Supplemental table S1. Total sugar amounts in seed mucilage sequentially extracted from *sbt1.7-3*, *gl2-6*, *gl2-7*, *gl2-8*, *gl2-9*, *luh*-7, *luh-8* and *mum2-15* compared to wild-type. Intact seeds were extracted sequentially with 0.05 M HCl - 0.3 M NaOH and rhamnogalacturonan hydrolase. Values (mg g-1 of intact dry seeds) ±SD of two biological repeats. WT, wild type.

Genotypes	HCl-NaOH	Rhamnogalacturonan hydrolase
WTWs	29.08 ± 0.893	8.66 ± 0.135
sbt1.7-3	27.27 ± 0.445	8.32 ± 0.286
gl2-6	8.89 ± 0.188	6.78 ± 0.029
gl2-7	8.95 ± 0.197	5.14 ± 0.280
gl2-8	5.98 ± 0.343	5.45 ± 0.123
gl2-9	4.56 ± 0.056	5.66 ± 0.115
luh-7	15.14 ± 1.538	10.72 ± 0.024
luh-8	12.47 ± 0.311	11.31 ± 0.010
mum2-15	20.51 ± 0.127	11.47 ± 0.857

Supplemental table S2. Monosaccharide Composition of Water-Extracted Mucilage.
Intact seeds were extracted with water for 3 h at room temperature with gentle shaking. Values (mg g^{-1} of intact dry seeds) ±SD of three biological repeats. n.d., not detected.

	WTCol-2	*mum5-1*
Rha	6.69 ± 0.225	9.92 ± 0.079
Fuc	n.d.	n.d.
Ara	0.15 ± 0.016	0.15 ± 0.007
Xyl	0.41 ± 0.014	0.23 ± 0.012
Man	0.23 ± 0.040	0.18 ± 0.031
Gal	0.30 ± 0.018	0.32 ± 0.028
Glc	0.74 ± 0.078	0.76 ± 0.031
GalA	10.15 ± 0.116	14.70 ± 0.113
Total	18.67 ± 0.114	26.26 ± 0.250
Rha/Xyl (molar ratio)	15	39

Supplemental table S3. Adsorption assays for three concentrations of enzymatically-tailored water-extracted mucilage from wild-type Col-0.

Water-extracted mucilage was partially degraded with rhamnogalacturonan hydrolase (3 h) and then precipitated with ethanol. The ethanol precipitate was recovered as enzymatically-tailored mucilage. The mass of bound material per mass of cellulose (q_e) and the concentration of free material remaining in solution at equilibrium concentration (C_e) were quantified. Values (C_e, µg/mL; q_e, µg.mg^{-1} cellulose) ±SD of two technical replicates.

	C_e	q_e
Rha	43.14 ± 1.807	3.25 ± 0.163
	70.25 ± 1.089	7.70 ± 2.711
	111.51 ± 7.445	13.78 ± 1.117
Xyl	0.00 ± 0.000	11.43 ± 1.835
	0.96 ± 0.099	15.48 ± 0.148
	2.89 ± 0.884	23.88 ± 1.326
GalA	62.79 ± 1.973	5.45 ± 0.296
	94.89 ± 1.973	7.11 ± 0.296
	153.50 ± 0.000	18.83 ± 0.000

Supplemental table S4. Sequences of primers used for identification of homozygous mutants.

mum5 mutant/ T-DNA line	Forward primer sequence flanking insertion site	Reverse primer sequence flanking insertion site	Insertion border primer sequence
mum5-2/ WiscDsLox 503F10	5’-ATGAGGCAGAATCTGAAAAAAG-3’	5’-GGTACTTCATGGATCACTTCGC-3’	p745 LB 5'-AACGTCCGCAATGTGTTATTAAGTTGTC-3'
mum5-3/ SALK_041744	5’-CAAGAACCGGGTCTCGAGGG-3’	5’-CACTTCAGTTTCCATTCATTAGG-3’	Sig LB1 : 5’-CGG AAC CAC CAT CAA ACA G-3’

Underlined primers were used to amplify insertion border PCR fragment.