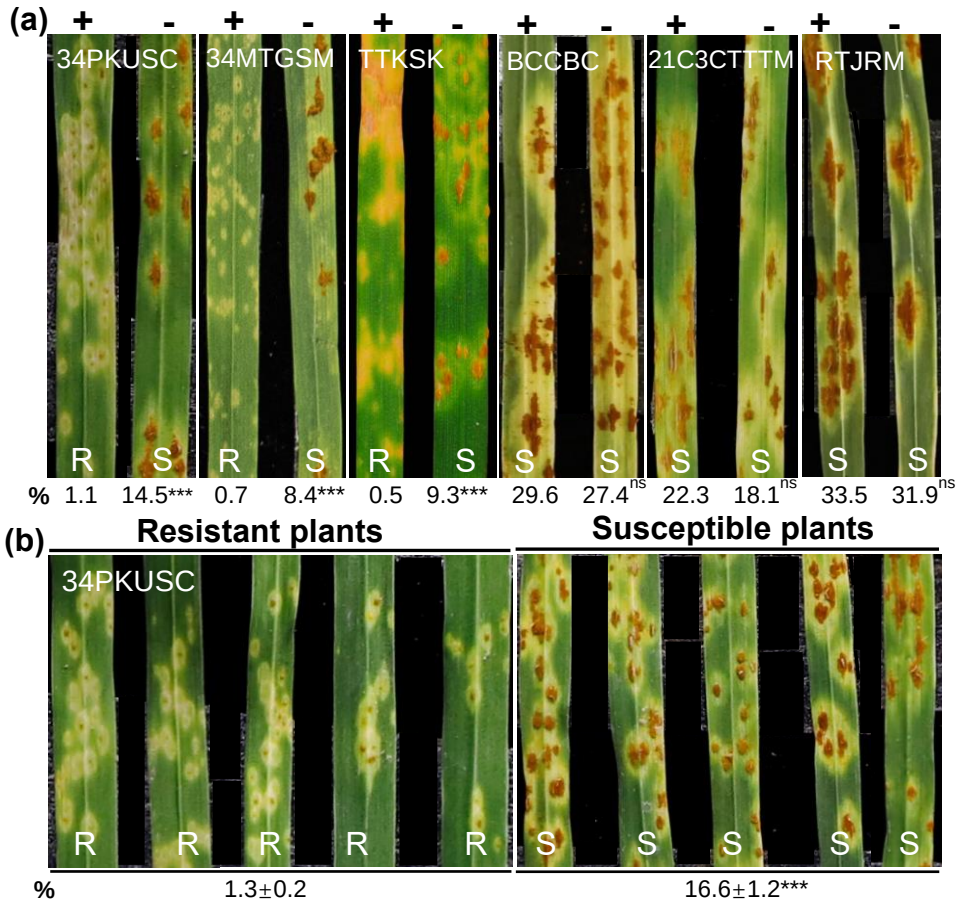

Figure S1 Reactions to six *Pgt* races 34PKUSC, 34MTGSM, TTKSK, BCCBC, 21C3CTTTM and RTJRM. (a) Infection types in *Triticum monococcum* F_5 lines TmR54-3 homozygous for *SrTm5* and its sister line TmS57-57 carrying no stem rust resistance gene. (b) Infection types on segregating resistant and susceptible plants when inoculated with race 34PKUSC. Numbers listed below leaves are average percentage of leaf area covered by *Pgt* pustules (n = 6). +, TmR54-3 (with *SrTm5*); -, TmS57-57 (without *SrTm5*); R, resistant; S, susceptible; ns= not significant (P >0.05), ***, $P < 0.001$.

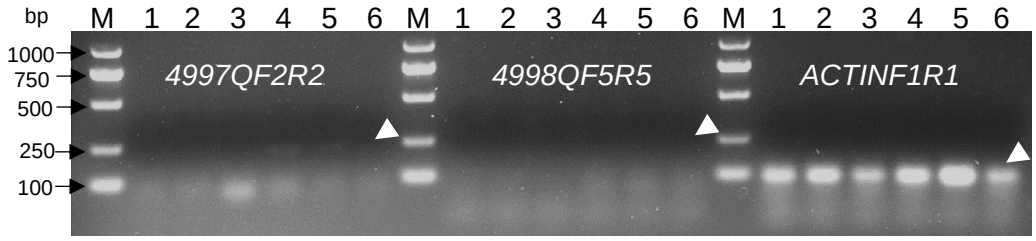

Figure S2 Semi-quantitative PCR products from markers *4997QF2R2* (260 bp, *TraesCS7A02G499700*), *4998QF5R5* (272 bp, *TraesCS7A02G499800*) and *ACTINF1R1* (*ACTIN*). RNAs were extracted from *Pgt*-inoculated leaves from *SrTm5* monogenic line TmR54-3. cDNAs were synthesized using the Applied Biosystems™ High-Capacity cDNA Reverse Transcription Kits. *ACTIN* was used as endogenous control. Six independent plants were evaluated. 1-3, samples collected at 3 dpi; 4-6, samples collected at 6 dpi; M, markers; Arrowheads indicate the expected band sizes.

```
SCHOMBURGK_R1      1  MAEVLVSASTGAMGSLLRKLGAMLTDEYKLLKNVRGDIKFLKDELEVMCAFLLKMSDVEEPDEPTKLRVTAVREMSYKIEDNIDKFMVLVEQEHGSSCSEAAHGVAKLMDKCKNLLPDIKARRRIAKEVKDIKKEIKDVSDRFSRYKIDDSSSSMP-AKD  160
IG44855_R2         1  MAEVLVSASTGAMGSLLRKLGAMLTDEYKLLKNVRGDIKFLKDELEVMCAFLLKMSDVEEPDEPTKLRVTAVREMSYKIEDNIDKFMVLV--EHGSSCSEAAHGVAKLMDKCKNLLPDIKARRRIAKEVKDIKKEIKDVSDRFSRYKIDDSSSSMP-AKD  160
IG44921_R3         1  MAEVLVSASTGAMGSLLRKLGAMLTDEYKLLKNVRGDIKFLKDELEVMCAFLLKMSDVEEPDEPTKLRVTAVREMSYKIEDNIDKFMVLV--EHESSCSEAAHGVAKLMDKCKNLLPDIKTRRRIAKEVKDIKKEIKDVSDRFSRYKIDESSSSMP-AKG  160
PI190945_R4        1  MAEVLVSASTGAMGSLLRKLGAMLTDEYKLLKNVRGDIKFLKDELEVMCAFLLKMSDVEEPDEPTKLRVTAVREMSYKIEDNIDKFMVLV--EHESSCSEAAHGVAKLMDKCKNLLPDIKTRRRIAKEVKDIKKEIKDVSDRFSRYKIDESSSSMP-AKG  160
PI289605_R5        1  MAEVLVSASTGAMGSLLRKLGAMLTDEYKLLKNVRGDIKFLKDELEVMCAFLLKMSDVEEPDEPTKLRVTAVREMSYKIEDNIDKFMVLVEQEHGSSCSEAAHGVAKLMDKCKNLLPDIKARRRIAKEVKDIKKEIKDVSDRFSRYKIDDSSSSMP-AKD  160
PI330550_R6        1  MAEVLVSASTGAMGSLLRKLGAMLTDEYKLLKNVRGDIKFLKDELEVMCAFLLKMSDVEEPDEPTKLRVTAVREMSYKIEDNIDKFMVLVEQEHGSSCSEAAHGVAKLMDKCKNLLPDIKARRRIAKEVKDIKKEIKDVSDRFSRYKIDDSSSSMP-AKD  160
PI306540_SrTm5     1  MAEVLVSASTGAMGSLLRKLGAMLTDEYKLLKNVRGDIKFLKDELEVMCAFLLKMSDVEEPDEPTKLRVTAVREMSYKIEDNIDKFMVLV--EHESSCSEAAHGVAKLMDKCKNLLPDIKTRRRIAKEVKDIKKEIKDVSDRFSRYKIDESSSSMP-AKG  160
DV92_S1            1  MAEVLVSASTGAMGSLLRKLGAMLTDEYKLLKNVRGDIKFLKDELEVMCAFLLKMSDVEEPDEPTKLRVTAVREMSYKIEDNIDKFMVLV--EHESSSSE-AHGVTKLMDKCKNLLPDIKTRRRIAKEVKDIKKEIKDVSDRFLRYKIDDSSSSMPAAKD  160
IG44878_S2         1  MAEVLVSASTGAMGSLLRKLGAMLTDEYKLLKNVRGDIKFLKDELEVMCAFLLKMSDVEEPDEPTKLRVTAVREMSYKIEDNIDKFMVLV--EHESSFSEAAHGVAKLMDKCKNLLPDIKTRRRIAKEVKDIKKEIKDVSDRFSRYKIDESSSSMP-AKG  160
PI355523_S3        1  MAEVLVSASTGAMGSLLRKLGAMLTDEYKLLKNVRGDIKFLKDELEVMCAFLLKMSDVEEPDEPTKLRVTAVREMSYKIEDNIDKFMVLVEQEHGSSCSEAAHGVAKLMDKCKNLLPDIKARRRIAKEVKDIKKEIKDVSDRFSRYKIDDSSSSMP-AKD  160
PI573523_S4        1  MAEVLVSASTGAMGSLLRKLGAMLTDEYKLLKNVRGDIKFLKDELEVMCAFLLKMSDVEEPDEPTKLRVTAVREMSYKIEDNIDKFMVLV--EHESSCSEAAHGVAKLMDKCKNLLPDIKTRRRIAKEVKDIKKEIKDVSDRFSRYKIDESSSSMP-AKG  160
WESTONIA_S5        1  MAEVLVSASTGAMGSLLRKLGAMLTDEYKLLKNVRGDIKFLKDELEVMCAFLLKMSDVEEPDEPTKLRVTAVREMSYKIEDNIDKFMVLV--EHESSCSEAAHGVAKLMDKCKNLLPDIKTRRRIAKEVKDIKKQIKDVSDRFSRYKIDESSSSMP-AKE  160
PI272557_S6        1  MAEVLVSASTGAMGSLLRKLGAMLTDEYKLLKNVRGDIKFLKDELEVMCAFLLKMSDVEEPDEPTKLRVTAVREMSYKIEDNIDKFMVLVEHE--SSCSEAAHGVAKLMDKCKNLLPDIKTRRRIAKEVKDIKKEIKDVSDRFSRYKIDESSSSMP-AKG  160

SCHOMBURGK_R1    161  KVDPRLRAVYKDAAELVGIDGPKDELVKWLNEKEGQSLKSVSIVGYGGLGKTTLANQIRVNLGATFDCGAFVSISRKPDMKAILRSILSQITKKDDACSRLDDIQLIIDKIREFLQDTRYFIIIDDIWELGTWETLKCAFVKNTLGSRIIITTRIVDVAK  320
IG44855_R2       161  KVDPRLRAVYKDAAELVGIDGPKDELVKWLNEKEGQSLKSVSIVGYGGLGKTTLANQIRVNLGATFDCGAFVSISRKPDMKAILRSILSQITKKDDACSRLDDIQLIIDKIREFLQDTRYFIIIDDIWELGTWETLKCAFVKNTLGSRIIITTRIVDVAK  320
IG44921_R3       161  KVDPRLRAVYKDAAELVGIDGPKDELVKWLNEKEGQSLKSVSIVGYGGLGKTTLANQIRVNLGATFDCGAFVSISRKPDMKAILRSILSQITKKDEACSRLDDIQLIIDKIREFLQDTRYFIIIDDIWELGTWETLKCAFVKNTLGSRIIITTRIVDVAK  320
PI190945_R4      161  KVDPRLRAVYKDAAELVGIDGPKDELVKWLNEKEGQSLKSVSIVGYGGLGKTTLANQIRVNLGATFDCGAFVSISRKPDMKAILRSILSQITKKDEACSRLDDIQLIIDKIREFLQDTRYFIIIDDIWELGTWETLKCAFVKNTLGSRIIITTRIVDVAK  320
PI289605_R5      161  KVDPRLRAVYKDAAELVGIDGPKDELVKWLNEKEGQSLKSVSIVGYGGLGKTTLANQIRVNLGATFDCGAFVSISRKPDMKAILRSILSQITKKDDACSRLDDIQLIIDKIREFLQDTRYFIIIDDIWELGTWETLKCAFVKNTLGSRIIITTRIVDVAK  320
PI330550_R6      161  KVDPRLRAVYKDAAELVGIDGPKDELVKWLNEKEGQSLKSVSIVGYGGLGKTTLANQIRVNLGATFDCGAFVSISRKPDMKAILRSILSQITKKDDACSRLDDIQLIIDKIREFLQDTRYFIIIDDIWELGTWETLKCAFVKNTLGSRIIITTRIVDVAK  320
PI306540_SrTm5   161  KVDPRLRAVYKDAAELVGIDGPKDELVKWLNEKEGQSLKSVSIVGYGGLGKTTLANQIRVNLGATFDCGAFVSISRKPDMKAILRSILSQITKKDEACSRLDDIQLIIDKIREFLQDTRYFIIIDDIWELGTWETLKCAFVKNTLGSRIIITTRIVDVAK  320
DV92_S1          161  KVDPRLRAVYKDAAELVGIDGPKDELVKWLNEKEGQSLKSVSIVGYGGLGKTTLANQIRVNLGATFDCGAFVSISRKPDMKAILRSILSQITKKDEACPRLDDIQLIIDKIREFLQDTRYFIIIDDIWELGTWETLKCAFVKNTLGSRIIITTRIVDVAK  320
IG44878_S2       161  KVDPRLRAVYKDAAELVGIDGPKDELVKWLNEKEGQSLKSVSIVGYGGLGKTTLANQIRVNLGATFDCGAFVSISRKPDMKAILRSILSQITKKDDACSRLDDIQLIIDKIREFLQDTRYFIIIDDIWELGTWETLKCAFVKNTLGSRIIITTRIVDVAK  320
PI355523_S3      161  KVDPRLRAVYKDAAELVGIDGPKDELVKWLNEKEGQSLKSVSIVGYGGLGKTTLANQIRVNLGATFDCGAFVSISRKPDMKAILRSILSQITKKDDACSRLDDIQLIIDKIREFLQDTRYFIIIDDIWELGTWETLKCAFVKNTLGSRIIITTRIVDVAK  320
PI573523_S4      161  KVDPRLRAVYKDAAELVGIDGPKDELVKWLNEKEGQSLKSVSIVGYGGLGKTTLANQIRVNLGATFDCGAFVSISRKPDMKAILRSILSQITKKDDACSRLDDIQLIIDKIREFLQDTRYFIIIDDIWELGTWETLKCAFVKNTLGSRIIITTRIVDVAK  320
WESTONIA_S5      161  KVDPRLRAVYKDVTELVGIDGPKDELVKWLNEKEGQSLKSVSIVGYGGLGKTTLANQIRVNLRASFDCGAFVSISRKPDMKAILRSILSQITKKDDAYSRLDDIQLIIDKIREFLQDTRYFIIIDDIWELGTWETLKCAFVKNTLGSRIIITTRIVDVAK  320
PI272557_S6      161  KVDPRLRAVYKDAAELVGIDGPKDELVKWLNEKEGQSLKSVSIVGYGGLGKTTLANQIRVNLGATFDCGAFVSISRKPDMKAILRSILSQITKKDDACSRLDDIQLIIDKIREFLQDTRYFIIIDDIWELGTWETVKCAFVKNTLGSRIIITTRIVDVAK  320

SCHOMBURGK_R1    321  SCSPSSEDLVYEMKPLSEADSKKLFFKRIFGCEESCPDSLKEAANDILKKCRGLPLAINAISSVLVTTRETKEEWDRVRHSIRSSKVKSDIIETMNYILSLSYFDLPHHLRSCLLYLALFPEDQLIGRKRLVRRWISEGFIHGESGQDLMELGEEYFHQL  480
IG44855_R2       321  SCSPSSEDLVYEMKPLSEADSKKLFFKRIFGCEESCPDSLKEAANDILKKCRGLPLAINAISSVLVTTRETKEEWDRVRHSIRSSKVKSDIIETMNYILSLSYFDLPHHLRSCLLYLALFPEDQLIGRKRLVRRWISEGFIHGESGQDLMELGEEYFHQL  480
IG44921_R3       321  SCSPSSEDLVYEMKPLSEADSKKLFFKRIFGCEESCPDSLKEAANDILKKCRGLPLAINAISSVLVTTRETKEEWDRVRHSIRSSKVKSDIIETMNYILSLSYFDLPHHLRSCLLYLALFPEDQLIGRKRLVRRWISEGFIHGESGQDLMELGEEYFHQL  480
PI190945_R4      321  SCSPSSEDLVYEMKPLSEADSKKLFFKRIFGCEESCPDSLKEAANDILKKCRGLPLAINAISSVLVTTRETKEEWDRVRHSIRSSKVKSDIIETMNYILSLSYFDLPHHLRSCLLYLALFPEDQLIGRKRLVRRWISEGFIHGESGQDLMELGEEYFHQL  480
PI289605_R5      321  SCSPSSEDLVYEMKPLSEADSKKLFFKRIFGCEESCPDSLKEAANDILKKCRGLPLAINAISSVLVTTRETKEEWDRVRHSIRSSKVKSDIIETMNYILSLSYFDLPHHLRSCLLYLALFPEDQLIGRKRLVRRWISEGFIHGESGQDLMELGEEYFHQL  480
PI330550_R6      321  SCSPSSEDLVYEMKPLSEADSKKLFFKRIFGCEESCPDSLKEAANDILKKCRGLPLAINAISSVLVTTRETKEEWDRVRHSIRSSKVKSDIIETMNYILSLSYFDLPHHLRSCLLYLALFPEDQLIGRKRLVRRWISEGFIHGESGQDLMELGEEYFHQL  480
PI306540_SrTm5   321  SCSPSSEDLVYEMKPLSEADSKKLFFKRIFGCEESCPDSLKEAANDILKKCRGLPLAINAISSVLVTTRETKEEWDRVRHSIRSSKVKSDIIETMNYILSLSYFDLPHHLRSCLLYLALFPEDQLIGRKRLVRRWISEGFIHGESGQDLMELGEEYFHQL  480
DV92_S1          321  SCSPSSEDLVYEMKPLSEADSKKLFFKRIFGCEESCPDSLKEAANDILKKCRGLPLAINAISSILATTRETKEEWDRVRHSIRSSKVKSDIIETMNYILSLSYFDLPHHLRSCLLYLALFPEDQLIERKRLVRRWISEGFIHGESGQALMELGEEYFHQL  480
IG44878_S2       321  SCSPSSEDLVYEMKPLSEADSKKLFFKRIFGCEESCPDSLKEAANDILKKCRGLPLAINAISSILVTTRETKEEWDRVRHSIRSSKVKSDIIETMNYILSLSYFDLPHHLRSCLLYLALFPEDQLIGRKRLVRRWISEGFIHGESGQDLMELGEEYFHQL  480
PI355523_S3      321  SCSPSSEDLVYEMKPLSEADSKKLFFKRIFGCEESCPDSLKEAANDILKKCRGLPLAINAISSILVTTRETKEEWDRVRHSIRSSKVKSDIIETMNYILSLSYFDLPHHLRSCLLYLALFPEDQLIGRKRLVRRWISEGFIHGESGQDLMELGEEYFHQL  480
PI573523_S4      321  SCSPSSEDLVYEMKPLSEADSKKLFFKRIFGCEESCPDSLKEAANDILKKCRGLPLAINAISSILVTTRETKEEWDRVRHSIRSSKVKSDIIETMNYILSLSYFDLPHHLRSCLLYLALFPEDQLIGRKRLVRRWISEGFIHGESGQDLMELGEEYFHQL  480
WESTONIA_S5      321  SCSPSSEDLVYEMKPLSEADSKKLFFKRIFGCEESCPDSLKEAANDILKKCRGLPLAINAISSILATTRETKEEWDRVRHSIHSSKVKSDIIETMNYILSLSYFDLPHHLRSCLLYLALFPEDQLIGRKRLVRRWISEGFIHGESGQDLMELGEEYFHQL  480
PI272557_S6      321  SCSPSSEDLVYEMKPLSEADSKKLFFKRIFGCEESCPDSLKEAANDILKKCRGLPLAINAISSILVTTRETKEEWDRVRHSIRSSKVKSDIIETMNYILSLSYFDLPHHLRSCLLYLALFPEDQLIGRKRLVRRWISEGFIHGESGQDLMELGEEYFHQL  480
```

```
SCHOMBURGK_R1    481  VNRSLIQPGNIGYDGKAMYCRVHDTILDFLIDKSSEENMCTVLKKQCKPNGIVRRLSLMGNEDEEIVEQLDLSHARSITAFGDIKLLPSLGRSKCLRVLDLQDCDQLENHHIKDIERLYQLRYLDISSTGITELPRQIGELLYLETLV--AY-GLRELPE  640
IG44855_R2       481  VNRSLIQPGNIGYDGKAMYCRVHDTILDFLIDKSSEENMCTVLKKQCKPNGIVRRLSLMGNEDEEIVEQLDLSHARSITAFGDIKLLPSLGRSKCLRVLDLQDCDQLENHHIKDIERLYQLRYLDISSTGITELPRQIGELLYLETLV--AY-GLRELPE  640
IG44921_R3       481  VNRSLIQPGNIGYDGKAMYCRVHDTILDFLIDKSSEENMCTVLKKQCKPNGIVRRLSLMGNEDEEIVEQLDLSHARSITAFGDIKLLPSLGRSKCLRVLDLQDCDQLENHHIKDIERLYQLRYLDISSTGITELPRQIGELLYLETLV--AY-GLRELPE  640
PI190945_R4      481  VNRSLIQPGNIGYDGKAMYCRVHDTILDFLIDKSSEENMCTVLKKQCKPNGIVRRLSLMGNEDEEIVEQLDLSHARSITAFGDIKLLPSLGRSKCLRVLDLQDCDQLENHHIKDIERLYQLRYLDISSTGITELPRQIGELLYLETLV--AY-GLRELPE  640
PI289605_R5      481  VNRSLIQPGNIGYDGKAMYCRVHDTILDFLIDKSSEENMCTVLKKQCKPNGIVRRLSLMGNEDEEIVEQLDLSHARSITAFGDIKLLPSLGRSKCLRVLDLQDCDQLENHHIKDIERLYQLRYLDISSTGITELPRQIGELLYLETLV--AY-GLRELPE  640
PI330550_R6      481  VNRSLIQPGNIGYDGKAMYCRVHDTILDFLIDKSSEENMCTVLKKQCKPNGIVRRLSLMGNEDEEIVEQLDLSHARSITAFGDIKLLPSLGRSKCLRVLDLQDCDQLENHHIKDIERLYQLRYLDISSTGITELPRQIGELLYLETLV--AY-GLRELPE  640
PI306540_SrTm5   481  VNRSLIQPGNIGYDGKAMYCRVHDTILDFLIDKSSEENMCTVLKKQCKPNGIVRRLSLMGNEDEEIVEQLDLSHARSISAFGDIKLLPSLGRSKCLRVLDLQGCDQLENHHIKDIERLYQLRYLDISSTGITELPRQIGELLYLETLV--AY-GLRELPE  640
DV92_S1          481  VNRSLIQPGNIGYDGKAEYCRVHDTILDFLIDKSSEENMCTVLKKQCKPNGIVRRLSLMGNEDEEIMEQLDLSHARSISAFGDIKLLPSLGRSKCLRVLDLQGCYQLKNHHIKDIERLYQLRYLDISFTGITELPRQIGELLYLETLV-TSY-GLRELPE  640
IG44878_S2       481  VNRSLIQPGNIGYDGKAKYCRVHDTILDFLIDKSSEENMCTVLKKQCKPNGIVRRLSLMGNEDEEIMEQLDLSHARSISAFGDIKLLPSLGRSKCLRVLDLQGCYQLKNHHIKDIERLYQLRYLDISFTGITELPRQIGELLYLETLVSTSY-GLRELPE  640
PI355523_S3      481  VNRSLIQPGNIGYDGKAMYCRVHDTILDFLIDKSSEENMCTVLKKQCKPNGIVRRLSLMGNEDEEIVEQLDLSHARSISAFGDIKLLPSLGRSKCLRVLDLQDCDQLENHHIKDIERLYQLRYLDISYTGITELPRQIGELLYLETLD--AS-GLRELPE  640
PI573523_S4      481  VNRSLIQPGNIGYDGKAEYCRVHDTILDFLIDKSSEENMCTVLKKQCKPNGIVRRLSLMGNEDEEIMEQLDLSHARSISAFGDIKLLPSLGRSKCLRVLDLQGCYQLKNHHIKDIERLYQLRYLDISFTGITELPRQIGELLYLETLVSTSY-GLRELPE  640
WESTONIA_S5      481  VNRSLIQPDYIGYDGKTEYCRVHDTILDFLIDKSSEENMCTVLKKQCKPNGIVRRLSLMGNEDEEIVEQLDLSHARSISAFGDIKLLPSLGRSKCLRVLDLQNCGQLRNHHIKDIERLYQLRYLDISFTGITELPRQIGELLYLETLV--TSDGLRELPE  640
PI272557_S6      481  VNRSLIQPDNIGYDGKAKYCRVHDTILDFLIDKSSEENMCTVLKKQCKPNGIVRRLSLMGNEDEETVEQLDLSHARSITAFRDIKLLPSLGRSKCLRVLDLQACNQLENHHIKDIERLYQLRYLDISFTGITELPRQIGELLYLETLV--TSYRLRELPE  640

SCHOMBURGK_R1    641  STSRLQRLARLFVYSGCKLPGGLGNLINLQELDCVDALHLKHVEELGKLTNLRKLSIKLDTGGIEGNKLEESKEKLVSSLCKLDECGLLSLSIDYYLREKDGEEPFLPALGCIQEVFVYGQDISRISRWLASLPNLHRLLLDDP--KIEQQDIEMIGLI-  800
IG44855_R2       641  STSRLQRLARLFVYSGCKLPGGLGNLINLQELDCVDALHLKHVEELGKLTNLRKLSIKLDTGGIEGNKLEESKEKLVSSLCKLDECGLLSLSIDYYLREKDGEEPFLPALGCIQEVFVYGQDISRISRWLASLPNLHRLLLDDP--KIEQQDIEMIGLI-  800
IG44921_R3       641  STSRLQRLARLFVYSGCKLPGGLGNLINLQELDCVDALHLKHVEELGKLTNLRKLSIKLDTGGIEGNKLEESKEKLVSSLCKLDECGLLSLSIDYYLREKDGEEPFLPALGCIQEVFVYGQDISRISRWLASLPNLHRLLLDDP--KIEQQDIEMIGLI-  800
PI190945_R4      641  STSRLQRLARLFVYSGCKLPGGLGNLINLQELDCVDALHLKHVEELGKLTNLRKLSIKLDTGGIEGNKLEESKEKLVSSLCKLDECGLLSLSIDYYLREKDGEEPFLPALGCIQEVFVYGQDISRISRWLASLPNLHGLLLDNP--KIEQQDIEMIGLI-  800
PI289605_R5      641  STSRLQRLARLFVYSGCKLPGGLGNLINLQELDCVDALHLKHVEELGKLTNLRKLSIKLDTGGIEGNKLEESKEKLVSSLCKLDECGLLSLSIDYYLREKDGEEPFLPALGCIQEVFVYGQDISRISRWLASLPNLHGLLLDYP--KIEQQDIEMIGLI-  800
PI330550_R6      641  STSRLQRLARLFVYSGCKLPGGLGNLINLQELDCVDALHLKHVEELGKLTNLRKLSIKLDTGGIEGNKLEESKEKLVSSLCKLDECGLLSLSIDYYLREKDGEEPFLPALGCIQEVFVYGQDISRISRWLASLPNLHGLLLDNP--KIEQQDIEMIGLI-  800
PI306540_SrTm5   641  STSRLQRLARLFVYSGCKLPGGLGNLINLQELDCVDALHLKHVEELGKLTNLRKLSIKLDTGGIEGNKLEESKEKLVSSLCKLDECGLRSLSIHYYLREKDGEEPFLPALGCIQEVCVYGQDISRISRWLASLPNLHRLFLNQP--KIEQQDIEMIGLI-  800
DV92_S1          641  STSRLQRLARLFVYHGCKLPDGLGNLVNLQELECVDALQLKHVEELGKLTNLRKLSIKLDTGGIEGNKLEESKEKLVSSLCKLDECGLRSLSIHYYLREKDGEEPFLPALGCIQEVCVYGQDISRISRWLASLPNLHRLFFNDPKMKIEQQDIEMIGLI-  800
IG44878_S2       641  STSRLQRLARLFVDSGCKLPDGLGNLINLQELDCVDALQLKHVEELGKLTNLRKLRIKLDTDGIEGNKLEQSKEKLVSSLCKLDECGLLSLSIYYYLREKDGEEPFLPALGCIQEVFVHGQDISRISRWLASLPNLHRLFLNQP--KIEQQDIEMIALRE  800
PI355523_S3      641  STSRLQRLARLFVDSGCKLPDGLGNLINLQELDCVDALQLKHVEELGKLTNLRKLKIKLDTGGIEGNKLEESKEKLVSSLCKLDECGLRSLSIRYYLREKDGEEPFLPALGCIQEVCVYGQDISRISRWLASLPNLHTLLLDYP--KIEQQDIEMIGLI-  800
PI573523_S4      641  STSRLQRLARLFVDSGCKLPDGLGNLINLQELDCVDALQLKHVEELGKLTNLRKLRIKLDTDGIEGNKLEQSKEKLVSSLCKLDECGLLSLSIYYYLREKDGEEPFLPALGCIQEVFVHGQDISRISRWLASLPNLHRLFLNQP--KIEQQDIEMIGLI-  800
WESTONIA_S5      641  STSRLQRLARLIVGCDCKLPDGLGNLMNLQELDCVGALHLKHAEELGKLTNLRKLKINLYTHGIEGNKLEESKEKLVSSLCKLDECGLRSLSIDYYLREKDGEEPFLPALGCIEEVFVYEQDISRISRWLASLPNLHRLVSYDP--KIEQQDIEMIGLI-  800
PI272557_S6      641  STSRLQRLARLFVDPGCKLPDGLGNLINLQELDWVDALQLKHVEELGKLTNLRKLRIKLDTDGIEGNKLEQSKEKLVSSLCKLDECGLRSLSIGYYLREKDGEEPFLPPLGCIQEVSVYGQDISRISRWLASLPNLHMLFFDYV--KIEQQDIEMIGLI-  800

SCHOMBURGK_R1    801  PNLIDLTLPPLYKTDDA-GRLIIRREGFQQLQKFEAYNTRMGVLMFEPGAMPRLKELKLHNFIEKPKSAAVDFDFGIQRLSSLARLTVSLSCGGWTVAEVEAAEDAFKSMAEANPNRPILEMTRYNTQHMLQDEQIGMTGSATTPAVKS  949
IG44855_R2       801  PNLIDLTLPPLYKTDDA-GRLIIRREGFQQLQKFEAYNTRMGVLMFEPGAMPRLKELKLHNFIEKPKSAAVDFDFGIQRLSSLARLTVSLSCGGWTVAEVEAAEDAFKSMAEANPNRPILEMTRYNTQHMLQDEQIGMTGSATTPAVKS  949
IG44921_R3       801  PNLIDLTLPPLYKTDDA-GRLIIRREGFQQLQKFEAYNTRMGVLMFEPGAMPRLKELKLHNFIEKPKSAAVDFDFGIQRLSSLARLTVSLSCGGWTVAEVEAAEDAFKSMAEANPNRPILEMTRYNTQHMLQDEQIGMTGSATTPAVKS  949
PI190945_R4      801  PNLIDLTL-YLRITDDA-GRLIIKREGFQQLQRFELSRIRMGDLMFEPGAMPRLKELILYHFIEKPKSGAVDFDFGIQHLSSLARLTVGLLCVGSTAAEVEAAEDAFKSMAEANPNRPILEMTRLYPQHMLQDEQIGMTGSATTPAVKS  949
PI289605_R5      801  PNLIDLTL-YLRITDDA-GRLIIKREGFQQLQRFELSRIRMGDLMFEPGAMPRLKELILYHFIEKPKSGAVDFDFGIQHLSSLARLTVGLLCVGSTAAEVEAAEDAFKSMAEANPNRPILEMTRLYPQHMLQDEQIGMTGSATTPAVKS  949
PI330550_R6      801  PNLIDLTL-YLRITDDA-GRLIIKREGFQQLQRFELSRIRMGDLMFEPGAMPRLKELILYHFIEKPKSGAVDFDFGIQHLSSLARLTVGLLCVGSTAAEVEAAEDAFKSMAEANPNRPILEMTRLYPQHMLQDEQIGMTGSATTPAVKS  949
PI306540_SrTm5   801  PNLIDLSL-SLYKTDDA-GRLIIRREGFQQLQSFRVYHTRMGVLMFEPGAMPRLKELKFYDFIGKPKSGAVDFDFGIQHLSSLARLTVDLSCVGWTAAEVEAAEDAFKSMAEANPNRPILEMTRLFPQDMLRDEQIDMAGSATTPAVKS  949
DV92_S1          801  PNLMDLTL-YLRITDDAMPRLIIKREGFQQLQRFELSRIRMGDLMFEPGAMPRLKELILHNFIEKPKSGAVDFDFGIQHLSSLARLTVGLLCVGSTAAEVEAAEDAFKSMAEANPNRPILEMTRLCPQHMLQDEQIGMTGSATTPAVKS  949
IG44878_S2       801  PNLMDLTL-YLCITDDA-GRLIIKREGFQQLQRFELSRIRMGDLMFEPGAMPRLKELILYDFIGKPKSGAVDFDFGIQHLSSLARLTVGLSCVGSTVAEVEAAEDAFKSMAEANPNRPILEMTRYNTQHMLQDEQIGMTGSATTPAVKS  949
PI355523_S3      801  PNLIDLTL-PLYKTDDA-GRLIIRREGFQQLQKFEAYNTRMGVLMFEPGVMPRLKELKLHNFIEKPKSAAVDFDFGIQHLSSLARLTVDLSCVGWTAAEVEAAEDAFKSMAEANPNRPILEMTRYNTQHMLQDEQIGMTGSATTPAVKS  949
PI573523_S4      801  PNLMDLTL-YLCITDDA-GRLIIKREGFQQLQRFELSRIRMGDLMFEPGAMPRLKELILYDFIGKPKSGAVDFDFGIQHLSSLARLTVGLSCVGSTVAEVEAAEDAFKSMAEANPNRPILEMTRYNTQHMLQDEQIGMTGSATTPAVKS  949
WESTONIA_S5      801  PNLIDLTL-SLPGTDDA-GRFIITREGFQQLQSFELSGSRMGVL-FEPGAMPRLKELILDDFIRKPKSAAVDFDFGIQRLSSLARLTVSLACYRSTAAEVEATEDAFKSMAEANPNRPILEMTRLYPQHMVRDEQIDMAGSATTPAVKS  949
PI272557_S6      801  PNLIDLSL-SLRKTDDA-GRLIIRREGFQHLHSFRVYDTRMGVLMFEPGAMPRLKELKLHNFIEKPESGAVDFDFGIQRLSSLARLTVSLFCVGSTAAEVEATEDAFKSMAEANPNRPILEMIRVNPHRMF-DEQIDMAGSATTPAVKS  949
```

Figure S3 SrTm5 protein sequence analysis. Multiple sequence alignment between SrTm5 and reported Sr22 resistant and susceptible protein sequences (Steuernagel et al. 2016). Highlighted in green are protein polymorphisms that discriminate perfectly between Sr22 susceptible and resistant haplotypes. Highlighted in yellow are Sr22b unique protein polymorphisms compared with other Sr22 resistant haplotypes.

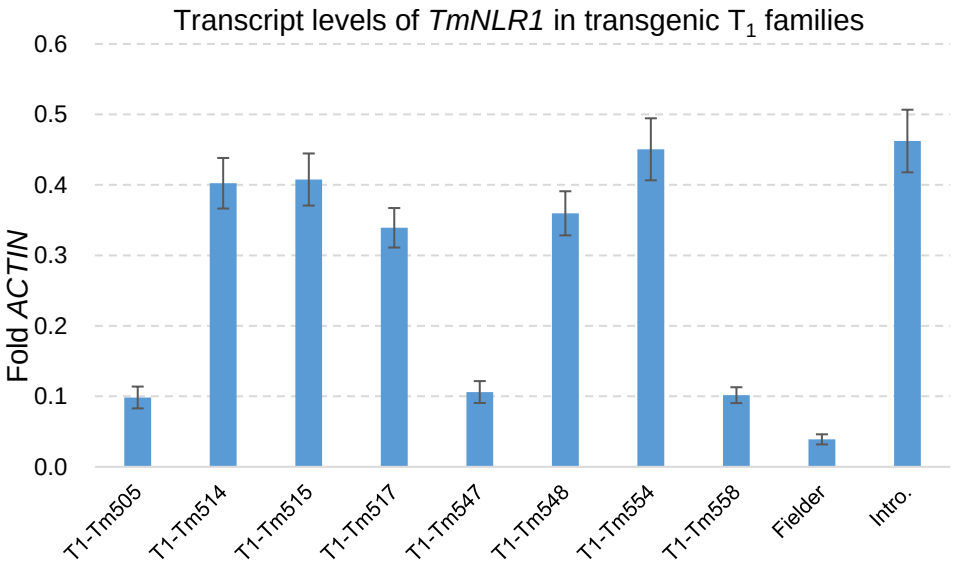

Figure S4 Transcript levels of *TmNLR1* in transgenic T_1 families (three positive plants per event, n = 3). Transcript levels are expressed as fold-*ACTIN* using the $2^{\Delta CT}$ method. Fielder, susceptible control; Intro., *SrTm5* introgression plants (BC_3F_2, positive control). Error bars are standard errors of the mean.

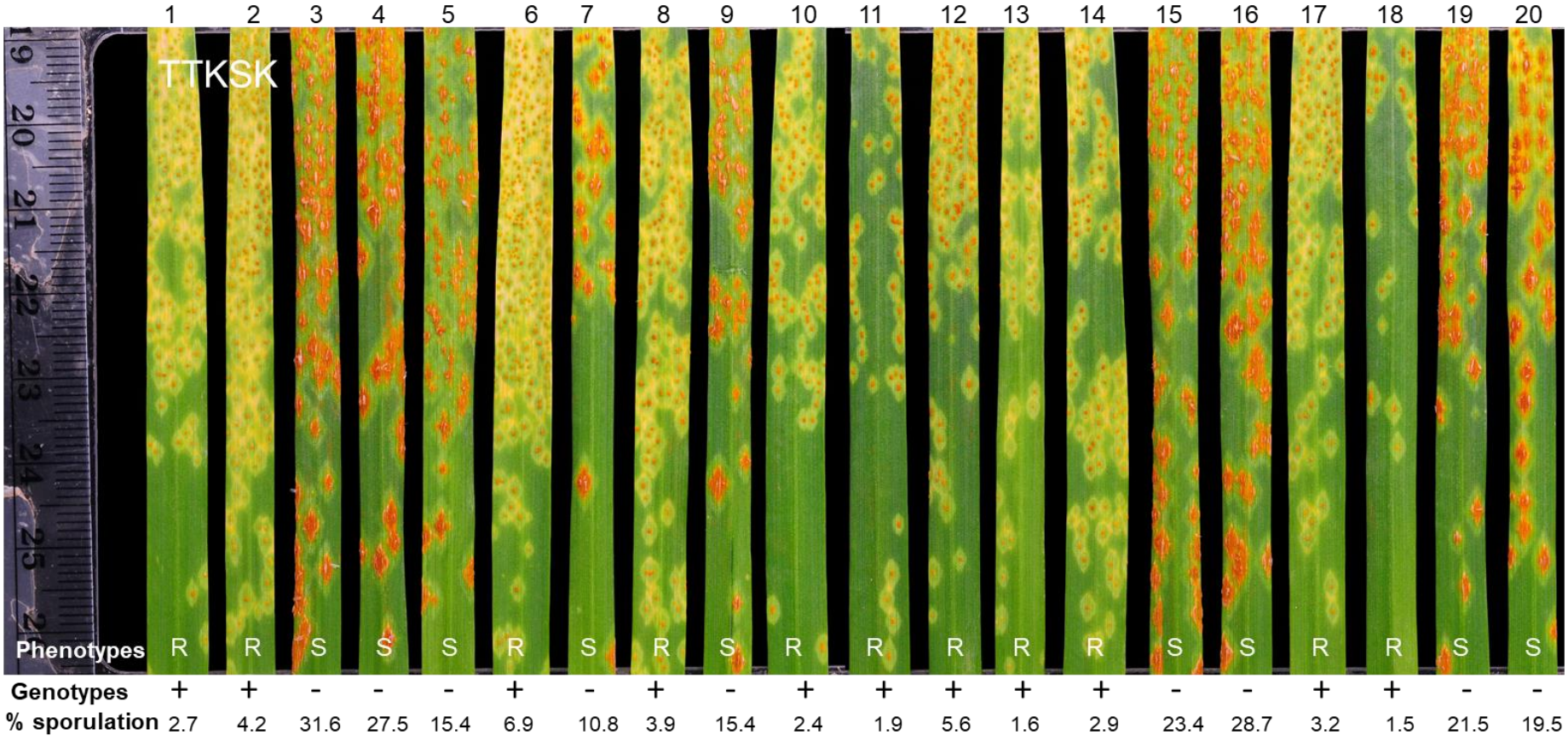

Figure S5 Reactions to *Pgt* race TTKSK (Ug99) in transgenic family T_2Tm515-6. This family showed segregation for resistance. Genotyping of the plants with markers *Tm5F3R4*, *TM5TF2R2*, and *TM5TF3R3* (Table 1) revealed a perfect co-segregation between the presence of transgene and the phenotypes. The numbers below the figure indicate the average percentage of the leaf area covered by *Pgt* pustules. S, susceptible; R, resistant; +, with transgene; -, without transgene.

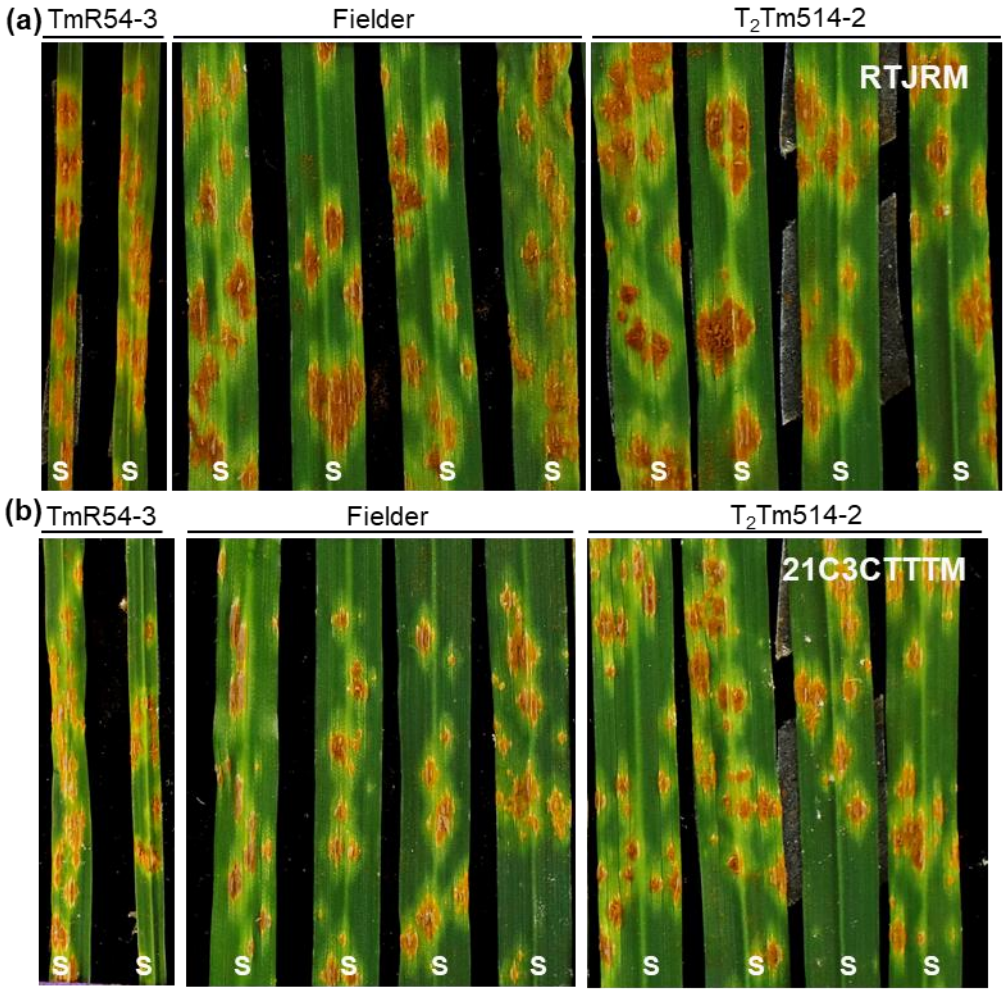

Figure S6 Transgenic family T_2Tm514-2 homozygous for the transgene were inoculated with two *SrTm5*-virulent *Pgt* races RTJRM and 21C3CTTTM. (a) Stem rust reactions to *Pgt* race RTJRM. (b) Stem rust reactions to *Pgt* race 21C3CTTTM. All the tested plants from transgenic family T_2Tm514-2 were susceptible to these two races suggesting similar race specificity between the transgene and natural *SrTm5* in *T. monococcum*. Figure 2a in the main text presents stem rust reactions from the same transgenic family T_2Tm514-2 against *Pgt* race TTKSK.

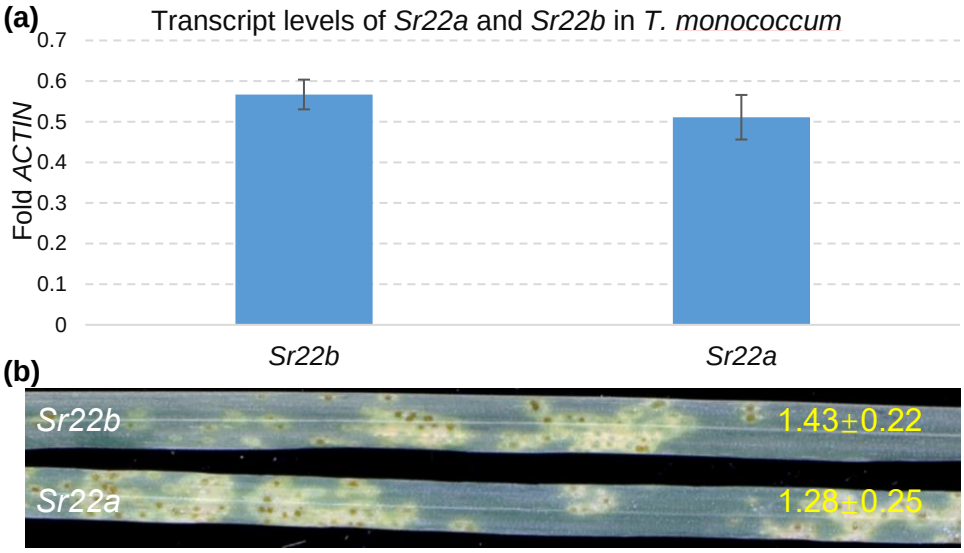

Figure S7 Transcript levels and infection types of *Sr22a* and *Sr22b* in *T. monococcum* background. (a) Transcript levels of *Sr22a* and *Sr22b* in *T. monococcum*. Leaves were collected from *T. monococcum* accession PI 190945 (*Sr22a*) and *T. monococcum* line TmR54-3 (*Sr22b*) without *Pgt* inoculation. Plants were grown in growth chambers at 22 ˚C day / 20 ˚C night with 16 hours light / 8 hours dark. Transcript levels were expressed as fold-*ACTIN* (n = 6). Error bars are standard errors of the mean. (b) Infection types on *T. monococcum* plants of PI 190945 (*Sr22a*) and TmR54-3 (*Sr22b*) when inoculated with *Pgt* race 34PKUSC. No significant differences were observed between the two genotypes in average percentage of leaf area covered by *Pgt* pustules using software ASSESS v2 (n = 5).

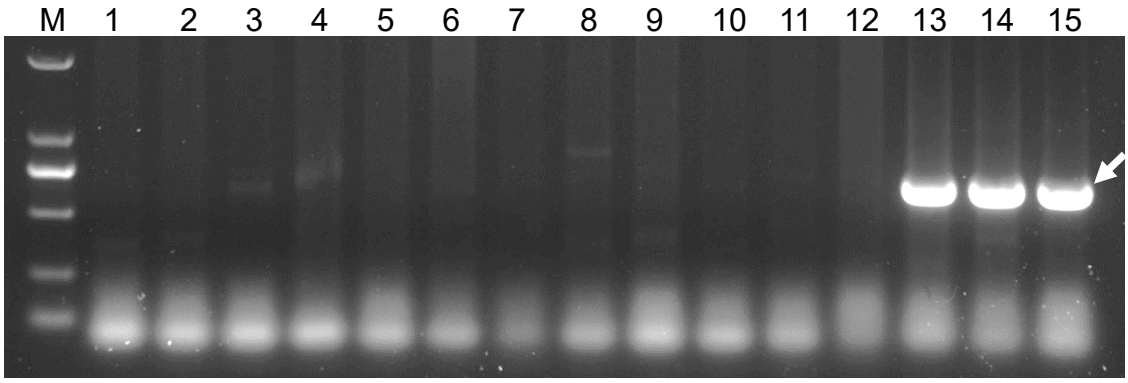

Figure S8 PCR products from the *Sr22b* diagnostic marker *TM5TF2R2*. The amplicons of 673 bp (white arrow) were present only in resistant *T. monococcum* accessions carrying *Sr22b*. 1, Xiaoyan22 (6x); 2, Chinese Spring (6x); 3, Chuanmai42 (6x); 4, Fielder (6x); 5, 8155B (4x); 6, Rusty (4x); 7, D447 (4x); 8, Kronos (4x); 9, PI 272557 (2x); 10, PI 418580 (2x); 11, PI 487249 (2x); 12, PI 427507 (2x); 13, PI 306540 (2x); 14, PI 377668 (2x); 15, PI 362610 (2x); M, markers.

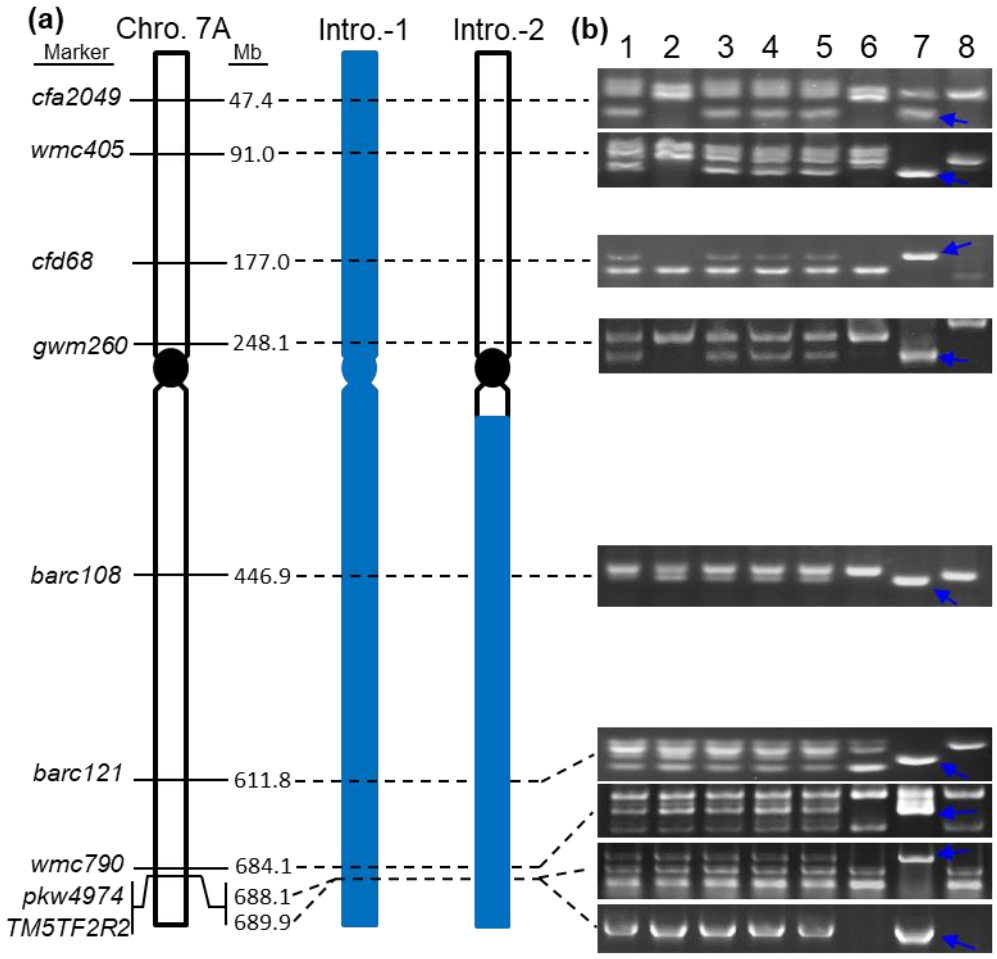

Figure S9 Markers across chromosome 7A were used to analyze the length of introgressed *T. monococcum* segments. (a) The physical positions of markers and the length of the introgression segments. Blue rectangles indicate *T. monococcum* chromatin. The positions were based on the reference genome of Chinese Spring Refseq v1.0. (b) PCR products from nine selected markers. 1-5, BC_3F_1 plants 1, 2, 3, 4 and 5; 6, Fielder; 7, PI 306540; and 8, Kronos. Blue arrows indicate the bands from PI 306540.

Table S1. Avirulence/virulence formulae of *Pgt* races, and their responses to *SrTm5*. The data shown here was based on the current study and several previous studies (Li et al. 2016; Chao et al. 2017; Li et al. 2018; Chen et al. 2018a; Chen et al. 2020).

Race (isolate)[#]	**Origin**	**Response to *SrTm5***	**Avirulence**	**Virulence**
BCCBC (09CA115-2)	USA	virulence	*Sr5 6 7b 8a 9a 9d 9e 9b 10 11 21 24 30 31 36 38 Tmp*	*Sr9g 17 McN*
TTKSK (04KEN156/04)	Kenya	**avirulence**	*Sr21 24 36 Tmp*	*Sr5 6 7b 8a 9a 9b 9d 9e 9g 10 11 17 30 31 38 McN*
MCCFC (59KS19)	USA	**avirulence**	*6 8a 9a 9d 9e 9b 11 21 24 31 30 36 38*	*5 7b 9g 10 17 McN Tmp*
TTKST (06KEN19-V-3)	Kenya	**avirulence**	*21 36 Tmp*	*5 6 7b 8a 9a 9b 9d 9e 9g 10 11 17 24 30 31 38 McN*
34MTGSM (20GSA1)	China	**avirulence**	*Sr9e 12 13 14 17 21 22 23 26 30 31 33 35 36 37 38 47 Tmp*	*Sr5 6 7b 8a 9a 9b 9d 9f 9g 10 11 15 16 18 19 20 24 25 27 28 29 32 34 39 McN*
QFCSC (06ND76C)	USA	virulence	*6 7b 9e 9b 11 24 31 30 36 38 Tmp*	*5 8a 9a 9d 9g 10 17 21 McN*
TRTTF (06YEM34-1)	Yemen	virulence	*8a 24 31*	*5 6 7b 9a 9b 9d 9e 9g 10 11 17 21 30 36 38 McN Tmp*
TTTTF (01MN84A-1-2)	USA	virulence	*24 31*	*5 6 7b 8a 9a 9b 9d 9e 9g 10 11 17 21 30 36 38 McN Tmp*
21C3CTTTM (20GH13)	China	virulence	*Sr5 9e 14 19 21 22 23 26 27 31 33 35 37 38 39 47*	*Sr6 7b 8a 9a 9b 9d 9f 9g 10 11 12 13 15 16 17 18 20 24 25 28 29 30 32 34 36 Tmp McN*
RTJRM (mutant strain, 20IAS11)	China	virulence	*Sr13 14 17 18 19 20 22 23 25 27 28 29 31 32 33 36 37*	*Sr5 8a 10 11 12 15 21 24 30 34 35 Tmp McN*

[#], Chinese race 34PKUSC (19IAS08) was provided by Dr. Jianhui Wu at Northwest Agriculture & Forestry University in China, and its responses to different *Sr* resistance genes is unknown.

Table S2. Comparison of SrTm5 protein with polymorphisms that discriminate perfectly between Sr22 susceptible and resistant haplotypes from Steuernagel et al. (2016). SrTm5 carries the same amino acids as the resistant haplotypes at all three positions 381, 605 and 655. BLOSUM62 scores were obtained from the following link (https://www.ncbi.nlm.nih.gov/IEB/ToolBox/C_DOC/lxr/source/data/BLOSUM62). The resistant (PI 306540) and susceptible (PI 272557) parents are indicated in red.

	Accessions													
Positions	SCHOMBURGK	IG44855	IG44921	PI190945	PI289605	PI330550	**PI306540**	DV92	IG44878	PI355523	PI573523	Westonia	**PI272557**	BLOSUM62
	R1	R2	R3	R4	R5	R6	***SrTm5***	S1	S2	S3	S4	S5	**S6**	
381	V	V	V	V	V	V	**V**	L	L	L	L	L	**L**	**1**
605	S	S	S	S	S	S	**S**	F	F	Y	F	F	**F**	**-2**
655	G	G	G	G	G	G	**G**	D	D	D	D	D	**D**	**-1**
Phenotypes	Res.	Res.	Res.	Res.	Res.	Res.	**Res.**	Sus.	Sus.	Sus.	Sus.	Sus.	**Sus.**	

Table S3. Segregation ratios in T_1 and T_2 transgenic families detected using PCR markers *Tm5F3R4*, *TM5TF2R2*, and *TM5TF3R3* (Table 1). We genotyped more than 20 T_1 plants from each transgenic family. All transgenic T_1 families except T_1-Tm505 showed significant segregation distortion with an excess of non-transgenic plants. Genotyping of T_2 plants from one positive T_1 plant for each transgenic event revealed that the transgene was fixed in families T_2-Tm505-15, T_2-Tm514-2, T_2-Tm517-1, T_2-Tm548-3, T_2-Tm554-2 and T_2-Tm558-7, and segregating in families T_2-Tm515-6 and T_2-Tm547-3.

Genotyping	Transgenic T_1 families							
	T_1-Tm505	T_1-Tm514	T_1-Tm515	T_1-Tm517	T_1-Tm547	T_1-Tm548	T_1-Tm554	T_1-Tm558
Present (+)	22	8	6	10	15	12	8	3
Absent (-)	3	20	16	88	45	20	20	18
χ^2 *P* value 1 copy	0.133	1.4E-08	2.3E-07	1.2E-49	3.7E-19	9.6E-07	1.4E-08	1.3E-10
Genotyping	Transgenic T_2 families							
	T_2-Tm505-15	T_2-Tm514-2	T_2-Tm515-6	T_2-Tm517-1	T_2-Tm547-3	T_2-Tm548-3	T_2-Tm554-2	T_2-Tm558-7
Present (+)	23	33	23	39	12	22	24	21
Absent (-)	0	0	16	0	12	0	0	0
χ^2 *P* value 1 copy	0.006	9.1E-04	0.021	3.1E-04	0.005	0.007	0.005	0.008

Table S4. Resistance profiles of *Sr22b* (=*SrTm5*) and *Sr22a* (haplotypes R1 and R4) to multiple *Pgt* races. Infection types for *Sr22b* are based on the selected F_5 line TmR54-3, whereas *Sr22a* infection types are from *T. aestivum* lines Schomburgk / PI 660256 (R1) and *T. monococcum* accession PI 190945 (R4). PI 272557 was used as susceptible control.

Pgt race	*Sr22b* 2x[a] TmR54-3	*Sr22a* (*Sr22TB*, R1) 6x[a] Schomburgk/PI 660256	*Sr22a* (R4) 2x[a] PI 190945	No *Sr* gene 2x[a] PI 272557
TTKSK[b]	;1	2-	1	4
MCCFC[b]	1;	2-	;1	4
TTKST	;	Not available	Not available	Not available
34PKUSC	1	2-	;1	3+
34MTGSM	1;	2-	;1	3+
BCCBC	3+	2-	;1	3+
QFCSC[b]	3+	;2-	;1-	4
TRTTF[b]	3+	2-;	1;	3+
TTTTF[b]	3+	2	2-	4

[a], 2x = diploid wheat (*T. monococcum*), 6x= hexaploid wheat (*T. aestivum*).

[b], Based on previous studies (Steuernagel et al. 2016, Rouse & Jin, 2011 and Chen et al. 2018a)

Table S5. A collection of 92 accessions of *T. monococcum*, 23 of *T. turgidum*, and 53 of *T. aestivum* was used to test the presence of *Sr22b*. All these accessions were screened using the diagnostic marker *TM5TF2R2* and the other two sequence-based markers *TM5AF6R8* and *TM5AF4R4*. PI, CItr and GSTR numbers correspond to Germplasm Resources Information Network (GRIN) numbers.

Accessions	Acc. No.	With/without *Sr22b*
***T. monococcum*:** PI 306540, PI 277130, PI 306545, CItr 17657, PI 277131-2, PI 306544, PI 306547, PI 352480, PI 355536, PI 355541, PI 435000, PI 435001, PI 221414, **PI 355538, PI 362610, PI 377668**	16	with (+)
***T. monococcum*:** PI 418580, PI 487249, CItr 17671, PI 427507, PI 272560, PI 427580, CItr 17674, PI 245726, PI 272557, PI 573520, PI 560720, G3116, DV92, PI 573523, PI 427464, PI 427444, PI 352273, PI 427465, PI 272556, CI2433, PI 427498, PI 352505, PI 190942, PI 277121, CItr 14520, CItr 13963, PI 427662, PI 427478, CItr 13964, CItr 17655, PI 168803, PI 168806, PI 190940, PI 289605, PI 352486, PI 355517, PI 355524, PI 428158, PI 503874, PI 427452, PI 330528, PI 554480, PI 427467, PI 428012, PI 538540, PI 362554, PI 427497, PI 427993, PI 427476, CItr 17741, PI 427450, PI 554519, PI 427661, PI 427405, PI 427540, PI 352504, PI 427453, PI 427510, PI 427603, CItr 17665, PI 355453, PI 427477, PI 427484, PI 427488, PI 554517, PI 401412, PI 427994, PI 427472, PI 427468, PI 352270, PI 427592, PI 427796, PI 427527, PI 427808, PI 190945, PI 362553	76	without (-)
***T. turgidum*:** 8155B, Rusty, D447, Kronos, Svevo, LineE, CItr 15326, PI 478298, PI 584833, CItr 13768, PI 331260, PI 480016, CItr 15892, PI 510696, Zavitan, PI 94701, PI 606286, PI 480148, PI 191365, CItr 13165, PI 496260, PI 560877, PI 428016	23	without (-)
***T. aestivum*:** Xiaoyan22, Zhengzhou5389, Chinese Spring, Cadenza, Lassik, PI 675640, Patwin, UC1110, PI 660056, ISr8a-Ra, CItr 15082, PI 660060, PI 178759, PI 648419, PI 679621, PI 181434, PI 660059, PI 182527, PI 189747, PI 430067, PI 660057, PI 648417, PI 442904, PI 603918, PI 600683, GSTR434, GSTR429, GSTR428, GSTR420, GSTR501, GSTR522, GSTR425, PI 679605, GSTR409, PI 679598, PI 679603, GSTR437, PI 566596, GSTR441, Avocet-S, Pavon, Fielder, PI 638738, Taichang29, SY95-71, PI 675564, PI 672538, PI 277012, PI 596533, Chuanmai42, Xinong511, Taimai198, PI 634936	53	without (-)

Table S6. Geographic distribution of *T. monococcum* accessions, and their reactions against *Pgt* races TTKSK, MCCFC and 34PKUSC. The data for races TTKSK and MCCFC was based on the previous study (Rouse & Jin, 2011). Gene postulations were based upon infection types and genotypes from the diagnostic markers of cloned *Sr* genes *Sr21*, *Sr22*, *Sr35* and *Sr60* (Saintenac et al., 2013, Steuernagel et al., 2016, Chen et al., 2018b, Chen et al., 2020). +, with *Sr22b*; -, without *Sr22b*.

Accession	With / without *Sr22b*	Source	Species[a]	TTKSK	MCCFC	34PKUSC	Gene Postulation
TmR54-3	(+)	-	*T. m. m*	;1	**1;**	**1**	***Sr22b***
PI 306540	(+)	Romania	*T. m. m*	**0;**	**0**	**0**	*Sr21*, *SrTm4*, *Sr60*, ***Sr22b***
PI277131-2	(+)	Albania	*T. m. m*	**;**	**;1/;**	**;1**	*Sr21*, *Sr60*, ***Sr22b***
PI 277130	(+)	Albania	*T. m. m*	**;**	**0;**	**;1**	*Sr21*, *Sr60*, ***Sr22b***
PI 306545	(+)	Romania	*T. m. m*	**;1-**	**0;**	**;1**	*Sr21*, *Sr60*, ***Sr22b***
CItr 17657	(+)	United States	*T. m. m*	**;**	**0;**	**;1**	*Sr21*, ***Sr22b***
PI 306544	(+)	Romania	*T. m. m*	**0;**	**0;**	**;1**	*Sr21*, *Sr60*, ***Sr22b***
PI 306547	(+)	Romania	*T. m. m*	**;**	**0;**	**;1**	*Sr21*, *Sr60*, ***Sr22b***
PI 352480	(+)	Albania	*T. m. m*	**0;**	**0;**	**;1-**	*Sr21*, *Sr60*, ***Sr22b***
PI 355536	(+)	Italy	*T. m. m*	**0**	**;1**	**0**	*Sr21*, *Sr35*, ***Sr22b***
PI 355541	(+)	Albania	*T. m. m*	**0;**	**0;**	**;1-**	*Sr21*, *Sr60*, ***Sr22b***
PI 435000	(+)	Yugoslavia	*T. m. m*	**0;**	**;**	**;1-**	*Sr21*, *Sr60*, ***Sr22b***
PI 435001	(+)	Bosnia and Herzego.	*T. m. m*	**;**	**;**	**0;**	*Sr21*, *Sr60*, ***Sr22b***
PI 221414	(+)	Yugoslavia	*T. m. m*	**0**	**0;**	**;1-**	*Sr21*, *Sr60*, ***Sr22b***
PI 355538	(+)	Balkans	*T. m. m*	**;1-**	**;1-**	**1**	***Sr22b***
PI 377668	(+)	Former Yugoslavia	*T. m. m*	**;**	**0;**	**1**	***Sr22b***
PI 362610	(+)	Macedonia	*T. m. m*	**;1-**	**0;**	**1**	***Sr22b***
PI 418580	(-)	Azerbaijan	*T. m. a.*	3+	4	-	*Susceptible*
PI 487249	(-)	Syria	*T. m. a.*	2+/3/12+Z	;1	-	*Sr21*
CItr 17671	(-)	Turkey	*T. m. a.*	1/12Z	;1	-	*Sr21*
PI 427507	(-)	Turkey	*T. m. a.*	3-	1	-	*Sr21*
PI 272560	(-)	Hungary	*T. m. m*	0	4	-	*Sr35*
PI 427580	(-)	Turkey	*T. m. a.*	123Z	;1	-	*Sr21*
CItr 17674	(-)	Iran	*T. m. a.*	2++	1	-	*Sr21*
PI 245726	(-)	Turkey	*T. m. a.*	-	4	-	*Susceptible*
PI 272557	(-)	Hungary	*T. m. m*	4	4	4	*Susceptible*
PI 573520	(-)	Turkey	*T. m. a.*	2-	;1	-	*Sr22*
PI 560720	(-)	Turkey	*T. m. m*	2-	4	-	*Susceptible*
G3116	(-)	Lebanon	*T. m. a.*	2,2+	1	-	*Sr21*
DV92	(-)	-	*T. m. m*	0;	1	-	*Sr21*, *Sr35*
PI 573523	(-)	Turkey	*T. m. m*	;N	;1-	-	*Sr22*
PI 427464	(-)	Azerbaijan	*T. m. a.*	2+3Z	;1	-	*Sr21*

PI 427444	(-)	Turkey	*T. m. a.*	22+Z	1	-	*Sr21*
PI 352273	(-)	Asia Minor	*T. m. a.*	12Z	1	-	*Sr21*
PI 427465	(-)	Armenia	*T. m. a.*	2+3Z	2	-	*Sr21*
PI 272556	(-)	Hungary	*T. m. a.*	4	4	4	*Susceptible*
CI 2433	(-)	Germany	*T. m. m*	2+	;1	-	*Sr21*
PI 427498	(-)	Turkey	*T. m. a.*	3	22+	-	*Sr21*
PI 352505	(-)	Switzerland	*T. m. a.*	;1	;1	-	*Sr22*
PI 190942	(-)	Spain	*T. m. m*	1	;1	-	*Sr21*
PI 277121	(-)	Germany	*T. m. a.*	2+3Z	;1	-	*Sr21*
CItr 14520	(-)	Canada	*T. m. m*	2	;1	-	*Sr21*
CItr 13963	(-)	United States	*T. m. m*	2+	;1	-	*Sr21*
PI 427662	(-)	Iraq	*T. m. a.*	3+	33+	-	*Susceptible*
PI 427478	(-)	Turkey	*T. m. a.*	1/12Z	;1	-	*Sr21*
CItr 13964	(-)	United States	*T. m. m*	3-	;1	-	*Sr21*
CItr 17655	(-)	United States	*T. m. m*	3-	;1	-	*Sr21*
PI 168803	(-)	United States	*T. m. m*	3-	;1	-	*Sr21*
PI 168806	(-)	United States	*T. m. m*	22+3Z	;1	-	*Sr21*
PI 190940	(-)	Spain	*T. m. m*	3-	;1	-	*Sr21*
PI 289605	(-)	United Kingdom	*T. m. m*	2-	;1	-	*Sr22*
PI 352486	(-)	Switzerland	*T. m. m*	2-	;1	-	*Sr22*
PI 355517	(-)	Asia Minor	*T. m. m*	12-	;1	-	*Sr22*
PI 355524	(-)	Germany	*T. m. m*	;1	;1	-	*Sr22*
PI 428158	(-)	United Kingdom	*T. m. m*	;12-	;1	-	*Sr21, Sr60*
PI 503874	(-)	South Africa	*T. m. m*	3+	;1	-	*Susceptible*
PI 427452	(-)	Turkey	*T. m. a.*	12Z	1	-	*Sr21*
PI 330528	(-)	United Kingdom	*T. m. a.*	1;	;1	-	*Sr22*
PI 554480	(-)	Turkey	*T. m. a.*	3-	;1	-	*Sr21*
PI 427467	(-)	Azerbaijan	*T. m. a.*	2+3Z	2	-	*Sr21*
PI 428012	(-)	Armenia	*T. m. a.*	12+Z	;1	-	*Sr21*
PI 538540	(-)	Turkey	*T. m. a.*	33+	4	-	*Susceptible*
PI 362554	(-)	Yugoslavia	*T. m. m*	;1	;1	-	*Sr22*
PI 427497	(-)	Turkey	*T. m. a.*	22+Z	1	-	*Sr21*
PI 427993	(-)	Lebanon	*T. m. a.*	123Z/1;/12Z	;1	-	*Sr21*
PI 427476	(-)	Turkey	*T. m. a.*	1	;1	-	*Sr21*
CItr 17741	(-)	United States	*T. m. a.*	2++	;1	-	*Sr21*
PI 427450	(-)	Turkey	*T. m. a.*	3-	;1	-	*Sr21*
PI 554519	(-)	Former Soviet Union	*T. m. a.*	3+	4	-	*Susceptible*
PI 427661	(-)	Iraq	*T. m. a.*	3	3+	-	*Susceptible*
PI 427405	(-)	Iraq	*T. m. a.*	2+3Z	1	-	*Sr21*
PI 427540	(-)	Turkey	*T. m. a.*	2+3Z	1	-	*Sr21*
PI 352504	(-)	Germany	*T. m. a.*	2-	1	-	*Sr22*
PI 427453	(-)	Turkey	*T. m. a.*	22+Z	1	-	*Sr21*
PI 427510	(-)	Turkey	*T. m. a.*	3	22+	-	*Sr21*
PI 427603	(-)	Turkey	*T. m. a.*	2+3Z	;1	-	*Sr21*

Cltr 17665	(-)	Iran	*T. m. a.*	1;	1	-	*Sr21*
PI 355453	(-)	Asia Minor	*T. m. a.*	2	1	-	*Sr21*
PI 427477	(-)	Turkey	*T. m. a.*	12-Z	;1	-	*Sr21*
PI 427484	(-)	Turkey	*T. m. a.*	2/2+Z	;1	-	*Sr21*
PI 427488	(-)	Turkey	*T. m. a.*	22+Z	22+	-	*Sr21*
PI 554517	(-)	Former Soviet Union	*T. m. a.*	1	;1	-	*Sr22*
PI 401412	(-)	Iran	*T. m. a.*	3	3+	-	*Susceptible*
PI 427994	(-)	Lebanon	*T. m. a.*	12+Z	;1+	-	*Sr21*
PI 427472	(-)	Turkey	*T. m. a.*	1	;1	-	*Sr21*
PI 427468	(-)	Azerbaijan	*T. m. a.*	2+3Z	1	-	*Sr21*
PI 352270	(-)	Germany	*T. m. a.*	2+3Z	1	-	*Sr21*
PI 427592	(-)	Turkey	*T. m. a.*	12+Z	;1	-	*Sr21*
PI 427796	(-)	Iran	*T. m. a.*	1	;1	-	*Sr21*
PI 427527	(-)	Turkey	*T. m. a.*	12+Z	;1	-	*Sr21*
PI 427808	(-)	Iran	*T. m. a.*	1	;1	-	*Sr21*
PI 190945	(-)	Spain	*T. m. m*	1	;1	-	*Sr22*
PI 362553	(-)	Yugoslavia	*T. m. m*	1	;1	-	*Sr22*

[a], *T. m. m. = Triticum monococcum* subsp. *monococcum*; *T. m. a. = Triticum monococcum* subsp. *aegilopoides*.

References

Li, T., Wu, X., Xu, X., Wang, W. and Cao, Y. (2016) Postulation of seedling stem rust resistance genes of Yunnan wheat cultivars in China. *Plant Protect Sci*, **52**, 242-249.

Chao, S., Rouse, M.N., Acevedo, M., Szabo‐Hever, A., Bockelman, H., Bonman, J.M., Elias, E., Klindworth, D. and Xu, S. (2017) Evaluation of genetic diversity and host resistance to stem rust in USDA NSGC durum wheat accessions. *The plant genome*, https://doi.org/10.3835/plantgenome2016.07.0071.

Li, T.Y., Ma, Y.C., Wu, X.X., Chen, S., Xu, X.F., Wang, H., Cao, Y.Y. and Xuan, Y.H. (2018) Race and virulence characterization of *Puccinia graminis* f. sp. *tritici* in China. *Plos One*, **13**, e0197579.

Chen, S., Guo, Y., Briggs, J., Dubach, F., Chao, S., Zhang, W., Rouse, M.N. and Dubcovsky, J. (2018a) Mapping and characterization of wheat stem rust resistance genes *SrTm5* and *Sr60* from *Triticum monococcum*. *Theor Appl Genet*, **131**, 625-635.

Chen, S., Rouse, M.N., Zhang, W., Zhang, X., Guo, Y., Briggs, J. and Dubcovsky, J. (2020) Wheat gene *Sr60* encodes a protein with two putative kinase domains that confers resistance to stem rust. *New Phytol*, **225**, 948-95

Rouse M, Jin Y. 2011. Stem rust resistance in A-genome diploid relatives of wheat. *Plant Dis* **95**: 941-944.

Saintenac, C., Zhang, W., Salcedo, A., Rousse, M., Trick, H., Akhunov, E. and Dubcovsky, J. (2013) Identification of wheat gene *Sr35* that confers resistance to Ug99 stem rust race group. *Science*, **341**, 783-786.

Steuernagel, B., Periyannan, S.K., Hernandez-Pinzon, I., Witek, K., Rouse, M.N., Yu, G., Hatta, A., Ayliffe, M., Bariana, H., Jones, J.D., Lagudah, E.S. and Wulff, B.B. (2016) Rapid cloning of disease-resistance genes in plants using mutagenesis and sequence capture. *Nat Biotechnol*, **34**, 652-655.

Chen, S., Zhang, W., Bolus, S., Rouse, M.N. and Dubcovsky, J. (2018b) Identification and characterization of wheat stem rust resistance gene *Sr21* effective against the Ug99 race group at high temperature. *PLoS Genet*, **14**, e1007287.