Suppl. Figure 6: Predicted amino acid consequences of the CRISPR Cas9 mutations in the *TaRPG1-A* homoeologue of all of the sterile plants produced.

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                                   20                                  40                                  60                                  80                                  100
RPG Wt A        MVSADAARNV VGIIGNVISF GLFLSPTPVF WRIIKAKDVE EFKPDPYLAT LLNCMLWVFY GLPIVHPNSI LVVTINGIGL VIEGSYLIIF FLYSTNNKRL 100
RPG 9 allele 1  MVSADAARNV VGIIGNVISF GLFLSPTAVV ---------- ---------- ---------- ---------- ---------- ---------- 30
RPG 9 allele 2  MVSADAARNV VGIIGNVISF GLFLSP---- ---------- ---------- ---------- ---------- ---------- ---------- 26
RPG 10          MVSADAARNV VGIIGNVISF GLFLSPTPVF WRIIK----- ---------- ---------- ---------- ---------- ---------- 35
RPG 12 allele 1 MVSADAARNV VGIIGNVISF GLFLSPT--- --------RG ---------- ---------- ---------- ---------- ---------- 29
RPG 12 allele 2 MVSADAARNV VGIIGNVISF GLFLSPTPVF WRIIKA--RG ---------- ---------- ---------- ---------- ---------- 38
RPG 13          MVSADAARNV VGIIGNVISF GLFLSPTPVF WRIIKAKVRG ---------- ---------- ---------- ---------- ---------- 40
RPG 15          MVSADAARNV VGIIGNVISF GLFLSPTPVF WRIIKAKARG ---------- ---------- ---------- ---------- ---------- 40
RPG 16          MVSADAARNV VGIIGNVISF GLFLSPTPVF WRIIKAKARG ---------- ---------- ---------- ---------- ---------- 40
RPG 17          MVSADAARNV VGIIGNVISF GLFLSPTPVF WRIIK----- ---------- ---------- ---------- ---------- ---------- 35
Consensus       MVSADAARNV VGIIGNVISF GLFLSPTPVF WRIIKA--RG ---------- ---------- ---------- ---------- ---------- ----------
100%
Conservation
0%

                                   120                                 140                                 160                                 180                                 200
RPG Wt A        KMIGVLAAEA AFMVAVVLGV LLGAHTHEKR SMIVGILCVI FGTIMYASPL TIMGKVIKT- KSVEYMPFTL SLVNFLNGCC WLAYALIKFD LYVTIPNG-- 197
RPG 9 allele 1  ---------- -------LGV LLGAHTHEKR SMIVGILCVI FGTIMYASPL TIMGKVIKT- KSVEYMPFTL SLVNFLNGCC WLAYALIKFD LYVTIPNG-- 110
RPG 9 allele 2  ---------- ---------- ---------- ------FCVI FGTIMYASPL TIMGKVIKT- KSVEYMPFTL SLVNFLNGCC WLAYALIKFD LYVTIPNG-- 87
RPG 10          ---------- -------AGP LPGD------ ---------- ------AAQL HALGLLRPPH RPSQQHPRRH HQRDRARHRG LLPHHLLPL- LHQQQAAEDD 95
RPG 12 allele 1 ---------- ----GVQAGP LPGD------ ---------- ------AAQL HALGLLRPPH RPSQQHPRRH HQRDRARHRG LLPHHLLPL- LHQQQAAEDD 92
RPG 12 allele 2 ---------- ----GVQAGP LPGD------ ---------- ------AAQL HALGLLRPPH RPSQQHPRRH HQRDRARHRG LLPHHLLPL- LHQQQAAEDD 101
RPG 13          ---------- ----GVQAGP LPGD------ ---------- ------AAQL HALGLLRPPH RPSQQHPRRH HQRDRARHRG LLPHHLLPL- LHQQQAAEDD 103
RPG 15          ---------- ----GVQAGP LPGD------ ---------- ------AAQL HALGLLRPPH RPSQQHPRRH HQRDRARHRG LLPHHLLPL- LHQQQAAEDD 103
RPG 16          ---------- ----GVQAGP LPGD------ ---------- ------AAQL HALGLLRPPH RPSQQHPRRH HQRDRARHRG LLPHHLLPL- LHQQQAAEDD 103
RPG 17          ---------- ---------- ---------- ---------- ---------- -------ATW RSSSRTPTWR RCSTACSGSS TASPSSIPT- ASSSSPST-- 75
Consensus       ---------- ----GVQAGP LPGD------ ---------- ------AAQL HALGLLRPPH RPSQQHPRRH HQRDRARHRG LLPHHLLPL- LHQQQAAEDD
100%
Conservation
0%

                                   220                                 240
RPG Wt A        -----LGAFF GLMQLILYGC YYKRTPKEEK SVEL-----P TSNPAGAGNV SVTVDR-- 243
RPG 9 allele 1  -----LGAFF GLMQLILYGC YYKRTPKEEK SVEL-----P TSNPAGAGNV SVTVDR-- 156
RPG 9 allele 2  -----LGAFF GLMQLILYGC YYKRTPKEEK SVEL-----P TSNPAGAGNV SVTVDR-- 133
RPG 10          RRARRRGGVH G-------GR RARRAPRCPH PREALHDRRH PRRHLRNHHV CLPAHHHG 146
RPG 12 allele 1 RRARRRGGVH G-------GR RARRAPRCPH PREALHDRRH PRRHLRNHHV CLPAHHHG 143
RPG 12 allele 2 RRARRRGGVH G-------GR RARRAPRCPH PREALHDRRH PRRHLRNHHV CLPAHHHG 152
RPG 13          RRARRRGGVH G-------GR RARRAPRCPH PREALHDRRH PRRHLRNHHV CLPAHHHG 154
RPG 15          RRARRRGGVH G-------GR RARRAPRCPH PREALHDRRH PRRHLRNHHV CLPAHHHG 154
RPG 16          RRARRRGGVH G-------GR RARRAPRCPH PREALHDRRH PRRHLRNHHV CLPAHHHG 154
RPG 17          ---------- G-------SG SSSRAPTSSS SSST------ ---------- --PPTTSG 98
Consensus       RRARRRGGVH G-------GR RARRAPRCPH PREALHDRRH PRRHLRNHHV CLPAHHHG
100%
Conservation
0%
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