCVGKKE-----AAEFAGEP-----
WDRRLDQLTKCVSAGQERVVSCDPFDTVVKNIRVNQEIENKADELTCDRTT-----
WDHRLINASTLHKLENSDDTKREENEKPLAKSQTLPEMNAGTNSLLTGSEVNLNPDGDS
**:*: : . . :.: : .:

-----AATGESAVPFENGYIKEMQYSSET-----LTDENSRREEQ-----
----SVLSAVGLTECPSNRNYIDHQSVDIEAPVLTENQGAGCAQFSSTGGRNDEDSYAP
TGDTGSLNNVQKEADTNSDLYQEKDDGGEVSPSKTLPDTSYPLENKVDVVRTQSDGQIVM
. . . * . . . : . *

-----HITKVPSFRVLEG-TDTQLINPECGDNR-----ETWIWS
CQLEVDSMAQTKEVPSFEISEVQGDGIVVHPISLDQEPSNAPNHFRKIPDWDTGEGWIWN
KNLSATLDAAWIGERQTSVEIPTNNKVSLPPSTMSNSSTFPPISEGLMPIDLPEQQNEFK
. : : : * .: : .:

PLHELRESYRHELQAGYLERFELVNNYSPSHLSPLHKQ---SSAEFIVGPGGNVLCISE
SFHECQLAYRKDIQNEILDKFEIVNRYSPSHMSPLFEQHHEEVSSPQFTVGPNGNLSVLE
VAYPVSPALPSKNYENSEDSVSWLSVPFLNFYRSINKNFLSSQKLDTFGEHSPIYISSF
: : . :.. :. . :.: * . * .:

DEISSIISRALAISEERRHLLLDALMVEGEAAYSRGSESSKMEKSYSSLSEASSASSWS
DEISSIARALAVSGEHRHL-----VENETEGARLEHAKTMEKSYFMSGSSLDSSPWS
REAEQGGPRLLLPVGLNDIVVPVYDDEPTSMIAYALMSPEYQRQTSAGESLSVSYSEL
* . . * :. .: * : : : :. * . : .:

SIGSSSDASFS-----SDDLFSYDSSLSSLLHPEVSVNGKSSL-KG
SIGSLDSEASFLSLGSS-----VSSDDLSGYDSLPLFSSIHPEVAVNGKVAL-RG
NIPRPVDDTIFDPSRNGSVDESILSISSSRSTSLLDPLSYTKALHARVSYGEDGTLGKV
.* :.: * . * * . :*. *: . . :* :

KYSVICVHANQFYTLRKKCCPSELAYITSLSRCMKWDAQGGKSKAFFAKTLDDRFIKQI
KYSVTSIYAKQFQDLRKKCCPSELAYITSLSRCKKWDAQGGKSKAFFAKTVDDRFIKQI
KYTVTCYYAKRFEALRGICLPSELEYIRSLSRCKKWGAQGGKSNVFFAKTLDDRFIKQV
:* . :.:* ** * *** ** ***** ** .*****:*****:*****:

KKTEFESFIEFAPDYFKHVYHSLDTGSQTCLAKILGIYQ0VK--QIRHGKEVKLDLMVME
KKTEFESFIKFAPDYFKHVYHSLDTGSQTCLAKILGIYQ0VK--QTRHGKEIKIDLLVME
TKTELESFIKFAPAYFKYLSSESISTKSPTCLAKILGIYQ0VATKQLKSGKETKMDVLIME
.***:***:*** **:.: .*: * ***** * * : *** *:.:**

NLLFGHKLSRIYDLKGVVFSRHVSDSNHGTVYLDQNFVDDMRVSPYVGGRTKHLQRA
NLLFGHNISRIYDLKGAIFSRHVAHSNDRNTVYLDQNYVEDMRVSPYVGGRTKHLQRA
NLLFGRTVKRLYDLKGSSRARNPDSSGSNKVLLDQNLIEAMPTSPIFVGNAKRLLERA
*****:.:*:***** :*: ..* . * ***** :*: * .*****:*****:*****:

IWNDAFLT0SINVM DYSLLVGV DKEKHEFVFGI IDYLRQYTWDKQLETWVKTS--LVVP
IWNDSFLT0SVNVM DYSLLVGV DKEKHELVFGI IDYLRQYTWDKQLETWVKSS--LVVP
VWNDAFLA0LGDVM DYSLLVGV DEEKNEVLVGI IDFLRQYTWDKHLESWKFTGILGGP
:***:***: :*****:***:***:*****:*****:***:*** : * *

KNASPTVISPKKEYKKRFRKFMKYFLTPDDWST-----
KNVSPTTVSPKEYKKRFRKFMKHFLTPDTSSENSSGSPKSFSGHSNNMLVEVHSDNLL
KNEAPTVISPKQYKRRFRKAMTTYFLMVPDQWSPPNVANNKSDQPEETSQAGTQAE--

** :***:***:***:***** *:.:** *** **.

LQHPIEAETVV

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: LOC_Os11g01820.1 801 aa

Sequence 2: LOC_Os05g39600.1 834 aa

Sequence 3: At2g13620.1 821 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 34

Sequences (1:3) Aligned. Score: 35

Sequences (2:3) Aligned. Score: 38

Guide tree file created: [/tmp/3MLr1SjSp3/hixpyoEVK3.dnd]

Start of Multiple Alignment

There are 2 groups

Aligning...

Group 1: Sequences: 2 Score:11864

Group 2: Sequences: 3 Score:8884

Alignment Score 4887

GCG-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

MAGANASTVKPVVAACYDNNLVNSQG--MFLGDEPLRFALPLLLVQVSIILILSAAAHV
-----MDKIDCYVVPQTTGTGRNIFQGGSPLSASLPLLVQLVLIVAVTRVLYFL
-MATSEEPSTDASIICYAPSMITTNG--VWQGDNPLDFSLPLFVLQLTLVVVVTRFFVFI
** . * :. *.** :***: **: :. :.

LRRLGQCRFVTHML~VGIFLGPSVLGRNPHLRTALFSERGTYILESLSLVALILFLFSMA
LKPLKQPRVVSEIMGGIILGPSVLSRHAAFREVVFPARGEPVLNTVATFGLMYVIFLIG
LKPFQRPRVISEILGGIVLGPSVLGRSTKFAHTIFPQRSVMVLETMANVGLLYFLFLVG
*: : * *. :. :. *.**.*. :. :. *. :* :. :. :. :.

VKTDLTLLRRPTARALAVGLAGSLVPLAVTLPVFHALSPSLPADLRG-SSLITELAVRLS
VRMDPRLVVRSGRKGVIIGLSGFLPLAMTGAGSSGEAMATEPDVSRRSTFLFALATSLS
VEMDIMVVRKTGKRALTIAIGMVLPLFLIGAAFS--FSMHRSEDHLGQGTIILFLGVALS
* . * :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :.

LSSFPVADALAELDLLNSELGRVALNASLITDVTWFLRACFAAFLITQAKSPLFTAK
VTSFAVLSPILSELSLLNSDLGRIAMSASMTTDGIAWIIMVVYILAEAF--LVSPATSIW
VTAFPVLARILAEKLINTEIGRISMSAALVNDMFAWILLALAIALAES--DKTSFASLW
: : *. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :.

VLASFAAFVLVFFVVARPAGRYIARKRTPPGDLLSEGSFVLVIAALLSALVTDVIGFKF
AFLSLAVLAAFILFVVRPVALRVIER-TPPGKPEETYVFVFLVLLVGFYSDVIGTNS
VMISSAVFIAVCVFVVRPGIAWIIRK-TPEGNFSEFHICLILTGMISGFITDAIGTHS
. : * *. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :.

MIGPMMLGLALPGMPIGATLTERLDSFFIALFLPVYMALAGYRTDLAELSLIGVSAEHE
FHGALMLGLAIPDGPPLGTALGEKIEAMVSGLILPLYAMTGLSTDVWRMH-----
VFGAFVFGVLIPNGP-LGLTLIEKLEDFVSGLLPLFFAISGLKTNIAAIQGP-----
. * :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :.

EKFCALELFVALCVAGKMVGCVAAGLFFSMPFREATVLALMLNIRGIVEVAAINNWGDTM
--WGRLQVVMFLAWVGKLVGMVSSLYLEIPLRDAVSLSLFMNSKGIVEVITFNFFLTNK
ATWLTFLVIFLACAGKVIGTVIVAFFHGMPPVREGITLGLLLNTKGLVEMIVLNVGKDQK
: * :.: *. :*:.* : .: :*.*. *. :*:.* :*:.* :.*

~KATAEHYSTLTLSMVVITAVATPLIKLLYDPSGRFARAKRRTMEESRPNAELRVMACLF
0LIGKNTFSILICLSVAITAVSVPVAGWLYDPARRYAVYKRRTVQHLKADADLRILACVH
~VLDDETFATMVLVALVMTGVITPIVTILYKPVKKSVSYSKRRTIQQTKPDSELRLVLCVH
: :.: : :*:.* :*. :*. :. :*:.* :.:*:.* :.*

SEDHAAPLLDLIEASGSSRDAPVSLIVLHTELVGHAASVLKPHRKSRSSCG-----
DQSHVPGTLAVLEASNATPQTPLSLYLLQLVEIAGRSAPVFIPHKLRHSASRAGAAAASA
TPRNVPTIINLLEASHPTKRSPICIVLHLVELTGRASAMLIVHNTRKSGR-----PALN
:.. : :*:.* :. :*:.* :*:.* :*:.* :*. :.*

-NPTPSDRIVNAFRYFEQQAPLGAVTVSPYVVASPYSSMQHDVCLLAHSRKANLILLPFH
APPTDSRIINAFFQYELKHPEGAVSVHPFTTISPYSSMHDEVCRlaveKRTSLILLHYH
RTQAQSDHIINAFENYEQA- -AFVAVQPLTAISPYSTMHEDVCslaEDKRVSFIIIPFH
: :*:.* :* :. :*. * .. :*:.* :*:.* :*:.* :*:.* :*

K--SSDGARSTANNAIRGINRSVMQYAPCSVGILIDH-----GVAAG
KRHMLAGGVR-AAVGLRVVNRKVLEVAPCSVAVFVDRNAGSVGLCAFIPGPVQDQSTSSR
KQQTVDGGMESTNPAYRLVNQNLLENSPCSVGILVDR-----GLNGA
* * :. * :*:.* :*:.* :*:.* :.*

SACATASNS----TLQRVALYFLGGADDREALAYVARMAECGLVAVTVVRLKLRDWVGM
SRSGGHAASGSGQGFKAAVASLFFGGGDDREALAYATRMARHEGVAVGVIRFLPARGIKD
TRLNSNTVS-----LQVAVLFFGGPDDREALAYAWRMAQHPGITLTVLRFIHDEDEAD
: : * ** :*:.* :*:.* :*:.* :*:.* :*:.* :*:.*

GGRD-----EMRDEEALQEFWQRYSCAGAERVAYVEKTVEDGEGTASV
EPSD-----RRIDNRAIEEVKALAARSRNIKVQEELVGDMERIVQVL
TASTRATNDSLKIPKMDHRKQRLDDDYINLFRAENAEYESIVYIEKLVSNGEETVAAV
* : : * . : * : * : * . .

RAMSDK-FDLLVVGRRREGGDDGAEGSSAAALTSGLSEWSEFPELGVLDMLASADFAAKV
RGLDEAGYDLVLVGMRRH-----WYPVMPANGMSDWSECPGLVIGDLLASSDFDTPY
RSMDSHDLFIVGRGEG-----MSSPLTA-GLTDWSECPGLGAIGDLLASSDFAATV
* :.. :*. :* :. : :*:.* :*:.* :*:.* :*:.* :*

SILVVQQAATRNDADY-----
SVLIMKQQD-QGGLNAAVPGAQDVWHVNDGGAEDAPAPPRNMSTAGS
SVLVVQYVGSWAQEDDMDFPESPVHSHETKVTYGLENPR-----
::.*

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: LOC_0s03g25480.1 518 aa
Sequence 2: LOC_0s07g44140.1 517 aa
Sequence 3: At2g46950.1 572 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 52
Sequences (1:3) Aligned. Score: 47
Sequences (2:3) Aligned. Score: 47

P2DGKSAASTSTASKSTASAI PRNSTAPATATESNSTAPATPSNSTAPVTASNSTAPATA
P~--KSM-----
P~--SF-----
* *

SSSNPPATKSYSGPPATPSASSTPAKASR

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: LOC_0s01g74320.1 446 aa
Sequence 2: LOC_0s05g02130.1 450 aa
Sequence 3: At2g28840.1 456 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 64
Sequences (1:3) Aligned. Score: 53
Sequences (2:3) Aligned. Score: 63
Guide tree file created: [/tmp/3MLr1SjSp3/ZJz3WE9EjV.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:7901
Group 2: Sequences: 3 Score:7437
Alignment Score 5223
CGC-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

MGHGLSCSRDTDEYDLFRAAQLGDIHALSALLAADPALARRATVYDRFTALHIAAANGRL
MGHGVSCARTGDEHDFRAAQLGDLALAALLAADPSLARRATLYDRLSVLHIAAANGRI
MGQSMSCG-SRPEHGIFASVQCGDIITIRVMATEPSLLNQTPYDRHSVLHVAAANGQI
:..: *:..* :.* **: : : :*:*:*. :.* *** :.**:*****:.

Q~VLSMLLDRDGDVDVLSRKKQ~TPLMVAAMRGNTECVVRLLRGGAN~VLTFDSPRARTC
E0VLSMFLDRGAPPDVNRHKQ0TPLMLAAMHGKIDCVLKLQADAN0ILMFDSVHARTC
E0ILSLLERFTNPDLLNRHKQ0TPLMLAAMYGRISCVKKLAEVGAN0ILMFDSVNRRTC
: :*:*:*: * :*:*: *****:*** *. :. ** :* . :. ** :* *** . ***

LHHAAYYGHAECQLAILGAAAQAQGPVAAS~WGFARFVNVRDERGATPLHLAARHARASC
LHHAAYYGHVDCLQAIL-AAAQTT-PVADS2WGFARFVNVRDDHGATPLHLAARQGRPGC
LHYAAYYGHANCVQAIL-SAAQSS-PVAVH2WGYARFVNIRDDKGATPLHLAARQRPEC
*:*****.:*:***** :***: *** *:*****:*.:*****: * . *

VRLLLDKGAIVSAPTAVY~GFPGSTALHLAARAGSMCEIRELLAWGADRLQRDSA~GRIA
VQVLENGAIVSALTGSY2GFPGSTSLHLAARSGNLDCIRKLLAWGADRLQRDSA2GRIP
VNVLLDSGSLVCASTSVY2GSPGSTPLHLAARSGSIDCVRKLLAWGADRLQRDAS2GRIP
.::*:*:*. * * * * * *:*****:*.:*****: * * * .

YAVAMRRGHRACAALLNPAAAEPIVWPSPLKFIGELEADAKALLEALMEANREREKRIL
YSVALKRNHGACAALLNPSTAEPMVWPSPLKFISELEPEAKALLEALMEANREREKKIL
YVAMKHKHGACGALLNPSSAEPLVWPSPLKFISELNDEAKLLEALMEANREREKTIL
* * *: : : * * * .*****: :*:*****: *: * * * ***** * *

HGSDINIKGGDEEESEDEE----~----EACNICFEQACSMVEKCGHQMCAACTLAIC

NGTKYSLPSPSPGDDSDACSE0VSDTELCCICFDQACTIEVQDCGHQMCAPCTLALC
KGTAYSLPSPSFDSDTDNMS--E0VSDTELCCICFEQVCTIEVKDCGHQMQAQTALC
*: : . . : . : * * *:*.*:*:*****:*

CHSKPNPKTLLHPPACPF CRTTISRLLVATTNS-----NKTN----S
CHNKPNPTTLTPSPACPF CRGSISRLLVQAQTRSA-----CDPDKPSSLQLT
CHNKPNPTTSTVTPPVCPFCRSTIACLVAQNNNNNNEKSKSLDDVVVVVDREAGDVSSSK
*.****.* .*.*****:*.****... : . .

RRRSR-----SRSSSFKGGLSSAMGSFSRI-GRGSGRLVVDGSSV GELADKPDHDFSSV
RKRSRRSHNLSEGSSSFKG-LPSAMGSFSKL-GRGSSRMADSDSSN---LDKPEHDL---
FRKHRRSINLGESSSFMG--LSTIGSFGRITGRGSGRIAENELM----DKPIL-----
: : * . ***** *:*****: *****:*. . . . ***

AAAAAICDT

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: LOC_0s01g09540.1 303 aa
Sequence 2: LOC_0s05g10210.1 265 aa
Sequence 3: At4g25150.1 260 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 46
Sequences (1:3) Aligned. Score: 33
Sequences (2:3) Aligned. Score: 38
Guide tree file created: [/tmp/3MLr1SjSp3/iS0FXUpygq.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:4129
Group 2: Sequences: 3 Score:3749
Alignment Score 1815
GCG-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

MAPKRLVCFLAVAAALATTCHGWGAGAGDVVSSSAAALSFVDRLRQMMIPAAVGDGDYCD
MATARLILLTVA AAAAGSCC-FCSAQEVIVGGVGEQLATAP----PAAPAPSPPPPYCG
---MRILVNLILFSLIPLAFSNNSSSYLIARPLIFETQLKN-----INDNVN--LHCT
*: : * : : . : :. :. :*

SWRVGVEANNVRGWTAAPRKCDNYVENYMRGHYRRDSKVVVDEAAAYAEA AVLSGDPAA
SVRTAVEAHNIIIGWKTVPADCAEYVSDYLTGERYGRSDVVINEAIAYAESLKLSG----
SWRFAAETNNLAPWKTIPAECADYVKDYLMGEGYVVDVERVSEEAKVYASSFESNG----
* * .*:*: *. : * .*:*:*: * . * * . * :*:*.***: .*

DANATWVFDVDETALSHVKFYKKHGF~GYHRTDEPAFMEWLIAGRASALPNTVTLYKKLL
HGKEIWVFDVDETALSTLPYQAKHGY2GTKPYDHASFVQYVAGGSAPALQGTLRLYRRL
DGKDIWIFDIDETLLSNLPYMEHGC2GLEVFDHSKFDMWVEKGIAPAIAPSLKLYQKVI
...*:***:*** ** : : :** * . *.. * : : * *.*: : :*:***:

LLGVKIVFLSDRPDTPELRNATATNLIKEGFD CWDELIL2RSENSTATGSVVEYKSGERK
QLGIKPVFLTDR--TEDQRAVTTHNLLSQGYYSWEKLLL~QPVGLQTT--TQAFKTGERQ
HLGYKVILLTGR--RENHRVITVENLRNAGFHNWDKLIL2RSLDRNK-TATMYKSEKRE

```

** * :*:.*      : * *. ** . *: *::*:* :. . . . :*: **:
KLEEEKGMVVIIGNIGDQWSDLLGSPEGRRTFKLPNPAYYIDNYKRAGAAVRAAVAITASS
KLVS-AGYVIVGNIGDQWSDILGSPEGYRTFKYPNPIYYVA-----
EMVK-EGYRIRGNSGDQWSDLLGSAMSERFSKLPNPMYYIP-----
:: . * * ** *****:***. . *:** *** **:

```

SSSSS

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: LOC_0s11g09020.1 476 aa

Sequence 2: LOC_0s12g08090.1 475 aa

Sequence 3: At5g63850.1 466 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 83

Sequences (1:3) Aligned. Score: 68

Sequences (2:3) Aligned. Score: 66

Guide tree file created: [/tmp/3MLr1SjSp3/lNRKwQFQFI.dnd]

Start of Multiple Alignment

There are 2 groups

Aligning...

Group 1: Sequences: 2 Score:9610

Group 2: Sequences: 3 Score:8545

Alignment Score 6650

GCG-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

```

MGKAAAMEVSASAAAEAGMMVGHGEWRDDDGRRARM~GTVWTASAHITAVIGSGVLSLA
MASGQKVVPKMEVSVEAG-NAGEAAWLDDDGRRART~GTFWTASAHITAVIGSGVLSLA
-----MDVPRPAF-----KCFDDDGRLKRS1GTVWTASAHITAVIGSGVLSLA
... * *****:*. ** .*****:*****

```

```

WAIACLQGWVAGPAVMLLFAFVIYYTSTLLAECYRSGDPCTGKRNYTYMDAVRANL~GGSK
WAIACLQGWVAGPAVMLLFAFVIYYTSTLLAECYRTGDPATGKRNYTYMDAVRANL~GGAK
WAIGQLGWIAGPTVMLLFSFVTTYSSSTLLSDCYRTGDPVSGKRNYTYMDAVRSIL1GGFR
***.***:***:***:***:*** **:*:***:***:***:***:*****: * ** :

```

```

VRLCGVIQYANLFGVAIGYTIAASISM2LAIKRADCFHEKGHNKPCRSSSNPYMILFGVV
VTFCGVIQYANLVGVAIGYTIAASSISM1RAIRRAGCFHHNGHGDPCRSSSNPYMILFGVV
FKICGLIQYLNLFGITVGYTIAASISM2MAIKRSNCFHESGGKNPCHMSSNPYMIMFGVT
.:**:* **.*:***:*** **:*:*.***.* :*: *****:***.

```

```

QIVFSQIPDFDQIWWLSIVAAIMSFTYSTIGLSLGIAQTV~ANGGFMGSLTGISVGTGVT
QIVFSQIPDFDQIWWLSIVAAMVSFTYSGIGLSLGIVQTI1SNGGIQGS�TGISIGVGS
EILLSQIKDFDQIWWLSIVAAIMSFTYSAIGLALGIIQVA1ANGVVKGSLTGISIG-AVT
*:**:* *****:***** **:* **.* :** . *****:* .*:

```

```

SMQKVWRSLQAFGDIAFAYSYSIILIEIQ0DTIKAPPSEAKVMKRATMVSVATTTVFYM
STQKVWRSLQAFGDIAFAYSFSNIIIEIQ0DTIKAPPSEAKVMKSATRLSVATTTVFYM
QTQKIWRTFQALGDIAFAYSYSVVLIEIQ0DTRSP- AESKTMKIATRISIAVTTTFYM
. **:*:***:*****:* :***** **:*:*** :*: **.* ** :*:**.* **

```

LCGCMGYAAFGDKSPDNLLTGFGFYEPFWLLDVANAAIVVHLVGAYQVFVQPIFAFVERW
LCGCMGYAAFGDAAPDNLLTGFGFYEPFWLLDVANVAIVVHLVGAYQVFVQPIFAFVERW
LCGCMGYAAFGDKAPGNLLTGFGFYNPFWLLDVANAAIVIHVLVGAYQVFAQPIFAFIEKQ
***** :*.*****:*****.***:*****.*****:*.:

AAARWPDGGFISRELRV-----GPFSLSVFRLTWRTAFVCATTVVSMLLPFFGDVVGLL
ASRRWPDSAFIAKELRV-----GPFALSLFRLTWRSFVCLTTVVAMLLPFFGNVVGLL
AAARFPDSDLVTKEYEIRIPGFRSPYKVVNFRAVYRSGFVVLTTVISMLMPFFNDVVGIL
*:***. :*: * . :*. :*: * :*: * :*: * :*: * :*: *

GAVSFWPLTVYFPVEMYIAQRGVRRGSARWLCLKVLSAACLVVSAAAAAGSIADVVDAK
GAVSFWPLTVYFPVEMYIAQRGVPRGSARWVSLKTLSCCLVVSIAAAAGSIADVIDAK
GALGFWPLTVYFPVEMYIRQRKVERWSMKWVCLQMLSCGCLMITLVAGVGSIAGVMLDLK
*:.***** ** * * * :*:. * : * . * : : : . * . * : * : * *

VYRPFSG--
VYRPFSG--
VYKPFKTTY
:.

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: LOC_0s12g02840.1 839 aa
Sequence 2: LOC_0s05g40650.1 874 aa
Sequence 3: At2g13620.1 821 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 39
Sequences (1:3) Aligned. Score: 40
Sequences (2:3) Aligned. Score: 55
Guide tree file created: [/tmp/3MLr1SjSp3/MAa124iJfY.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:13924
Group 2: Sequences: 3 Score:12341
Alignment Score 6918
CGC-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

-----MAAHTVTDPLEELWNHTMSMDKTHLMCFYPSKITMGGVWTGD
MAPIMSGAAAAAGGTGGAVPLIKNATSASQMSRGKAGTGAGAVVCYSPMMVTAYGIWQGA
-----MATSEEPSTDASIICYAPSMITTNGVWQGD
: :*: * :* *:* *

NPLDFSIPLLLFQILLITSTTRAATLLLSPLRLPTYISQIL~AGFLLGPSVLGHLPHFSN
SPLDFSLPLFLLQVAIIIVATTRLLVILLKPFQPRVIAEILGAGVILGPSVMGQVSTWAV
NPLDFSLPLFVLQLTLVVVVTRFFVFILKPFQPRVISEILGGIVLGPSVLGRSTKFAH
.*****:***: * :. . * . :*. * : * : * : * : * : * : * : * : *

LVFPVRSFLVLESMALLGLVYYTFIVGVEIEVSAITRAGIRSFGFAIGCTLPPFLVGALT
KVFPERSLLTLETVAHLGLLYFLFLVGLEMDVNTIRRSKKALIIAVAGMALPFCIGTAT
TIFPQRSVMVLETMANVGLLYFLFLVGEMDIMVVRKTGKRALTIAIGGMVLPFLIGAFAF
:* * : : * : * : * : * : * : * : * : * : * : * : * : * : *

QAYGRPAAVVGAGAGAMSVDFGGDSVMAAERTASGRRPWARPGV-----
QOYVITAPLPPP--VALAGPPTDDPVRQYLTNANQRPSVAIGGNQMGAAGRGGWSGGAGG

Sequences (2:3) Aligned. Score: 34
Guide tree file created: [/tmp/3MLr1SjSp3/S8BXCLM0Ml.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:14068
Group 2: Sequences: 3 Score:12801
Alignment Score 6051
GCG-Alignment file created [/tmp/3MLr1SjSp3/P5W730m2jT]

MARRSCFFFLPLLLVAALAGSP-----VVTARQNALPAAAAAASVRVGVILNLTSAV
MEAGARLAFVMPPLVVLLLMIFSLGVRGVDVVVDDGGGGGAAAARRRRVEVGVILDRRTWL
MRTEKLFFCILLVFFFL--EFN-----RGQNGKTLVDVGVTVDVDTSH
* : :: :.. * . * ***: : :

GVRRRVGIQMAVEDYYAANPGS--ATRVELHFRDSAGDVLPAASA1AVDLIKNVQVQAMI
GNISWACMELAVEDFYADEERASYTTALRLHLRDLRLDAVDAASA1GVDLLKNVHVQAI
SKVVMCINMSISDFYSSNPQF--ETRLVVNVGDSKSDVVGAAIA1ALDLIKNKQVKAIL
. : : : :. * : : : * : : * * : : * : : * : : * : : * : : * : : *

GPPSSAATEFVAHIGSHSRVPVLSYSATSPSLSPAQTFFVRAAVNDSFQAAPVAAVLDA
GPQTSAAKFLAELGEKSSVPVVSFSANSPCRTASQTPYFIRTAWNDSQAIAIASLVQR
GPWTSMQAHFLIEIGQKSRVPIVSYSATSPILTSRSPYFLRATYEDSFQVQPIKAIKIL
* * : * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : *

FRWRAAAVVYEDSPYGGILPALADALQGAGAKIMDRTAVPVDATDDRLDALLYRLRAMP
FNWRDVIPIEDDDSNTRFIPDLVDALRNAEIRVTHRCKIHPSAGADDIKKVVLSLKEKW
FGWREVVPVYIDNTFEGIMPRLTDALQDINVRIPIYRSVIAINATDHEISVELLKMMNMP
* * * . * * . : : * * . * : : : * : : . * : : : : :

TRVFVHMLHNVAGRLFRRAKMLGMMSDGYIWWATDGVATFMDRFSPEEVDAMQGVVSLR
TSVFVVRMSYQLALSFFKHAKDEGMMGQGFVWIAAYGLTDIFDVVGSPAFDVMQGVIGMK
TRVFLVHMYDLASRFFIKAKELGLMEPGYVWILTNGVIDDLSLINETAVEAMEGVLGK
* * : * : * : : * : : * : : * : : * : : * : : * : : * : : * : : *

PYVQETDAVKNFSAKFARLRDHTVDDVREPTVLRFWAYDTAWAIAAAAESAGVAGPA
PYVNDTKQLQNRQRWRKMYKSENP-GTTLSEPTLSGLYAYDTVWALALAAEKAGYVNSD
TYIPKSPDLEKFRSRWRSFLP-----RVELSVYGLWAYDATTALAVAIIEEAGTNMT
. * : : : : * : : : : * : : : : * : : : : * : : : : *

F-QTPQTSAPLTDLRLGVSATGTALLNAVLSTTFDGLAGKFRLVDGQLQPPAYEVVNII
F-LLSEKNGSTDFDRINTSNAKKLQSTLLNIDFQGMGKFQFQDMHLLSMTYEIINIV
FSKVVDTEGRNVSELEALGLSQFGPKLLQTLTVQFRGLAGEFRFFRGQLQPSVFEIVNII
* : : : : : : : * : : * : : * : : * : : * : : * : : * : : *

GKGARTVGFWTPEFGITQDLNAGS-----AKTLRQILWPGEPRDTPRGWTVSPSGL
GEEQRVVGFWTPEFNISRGLNT-----KADVNEIIWPGGETTVPRGWLF-PMNK
NTGEKSIGFWKEGNLVKKLDQASSISALSTWKDHLKHIVWPGEADSVPKGWIPTKKG
. : : * : : : : * : : : : * : : : : * : : : : * : : : : *

PLRVSVPTKRGFTQFVDVGNVTATGRRNITGYCIDVFDEVMKIMPYPVSYVYDPYP----
TLKIGVPAKPGFSGFIK-----EKYNFTGLCIEVFEEVLNGLPYKIPHDYVEFGNGKG
KLRIGVPKRTGYTDLVKVTRDPITNSTVVTGFCIDFFEAVIRELPYDVSYEFIPFEKPDG
* : : * : : * : : * : : * : : * : : * : : * : : * : : *

DSPESYEKLVDQVSSQ0KADAVVGDTVITASRMEEVDFTMPFTESGWSMVAVQKETSTS
ESNGTYDELIYKVYQN0DFDAVGDITILANRSlyVDFTLPYTESGVRMLVPVQDQRQKT

KTAGNYNDLVYQVYLGRYDAVVGDTTILVNRSSYVDFTFPFIKSGVGLIVEMTDPVKRD
. : . * . * : : * * * . * * * * * . * * * * : : * * : : * : . .

MWIFLQPLTTSLWLASLAFFCFTGFVWVWIEHRINEEFRGTPWQQFGLIFYFSFSTLVFS
AWTFLQPLTADLWLGTAAFFVLTGFVWVWIEHRTNEDFRGPPVNQIGSVFYFAFSTLVFA
YILFMKPLSWKLWLTSFISFVLVGCTVWVLEYKRNPDFSPPRFQASTICWFAFSTMVFA
* : : * : . * * : * : . * . * . : : * : * . * * . : : * : * * : * :

H1KEKLESNLSRFVWIIWVFWLILTSSYTASLTSMLTVQKLQPTVTDVRELLRRGDYIG
H-RQKIVNNLSRVLLVIWLFVVLILQRSYTASLSSILTVEQLQPTVTNLDEVIRKGANVG
P1RERVFSFWARALVIWYFLVLVLTQSYTASLASLLTSQKLNPTITSMSSLLEKGETVG
: : : . : * : : * * : * : * * : * : * : * : * : * : * : * : * : *

FQEGTFIVPVLEKMGFEG-RMRSYSTVDQYADALSKGSANGGVAAIFDEIPYLKFLFSQY
YLNDSEMPPELLKRLKIDESKLIALDSPDEYNEALSTG---RVAVVDEIPYLKVFLSKY
YQRTSFILGKLKERGFQSSSLVPFDTAEECDLLSKGPKKGGVSGAFLEIPYLRFLGQF
: . : * : * : : : . : : : : * * . * : . * * * : * * : :

CNGYTMVGPIYKTDGFGF-VFPRGSPMVADVSRAILTLAEGEKMAQIEKKWFGEPGACQS
CHNYTMVGPTYKFDGFGFAFPLGSPLTAEISRGILNFTSSNRMAQLERELYNN-RTCPD
CNTYKMVEEPFNVDGFGFVFPIGSPLVADVSRAILKVAESPKAMELERAWFKKKEQSCP
* : * . * : : * * * . * * * : : * * . * . . . : : * : : : .

QGSAGSSNLSFRSFGGLFLITGVVTSAMLLIYLAVFFYRERDELRAAEAAAAASGSGSG
KDDSQTSSSLTLRSFLGLFIITGASSLLALFLHVITLYNHRHDL-----SSASSQSSW
DPITNPDNPNSFTSRQ-----LDIDSFLFLVGVLLVCVMA-----
. : . . : : * . : * : : :

SGSRSLRRLRAWARHYDQKDLKSPTFKRRWSDSVRNGSEYAASRTPRWGDESPCNVAGA
CG-----WFAILLKIFHEGDRPN---APQLDEPAVSNANTTADTPWSTPDHHIIENVDSG
-----LGNFTYCFLAKDQVS-----YLDKVESPCSSSQMPVKR---KTQLNMSQV
: : * . . : . . * :

ADADAGRIP--EEVVGGMSPFSISTSSEERNGAVSPAAAEFDNSSDRAAVVAGTSQPR
SDVESVREEDREDFVQGPDPSPFAYMHSERGQ-----
HDQDSL-----
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