```
Vf Inh3 (AB372570)        MDRRRGTTRQVVLSSPSATGTTTITIESSV------------------PSSSSSQQEQQQP---EVLFLPLNRK-KKKVSWKDGTVDNEF  [ 68]
Mt Inh3 (ABN09808)        MDRRRNSTRPVALSPPSITATTTITIQNSD------------------ASSSSSQHEQQQP---EVLYLPLNRK-KKKVSWKEGTVDNEF  [ 68]
At Inh3 (At2g31305)       MS---TATR------PSSSATTSVILENPV------------------SQS-------QPT---ERLVLRLNRK-KKKVSWKDGTVDNEF  [ 52]
Os Inh3a (NP_001052397)   -----MATR------APATGSATVTVDPTP------------------SSS--APASSAPPPAAETVVLRLKRRAKKKVTWKEGTVDNES  [ 59]
Os Inh3b (NP_001055058)   -----MATR------APATGSTTVTVDPSP------------------SSSSSAPASSAPPPAAESVVLRLKRRPKKKVTWKEGTVDNES  [ 61]
P.falciparum (Q8IJ88)     --------------MCPMHSSSTTTTTYVQ------------------DTNTQN----DTNENSSTIVRILKLAPQKVVRWDENTIDNEN  [ 54]
N.crassa (EAA27640)       --------------MTSVAQRQAQPAQPST------------------SQTAAPTRTQTETSSPAILRLRGAHSNGRSVQWRSDVVDNEG  [ 58]
S.cerevisiae (BAA09242)   ----------MSGNQMAMGSEQQQTVGSRT------------------VSVEEVPAVLQLRATQDPPRSQEAMPTRHNVRWEENVIDNEN  [ 62]
S.pombe (O14218)          ---------------MELTRPLGDISSSAT------------------VTIESTEESASISHEESENVLHLQPEPVRRVRWTVSTVDNEH  [ 57]
C.elegans (NP_498652)     ---------------MSHTQQQTASSTETS------------------TVTVPPSREQNLVLHLSPNPAQPSTSERRHVVWATETVDNEG  [ 57]
C.elegans (NP_497013)     --------------MAQSNTTT---------------------------TTLVVKSEDQEEVQEEHVLRLRAPPSPPHVTWAEGVVDNEH  [ 49]
C.elegans (NP_496183)     ---------------MQAPVVT---------------------------ETCQTNEEG-----EQLVLRLRAPVERPRVTWGAGVIDNEH  [ 43]
D.melanogaster (AAF50877) ------MDSNCDLSMVNGQTEPKDPKWASSSTQITSRASETFSGVGSAISTETSLQPVAAPTMYCLRLAQQRPITERHVHFHAGVIDNEH  [ 84]
D.melanogaster (AAF52335) --------------MAHKQSTNNETSNGSTTEIID--------------ETDARAQLESGRTTPTLLLRLEHPRNERRVAFHAGIIDNEH  [ 62]
D.rerio (CAM56331)        --------------MAEVPGTSSET-ITET------------------VQTGTP--PPPQQEGRSLTIKLRKRKTEKKVEWSSDTVDNEH  [ 55]
X.laevis (Q6DDH0)         --------------MAETSGPTAAGGSTSS------------------TVTTES---ETQPEHRSLTLKLRKRKPDKKVEWTCDTVDNEN  [ 55]
M.musculus (Q8K1L5)       --------------MAETGAGISET-VTET------------------TVTETTVTETTEPENQSLTMKLRKRKPEKKVEWSSDTVDNEH  [ 57]
H.sapiens (CAC16920)      --------------MAEAGAGLSET-VTET------------------TVTVT-----TEPENRSLTIKLRKRKPEKKVEWTSDTVDNEH  [ 52]


Vf Inh3 (AB372570)        MQKKSSKKCCIFHKEKPFDEDD------------SDE-DDVAHGSDKHP-------------------------HDLGD-----NGFCCK  [115]
Mt Inh3 (ABN09808)        MQKKSSKKCCIFHKEKPFDEDD------------SDE-DDIPHHSDHHP-------------------------HDHGD-----GGFCCK  [115]
At Inh3 (At2g31305)       MQKKSSKKCCIFHKQKPFDEDD------------SEEEDDNNHHCDHN--------------------------HEHSE-----SGEASS  [ 99]
Os Inh3a (NP_001052397)   LGRKSSKKCCIFHKDVPFDEDC------------SDDDPDGG--RRSPP-------------------------GDAGEGTSGGGGGCCS  [110]
Os Inh3b (NP_001055058)   LGRKSSKKCCIFHKEVPFDEDC------------SDDEPDGGGGRRSPP-------------------------GDAGEGTSGGGG-CCS  [113]
P.falciparum (Q8IJ88)     AQKKSSKVCCIYHKPKNFGESSD-----------SESDLDSDVELPDTQ-------------------------RMKN------------  [ 96]
N.crassa (EAA27640)       LGRKKSKVCCIYHRPKGVDESSDDSSSSSDSSSSSDSDSDPEPDQDKRITSGGGSSGRGHRHSHDHDHDGREGGCNHDHGRGRKHGNKGK  [148]
S.cerevisiae (BAA09242)   MNKKKTKICCIFHPQNEDEEECN-----------HHSDDDGSSSSGSSSS------------------------ESENEKDLDFNERRQR  [117]
S.pombe (O14218)          MNKKKSKVCCIFHKQRKFDESS------------SDSDSDSDSDSSCSS-------------------------CCSRN-----------  [ 99]
C.elegans (NP_498652)     MGKKKSKCCCIYKKPKNWQDSS------------SDSDSD----------------------------------CETGHCRG--HVEHKK  [ 99]
C.elegans (NP_497013)     MGRLKSNCCCIYVAPRQWDDPSTWEP--------NEYETEHCRGHTLPER------------------------KKKKEDGGDEGDDENK  [107]
C.elegans (NP_496183)     MGRLKSNCCCIYTPPRVWDDPSTWEP--------EEHETEHCRGHTLPE-------------------------KKQKPQGG-HGSDKD-  [ 98]
D.melanogaster (AAF50877) MNRRKSKCCCIYRKPHPFGESSSS----------TDDECEHCFGHPEVRT------------------------RNRLEKQRIQEQQNGC  [140]
D.melanogaster (AAF52335) LNRKKSKCCCIYKKPLAFGESSSE----------DDEDCEHCFGHPEKRQ------------------------RN--AKHNHNHGDKPC  [116]
D.rerio (CAM56331)        LGRRSSKCCCIYEKPRQFGESS------------SESEGDDEEGCGSAH-------------------------CILGHGRRGHGQREGG  [108]
X.laevis (Q6DDH0)         LGRRSSKCCCIYEKPRPFGESS------------SESE-DDDDCCESAH-------------------------CIRGHKKATSGSKETP  [107]
M.musculus (Q8K1L5)       MGRRSSKCCCIYEKPRAFGESS------------TESDEDEEEGCSHKH-------------------------CVRGHRKGRRPTTPAP  [110]
H.sapiens (CAC16920)      MGRRSSKCCCIYEKPRAFGESS------------TESDEEEEEGCGHTH-------------------------CVRGHRKGRRRATLGP  [105]


Vf Inh3 (AB372570)        NHDEAGPSS------------------------------------------------------------------------ [124]
Mt Inh3 (ABN09808)        NHDEAGPSS------------------------------------------------------------------------ [124]
At Inh3 (At2g31305)       SNDSKAVD------------------------------------------------------------------------- [107]
Os Inh3a (NP_001052397)   SSSDGHGH------------------------------------------------------------------------- [118]
Os Inh3b (NP_001055058)   SSSHGHGHGHDH--------------------------------------------------------------------- [125]
P.falciparum (Q8IJ88)     --------------------------------------------------------------------------------- [ 96]
N.crassa (EAA27640)       KTERRPSPNAYEKMPKYKPKDGGAGPSNSETQGPGGSK------------------------------------------- [186]
S.cerevisiae (BAA09242)   RLERRHRKLEKKRSYSPNAYEIQPDYSEYRRKQQEKKD------------------------------------------- [155]
S.pombe (O14218)          AYERA---------------------------------------------------------------------------- [104]
C.elegans (NP_498652)     NEEPKSSN------------------------------------------------------------------------- [107]
C.elegans (NP_497013)     ENKDNKDN---------------------------KDNKDNKDNNGCGCDHC----------------------------- [132]
C.elegans (NP_496183)     EDKGN-----------------------------------------CGCDHC----------------------------- [109]
D.melanogaster (AAF50877) SCCHHHHRLHSNRNNRPPTEEIAQHKDDLAKEEPKSVVNNESSLKLLNEENVKSSKPEKKNNSNNRLEPFSQAKKSRRKPA [221]
D.melanogaster (AAF52335) TEASHPE--------GPSTSTQAAHISQPPAEPVESKTDPKPPTPGVDFEQTGSS-------------------------- [163]
D.rerio (CAM56331)        GTTVPP-------SSGGTNPH------------------------------------------------------------ [122]
X.laevis (Q6DDH0)         SSHHDK---------TGSMQH------------------------------------------------------------ [119]
M.musculus (Q8K1L5)       TPTTPPQPPDPSKPPPGPMQH------------------------------------------------------------ [131]
H.sapiens (CAC16920)      TPTTPPQPPDPSQPPPGPMQH------------------------------------------------------------ [126]
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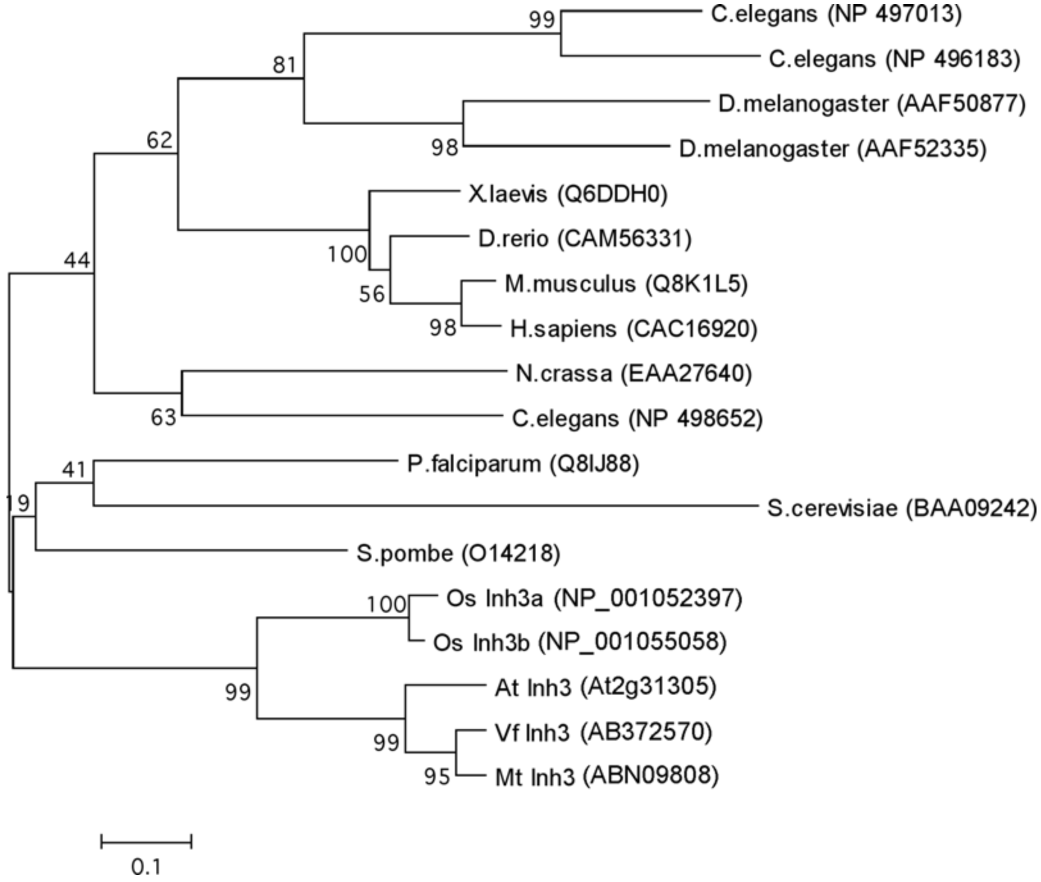
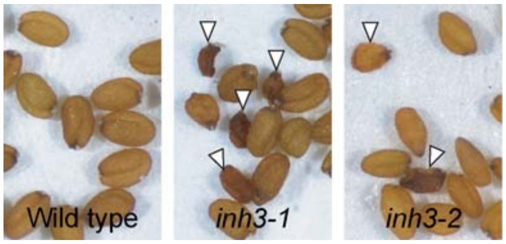
Supplemental Figure S1. Multiple Alignments of the Inh3 Protein Sequences by CLUSTAL W.

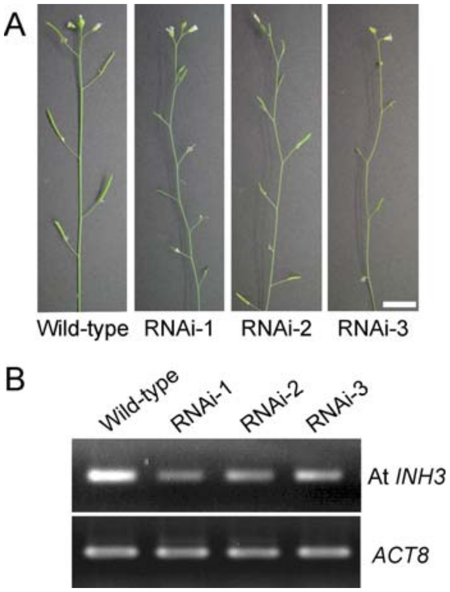


Supplemental Figure S2. Neighbor-Joining Phylogenetic Tree of Inh3 Protein Sequences with Bootstrap Values (1000 replicates).



Supplemental Figure S3. Dry Mature Seeds from Siliques of Wild-type and Heterozygous *inh3* Mutants.

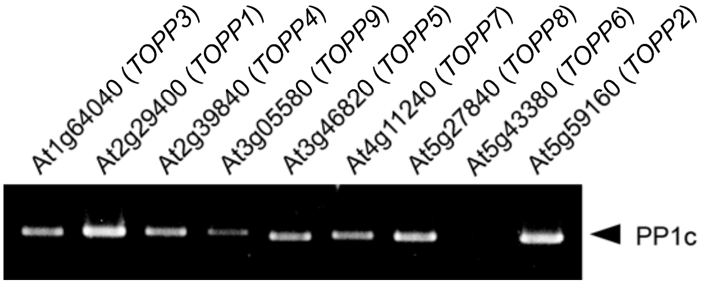
Arrowheads indicate shriveled and dark brown seeds.



Supplemental Figure 4. Seed Development Defect by RNAi-mediated Suppression of At *INH3* Expression

(A) Phenotypes of inflorescence in wild-type and At *INH3*-RNAi T2 lines (RNAi-1, RNA-2, and RNAi-3). The bar represents 1 cm.

(B) Expression of At *INH3* transcripts in wild-type and three At *INH3*-RNAi T2 lines determined by RT-PCR. Total RNA was extracted from immature siliques of both wild-type and RNAi lines. *ACT8* was used as an internal control.



Supplemental Figure S5. RT-PCR Analysis of the Expression of the Arabidopsis PP1c Isoforms in Young Green Siliques.