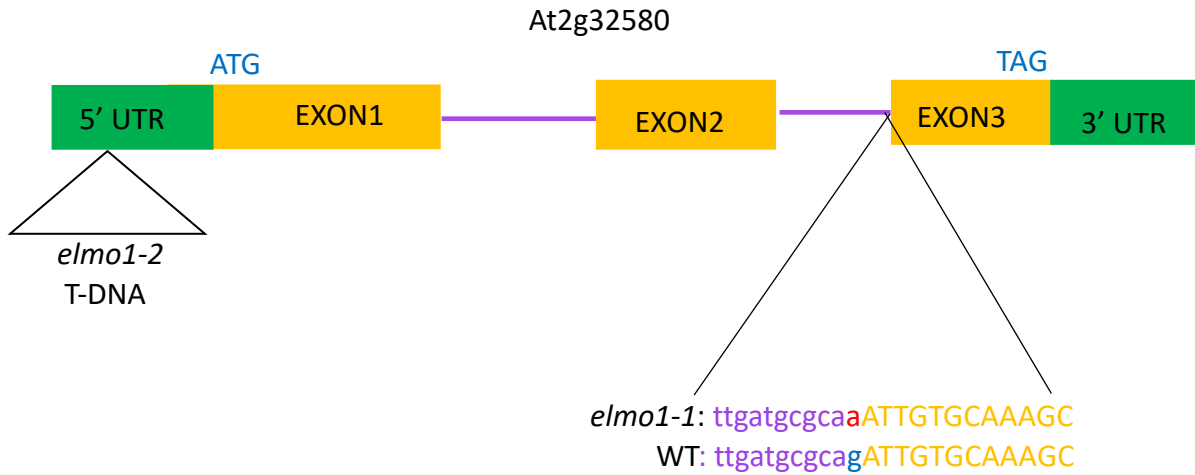


Fig S1

Position	Mutation	Frequency	Depth	Gene ID	Change	
14508965	G→A		1	10 AT1G38460		TE
13828788	G→A		1	12 AT2G32580	3' splice jct	
4002170	C→G T A		1	11 AT4G06716		TE
9914031	C→T A		1	14 AT4G17820		TE
13591422	C→T A	0.97530864		81 AT3G33055		TE
11733672	G→A T	0.97222222		36 AT5G31804		TE
17391851	G→A	0.94736842		22 AT2G41700		
15849518	G→A	0.93333333		21 AT2G37810		
9926214	G→A	0.92307692		27 AT2G23320		
3626169	G→AC	0.92063492		63 AT2G08986		
15345067	G→A	0.89473684		22 AT2G36600		
19484935	G→A	0.88235294		21 AT2G47480		
16523746	C→T	0.84444444		98 AT1G43755		
3951473	C→G A T	0.84210526		20 AT4G06698		
17596170	G→A	0.83333333		22 AT2G42230	Pro132Ser	
14494092	C→T	0.82608696		25 AT3G42350		
17356722	G→A	0.82352941		19 AT3G47120		
17141475	C→T	0.80487805		91 AT1G45223	Asp68Asp	

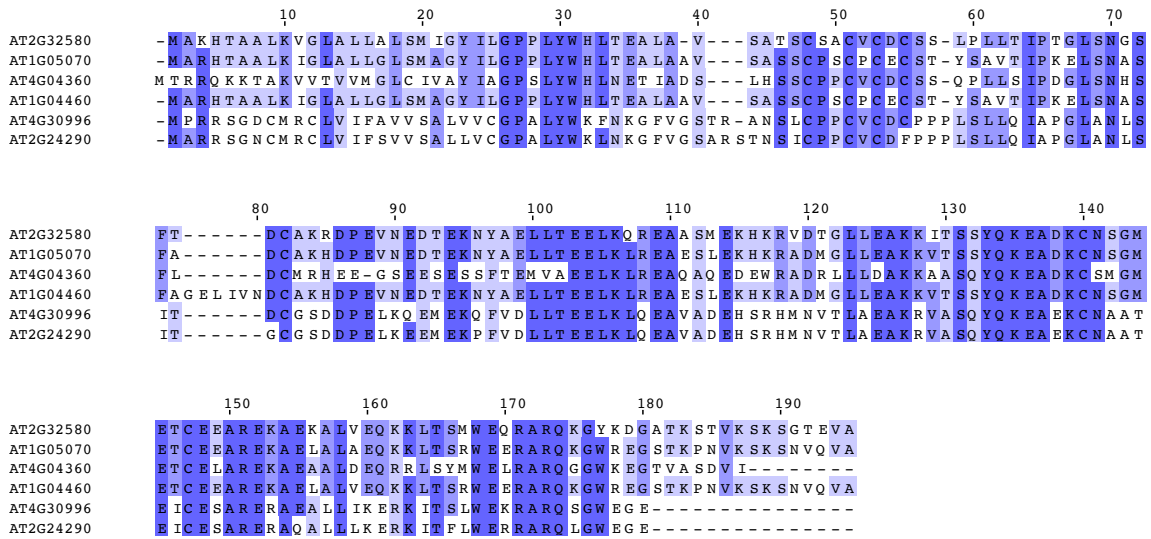
**Fig S1.** Allele frequency from DNA sequencing of *elmo1*<sup>-/-</sup> x WT pooled F2. The artMAP program produces a frequency table that maps the location of single nucleotide mutations and their frequency. Only mutations with a frequency of 80% and higher are shown. Position is on the *Arabidopsis thaliana* Col0 version 10 genome. Mutation indicates the WT allele changed to the indicated base. Change indicates the predicted effect of the mutation if there is one. TE indicates predicted transposable element.

Fig S2



**Fig S2.** Cartoon of At2g32580 identified by genomic sequencing. Location of UTR (green), exons (mustard), introns (purple) and the stop and start codon as indicated. Sequence shows the 3' splice junction of intron 2 with the WT allele G shown in blue and the mutant A in red of the *elmo1-1* allele. The position of the T-DNA insertion in the 5'UTR is indicated for the *elmo1-2* allele.

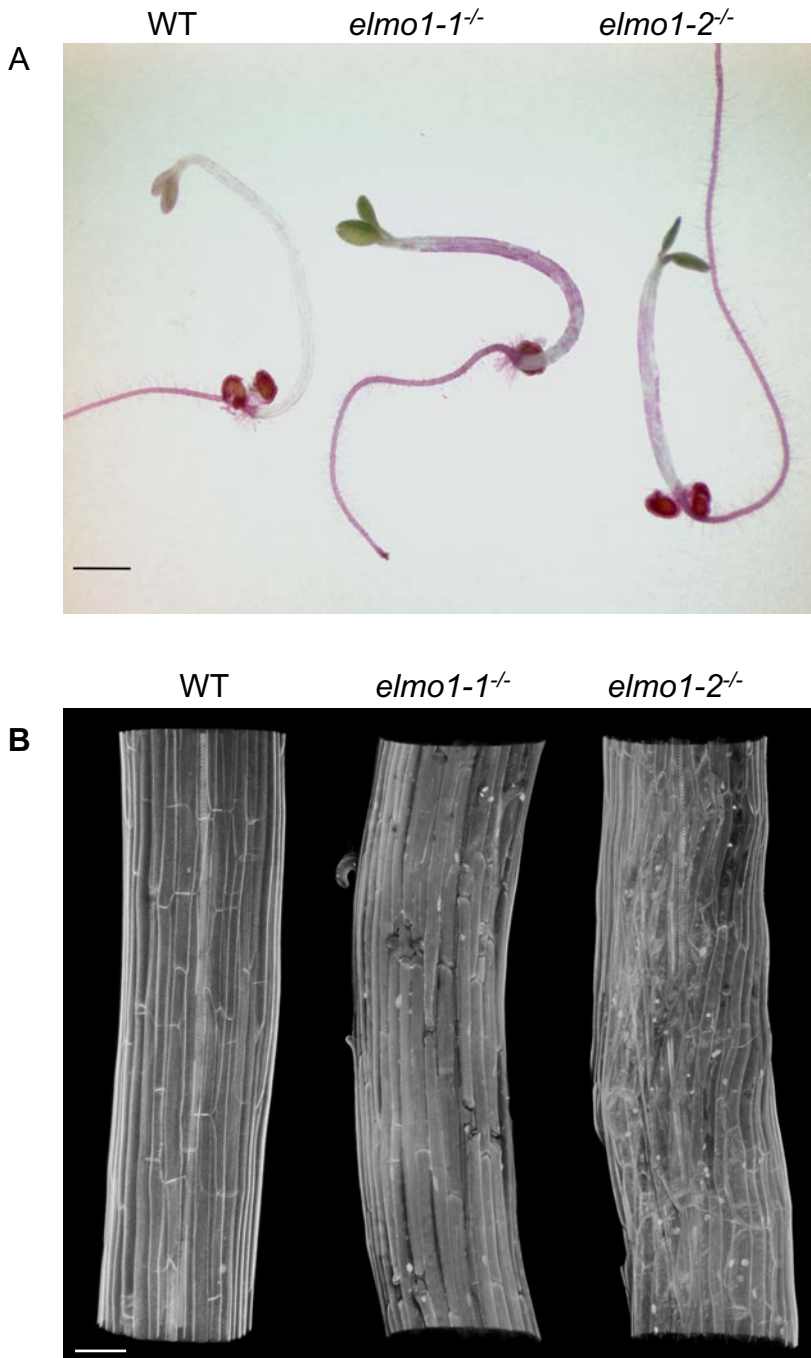
Fig S3A



**Fig S3.** Amino acid sequence alignment of At2g32580 (*ELMO1*) and homologs. Exact sequence overlap with At2g32580 is highlighted in blue where darker shades have higher similarity. A) Sequence alignment of Arabidopsis homologues. B) Alignment of Angiosperm homologues with *ELMO1* (At2g32580).

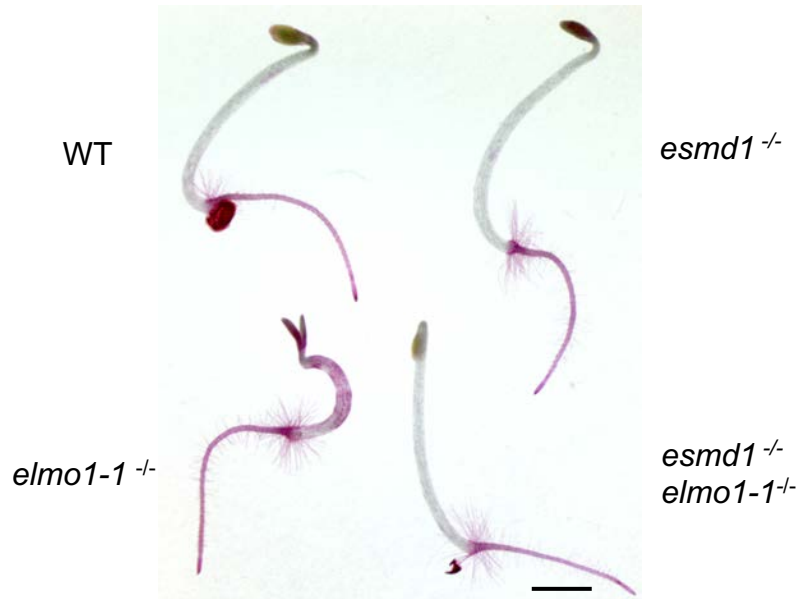


Fig S4



**Fig S4.** An additional allele *elmo1-2* displays cell adhesion defects. A) Shown are 4 day-old dark grown seedlings of the indicated genotype stained with Ruthenium Red. Bar indicates 1 mm. B) Confocal microscopy imaging of propidium iodide stained dark grown hypocotyls of the indicated genotype, bar indicates 50  $\mu$ m.

Fig S5



**Fig S5** . *esmd1* suppresses *elmo1*. Dark grown seedlings of the indicated genotype stained with Ruthenium Red. Bar indicates 1 mm.