

Supplemental Figure 1. Protein alignment of the NBS-LRR paralogues A, B and C of the *Pc* gene family from the cultivar *Pc/Pc* Colby. The region deleted in mutant M12 is inside the two opposing arrows. The region with a high unequal recombination rate (bp 3062-3622 on the consensus nucleotide sequence) is marked with asterisks (*).

Colby_B 1 -----MEALASGVLKAAGDKLVSLATEFAAIVGKRDLC
Colby_A 1 MAASAGPGGGVACNSQIFCRPLIYSRVENYYWNI SAATFPKKGLGNSFFDIMSGMEALASGVLKAAGDKLVSLATEFAAIVGKRDLC
Colby_C 1 -----MEALASGVLKAAGDKLVSLATEFAAIVGKRDLC

Colby_B 37 QLQDIHADITGWL SACHDRAIQSETQSHWVVKLKDVA YDIDDILQEVQLEAEKQKMERDDDKSGIAGCFCAKPKSFAFRYKMAHK IKAIK
Colby_A 91 QLQDIHADITGWL SAAYDRAIQSETQSHWVVKLKDVA YDIDDILQEVQLEAEKQKMERDDDKSGIAGCFCAKPKSFAFRYKMAHK IKAIK
Colby_C 37 QLQDIHADITGWL SAAYDRAIQSETQSHWVVKLKDVA YDIDDILQEVQLEAEKQKMERDDDKSGIAGCFCAKPKSFAFRYKMAHK IKAIK

Colby_B 127 VRFAAVVKQRSDFNTLVPTRDQHVGTR YKTVGEMTWL SKVPESKIPLRDQEKDEIISKLVECNAGENNMIVSIIIGLGGSGKTTLAKHICH
Colby_A 181 VRFAAVVKQRSDFNTLVPTRDQHVGAR YKTVGEMTWL SKVPESKIPLRDQEKDEIISKLVECNAGENNMIVSIIIGLGGSGKTTLAKHICH
Colby_C 127 VRFAAVVKQRSDFNTLVPTRDQHVGAR YKTVGEMTWL SKVPESKIPLRDQEKDEIISKLVECNAGENNMIVSIIIGLGGSGKTTLAKHICH

Colby_B 217 DVKIKEHFHGGEIFWVHV SQEFDVQKLI GKL FETIVGDN SDRHPPQH MVQKISEKLSNKKFLLI LDDAWHEDHRDWEQFMVQLKCGAPETR
Colby_A 271 DVKIKEHFHGGEIFWVHV SQEFDVQKLI GKL FETIVGDN SDRHPPQH MVQKISEKLSNKKFLLI LDDAWHEDHRDWEQFMVQLKCGAPETR
Colby_C 217 DVKIKEHFHGGEIFWVHV SQEFDVQKLI GKL FETIVGDN SDRHPPQH MVQKISEKLSNKKFLLI LDDAWHEDHRDWEQFMVQLKCGAPETR

Colby_B 307 IMLTTRDRKVAQAVESRYTFELAF LSESESWNLF LKGSGLAEQLSSDEVQV GKEIIKGC GGVP LAIQTLGAVLRD KKKQISTWRAIRENN
Colby_A 361 IVL TTRDRKVAQAVESRYTFELAF LSESESWNLF LKGSGLAEQLSSDEVQV GKEIIKGC GGVP LAIQTLGAVLRD KKKQISTWRAIRENN
Colby_C 307 IVL TTRDRKVAQAVESRYTFELAF LSESESWNLF LKGSGLAEQLSSDEVQV GKEIIKGC GGVP LAIQTLGAVLRD KKKQISTWRAIRENN

Colby_B 397 LKWKVQSIKDRVFASL KLSYIHLADEL KQCFTFC SIFPKGYGIRKDR LIAQWIAHGF INAMNGEQPEDVGRDYLD SLVVKVRF LQEVYGSWN
Colby_A 451 LKWKVQSIKDRVFASL KLSYIHLADEL KQCFTFC SIFPKGYGIRKDR LIAQWIAHGF INAMNGEQPEDVGRDYLD SLVVKVRF LQEVYGSWN
Colby_C 397 LKWKVQSIKDRVFASL KLSYIHLADEL KQCFTFC SIFPKGYGIRKDR LIAQWIAHGF INAMNGEQPEDVGRDYLD SLVVKVRF LQEVYGSWN

Colby_B 487 TDIYTMHDLI HDLTRQILKDEL VTCVP IHTTEEFTHRYR YLSLTSFTENVDKGV FDKVRALYISDSKTSFDTTVKSSCCMR SVVLDY AID
Colby_A 541 TDIYTMHDLI HDLTRQILKDEL VTCVP IHTTEEFTHRYR YLSLTSFTENVDKGV FDKVRALYISDSKTSFDTTVKSSCCMR SVVLDY AID
Colby_C 487 TDIYTMHDLI HDLTRQILKDEL VTCVP IHTTEEFTHRYR YLSLTSFTENVDKGV FDKVRALYISDSKTSFDTTVKSSCCMR SVVLDY AID

Colby_B 577 TPFSLF ILKFEYLGYLE IHNVSCTTVPEAISR CNWQLSHFVNCKGFVTLPE SVGKLRKLR TLELRG IITDLESLES PQSIGDCYV LQSLQLY
Colby_A 631 TPFSLF ILKFEYLGYLE IHNVSCTTVPEAISR CNWQLSHFVNCKGFVTLPE SVGKLRKLR TLELRG IITDLESLES PQSIGDCYV LQSLQLY
Colby_C 577 TPFSLF ILKFEYLGYLE IHNVSCTTVPEAISR CNWQLSHFVNCKGFVTLPE SVGKLRKLR TLELRG IITDLESLES PQSIGDCYV LQSLQLY

Colby_B 667 DC SMLREIPSS LGRIGSL CVL DIERCSSLQQLPSDI IGEFKNLRTIN FNGCTGLQDLPSTL SCPTLR TLNLSETKV TMLPQWVTSIDTLE
Colby_A 721 KCRKQREIPSS LGRIGNL CVL D-----FNGCTGLQDLPSTL SCPTLR TLNLSETKV TMLPQWVTSIDTLE
Colby_C 667 DC WKLREIPSS LGRIGNL CVL D-----FNGCTGLQDLPSTL SCPTLR TLNLSETKV TMLPQWVTSIDTLE

Colby_B 757 CIDLKG CNELR ELPKGIANLKR LIAV LNI EHC SBL CCLPSGLQLTR LRKLG LFFVVGCGADDAR ISELENLDMIGGRLEITNL KYLKDPSD
Colby_A 786 CIDLKG CNELR ELPKGIANLKR LIAV LNI EHC SBL CCLPSGLQLTR LRKLG LFFVVGCGADDAR ISELENLDMIGGRLEITNL KYLKDPSD
Colby_C 732 CIDLKG CNELR ELPKGIANLKR LIAV LNI EHC SBL CCLPSGLQLTR LRKLG LFFVVGCGADDAR ISELENLDMIGGRLEITNL KYLKDPSD

Colby_B 847 AEKACLKRKSNIQHLEL IWSLSDAE EELVSDMEHDWGV LNALEPPSQIESLDIYGYRG PCLPGWMMKQNDSSYCEGGIMLKQT VASHFLC
Colby_A 876 AEKACLKRKSNIQHLEL IWSLSDAE EELVSDMEHDWGV LNALEPPSQIESLDIYGYRG PCLPGWMMKQNDSSYCEGGIMLKQT VASHFLC
Colby_C 822 AEKACLKRKSNIQHLEL IWSLSDAE EELVSDMEHDWGV LNALEPPSQIESLDIYGYRG PCLPGWMMKQNDSSYCEGGIMLKQT VASHFLC

Colby_B 937 LTL LSLVRF PNLRHMRGFVELPSLKTLE LAEMP NLEELWTTSSGFETGEKELAAQH LFPVLSSEIYGC PKLNVSPYFP PSLVHMSLNRI
Colby_A 966 LTL LSLVRF PNLRHMRGFVELPSLKTLE LAEMP NLEELWTTSSGFETGEKELAAQH LFPVLSSEIYGC PKLNVSPYFP PSLVHMSLNRI
Colby_C 912 LTL LSLVRF PNLRHMRGFVELPSLKTLE LAEMP NLEELWTTSSGFETGEKELAAQH LFPVLSSEIYGC PKLNVSPYFP PSLVHMSLNRI

Colby_B 1027 NGQLLSTGRF SHQLPSMHAMV--LQSLV LSEVTGSSSGWELLQHL TELKELYIDTCNDLTQLPESMRNLT-----
Colby_A 1056 NGQLLSA GRF SHQLPSMHALVPR LKSLV LSEVTGSSSGWELLQHL TELKELYIYRCNDLTQLPESMRNLTSLERLR IDECPAVGTL PDWL
Colby_C 1002 NGQLLSTGRF SHQLPSMHALVPR LKSLV LSEVTGSSSGWELLQHL TELKELYIYRCNDLTQLPESMRNLTSLERLR IDECPAVGTL PDWL

Colby_B 1095 -----SLEHLELSSG PALTVLPEWIGQLSALRS LYI QHSPALQYLPQSIQR LTALELLCIYGC PGLAE
Colby_A 1146 GELHSLRDLV LGMGDLKQFPEAI QHLT SLEHL D LSGPALTVLPEWIGQLSALRS LYI QHSPALQYLPQSIQR LTALELLCIYGC PGLAE
Colby_C 1092 GELHSLRDLV LGMGDLKQFPEAI QHLT SLEHLELSSG PALTVLPEWIGQLSALRS LYI QHSPALQYLPQSIQR LTALELLCIYGC PGLAE

Colby_B 1158 RYKRGE GPDWHLVSHIPLVVIDFV VNTAN----ATVGT DAL--
Colby_A 1236 RYKRGE GPDWHLVSHIPLVVIDFV VNTAN----ATVGT DAL--
Colby_C 1182 RYKRGE GPDWHLVSHIPLVVIDFV VNTAN----ATVGT DAL--