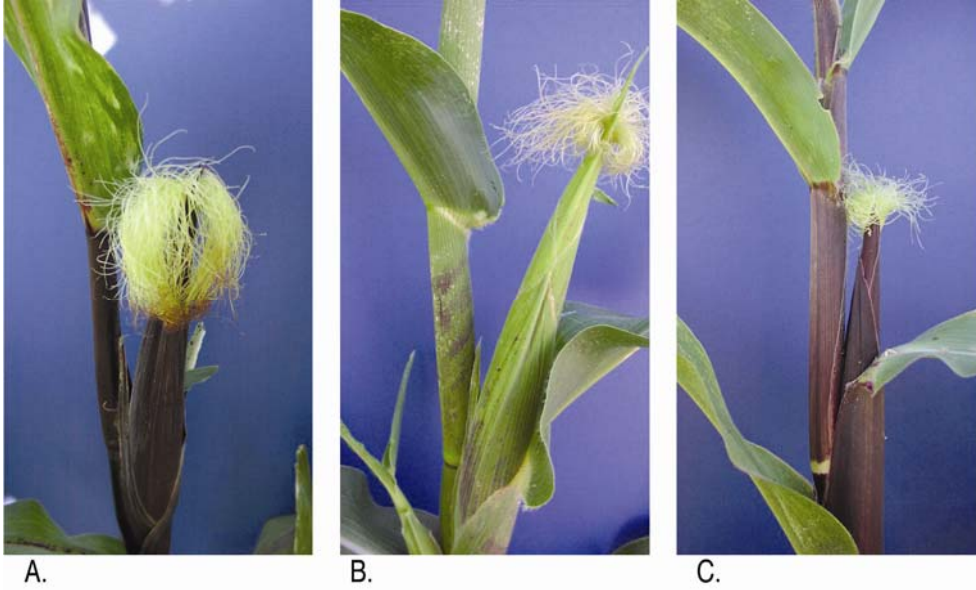
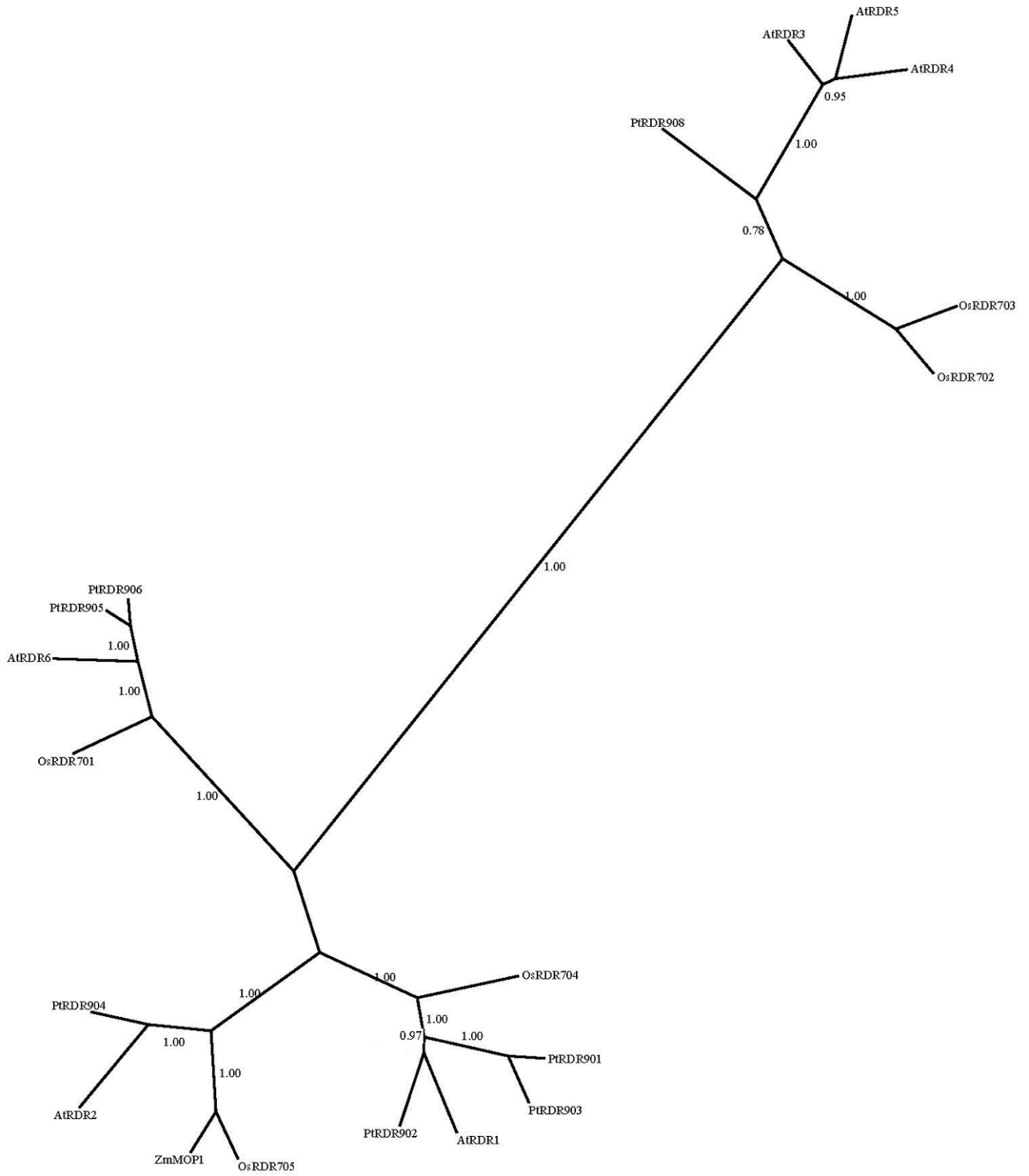


Supplementary Figure 1. Phenotypes of *mop1* mutations and *b1* paramutation used for mapping. *B-l/B-l* plants (**A**) are strongly pigmented with anthocyanin due to the high expression of the bHLH transcription factor encoded by *b1*. Plants homozygous for the paramutagenic (silenced) *B'* allele and either heterozygous *Mop1-B73/mop1-1* (**B**) or homozygous *Mop1-B73* (not shown) produce a weakly pigmented phenotype. Homozygous *mop1-1/mop1-1*, *B'/B'* plants (**C**) are darkly pigmented due to the loss of *B'* silencing in the presence of homozygous *mop1-1*.



Supplementary Figure 2. Maize RDR101 is most closely related to Arabidopsis RDR2. (A) The predicted maize RDR101 (MOP1) protein was compared to Arabidopsis (AtRDR1-6), rice (OsRDR701-705), and poplar (PtRDR901, 906, and 908) RNA dependent RNA polymerases. Phylogenetic analysis was performed as described in supplemental methods. Posterior probability is indicated on each branch. (B) Edited alignment used to generate tree.



0.1

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                *           20           *           40           *           60           *           80
OsRDR702 : LEELEGRKIFMVFAYLASEKII-ENVLSV-DYIRSLKFLS-----MAQFESQIWRITFG--HKYIAASDRAKN-- : 62
OsRDR703 : LGELEFRKIFMVFAYLPKSSKIEDVLSV-DSIRSLKSMS-----MAQFESRIWRITFG--HDNISSDRAKN-- : 63
PtRDR908 : LGELEFRKAFLLLSYLGKNTI-EEVLSA-DQIRGYKDLF-----METFESKIWEAFGCRRDYIKEEDRVKY-- : 64
AtRDR5 : LGELEFKKVFLLSYLPGQHV-GQVITA-DEIRLWKDLP-----MVEYEAAVWDRLG--RHYPCKQDRRM-- : 61
AtRDR3 : LGELEFKKAFLLLSYLGGESI-VEEVLG-DQIRKWKDLP-----MVSYEAAVWNLRG--QRYCSPKERRRP-- : 63
AtRDR4 : LGELEFKKAFLLLSYLGKSTI-GEVLSG-DEIRQWKDLP-----MVAYERAVWFKLQNEERMQ----- : 57
OsRDR701 : AEGLEKPEPLFMVNALVHKGIINQHQITP-EFFSLGRSEENVV--AALRDFWGDKFPVFDACGRLKALNRVARNPK-- : 75
AtRDR6 : KEGISFETIMFVNSVLRHGVSFNQFQITE-RFFDLRLNQPKDVNI--ASLKHICTYKRPVFDAYKRLK-LVQEWIQKNP-- : 74
PtRDR905 : KEGIAFQEVLFVNAVAMHKGIFNQHQLSN-DFFDLRLNQHTVENV--SALKHICTYRRPVFNAYRRLK-AVQEWLLKNPNL : 76
PtRDR906 : KEGIAFDVLFVNAVAMHKGIFNQHQLSN-DFFDLRLNQHTVENV--AALKHICYRRPVFDAYKRLK-LVQEWLLKNPKF : 76
OsRDR704 : RGYVPYELFKINHLVQNGTISGPTVDD-SFFRLVSPAFVPIDHIKRALEMYSYLKKTCLNP----- : 61
PtRDR901 : GIELPMDIVFKVNSLVQHGYLPGPALDA-SFYRLINPVRVNIHAIQNALEKMHHSMECCYDPVRWLRREYRKCISTGR-- : 77
PtRDR903 : VSELPMYDIVFKVNSLVQHGYLPGPALDA-RFRLINPVRVNIHAIQNALEKMHSHLKECCYDPAWLRREYQYKYLTTGR-- : 77
AtRDR1 : GFSLPPELFLFKINHLVQNGTISGPTVDD-SFYRLINPVRVNIHAIQNALEKMHSHLKECCYDPAWLRREYQYKYLTTGR-- : 77
PtRDR902 : GYNLPMYLLFRVNLVQNGCAGSMDD-IFVRLVDPNRMVRCIEYALEKMHSHLKECCYDPAWLRREYQYKYLTTGR-- : 77
OsRDR705 : DYSVPYEVLFRLNLSLHMGMKIVAKHUNA-DLFKALQELPVDVSR--RIFEKMHKLESTCYGPLQFIQOEAYSMMKRSHNVL : 77
ZmMOP1 : GFSVPYEVLFRLNLSLHMGMKIVARHUNA-DLFKALQELPVDVSR--RIFEKMHKLESTCYGPLQFIQOEAYSMMKRSHNVL : 75
AtRDR2 : GLEFPYELFLQNLALVHAQKISLFAASDMELIKILRGMSLETAL--VILKHLHQSSICYDPVFFVKTMQMSVVKMKHS : 78
PtRDR904 : SDKLAMEVLFQNLALVHTQKISLAAVDS-DLILKILRLNLTVTNTAI--IILQKHLKLMTCYDPLSFVKQSLRESLSSPP-- : 75
          5   F 6   6

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                *           100          *           120          *           140          *           160
OsRDR702 : -----LDSDPGMTKVYHCNVAIRGDTVVGPIYENRTRHLQKVVGD-DNVLVVKFVMEI-----LSDT : 117
OsRDR703 : -----LDSGPMKSKVYHCNVEIRGGTVVGPIYENRTRHLQKVVGD-DNVLVVKFVMEI-----SSDT : 118
PtRDR908 : -----LDWDSGKTHIYHCHVDFDGSVRFGLVSKLRNLRQRTLGD-DNLMVVKFGEV-----KDDR : 119
AtRDR5 : -----LQWDSGKTHYQCNVAENGSTYTFGLLEHTGTHLHKVVLGD-DNVLTVKFFADV-----QKSS : 116
AtRDR3 : -----LEGDSGKTHYQCHVATDGSYKFGHLENTGTHLHKVVLGD-DNVLTVKFFADV-----LGVE : 118
AtRDR4 : -----LESDSGKTHYQCHVATDGSYKFGHLENTGTHLHKVVLGD-DNVLTVRFDQL-----PKES : 112
OsRDR701 : ---LLCSKVGDDHAEVRRLLVITPTRANCLPPEVELSNRVLRRYKVAERFLRVTFMDEGMQVLLNNVLSNFTAPIVKDLM : 152
AtRDR6 : -KLLGSHEQSEDISEIRRLVITPTRANCLPPEVELSNRVLRRYKVAERFLRVTFMDESMQITNSNVLVSYFVAPIVKDLT : 153
PtRDR905 : FKNPKQL---GDVVEIRRLVITPTRANCLPPEVELSNRVLRRYKVAERFLRVTFMDEGLQRMNSNVLNYYVAPIVRDTIT : 153
PtRDR906 : FKNQKKL---DDIAEIRRLVITPTRANCLPPEVELSNRVLRRYKVAERFLRVTFMDEGLQTMNSNALNYFAAIVRAIT : 153
OsRDR704 : -----TMVYFGEINVSNRVVRNFSSDIENFLRISFVDEDEKLRATDLS-----PRSA : 110
PtRDR901 : LPTPPAVAVDDGLVHVRVQITPTKVYFRGPEVNLNLRVLRKYPPDDIDNLRVSVFVDEDLKLFSTNIS-----PRTF : 150
PtRDR903 : LPTPPAVAVDDGLVFLRRVQITPTKVYFRGPEVNLNLRVLRKYPPDDIDNLRVSVFVDEDLKLFSTNIS-----PRTF : 150
AtRDR1 : LPLSPTLSLDDGLVYMYRVQITPARVYFSGPEVNVSNRVLRRYKVAERFLRVTFMDEGLQRMNSNVLNYYVAPIVRDTIT : 153
PtRDR902 : PPRSPVLSLDAGLVVYKVVQITPCKVYFCGPEVNVSNRVLRRYKVAERFLRVTFMDEGLQRMNSNVLNYYVAPIVRDTIT : 150
OsRDR705 : LSNEGEGEGERKLMKCYRVIITPSKIYCLGPEEIVNYVVVHSEYASDFRVTFVDEDEKLRATDLS-----ARIE : 150
ZmMOP1 : --ALSNKRESGKLMKCYRIHITPSKIYCLGPEEIVNYVVVHSEYASDFRVTFVDEDEKLRATDLS-----ARTE : 146
AtRDR2 : PASAYKRLQENIMSCQRAYITPSKIYCLGPEEIVNYVVVHSEYASDFRVTFVDEDEKLRATDLS-----VNSK : 151
PtRDR904 : -----KSLTENNIMSCHRALITPSKIYCLGPEEIVNYVVVHSEYASDFRVTFVDEDEKLRATDLS-----TSIQ : 143
          p           gp           6           6 F

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                *           180          *           200          *           220          *           240
OsRDR702 : KTFD-----STYCEHYHKVAEDGIVLGLRRYRFFVYKDKCTSPVMQVFRVTESGRTVQARELFMHISSAPTLAKYMARF : 192
OsRDR703 : ETDL-----STYLEHYHKVAEBGIVLGLRCYRFFLYKDKCTSSVRCVFRVTESGRTIQAARDLFMHIARTVTLAKYMLRF : 193
PtRDR908 : DSGSRS---LDDYFASKYNKVLGECIHVGLRCYRFFVYKDKCTSSVRCVFRVTESGRTIQAARDLFMHIARTVTLAKYMLRF : 197
AtRDR5 : STYS-----IDHYFTYKGIKAKNGIMIGLRRYRFFVYKDKCTSSVRCVFRVTESGRTIQAARDLFMHIARTVTLAKYMLRF : 191
AtRDR3 : TY-----CNDLYSTYKGIKAKNGIMIGLRRYRFFVYKDKCTSSVRCVFRVTESGRTIQAARDLFMHIARTVTLAKYMLRF : 192
AtRDR4 : TY-----CDNPYSKYKGIKAKNGIMIGLRRYRFFVYKDKCTSSVRCVFRVTESGRTIQAARDLFMHIARTVTLAKYMLRF : 186
OsRDR701 : SNFFQQ---KTTVYKRVRLLETCFHMCCRKYSFLAFSSNQLRDKSAMFFAEDRKTITVEAIRKWMGRFTS-KNVAKHAARM : 229
AtRDR6 : SSSFSQ---KTYVFKRVKSIILTECFKLCGRKYSFLAFSANQLRDKSAMFFAEDRKTITVEAIRKWMGRFTS-KNVAKCAARM : 230
PtRDR905 : SNSFPQ---KTRIFKRVRSILTECFYLCCRYSFLAFSANQLRDKSAMFFAEDRKTITVEAIRKWMGRFTS-KNVAKCAARM : 230
PtRDR906 : SYSFPQ---KTRIFKRVRSILTECFYLCCRYSFLAFSANQLRDKSAMFFAEDRKTITVEAIRKWMGRFTS-KNVAKCAARM : 230
OsRDR704 : SGHDAN---RTALYKRVLSVLSDGITIGCKNFYFLAFSSSQRDKSAMFFASRQGLAASDIRTWMGDFRNIRNVAKYAARL : 188
PtRDR901 : SAIEGR---QTKIYQRILSTQRNCIVIGSKKFBFLGFSQSQVSESSLWMFASRQGLAASDIRTWMGDFRNIRNVAKYAARL : 228
PtRDR903 : SAIEGR---QTNLYQRILSVQRNGITIGSKKFBFLGFSQSQVSESSLWMFASRQGLAASDIRTWMGDFRNIRNVAKYAARL : 228
AtRDR1 : TOR-----RTKLYDRIVSVLRDGIIVIGDKKFBFLAFSSSQRDKSAMFFASRQGLAASDIRTWMGDFRNIRNVAKYAARL : 225
PtRDR902 : SRNELR---RTALYNRILSTLQNCIVIGDKKFBFLAFSSSQRDKSAMFFASRQGLAASDIRTWMGDFRNIRNVAKYAARL : 228
OsRDR705 : QGFFSKPFKTGLYRILSLKKGFSICPKNFYFLAFSSSQRDKSAMFFASRQGLAASDIRTWMGDFRNIRNVAKYAARL : 230
ZmMOP1 : QGFFSKPLKTLGLYRILSLKKGFSICPKNFYFLAFSSSQRDKSAMFFASRQGLAASDIRTWMGDFRNIRNVAKYAARL : 226
AtRDR2 : EGYFVKPRTNLYNRVLSILGBCITVCPKRFYFLAFSSSQRDKSAMFFASRQGLAASDIRTWMGDFRNIRNVAKYAARL : 231
PtRDR904 : RGIFAKPFRITGLYRILSLKKGFSICPKNFYFLAFSSSQRDKSAMFFASRQGLAASDIRTWMGDFRNIRNVAKYAARL : 223
          G 6g 4 5 F 5           5           4           aR

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OsRDR702 : A-LILSKTITWDADLSAVYVRRKDEPCMDRHHGNVNH-KDQEPLEHFDGTGLVSVDLALNCPSTIFKGGKFLKQGERIFLY : 270
 OsRDR703 : A-LIVSKTITLDVLDSEVLVKLIDDEPCLDEHGKEVF-RDGERLHFDGTGLISEDLAQKCTYSNSKGLLEQDLRIFLY : 271
 PtRDR908 : S-LILSKTMNLVLDLSEVVDIKPLADEPCRDKDGNVYGTDEKPLHFDGTGFI SHDLALKCPKNQVKGTCLQASNFRIFN : 276
 AtRDR5 : S-LILSKTKTLEVDMTGITTFDQDDHCHDQDGDVLDKKNKPCIHSDGTGYISEDLARMCPVNIKFKGSMRNNFRIFY : 270
 AtRDR3 : S-LILSKTKTLEVDMTGITTFEQDDHCHDQDGDVLDKKNKPCIHSDGTGYISEDLARMCPVNIKFKGSMRNNFRIFY : 272
 AtRDR4 : S-LILSKTKKLEVDMTGITVMQDDHCHDQSNNDVLDKKNKPRIHSDGTGYISEDLARMCPVNIKFKGSMRNNFRIFN : 265
 OsRDR701 : GQCFSSYATVTVMPPEVDES-FDDVW-----HNEYIFSDGIGKITPDLALEVAERLQLT-DNPEFAVQIRF : 294
 AtRDR6 : GLCFSSYATVTVMPPEVDE-VPDIE-----RNG--YVFSDGIGITPDLADEVMEKLLKLDVHYSECAVQIRY : 296
 PtRDR905 : GQCFSSYATVTVMPPEVNSD-LPDIE-----RNG--YVFSDGIGITPDLAREVAEKLLD-IDPECAVQIRY : 295
 PtRDR906 : GQCFSSYATVTVMPPEVNSD-LPDIK-----RNG--YVFSDGIGITPDLAREVAEKLLD-FDPECAVQIRY : 295
 OsRDR704 : GQSFSSSTETLKVQKYEVEE--ISDI-----KNGTQHVFSDGIGKISSAFANEVAMKCNLK-RFAFAVQIRY : 253
 PtRDR901 : GQSFSSSRESFNIDEKEIEK--TPDIEVR-----SGVDYVFSDGIGKISSAALAHSTIAQKFGFL-SFTPEAVQIRY : 296
 PtRDR903 : GQSFSSSRESFNIDRHETIEI--TPDIEVK-----SGVNYVFSDGIGKISSAELADSIARKLRLR-SFTPEAVQIRY : 296
 AtRDR1 : GQSFSSSRETNLNVRSDIEV--TPDIEVI-----SLTRYVFSDGIGKISSAEFARKVARKCGLT-EFSEAVQIRY : 293
 PtRDR902 : GQSFSSSTETLKVQKYEVEE--TPDIEVS-----RGETRYLFSDGIGKISSAEFARKVAIKCGCK-GFTPEAVQIRY : 296
 OsRDR705 : GQLFSSSRQTFEVLRWVVEV--TPDIEIT-----TDGSKYIFSDGIGKISLRFARVAHHVGLDPTNL-FAVQIRY : 299
 ZmMOP1 : GQLFSSSRQTFEVSVDVVEV--TPDIEVT-----TDGTYKIFSDGIGKISLRFARQVAKLIGLDPAPH-FAVQIRY : 295
 AtRDR2 : GQLFSSSRQTLIVRAQDVEQ--TPDIEVT-----TDGADYCFSDGIGKISLAFARQVAQKCGL--SHVPEAVQIRY : 295
 PtRDR904 : GQLFSSSLQTFVVPVQDVEI--TPDIEVT-----TDGIDYCFSDGIGKISLSFAKQVAHKCGL--SHTPEAVQIRY : 290

OsRDR702 : NCSAVKGTIVLDRRLPP-ATLIRPSMVKVQSVNSFEIVSTSNRPRRTLTSFLITLLCYGVPPEEYFLELLQSALEGAE : 349
 OsRDR703 : NCSAVKGTIVLDRRLPP-RTLIRPSMLKQVSVNSFEIVSTSNRSGRTFTSNLLIALLHYGVPPEEFMELLQATATEAD : 350
 PtRDR908 : NCSAVKGTIVLDRRLPP-ATLIRPSMVKVQSVNSFEIVSTSNRPRRTLTSFLITLLCYGVPPEEYFLELLQSALEGAE : 355
 AtRDR5 : DCSAVKGTIVLDRRLPP-RTVQVRPSMIKFSIFNALEVVTTSNPPKRTKLSKNLVALLSYGVPNDFFLDLILLNTEESK : 349
 AtRDR3 : NCSAVKGTIVLDRRLPP-RTVQVRPSMIKFSIFNSLEVVTTSNPPKARLSKNLVALLSYGVPNDFFLDLILLNTEESK : 351
 AtRDR4 : DCSAVKGTIVLDRRLPP-QTVQVRPSMIKFSIFNSLEVVTTSNPPKRAKLSKNLVALLSYGVPNDFFLDLILLNTEESK : 344
 OsRDR701 : ACF--KGVVAVWQGHGDTLRLSLRPSMRKFESENHLVLEVVSWTKFQPGFLNRQIITLLSVLVGVPDETFWDMQESMLYKLN : 372
 AtRDR6 : ACF--KGVVAVWQGHGDTLRLSLRPSMRKFESENHLVLEVVSWTKFQPGFLNRQIITLLSVLVGVPDETFWDMQESMLYKLN : 374
 PtRDR905 : ACF--KGVVAVWQGHGDTLRLSLRPSMRKFESENHLVLEVVSWTKFQPGFLNRQIITLLSVLVGVPDETFWDMQESMLYKLN : 373
 PtRDR906 : ACF--KGVVAVWQGHGDTLRLSLRPSMRKFESENHLVLEVVSWTKFQPGFLNRQIITLLSVLVGVPDETFWDMQESMLYKLN : 373
 AtRDR704 : GSY--KGVVAVDPTSR--WKLRLRSMKFKFSDNITVDVLAISKYQPCFLNRQIITLLSVLVGVPDETFWDMQESMLYKLN : 329
 PtRDR901 : GSY--KGVVAVDPTSL--KKLRLRSMKFKFSDNITVDVLAISKYQPCFLNRQIITLLSVLVGVPDETFWDMQESMLYKLN : 372
 PtRDR903 : GSY--KGVVAVDPTSS--MKLRLRSMKFKFSDNITVDVLAISKYQPCFLNRQIITLLSVLVGVPDETFWDMQESMLYKLN : 372
 AtRDR1 : GSY--KGVVAVDPTSS--MKLRLRSMKFKFSDNITVDVLAISKYQPCFLNRQIITLLSVLVGVPDETFWDMQESMLYKLN : 369
 PtRDR902 : ACF--KGVVAVDPTSS--MKLRLRSMKFKFSDNITVDVLAISKYQPCFLNRQIITLLSVLVGVPDETFWDMQESMLYKLN : 372
 OsRDR705 : GSY--KGVVAVDPTSS--MKLRLRSMKFKFSDNITVDVLAISKYQPCFLNRQIITLLSVLVGVPDETFWDMQESMLYKLN : 375
 ZmMOP1 : GSY--KGVVAVDPTSF--FNLRLRSMKFKFSDNITVDVLAISKYQPCFLNRQIITLLSVLVGVPDETFWDMQESMLYKLN : 371
 AtRDR2 : GSY--KGVVAVDPTSS--MKLRLRSMKFKFSDNITVDVLAISKYQPCFLNRQIITLLSVLVGVPDETFWDMQESMLYKLN : 374
 PtRDR904 : GSY--KGVVAVDPTSS--MKLRLRSMKFKFSDNITVDVLAISKYQPCFLNRQIITLLSVLVGVPDETFWDMQESMLYKLN : 366

OsRDR702 : NACYDYEDALRIFAFSYADMEDSMS-ARMILSGLI-PLDESYLQHRLDFAQQERKGIKQ-GKIPIDECYLLMDDTTPGTGL : 426
 OsRDR703 : NARFDYAGALNIFAFNYADMEDSMP-ARMILSGLI-PLDESYLQHRLDFAQQERKGIKQ-GKIPIDECYLLMDDTTPGTGL : 427
 PtRDR908 : GILSNKNAALRNVALNYGMDNDNIV-ATMIGCCI-PLDESYLQHRLDFAQQERKGIKQ-GKIPIDECYLLMDDTTPGTGL : 432
 AtRDR5 : SIFYNKRAALRNVALNYGEMDDQNA-AQMILVCI-PLDEPHLKNYLSILLKTEKNDLKA-GKIPVTESYLLMDDTTPGTGL : 426
 AtRDR3 : TIFYSERAAFKAAINYG--DDQYT-ADMILVCI-PLDEPHLKNYLSILLKTEKNDLKA-GKIPVTESYLLMDDTTPGTGL : 426
 AtRDR4 : TIFFFKVAAGKAAALHYGNMDDKNA-LQMIMAGI-PLDEPHLKNYLSILLKTEKNDLKA-GKIPVTESYLLMDDTTPGTGL : 421
 OsRDR701 : NILSDRDVAFVLTTCADDGNTA-ALMLSAFEPRTPEHLKAMLLAIRSAQLQDLLEKARIFVVPKGRWLMCCLDELGVL : 451
 AtRDR6 : RLDDTDVAFVLTASCAEQGNTA-AIMLSAFAKPKTEPHLRGMLTCVRAAQLWDLREKTRIFVVPKGRWLMCCLDELGVL : 453
 PtRDR905 : QMIVSDVAFVLTASCAEQGNVA-AIMLSAFAKPKTEPHLRGMLTCVRAAQLWDLREKTRIFVVPKGRWLMCCLDELGVL : 452
 PtRDR906 : QMIVSDVAFVLTASCAEQGNVA-AIMLSAFAKPKTEPHLRGMLTCVRAAQLWDLREKTRIFVVPKGRWLMCCLDELGVL : 452
 OsRDR704 : KVVTDPAQAIEALELMPMGEITNAVKBLLCYQPDDEPYLSMMLQTFRASKLLELTKSRILIPKGRAMMCLDETRTL : 409
 PtRDR901 : ALLTDPSSAQEALELMPMGEITNAVKBLLCYQPDDEPYLSMMLQTFRASKLLELTKSRILIPKGRAMMCLDETRTL : 452
 PtRDR903 : ALLTDPPIKAQEALELMPMGEITNAVKBLLCYQPDDEPYLSMMLQTFRASKLLELTKSRILIPKGRAMMCLDETRTL : 452
 AtRDR1 : ALLTHPLEAHEALGLMAGENTNLIKALILCYKPDDEPYLSMMLQTFRASKLLELTKSRILIPKGRAMMCLDETRTL : 449
 PtRDR902 : ALLTDPPIKAQEALELMPMGEITNAVKBLLCYQPDDEPYLSMMLQTFRASKLLELTKSRILIPKGRAMMCLDETRTL : 452
 OsRDR705 : EMLTNKEVALSVLGLKGGSETKTA-VKMLLQYEPSEPEYLSMMLKAHQENRITDIRTRCKIHVPKGRVILCCLDETGVL : 454
 ZmMOP1 : GMLTNKBAALSVLGLKGGGDTKTA-ADMMLQYEPSEPEYLSMMLKAHQENRITDIRTRCKIHVPKGRVILCCLDETGVL : 450
 AtRDR2 : NMLNEDRAALNVLQKLSGENSKNLLVKMLLQYAPSEPEYLSMMLRVHHESELKSRILIPKGRVILCCLDETGVL : 454
 PtRDR904 : KMLTNKESALDVLNLAWADSKNILLVQMLLQYEPSEPEYLSMMLQYAHENSLMELKSRILIPKGRVILCCLDETGVL : 446

OsRDR702 : RPNEVCIILENGQ-----500-----*-----FSDVLYVKHPGLHFGDIHVLKATYIRDLEKEYVGYAKYAILFFPIS : 485
 OsRDR703 : GPNEVCIILDYQ-----VSADVLYKYPGLHFGDIHVLKATYSSDI EK-VVGNKSHAILFFTT : 485
 PtRDR908 : ESDEVCIILDCGQ-----ISEVLYVRNPGHLHFGDIHVLKATYVRELED-FVGNKAYAIFFPCK : 490
 AtRDR5 : KEDEVCIILESGQ-----ISEVLYVRNPGHLHFGDIHVLKATYVKALEE-YVGNKFAVFFPQK : 484
 AtRDR3 : KENEICVILHSGQ-----ISADVLYVRNPGHLHFGDIHVLKATYVKALED-YVGNKFAVFFPQK : 484
 AtRDR4 : KEDEVSLGLAK-----SQDVLVVRNPGHLHFGDIHVLKATYVKSLEQ-YVGNKSYGVFFPQK : 475
 OsRDR701 : EQQCQCFTRATVPSLNSYFVKHGSRFSSTDKNTEVILCTVVIKAKNPCLHPGDVVRILEAVDVPDLHH--LVDC---LVFPQK : 526
 AtRDR6 : EHGQCFIQVSKPSIENCFSKHGSRFKETKTDLEVVKEVVAIAKAKNPCLHPGDVVRILEAVDVPDLHH--MYDC---LVFPQK : 528
 PtRDR905 : EQQCQCFIQVSNSSLEKCFMKHGAKFSEAEKNLQVVIKCTVVIKAKNPCLHPGDVVRILEAVDVPDLHH--LYDC---LVFPQK : 527
 PtRDR906 : EQQCQCFIQVSNNSYLENCFVKHGSKFSETKKNLQVVIKCTVVIKAKNPCLHPGDVVRILEAVDVPDLHH--LYDC---LVFPQK : 527
 OsRDR704 : KYGOVFRATSGV-----NDNDRFTVTEKVVIAKAKNPCLHPGDVVRILEAVDVPDLHH--MFNC---VVFQQ : 470
 PtRDR901 : GYGOAFVQGGQAV-----RNTQILKIKLIVAKNPCLHPGDVVRILEAVNVPALHH--MVDC---LVFPQK : 511
 PtRDR903 : EYGOAFVQYSRAR--LSKSHDHFKGGKTDQHTLIVRKEIVVAKNPCLHPGDVVRILEAVDVPDLHH--MVDC---LVFPQK : 525
 AtRDR1 : EYGOVVFQYSDPM-----RPGRRFIITKPVVIAKAKNPCLHPGDVVRILEAVNVPALNH--MVDC---VVFQK : 510
 PtRDR902 : EHGQVFKFSGSRFRNLYDSSDMFSESRGRGQCYLIKESVVIKAKNPCLHPGDVVRILEAVDVPDLHH--MVDC---VVFQK : 527
 OsRDR705 : EYGOVYRITKNS-KEQKDSNQSYFYNDGKTATVVKVAIAKAKNPCLHPGDVVRILEAVDVPDLVGG--MVDC---LVFPQK : 528
 ZmMOP1 : EYGOVYRITKNH-KEQKYSQPFPCNDGKTAVIVKVAIAKAKNPCLHPGDVVRILEAVDVPDLVGG--MVDC---LVFPQK : 526
 AtRDR2 : EYGOVYRVTLTK-AELKSRDQSYFRKIDEETSIVI KVVVIAKAKNPCLHPGDVVRILEAVDVPDLVGG--MVDC---LVFPQK : 530
 PtRDR904 : DYGOVYRITMTK-AELQCCDQSFRRKVDTESTIIEVVAIAKAKNPCLHPGDVVRILEAVDVPDLVGG--MVDC---LVFPQK : 522
 2 g 6 6 4nP LH GD6 6L A 6 FPq

OsRDR702 : GPRSLADEMANSDFDGDLYVWVSKNPKLLEHFKPSEPWVQAIAKPKKT-KQKKPQDCNESKLERLLFHEFLKTRTPSFALG : 564
 OsRDR703 : GORSLADEMANSDFDGDLYVWVSLNPKLLEHFKPKSKPWPAITPNGT-KQKGPEDFNESELERVLFHEFLKTRTPSPYARA : 564
 PtRDR908 : GPRSLADEMANSDFDGDLYVWVSRNPQLLENFKQTEPWPSTSTPNV-PNRKPEFSDLELEVELEFLFLRNRQPSFTVG : 569
 AtRDR5 : GPRSLGDEIAGCDFDGDYFYI SRNPKLLEHFKPSEPWVSLTPPSKNSNGRAPSQLSPELELEELFKMFLTAGFHASNVIG : 564
 AtRDR3 : GPRSLGDEIAGCDFDGDYFYI SRNPKLLEHFKPSEPWVSSSKPSKIYCGRKPSELSELELEELFKMFLKARCKRDVIG : 564
 AtRDR4 : GPRSLGDEIAGCDFDGDYFYI SRNPKLLEHFKPSEPWVSSSPRSKIYTRGQPSSELSPQLELEELFKIFLKTGFSPSSVIG : 555
 OsRDR701 : GBRPHANEASGSDLDGDLYFVFWDEKLIIPGKKSWNPMDYSPPE---AKQLPRQVSOHDIIDFF-----LKNMISENLG : 597
 AtRDR6 : GDRPHTNEASGSDLDGDLYFVFWQKLIIPNRKSYPAHYDAE---EKSLGRAVNHODIIDFF-----ARLANEQLG : 599
 PtRDR905 : GBRPHANEASGSDLDGDLYFVFWDENLIPPSKRSWIPM QYDAE---AKLLARPVNHOIIEFF-----AKNMVNDNLG : 598
 PtRDR906 : GBRPHANEASGSDLDGDLYFVFWDENLIPPSKRSWIPM QYDAE---AKQLTRPVNHODIIEFF-----AKNMANENLG : 598
 OsRDR704 : GBRPHANEASGSDLDGDLYFVSWDPSLIPP--RMVTPDYTPAP---TETLDHDVTIEEVEEYF-----TNMIVNENSLG : 539
 PtRDR901 : GBRPHANEASGSDLDGDLYFVFWDPDLIPP--RTFPMDYTAAP---TTILDHDVTIEEVEEYF-----TDMLLNDSLG : 580
 PtRDR903 : GBRPHANEASGSDLDGDLYFVFWDPDLIPP--KQFPMDYTAAP---TTILDHDVTIEEVEEYF-----ADMLLNDSLG : 594
 AtRDR1 : GBRPHANEASGSDLDGDLYFVFWQELVPP--RTSEPMDYTPAP---TQILDHDVTIEEVEEYF-----ANMIVNENSLG : 579
 PtRDR902 : GBRPHANEASGSDLDGDLYFVFWDPDLIPP--QQISPMDYTPAP---PLQLDHDVTIEEVEEYF-----TNMIVNENSLG : 596
 OsRDR705 : GBRPHANEASGSDLDGDLYFVFWDDKLIPE--KVDTPMDYTAAT---PRIMDHVTLIEEIQKHF-----VDMINDTLG : 597
 ZmMOP1 : GBRPHANEASGSDLDGDLYFVFWDDKLIPE--KVDAPMDYATR---PRIMDHVTLIEEIQKHF-----VDMINDTLG : 595
 AtRDR2 : GBRPHANEASGSDLDGDLYFVFWDEKLIIPS--EMDPMDYAGSR---PRIMDHVTLIEEIQKHF-----VDMINDTLG : 599
 PtRDR904 : GBRPHANEASGSDLDGDLYFVFWDEGLLPC--HTEAPMDYVGR---QRIMDHVTLIEEIQKHF-----VDMINDTLG : 591
 G R 1E g D DGD 556 1 66 6 g

OsRDR702 : TAADSWIAYMDRLTDSLDE-IEKKLIEEKMKLVDLYYALDAPKMG-NKVNIPSDLMVKQYPHFMDRS---FSYHSSS : 639
 OsRDR703 : TAATNWLAYMDRLTDSLDE-SEKKLIEEKMKLVDLYYALDAPKMG-NKVNIPRDLMDVKQYPHFMDRS---PSYHSSS : 639
 PtRDR908 : VAADSWIAYMDRLTGNDCTEEIIACVKKNINLLIDLYYDALDAPKMGGRKIEVPEGLKAELEFPHFMDCKN-EKKTYSRSTS : 648
 AtRDR5 : IAADSWITIMDRFLILGDDRAEKAEMKKMMLKLDLYYDALDAPKMG-DKVVLPNKLKPPDFPHYMERD---KKFQSTS : 640
 AtRDR3 : MAADSWIGIMDRFLLGDESAAEKYERKKNIKLIDLYYDALDAPKMG-AKVDLPDLEIKNFPHYMERD-PKRDFRSTS : 642
 AtRDR4 : QAADSWIAYMDRFLTLGDENVKEKAEMKKMMLKLDLYYDALDAPKMG-TEVNLPLDVKVDFPHYMERD---KTFKSTS : 631
 OsRDR701 : RICNAHVHADL-----SEYGAMDEKCTLAELAAATAVDFPKTG-KLAIMPPLKPKVYPDFMCKE-DGQSYKSEK : 666
 AtRDR6 : TICNAHVHADL-----SEYGAMDEECLLAEELAAATAVDFPKTG-KIVSMPPHLKPKVYPDFMCKE-DYQTYKSNK : 668
 PtRDR905 : AICNAHVHADL-----SEYGATDKNCTLAELAAATAVDFPKTG-KVSMPPYLPKPKVYPDFMCKE-EYQSYKSEK : 667
 PtRDR906 : AICNAHVVRADL-----SEYGALDEKCTLAELAAATAVDFPKTG-KIVSMPSDLKPKVYPDFMCKE-EHQSYKSKK : 667
 OsRDR704 : MIANAHVVFADK-----EDLKAESSPELAKLFSIAVDFPKTG-VPALIPPLHVKVYPDFMCKE-DKVTYBSKG : 608
 PtRDR901 : IICNAHVVFADL-----DPLMARSEKCTELARLSSIAVDFPKTG-VPAKIPRLRVKVPDFMCKEAAKDRTYBSQR : 650
 PtRDR903 : IICNAHVVFADS-----EPDMARSEKCTELARLSSIAVDFPKTG-VPAKIPKBLRVKVPDFMCKEAAKHTTYVSR : 664
 AtRDR1 : IIANAHTAFADK-----EPLKAFSDPCTELAKKFSIAVDFPKTG-VAAVIPQHLVYKVPDFMCKE-DKPTYBSKN : 648
 PtRDR902 : VIANAHTAHADL-----ESLKAMSEPCTELARKFSIAVDFPKTG-VAEIPSNLRARVYPDFMCKE-DKPSYBSRN : 665
 OsRDR705 : AISTAHVIHADL-----SPLKARSPECQLATLHSMVDFAKTG-APAEMPRTLRPRVYPDFMCKE-EKPMYISNG : 666
 ZmMOP1 : AISTAHVIHADL-----DPLKARSPECQLALHSMVDFAKTG-APAEMPLALRPRVYPDFMCKE-ERPMPYISNG : 664
 AtRDR2 : VISTAHVHADL-----DPEKARSQKCTELANLHSMVDFAKTG-APAEMPLYLKPVPDFMCKE-EKPTYBSSES : 668
 PtRDR904 : AISTAHVIHADL-----EPDKARSEKCTELATLHSMVDFAKTG-APAEMPLYLKPVPDFMCKE-EKPMYISDNG : 660
 D L A6D pKtG 6P 6 5P 56 4 5 S

*

OsRDR702 : ILGQIYDKAEDV : 651
 OsRDR703 : ILGKIYDKAGDP : 651
 PtRDR908 : ILCKIYDKVKAY : 660
 AtRDR5 : ILGLIFDFVKSQ : 652
 AtRDR3 : ILGLIFDTVDSH : 654
 AtRDR4 : ILGLIFDTVDFH : 643
 OsRDR701 : ILGRLYRSIQEA : 678
 AtRDR6 : ILGRLYRRVKEV : 680
 PtRDR905 : ILGRLYRQIKDA : 679
 PtRDR906 : ILGRLYRQIKDA : 679
 OsRDR704 : VIGKLYREIKKH : 620
 PtRDR901 : VLGKLF RDV RDI : 662
 PtRDR903 : VLGKLFRAVRDI : 676
 AtRDR1 : VIGKLFREVKER : 660
 PtRDR902 : VIGKLFREVKDI : 677
 OsRDR705 : VLGKLYRSAMGH : 678
 ZmMOP1 : VLGKLYRAALRH : 676
 AtRDR2 : VFGKLYRAVKSS : 680
 PtRDR904 : VLGKLYRDIHDS : 672

6 G 65

Supplementary Table 1. Mapping *mop1* to the interval defined by the 5' *stk2* and *CL10221-1 prp2* markers.

Number of recombinant plants	<i>umc1541</i>	<i>stk2</i> 5' of coding	<i>stk2</i> coding	<i>rdr101</i>	<i>prp2</i> (<i>phi083</i>)	<i>prp2</i> (<i>CL10221-1</i>)	<i>bnlg1018</i>
26	MB ¹	MM	MM	MM	MM	MM	MM
2	MB	MB	MM	MM	MM	MM	MM
1	MM	MM	MM	MM	MM	MB	MB
7	MM	MM	MM	MM	MM	MM	MB

¹M indicates polymorphism associated with the *mop1-1* containing chromosome; B indicates polymorphism associated with the chromosome from inbred line B73 containing wild type *Mop1-B73*.

Supplementary Table 2. Comparison of map distances in *mop1-1* and the IBM2 mapping populations.

Mapping population	<i>umc1541</i>	<i>stk2</i> 5' of coding	<i>stk2</i> coding	<i>rdr101</i>	<i>prp2</i> (<i>phi083</i>)	<i>prp2</i> (<i>CL10221-1</i>)	<i>bnlg1018</i>
<i>mop1-1</i> ¹	0.61	0.05	0	0	0	0.02	0.16
IBM2 distance ²	9.2				0	0	10.1
(position) ³	(274.9)	n/a	n/a	n/a	(284.1)	(284.1)	(294.2)

¹Mapping distances (cM) are calculated by dividing the number of recombination events between two neighboring markers (as presented in Supplementary Table 1) by the total number of plants in *mop1-1* mapping population (4248) and multiplying by 100.

²The distance is given in cM relative to *prp2*, and is calculated by subtracting the map location of *prp2* from the map location of each marker on the IBM neighbors-2 (IBM2) map, the current genetic map for maize. IBM2 was generated after three generations of self-pollination of a B73 and Mo17 hybrid. Thus, the IBM2 map is expected to be expanded 6 fold relative to the map distances obtained in our backcross mapping experiment. The distance between *umc1541* and *phi083* on the IBM2 map is 9.2 cM, rather than the 3.96 cM predicted from our mapping (0.66×6); this discrepancy may reflect local chromosomal rearrangements that partially suppress recombination in the *mop1-1*, B73 hybrid plants relative to the lines used to generate the IBM2 map.

³Position on IBM2 genetics map (www.maizegdb.org). n/a: not applicable, indicates marker was not mapped in IBM2 population.

Supplementary Methods

Information on mapping population. The mapping population was created by crossing the B73 inbred line carrying a wild type *Mop1* and *b1* allele (*Mop1-B73 b1-B73*) with a homozygous *mop1-1* mutant carrying a *B'* allele in a mixed K55/W23/A188 genetic background (*mop1-1 B'*). The *b1* and *mop1* loci are approximately 20 map units apart (data not shown). Advantages of B73 include that it is highly polymorphic relative to the *mop1-1* background, it was used to develop the high resolution genetic and physical maps of maize^{32,33} and it is being sequenced. The heterozygous *Mop1-B73 b1-B73/mop1-1 B'* F₁ plants were backcrossed to homozygous *mop1-1 B'* plants to produce the BC₁. While plants with *B'* and a wild type *Mop1* allele are typically light purple, *mop1-1* homozygotes exhibit up-regulation of *B'*, resulting in a dark purple plant (Supplementary Figure 1). The 702 BC₁ individuals that exhibited the *mop1-1* homozygous phenotype were used for mapping. To further increase the mapping population, heterozygous and homozygous BC₁ plants were inter-mated producing the F₂ generation; 3546 *mop1-1* homozygous plants were used for mapping, resulting in a total of 4248 homozygous plants that were screened for recombinants. Because incomplete penetrance of the *mop1-1* phenotype has been observed, only plants with very dark purple pigmentation were sampled for mapping.

DNA extraction. For mapping experiments, DNA extraction³⁴ (from leaves using CTAB, N-Cetyltrimethylammonium Bromide) and PCR reactions were carried out in 96-well plates. PCR primer sequences were obtained from MaizeGDB³².

BAC clone selection, sequencing and analysis. Mapping markers *umc1541* and *phi083* constituted a minimum tiling path of 22 BACs for the *mop1-1* region on maize chromosome 2S. Two BACs, ZMMBBb0004G18 and ZMMBBb0178I03 were sequenced by the Arizona Genomics Institute (<http://genome.arizona.edu>) for a fee. The resulting 261 kbp contig was analyzed using BLAST³⁵ for homology searches (the sequence was divided into overlapping segments and searched against the nonredundant NCBI and public maize and rice est databases), FGESH (<http://www.softberry.com/>) for locating genes, and BAC-Breaker to locate retroelements³⁶.

Candidate gene sequencing. Sequencing of *rdr101* from *mop1* mutants and progenitor (W22) was by direct sequencing of PCR amplified segments (Supplemental Information). The TIR6 primer that amplifies all *Mutator* element termini³⁷ was used with *rdr101* primers described below. Sequencing was done by the University of Arizona GATC Facility.

Primers for mapping and gene sequencing. PCR amplification of the polymorphic DNA fragment upstream of the *stk2* gene was carried out with vc1427A (AAAACAACCGATGAGCAACC) and vc1427B (CCAGTGATGTTCTCCAAGCA) primers. Primers used to amplify the region of the *stk2* coding sequence containing a single nucleotide polymorphism were MAR464B (TGCTGGCTCTTCTCTCCTAACAC) and MAR502 (ATAGAGTTGCCACGTTTGACATTT). Primers used for amplification of fragments of *rdr101* were: MAR445F (GGCCACGGTGC GGGTATCC); MAR446B (AAAAGGGGTAGAGCAGTTGTGAGC); MAR447F (TAAGCAACAGTCACCGAAAGAACC); MAR448B (GGGCAGTCAACAAGAGGAACCA); MAR449F

(CACATTGCAATTTCTGGGTCTACA); MAR450B (TATCAGCTGCCGTCTTGGTATCA); MAR451F (CTTAGACCCAGCTCATCCTCCTTC); MAR452B (TCTTGTGCTCGTTATTGCCCTATC); MAR453F (GCAACGAGGCCACGCATAA); MAR454B (CCACTCGCATCACAGGCTCACTTC); MAR455F (CGGAGCGGAGGACGAGATT); and MAR462B (GTAGCGTTGGACTGTTGGAGGTTT). Primers were designed using PrimerSelect (DNAStar Inc.) and synthesized by MWG (www.mwg-biotech.com).

Primers for preparation of run-on probes. The primers used for amplification of the *b1* repeat DNA templates used for the nuclear run-on experiments are as follows: vc1100f (GCGTATCTATGTTTCGTGCGAAGG); vc1100r (CTGGTCACCCGCGAAAATCGCTC); vc1101f (GAGCGATTTTCGCGGGTGACCAG); vc1101r (CATATTCACGCTAGTCCAAATCG); vc1102f (GATTTGGACTAGCGTGAATATGG); vc1102r (CGGTAAATAGACATGAGTACAACCG); vc1131f (CCATGGGTTTGCTGCATCCTTG); vc1131r (TTCGCACGAACATAGATACGCGTAG). Synthetic RNA (Ambion, #7778) was used as a negative control, while a 975 bp fragment from the maize *ubiquitin2* gene (M13 and SP6 primers, plasmid pCA210³⁸) was used as a positive control.

Northern analysis of small RNA species. RNA was extracted from maize sheath tissue using TRIzol reagent as recommended by the manufacturer (Invitrogen, #15596-026). Total RNA was enriched for small RNA species³⁹, electrophoresed on 20% PAGE gel, and electro blotted. An equivalent of 100 µg of total RNA was loaded in each lane. RNA probes that were labeled with radioactive alpha ³²P UTP and alpha ³²P ATP and hydrolyzed to 25-30 nt by incubation in a hydrolysis buffer (80 mM NaHCO₃ and 120 mM Na₂CO₃) at room temperature for 2-3 hours depending on the length of the starting RNA probe, followed by neutralization with 3M Sodium Acetate, pH 5.0 (1/10 volume)⁴⁰. A published hybridization protocol was used⁴¹ with the exception that hybridizations were performed at 40°C.

Phylogenetic Reconstruction. FGENESH⁴² was used to predict an open reading frame in the genomic sequence of *rdr101*. The predicted protein was corrected by multiple species alignment using RDR2-like sequences from rice, poplar, and Arabidopsis. The RDRP domain of 381 amino acids was determined by conserved domain- (CD) search using the PFAM protein domain database^{43 44}.

Additional proteins used for phylogenetic analysis were obtained from the Plant Chromatin Database (www.chromdb.org). The Arabidopsis proteins are: RDR1 (At1g14790), RDR2 (At4g11130), RDR3 (At2g19910), RDR4 (At2g19920), RDR5 (At2g19930), and RDR6 (At3g49500). The rice proteins are: RDR701 (LOC_Os01g34350), RDR702 (LOC_Os01g10130; a truncated protein version of RDR702), RDR703 (LOC_Os01g10140.2; ChromDB splice model is different than TIGR v. 6 model and reflects curation from a multiple sequence alignment of rice, Arabidopsis and poplar proteins), RDR704 (LOC_Os02g50330; a truncated protein version of RDR704), and RDR705 (LOC_Os04g39160). RDR901 through RDR906 and RDR908 are *Populus trichocarpa* proteins derived from the sequences from version 1.0, the preliminary draft of the Populus genome sequence compliments of the Department of Energy Joint Genome Institute and the Poplar Genome Consortium (<http://genome.jgi-psf.org/Poptr1/Poptr1.download.html>).

Domains of protein sequences were aligned using Muscle 3.52⁴⁵. The alignments were visualized and edited using GeneDoc (<http://www.psc.edu/biomed/genedoc/>).

Bayesian phylogenetic analyses were performed using MrBayes 3.0B4⁴⁶. Searches were run using four different Markov chains for 3,000,000 generations setting the prior amino acid substitution rate matrix to average over all the models (i.e. aamodelpr = mixed). The first 10,000 trees were discarded and a consensus tree was built.

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