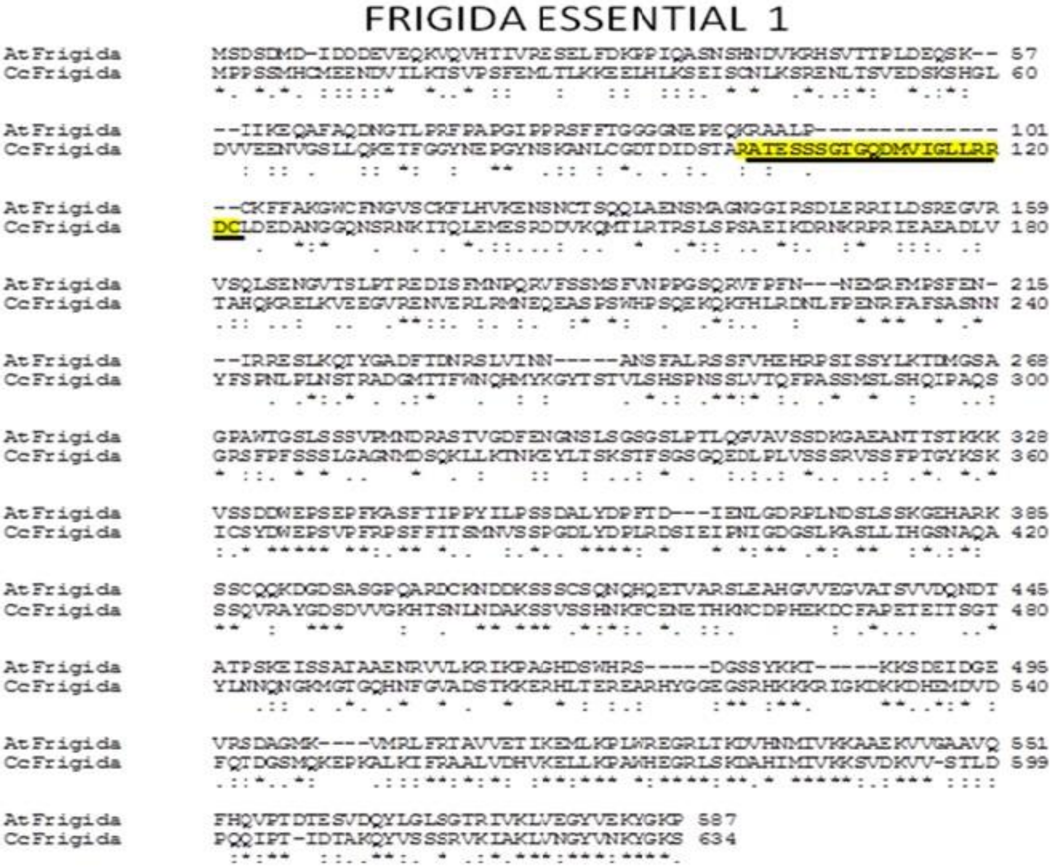
Supplementary data



FRIGIDA ESSENTIAL 1

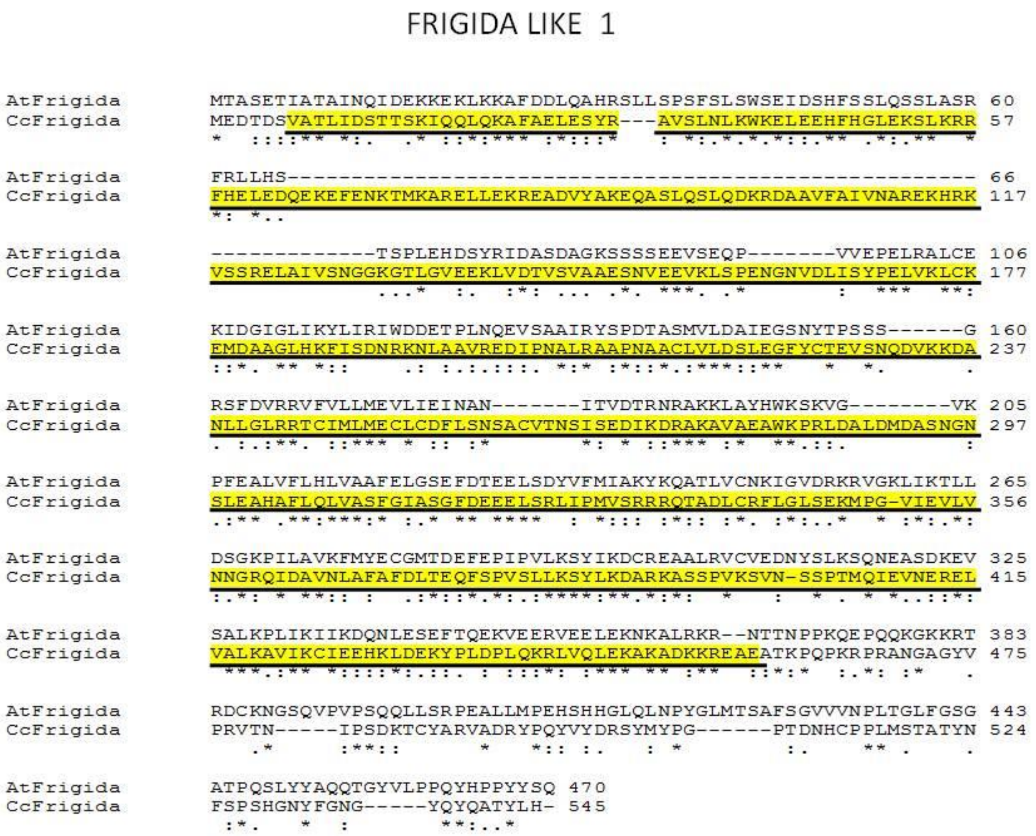
```
AtFrigida       MSDSIMD-IDDDEVEQKVQVHTIVRESELFDKPPIQASNSHNDVKRHSVTTPLDEQSK-- 57
CcFrigida       MPPSSMHCMEENDVILKTSVPSFEMLTLKKEELHLKSEISCNLKSRENLTSVEDSKSHGL 60
                *. *.*. :::::*  *..* ::    :    ::  :::. * *   .*..:*:  *.:*:

AtFrigida       --IIKEQAFAQDNGTLPRFPAPGIPPRSFFTGGGGNEPEQKRAALP-------------- 101
CcFrigida       DVVEENVGSLLQKETFGGYNEPGYNSKANLCGDTDIDSTARATESSSGTGQDMVIGLLRR 120
                  : ::  .    :: *:   :    **   .:: : *.  . :.   : :   .

AtFrigida       --CKFFAKGWCFNGVSCKFLHVKENSNCTSQQIAENSMAGNGGIRSDLERRILDSREGVR 159
CcFrigida       DCLDEDANGGQNSRNKITQLEMESRDDVKQMTLRTRSLSPSAEIKDRNKRPRIEAEADLV 180
                   .    *:*    .   .  . *.::...: ..    *    .*:: .. *:.   :*  :::. .:

AtFrigida       VSQLSENGVTSLPTREDISFMNPQRVFSSMSFVNPPGSQRVFPFN---NEMRFMPSFEN- 215
CcFrigida       TAHQKRELKVEEGVRENVERLRMNEQEASPSWHPSQEKQKFHLRDNLFPENRFAFSASNN 240
                .:: ..:  ..  .**::. :. :.  :* *:  .  .*:..   :     * **  * .*

AtFrigida       --IRRESLKQTYGADFTDNRSLVINN-----ANSFALRSSFVHEHRPSISSYLKTDMGSA 268
CcFrigida       YFSPNLPLNSTRADGMTTFWNQHMYKGYTSTVLSHSPNSSLVTQFPASSMSLSHQIPAQS 300
                    . .*:.* . .:*    .  : :      . *.: .**:* :. .*  *   :    ..:

AtFrigida       GPAWTGSLSSSVPMNDRASTVGDFENGNSLSGSGSLPTLQGVAVSSDKGAEANTTSTKKK 328
CcFrigida       GRSFPFSSSLGAGNMDSQKLLKTNKEYLTSKSTFSGSGQEDLPLVSSSRVSSFPTGYKSK 360
                * ::. * * ..    *  . :   ::  :  ..: * .  :.:.: *.. ..: .*. *.*

AtFrigida       VSSDDWEPSEPFKASFTIPPYILPSSDALYDPFTD---IENLGDRPLNDSLSSKGEHARK 385
CcFrigida       ICSYDWEPSVPFRPSFFITSMNVSSPGDLYDPLRDSIEIPNIGDGSLKASLLIHGSNAQA 420
                :.* ***** **:.** *..   :.*.. ****: *    * *:** .*: **   :*.:*:

AtFrigida       SSCQQKDGDSASGPQARDCKNDDKSSSCSQNQHQETVARSLEAHGVVEGVATSVVDQNDT 445
CcFrigida       SSQVRAYGDSDVVGKHTSNLNDAKSSVSSHNKFCENETHKNCDPHEKDCFAPETEITSGT 480
                **  :  ***     :  .  ** *** .*:*:. *. ::.          : .*...   ..*

AtFrigida       ATPSKEISSATAAENRVVLKRIKPAGHDSWHRS-----DGSSYKKT----KKSDEIDGE 496
CcFrigida       YLNNQNGKMGTGQHNFGVADSTKKERHLTEREARHYGGEGSRHKKKRIGKDKKDHEMDVD 540
                    .:: . .*. .*  * .   *    * : :.:      :** :**.      **..*:* :

AtFrigida       VRSDAGMK-----VMRLFRTAVVETIKEMLKPLWREGRLTKDVHNMIVKKAAEKVVGAAVQ 551
CcFrigida       FQTDGSMQKEPKALKIFRAALVDHVKELLKPAWHEGRLSKDAHIMIVKKSVDKVV-STLD 599
                .::*..*:     .:::**:*:*: :**:*** *:****:**.* *****:.:*** ::::

AtFrigida       FHQVPTDTESVDQYLGLSGTRIVKLVEGYVEKYGKP 587
CcFrigida       PQQIPT-IDTAKQYVSSSRVKIAKLVNGYVNKYGKS 634
                 :*:**  ::..**:. * .:*.***:***:****.
```

Fig. 1A. Amino acid sequence alignment of pigeon pea Frigida essential 1 (CcFrigida essential 1) with *Arabidopsis* Frigida essential 1 (AtFrigida essential 1)

FRIGIDA

```
AtFrigida       MSNYPPTVAAQPTTTANPLLQRHQSEQRRRELPKIVETESTSMDITIGQSKQPQFLKSID 60
CcFrigida       -------MATTDTSAPSSPPPGNETNEG-----------------------AAKLTKSVN 30
                       :*:  *::...    :::::                         .:: **::

AtFrigida       ELAAFSVAVETFKRQFDDLQKHIESIENAIDSKLESNGVVLAARNNNFHQPMLSP---PR 117
CcFrigida       ELNDLSIAIQTFKNRYDELQKHLEFIEQAIDARTKELQALRSNVENGVVEHDVKSDSNPN 90
                **  :*:*::***.::*:****:* **:***:: :.  .: :  :*.. :  :..   *.

AtFrigida       NNVSVETTVTVSQPSQEIVPETSNKPEGE---RMCELMCSKGLRKYIYANISDQAKLMEE 174
CcFrigida       QQVKAEEEEKEKEKEEEKEKEKEEEKEEEELVSLCKTMNSRGLRKHVLSHLTETTALREQ 150
                ::*..*   . .: .:*   *..:: * *    :*: * *:****:: ::::: : * *:

AtFrigida       IPSALKLAKEPAKFVLDCIGKFYLQGRRAFTKESPMSSARQVSLLILESFLLMPDRGKGK 234
CcFrigida       VSAALKSAPKPSRLVFECIGRFFLQGSKAYAKDSPMIPARQASVQVLEYYLLSGCVG-GE 209
                :.:*** * :*:::*::***:*:*** :*::*:*** .***.*: :** :**    * *:

AtFrigida       VKIESWIKDEAETAAVAWRKRLMTEGGLAAAEKMDARGLLLLVACFGVPSNFRSTDLLDL 294
CcFrigida       EDVEASLKREAESAAVAWRKRLIVEGGVARATKVDARGLVLFVAGFGIPDVFRDDDVFNL 269
                 .:*: :* ***:*********:.***:* * *:*****:*:** **:*. **. *:::*

AtFrigida       IRMSGSNEIAGALKRSQFLVPMVSGIVESSIKRGMHIEALEMVYTFGMEDKFSAALVLTS 354
CcFrigida       VRLSNVKEISDALCKSKPFLKRVSDIADGMMKKGMVVNAVDLGYTFGFEEKFSPQTALNS 329
                :*:*. :**:.** :*: ::  **.*.:. :*:** ::*::: ****:*:***.  .*.*

AtFrigida       FLKMSKESFERAKRKAQS-PLAFKEAATKQLAVLSSVMQCMETHKLDPAKELPGWQIKEQ 413
CcFrigida       FLRKSEETWKKAKQDARNFPSMLKEVHEKYLTVLKSVVNCLESHKIDFVKLLPGWQLKDK 389
                **: *:*::::**:.*:. *  :**.  * *:**.**::*:*:**:* .* *****:*::

AtFrigida       IVSLEKDTLQLDKEMEEKARSLSLMEEAALAKRMYNQQIKRPRLSPMEMPPVTSSSYSPI 473
CcFrigida       ISDLEKDISDANKKIEEKSAHKRKMDKSNLSNKMKIPETKRSRFVGNGKDASMLSPSLTA 449
                * .****  : :*::***:     *::: *:::*   : **.*:      .   *.  .

AtFrigida       YRDRSFPSQRDDDQDEISALVSSYLG-----PSTSFPHRSRRSPEYMVPLPHGGLGRSVY 528
CcFrigida       LQEQRLLSHMDGNSSYDGSLSAHLLDGRSYGYPNNYLTASAQVGSVSDSLAEKYLGSALT 509
                 ::: : *: *.:..  .:* :  *.      ...:   *  :  .   .*..  ** ::

AtFrigida       AYEHLAPNSYS---PGHGHRLHRQYSPSLVHGQRHPLQYSPPIHGQQQLPYGIQRVYRHS 585
CcFrigida       NGTNMLGGAIGGSYSGYQGGVIRDNVGTVLNSNSHLYRWHGIGEGALSHDRPVGQSYVGQ 569
                   ::  .: .   .*:   : *:   ::::.: *  ::    .*  .    : : *  .

AtFrigida       PSEERYLGLSNQRSPRSNSSLDPK------------------------ 609
CcFrigida       SPSALVNNLYGKTPTDNFSGVPEHLSIGASSRTGGPDLYSFADSVFDS 617
                ...    .* .: .. . *.:  :
```

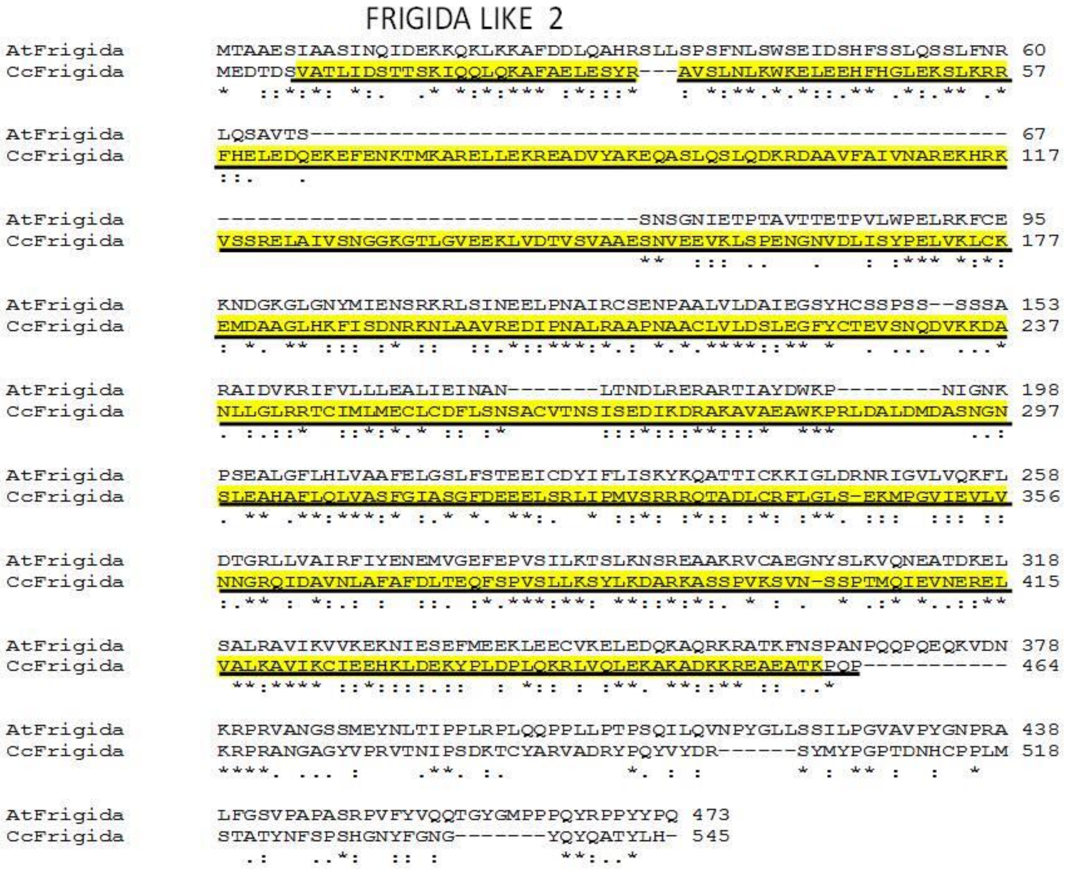
Fig. 1B. Amino acid sequence alignment of Frigida from *C. cajan* and *A. thaliana* showed relatively high sequence conservation



FRIGIDA LIKE 1

```
AtFrigida       MTASETIATAINQIDEKKEKLKKAFDDLQAHRSLLSPSFSLSWSEIDSHFSSLQSSLASR 60
CcFrigida       MEDTDSVATLIDSTTSKIQQLQKAFAELESYR---AVSLNLKWKELEEHFHGLEKSLKRR 57
                *  ::::** *:.  .* ::*:*** :*:::*   : *:.*.*.*::.** .*:.**  *

AtFrigida       FRLLHS------------------------------------------------------ 66
CcFrigida       FHELEDQEKEFENKTMKARELLEKREADVYAKEQASLQSLQDKRDAAVFAIVNAREKHRK 117
                *: *..

AtFrigida       -------------TSPLEHDSYRIDASDAGKSSSSEEVSEQP-------VVEPELRALCE 106
CcFrigida       VSSRELAIVSNGGKGTLGVEEKLVDTVSVAAESNVEEVKLSPENGNVDLISYPELVKLCK 177
                             ...*  :.  :*: ... .*. ***. .*       :  ***  **:

AtFrigida       KIDGIGLIKYLIRIWDDETPLNQEVSAAIRYSPDTASMVLDAIEGSNYTPSSS------G 160
CcFrigida       EMDAAGLHKFISDNRKNLAAVREDIPNALRAAPNAACLVLDSLEGFYCTEVSNQDVKKDA 237
                ::*. ** *::    .: :.:.:::. *:* :*::*.:***::**   *  *.      .

AtFrigida       RSFDVRRVFVLLMEVLIEINAN-------ITVDTRNRAKKLAYHWKSKVG--------VK 205
CcFrigida       NLLGLRRTCIMLMECLCDFLSNSACVTNSISEDIKDRAKAVAEAWKPRLDALDMDASNGN 297
                . :.:**. ::*** * :: :*       *: * ::*** :*  **.::.         :

AtFrigida       PFEALVFLHLVAAFELGSEFDTEELSDYVFMIAKYKQATLVCNKIGVDRKRVGKLIKTLL 265
CcFrigida       SLEAHAFLQLVASFGIASGFDEEELSRLIPMVSRRRQTADLCRFLGLSEKMPG-VIEVLV 356
                .:** .**:***:* :.* ** ****  : *::: :*:: :*. :*:..*  * :*:.*:

AtFrigida       DSGKPILAVKFMYECGMTDEFEPIPVLKSYIKDCREAALRVCVEDNYSLKSQNEASDKEV 325
CcFrigida       NNGRQIDAVNLAFAFDLTEQFSPVSLLKSYLKDARKASSPVKSVN-SSPTMQIEVNEREL 415
                :.*: * **:: :  .:*::*.*:.:****:**.*:*:  *   :  * . * *..::*:

AtFrigida       SALKPLIKIIKDQNLESEFTQEKVEERVEELEKNKALRKR--NTTNPPKQEPQQKGKKRT 383
CcFrigida       VALKAVIKCIEEHKLDEKYPLDPLQKRLVQLEKAKADKKREAEATKPQPKRPRANGAGYV 475
                 ***.:** *::::*:.::. : :::*: :*** ** :**  ::*:*  :.*: :*   .

AtFrigida       RDCKNGSQVPVPSQQLLSRPEALLMPEHSHHGLQLNPYGLMTSAFSGVVVNPLTGLFGSG 443
CcFrigida       PRVTN-----IPSDKTCYARVADRYPQYVYDRSYMYPG------PTDNHCPPLMSTATYN 524
                   .*     :**::      *   *:: :.   : *        :.    ** .    .

AtFrigida       ATPQSLYYAQQTGYVLPPQYHPPYYSQ 470
CcFrigida       FSPSHGNYFGNG-----YQYQATYLH- 545
                 :*.   *  :       **:..*
```

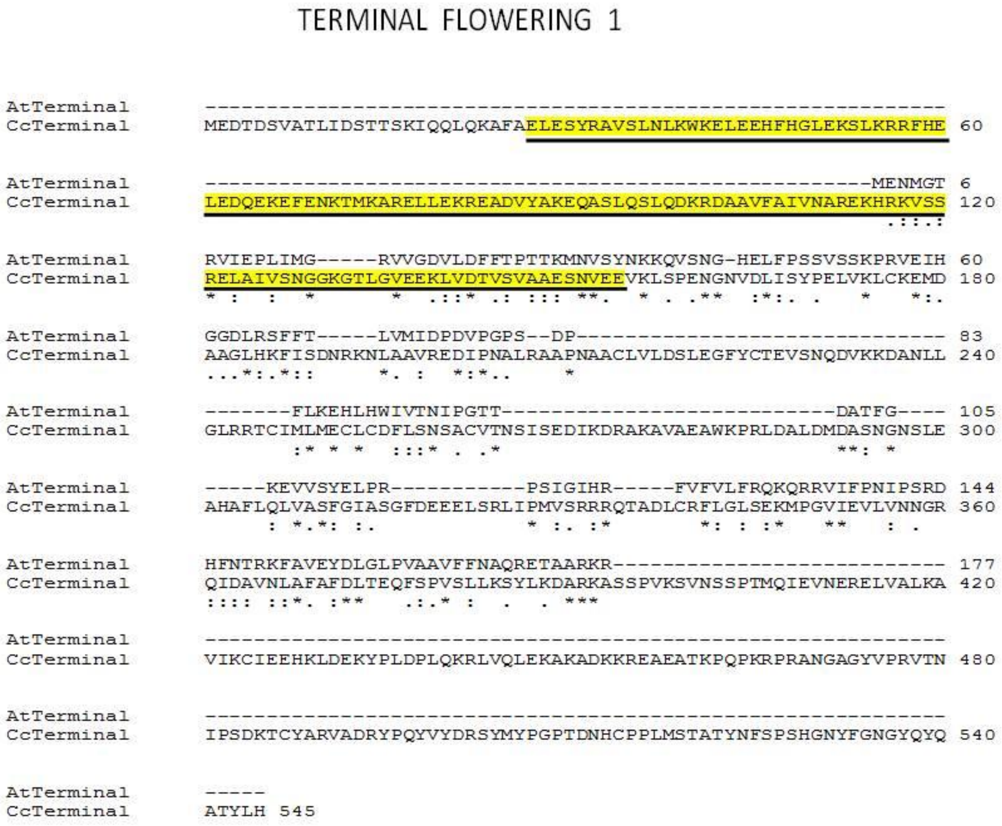
Fig. 1C. Amino acid sequence alignment of Frigida like 1 from *C. cajan* and *A. thaliana*



FRIGIDA LIKE 2

```
AtFrigida        MTAAESIAASINQIDEKKQKLKKAFDDLQAHRSLLSPSFNLSWSEIDSHFSSLQSSLFNR 60
CcFrigida        MEDTDSVATLIDSTTSKIQQLQKAFAELESYR---AVSLNLKWKELEEHFHGLEKSLKRR 57
                 *  ::*:*: *:.  .* *:*:*** :*:::*   : *:**.*.*::.** .*:.** .*

AtFrigida        LQSAVTS----------------------------------------------------- 67
CcFrigida        FHELEDQEKEFENKTMKARELLEKREADVYAKEQASLQSLQDKRDAAVFAIVNAREKHRK 117
                 ::.   .

AtFrigida        --------------------------------SNSGNIETPTAVTTETPVLWPELRKFCE 95
CcFrigida        VSSRELAIVSNGGKGTLGVEEKLVDTVSVAAESNVEEVKLSPENGNVDLISYPELVKLCK 177
                                                 **  ::: ..   .   : :*** *:*:

AtFrigida        KNDGKGLGNYMIENSRKRLSINEELPNAIRCSENPAALVLDAIEGSYHCSSPSS--SSSA 153
CcFrigida        EMDAAGLHKFISDNRKNLAAVREDIPNALRAAPNAACLVLDSLEGFYCTEVSNQDVKKDA 237
                 : *. ** ::: :* ::  ::.*::***:*.: *.*.****::** *  . ...  ...*

AtFrigida        RAIDVKRIFVLLLEALIEINAN-------LTNDLRERARTIAYDWKP--------NIGNK 198
CcFrigida        NLLGLRRTCIMLMECLCDFLSNSACVTNSISEDIKDRAKAVAEAWKPRLDALDMDASNGN 297
                 . :.::*  ::*:*.* :: :*       :::*:::**:::*  ***          ..:

AtFrigida        PSEALGFLHLVAAFELGSLFSTEEICDYIFLISKYKQATTICKKIGLDRNRIGVLVQKFL 258
CcFrigida        SLEAHAFLQLVASFGIASGFDEEELSRLIPMVSRRRQTADLCRFLGLS-EKMPGVIEVLV 356
                 . ** .**:***:* :.* *. **:.  * ::*: :*:: :*: :**. :::  ::: ::

AtFrigida        DTGRLLVAIRFIYENEMVGEFEPVSILKTSLKNSREAAKRVCAEGNYSLKVQNEATDKEL 318
CcFrigida        NNGRQIDAVNLAFAFDLTEQFSPVSLLKSYLKDARKASSPVKSVN-SSPTMQIEVNEREL 415
                 :.** : *:.: :  ::. :*.***:**: **::*:*:. * : .  * .:* *..::**

AtFrigida        SALRAVIKVVKEKNIESEFMEEKLEECVKELEDQKAQRKRATKFNSPANPQQPQEQKVDN 378
CcFrigida        VALKAVIKCIEEHKLDEKYPLDPLQKRLVQLEKAKADKKREAEATKPQP----------- 464
                  **:****  ::*::::.::  : *:: : :**. **::** :: ..*

AtFrigida        KRPRVANGSSMEYNLTIPPLRPLQQPPLLPTPSQILQVNPYGLLSSILPGVAVPYGNPRA 438
CcFrigida        KRPRANGAGYVPRVTNIPSDKTCYARVADRYPQYVYDR------SYMYPGPTDNHCPPLM 518
                 ****. ... :    .**. :.         *. : :       * : ** :  :  *

AtFrigida        LFGSVPAPASRPVFYVQQTGYGMPPPQYRPPYYPQ 473
CcFrigida        STATYNFSPSHGNYFGNG-------YQYQATYLH- 545
                   .:   ..*:  :: :         **:..*
```

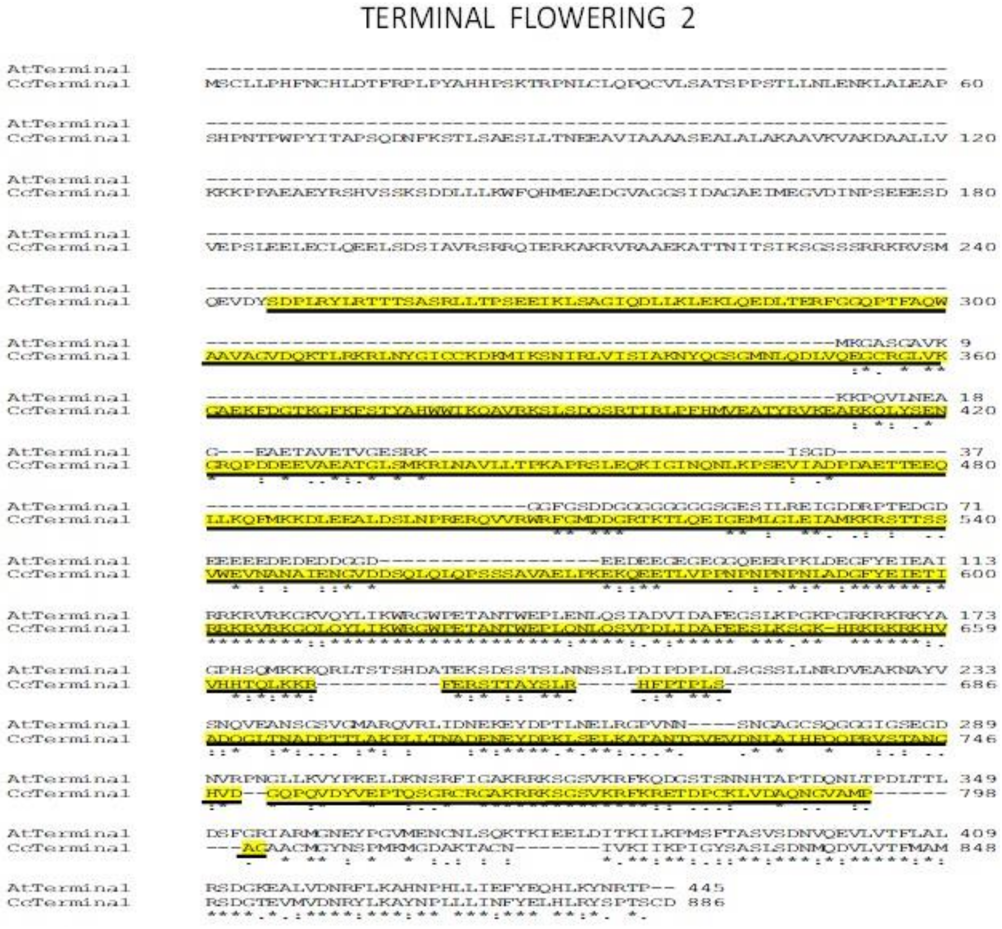
Fig. 1D. Amino acid squence alignment of Frigida like 2 from *C. cajan* and *A. thaliana*



TERMINAL FLOWERING 1

```
AtTerminal      ------------------------------------------------------------
CcTerminal      MEDTDSVATLIDSTTSKIQQLQKAFAELESYRAVSLNLKWKELEEHFHGLEKSLKRRFHE 60

AtTerminal      ------------------------------------------------------MENMGT 6
CcTerminal      LEDQEKEFENKTMKARELLEKREADVYAKEQASLQSLQDKRDAAVFAIVNAREKHRKVSS 120
                                                       .::.:

AtTerminal      RVIEPLIMG-----RVVGDVLDFFTPTTKMNVSYNKKQVSNG-HELFPSSVSSKPRVEIH 60
CcTerminal      RELAIVSNGGKGTLGVEEKLVDTVSVAAESNVEEVKLSPENGNVDLISYPELVKLCKEMD 180
                * :  :  *      *  .::* .: ::: **.  * . .**  :*:. .   *   *:.

AtTerminal      GGDLRSFFT-----LVMIDPDVPGPS--DP------------------------------ 83
CcTerminal      AAGLHKFISDNRKNLAAVREDIPNALRAAPNAACLVLDSLEGFYCTEVSNQDVKKDANLL 240
                ...*:.*::     *. :  *:*..    *

AtTerminal      -------FLKEHLHWIVTNIPGTT---------------------------DATFG---- 105
CcTerminal      GLRRTCIMLMECLCDFLSNSACVTNSISEDIKDRAKAVAEAWKPRLDALDMDASNGNSLE 300
                       :* * *  :::* . .*                           **: *

AtTerminal      -----KEVVSYELPR-----------PSIGIHR-----FVFVLFRQKQRRVIFPNIPSRD 144
CcTerminal      AHAFLQLVASFGIASGFDEEELSRLIPMVSRRRQTADLCRFLGLSEKMPGVIEVLVNNGR 360
                     : *.*: :.            * :. :*       *: : :*   **   : .

AtTerminal      HFNTRKFAVEYDLGLPVAAVFFNAQRETAARKR--------------------------- 177
CcTerminal      QIDAVNLAFAFDLTEQFSPVSLLKSYLKDARKASSPVKSVNSSPTMQIEVNERELVALKA 420
                :::: ::*. :**   .:.* :  .  . ***

AtTerminal      ------------------------------------------------------------
CcTerminal      VIKCIEEHKLDEKYPLDPLQKRLVQLEKAKADKKREAEATKPQPKRPRANGAGYVPRVTN 480

AtTerminal      ------------------------------------------------------------
CcTerminal      IPSDKTCYARVADRYPQYVYDRSYMYPGPTDNHCPPLMSTATYNFSPSHGNYFGNGYQYQ 540

AtTerminal      -----
CcTerminal      ATYLH 545
```

Fig. 1E. Amino acid sequence alignment of Terminal flowering 1 from *C. cajan* and *A. thaliana*



TERMINAL FLOWERING 2

```
AtTerminal      ------------------------------------------------------------
CcTerminal      MSCLLPHFNCHLDTFRPLPYAHHPSKTRPNLCLQPQCVLSATSPPSTLLNLENKLALEAP 60

AtTerminal      ------------------------------------------------------------
CcTerminal      SHPNTPWPYITAPSQDNFKSTLSAESLLTNEEAVIAAAASEALALAKAAVKVAKDAALLV 120

AtTerminal      ------------------------------------------------------------
CcTerminal      KKKPPAEAEYRSHVSSKSDDLLLKWFQHMEAEDGVAGGSIDAGAEIMEGVDINPSEEESD 180

AtTerminal      ------------------------------------------------------------
CcTerminal      VEPSLEELECLQEELSDSIAVRSRRQIERKAKRVRAAEKATTNITSIKSGSSSRRKRVSM 240

AtTerminal      ------------------------------------------------------------
CcTerminal      QEVDYSDPLRYLRTTTSASRLLTPSEEIKLSAGIQDLLKLEKLQEDLTERFGGQPTFAQW 300

AtTerminal      ---------------------------------------------------MKGASGAVK 9
CcTerminal      AAVAGVDQKTLRKRLNYGICCKDKMIKSNIRLVISIAKNYQGSGMNLQDLVQEGCRGLVK 360
                                                                   :*.  * **

AtTerminal      ---------------------------------------------------KKPQVINEA 18
CcTerminal      GAEKFDGTKGFKFSTYAHWWIKQAVRKSLSDQSRTIRLPFHMVEATYRVKEARKQLYSEN 420
                                                                   : *: .*

AtTerminal      G---EAETAVETVGESRK-----------------------------ISGD--------- 37
CcTerminal      GRQPDDEEVAEATGLSMKRLNAVLLTPKAPRSLEQKIGINQNLKPSEVIADPDAETTEEQ 480
                *   :  *  ..*:.* * *                           :  .*

AtTerminal      --------------------------GGFGSDDGGGGGGGGSGESILREIGDDRPTEDGD 71
CcTerminal      LLKQFMKKDLEEALDSLNPRERQVVRWRFGMDDGRTKTLQEIGEMLGLEIAMKKRSTTSS 540
                                          ** ***          ** :  **. .: :  ..

AtTerminal      EEEEEDEDEDDGGD------------------EEDEEGEGEGGQEERPKLDEGFYEIEAI 113
CcTerminal      VWEVNANAIENGVDDSQLQILQPSSSAVAELPKEKQEETLVPPNPNPNPNIADGFYEIETI 600
                  *  :  :   ::* *                *::**       . :  .*:* :*******:*

AtTerminal      RRKRVRKGKVQYLIKWRGWPETANTWEPLENLQSIADVIDAFEGSLKPGKPGRKRKRKYA 173
CcTerminal      RRKRVRKGQLQYLIKWRGWPETANTWEPLQNLQSVPDLIDAFEESLKSGK-HRKRKRKHV 659
                ********::*******************:****:.*:****** ***.**  ******:.

AtTerminal      GPHSQMKKKQRLTSTSHDATEKSDSSTSLNNSSLPDIPDPLDLSGSSLLNRDVEAKNAYV 233
CcTerminal      VHHTQLKKR-----------FERSTTAYSLR-----HFPTPLS----------------- 686
                 *:*:***:           *:* :: **.      .:* **.

AtTerminal      SNQVEANSGSVGMARQVRLIDNEKEYDPTLNELRGPVNN----SNGAGCSQGGGIGSEGD 289
CcTerminal      ADQGLTNADPTTLAKPLLTNADENEYDPKLSELKATANTGVEVDNLAIHEDQPRVSTANG 746
                ::*  :*:... :*: :     :*:****.*.**:...*.     .* *   *   :.: ..

AtTerminal      NVRPNGLLKVYPKELDKNSRFIGAKRRKSGSVKRFKQDGSTSNNHTAPTDQNLTPDLTTL 349
CcTerminal      HVD--GQPQVDYVEPTQSGRCRGAKRRKSGSVKRFKRETDPCKLVDAQNGVAMP------ 798
                :*   *  :*   *  :..*  ****************:: ...:    *  ..  :.

AtTerminal      DSFGRIARMGNEYPGVMENCNLSQKTKIEELDITKILKPMSFTASVSDNVQEVLVTFLAL 409
CcTerminal      ---AGAACMGYNSPMKMGDAKTACN-------IVKIIKPIGYSASLSDNMQDVLVTFMAM 848
                   .  * ** : *  * :.: : :       *.**:**:.::**:***:*:*****:*:

AtTerminal      RSDGKEALVDNRFLKAHNPHLLIEFYEQHLKYNRTP-- 445
CcTerminal      RSDGTEVMVDNRYLKAYNPLLLINFYELHLRYSPTSCD 886
                ****.*.:****:***:** ***:*** **:*. *.
```

Fig. 1F. Amino acid sequence alignment of Terminal flowering 2 from *C. cajan* and *A. thaliana*