

Figure S1

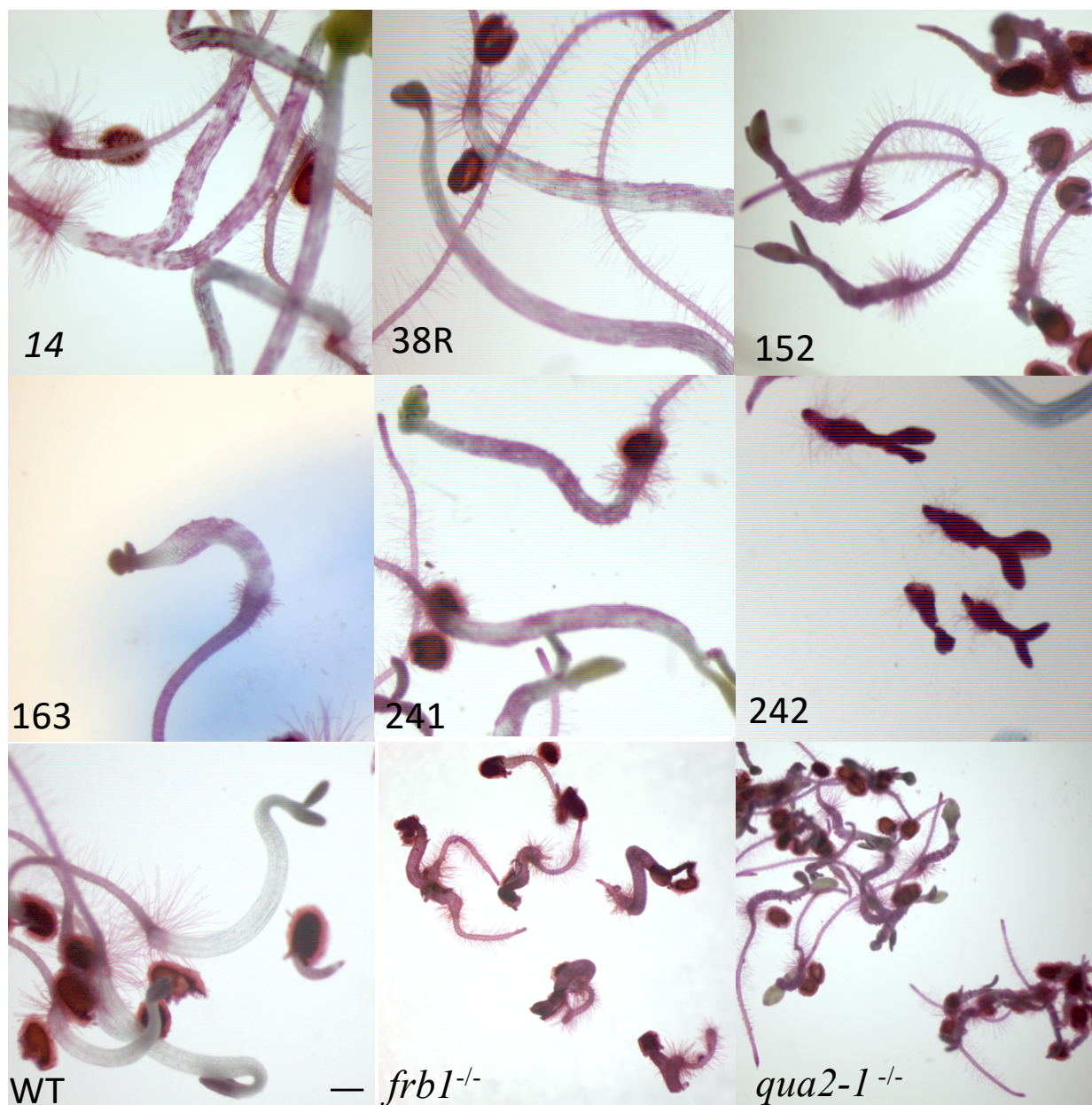


Figure S1. Ruthenium Red stained M2 dark grown hypocotyls from the indicated seed pool. Shown are red staining seedlings isolated from 192 M2 pools of seeds of 20-33-plants. WT, *frb1* and *qua2* are shown as controls. This report describes the characterization of mutant 38R, and 14, 152, 163 241 and 242 will be reported elsewhere. Bar indicate 0.5mm

Figure S2

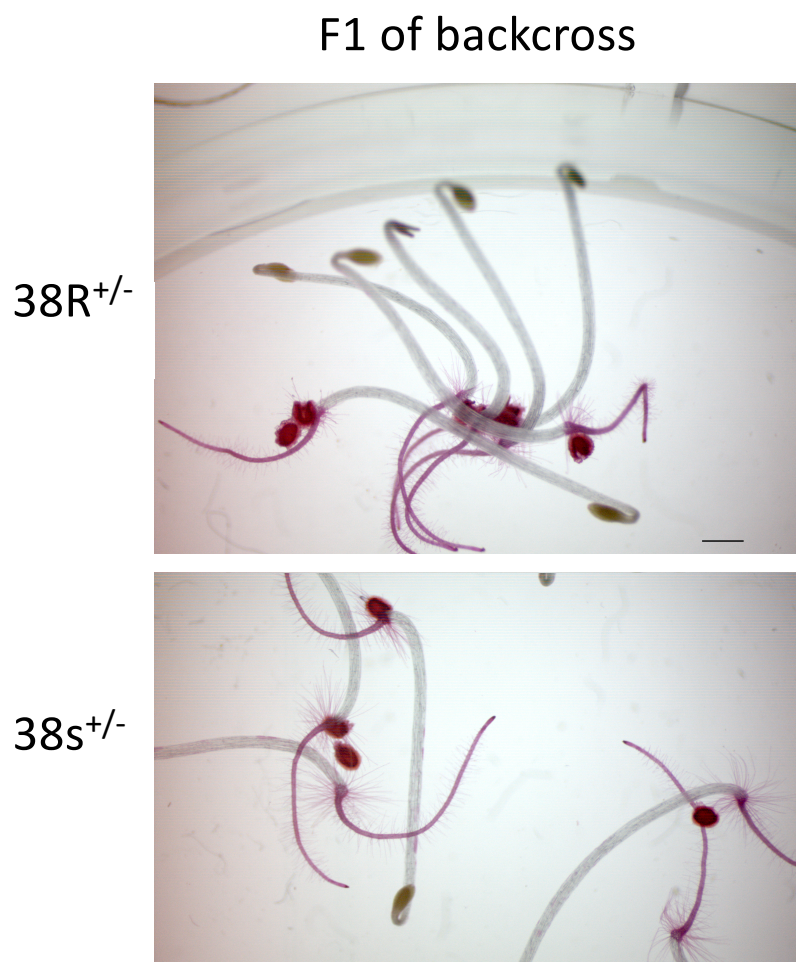
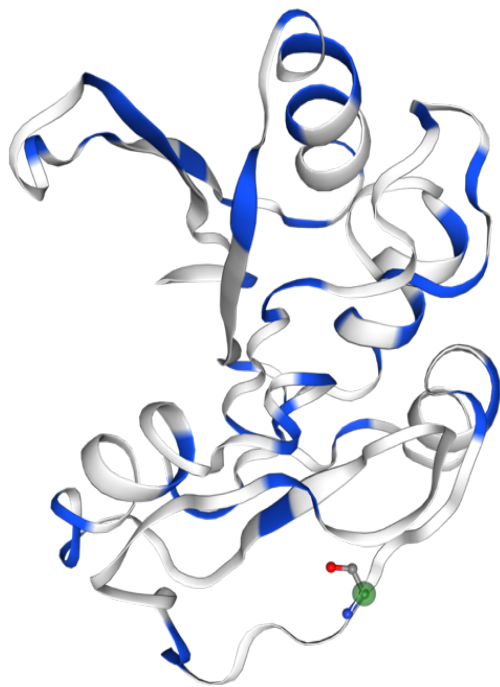


Figure S2. 38R and 38S are recessive alleles. Shown are Ruthenium Red stained dark grown hypocotyls of the F1 of the indicated mutant crossed to WT. Bar indicates 1 mm.

Figure S3



```

QUA2      _  MSMP LQRGISGVRRVSDSSDDL RDSQM KDKTERARSTENN NLT LRFPPFGFLFSNQSSSKHG 60
At1g13860 _  M-----KVASV----- 6
At2g03480 _  MRGSWYKSVSSV----- 12
          *          :.:*

QUA2      _  GGGENGFSADPY SARSRHRLMLLFLKISLV LIVVIALAGSFWWTISISTSSRGHVHYHNYR 120
At1g13860 _  -----IGLRPRISGLLFLTLGVIALITILV P NSDSSSTTSTTRVPPSN IYSNYG
At2g03480 _  -----FGLRPRIRGLLFFIVGVVALVTILAP L TSNSYDSSSSSTLVPNIYSNYR
          . *. * :.:* :.:* :.:* . * : :.:* **

QUA2      _  RLQEQLVSDLWDIG EISLGPNRWKELEYCNIESENFVPCFNVSENALGYSNGDENDRFC 180
At1g13860 _  RVKEQAADVLDLRF FSLGVNRLKEFPLCGKERDNYVPCYNVT-----ESDRNC 104
At2g03480 _  RIKEQAADVLDLRLSLSLGAS-LKEFPFCGKERESYVPCYNTGNLLAGLQEGEELDRHC 120
          :.:* * * * :.:* * * * :.:* * * * :.:* * * *

QUA2      _  GPGSKQE-CLELPPVKYRVPLRWPTGKDI I WHSNVKITAQEVVSSGSITKRM MMEDDQI 239
At1g13860 _  EFAREEBERCIVRPPRDYK I PLRWPVGRDI IWTGNVKITKDQFLSSGTMTKRMLLLENQI 167
At2g03480 _  EFEREKERCIVRPPRDYK I PLRWPVGRDI I WSGNVKITKDQFLSSGTVTTRMLLENQI 180
          :.:* * * * :.:* * * * :.:* * * * :.:* * * *

QUA2      _  SFRSASPMS-DEVEDYSHQIAEMIGIKKDN-FIEAGVRTILDIGCGYSGFGAHL LSKQIL 297
At1g13860 _  TFHSDGLIFDGVKDYAFQIAEMIGLGS DTEFPQAGIRTVLDIGCGFGSFGAHLVSLNVM 224
At2g03480 _  TFHSEDLVFDGVKDYARQIAEMIGLGS DTEFAQAGVRTVLDIGCGFGSFGAHLVSLKLM 240
          :.:* * * * :.:* * * * :.:* * * * :.:* * * *

QUA2      _  TMCIANYEASGSQVQLT LERGLPAMIGSFISKQLPYPSP LSFDMHLCLRCGIDWDQKDGLL 357
At1g13860 _  PICIAEYETSGSQVQLALERGLPAMIGNFFSKQLPYPALS FDMVHCAQCCTIWDIKDAML 284
At2g03480 _  PICIAEYATG SQVQLALERGLPAMIGNFFSKQLPYPALS FDMVHCAQCCTIWDIKDAML 300
          .: * * * :.:* * * * :.:* * * * :.:* * * *

QUA2      _  LVEIDRVLKPGGYFVWTSPLTNPR-NKDH LKRWNF---VHDFAESICW TLLNQDDETVVW 413
At1g13860 _  LLEVDRVLKPGGYFVLT SPTSKAQGN SPTKKTTSI STRVDEL SKKICWSLSGQDDETFW 344
At2g03480 _  LLEVDRVLKPGGYFVLT SPTNKAQGNL PDKTTSI STRVNELSKKICWSLTAQDDETFW 360
          *: * * * * * * * :.:* * * * :.:* * * * :.:* * * *

QUA2      _  KKTINTKCYSSRKPGVGPSVCTKGHDVESP YRPLQMCIGGTRSRRWIPIEGRTRWPSRS 473
At1g13860 _  QKTADPN CYSSRSQASIP-VCKDDDSV---PYHPLVPCISG TSKRWIPIQNRSR---AS 398
At2g03480 _  QKTS DSSCYSSRSQASIP-LCKDGD SV---PYHPLVPCISG TSKRWISIQNRSA---VA 414
          :.:* * * * * * * :.:* * * * :.:* * * * :.:* * * *

QUA2      _  NMNKTELSLYGLHPEVLGEDAENWKITVREYWSL LSP LIFS DHPKRPGEDDPSPPPYMLR 533
At1g13860 _  GTLSLELEI HGIKPEEFDEDIQV WRSALKNYWSL L TPLIFS DHPKRPGEDDPVPPY MIR 456
At2g03480 _  GTTSAGLEI HG-----KSALKNYWSL L TPLIFS DHPKRPGEDDPLPPFN MIR 459
          . . : *.:* * :.:* * * * :.:* * * * :.:* * * *

QUA2      _  NVLDMNAQFGGLNSALLEARKSVWVMNVVPTAGPNH LPMILDRGFVGV LHWNWCEPFPTY 593
At1g13860 _  NAMDMNARYGNL NQALLNQQGKSVWVMNVV PVKARNTLP I ILDRGFV G ALHDWCEPFPTY 518
At2g03480 _  NVMDMHARFGNLN AALLDEGKSAWVMNVV PVARNTLP I ILDRGFV G VLHDWCEPFPTY 521
          *: * * * :.:* * * * :.:* * * * :.:* * * *

QUA2      _  RTYDLVHADNLLSQT SQPRKTC LLIDIFTEI DRLLRPEGWVIIRD T AOLVEKARETITQ 653
At1g13860 _  RTYDMLHANEL LTHLSSE---RCSLMDL FLEMDRILRPEGWV VLSDKLGVIE M ARTLAAR 575
At2g03480 _  RTYDMLHANEL LTHLSSE---RCSLMDL FLEMDRILRPEGWV VLSDKVGVIE M ARALAAAR 578
          * * * :.:* * * * :.:* * * * :.:* * * *

QUA2      _  LKWEARVIEVESSEQRLLICQKPFTRQSI 684
At1g13860 _  VRWEARVIDIQDGS DQRLLCVCKP L LKK--- 603
At2g03480 _  VRWEARVIDIQDGS DQRLLCVCKP F I K--- 606
          :.:* * * * :.:* * * * :.:* * * *

```

38R/qua2-4
(Gly580→Glu)
qua2-1
(Ile625 → STOP)

Figure S3. CLUSTAL format alignment of QUA2 amino acid sequence to its two closest *Arabidopsis thaliana* methyl transferase homologous (9). An asterisk indicates positions which have a single, fully conserved residue, a colon indicates conservation between groups of strongly similar properties, and a period indicates conservation between groups of weakly similar properties (10). The location of *qua2-4* (G to E) is highlighted in green and *qua2-1* (I to STOP) is highlighted in red. Swiss-Model predicted structure of aa 532-678, which lie within the methyl transferase domain of QUA2, is shown to the left of the sequence. Hydrophobic regions are highlighted in white, while hydrophilic regions are highlighted in blue (11). *qua2-4* (green dot at amino acid 580) lies within a long hydrophobic region of QUA2 and is characterized by a change from a glycine (aa structure shown) to a glutamic acid.

Figure S4

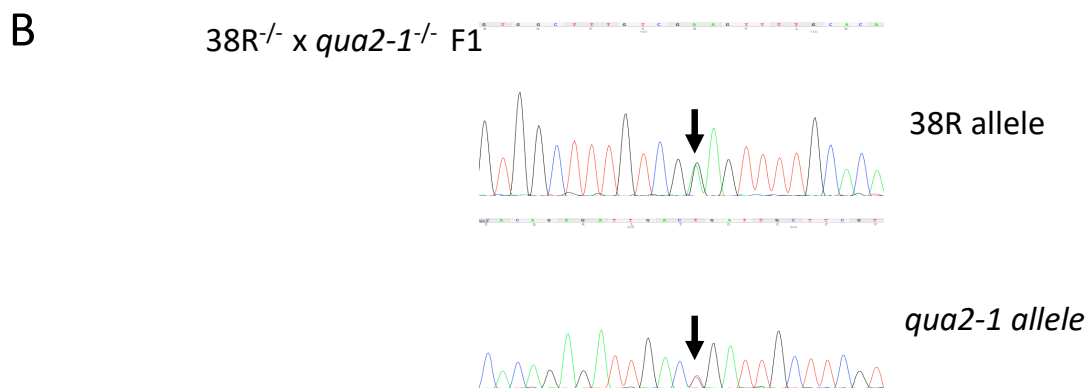
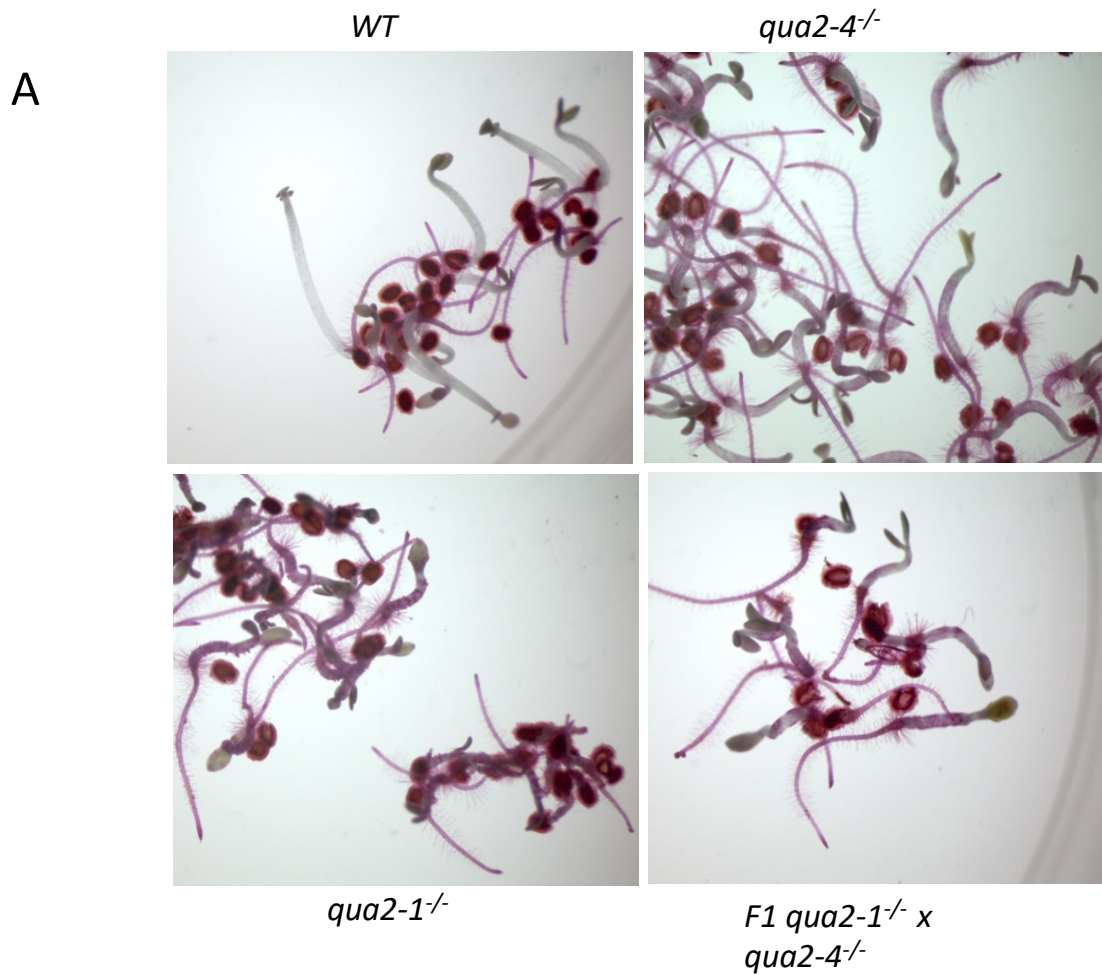


Figure S4. *qua2-1* does not complement 38R adhesion defect. **A)** 4 day old Ruthenium Red stained dark grown hypocotyls from the indicated genotype. **B)** The *QUA2* gene was PCR amplified and sequenced from DNA of an F1 *qua2-1^{-/+} qua2-4^{-/+}* seedling, and shown are the heterozygous loci for each allele.

Figure S5

$38S^{+/-}$ x $sab1-5^{+/-}$ F1



Figure S5. $38S$ and $sab1-5$ are alleles of the same gene. Shown are dark grown hypocotyls from F1 seeds of a $38S^{-/+}$ x $sab1-5^{-/+}$ cross. The presence of $1/7^{\text{th}}$ of the population of stunted progeny (arrows) indicates the lack of complementation. Bar indicates 1 mm.

Figure S6 . Excel file of RNA seq

List of differentially expressed genes related to the cell wall compared between *sab* and WT. Similar levels are seen in *sab/qua* vs WT. In addition the following genes were evaluated and found not to differ significantly between genotype; Cell Wall Integrity- *FER1*, *HERK1*, *HERK2*, *FEI1*, *FEI2*, *KIN13A*, *THE1*, *WAK1-5*. Biosynthesis; *CESA*, *GAE1-6*, *PMT*, *PG*, *PGIP*, *PGX1*, *MNA*, *ORT2*, *APG*.

Figure S7 (compressed) Additional Excel sheets 2-4 show Differential Expressed Genes (DEG) between WT and *sab*, *qua2* or *sab qua2*.