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# The tension-sensitive ion transport activity of MSL8 is critical for its function in pollen hydration and germination

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1 **The Tension-sensitive Ion Transport Activity of MSL8 is Critical for its Function in Pollen Hydration**  
2 **and Germination**

3

4 Running title:

5 Ion transport is required for MSL8 pollen function

6

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25

26 Abbreviations: cRNA, capped RNA; MS, mechanosensitive; MscL, Mechanosensitive channel of Large

27 conductance; MscS, Mechanosensitive channel of Small conductance; MSL8, MscS-Like 8; MSL10; MscS-

28 Like 10; PEG, polyethylene glycol; TM, transmembrane

29 **Abstract**

30 All cells respond to osmotic challenges, including those imposed during normal growth and development.  
31 Mechanosensitive (MS) ion channels provide a conserved mechanism for regulating osmotic forces by  
32 conducting ions in response to increased membrane tension. We previously demonstrated that the MS ion  
33 channel MscS-Like 8 (MSL8) is required for pollen to survive multiple osmotic challenges that occur during  
34 the normal process of fertilization, and that it can inhibit pollen germination. However, it remained unclear  
35 whether these physiological functions required ion flux through a mechanically gated channel provided by  
36 MSL8. We introduced two point mutations into the predicted pore-lining domain of MSL8 that disrupted  
37 normal channel function in different ways. The Ile711Ser mutation increased the tension threshold of the  
38 MSL8 channel while leaving conductance unchanged, and the Phe720Leu mutation severely disrupted the  
39 MSL8 channel. Both of these mutations impaired the ability of MSL8 to preserve pollen viability during  
40 hydration and to maintain the integrity of the pollen tube when expressed at endogenous levels. When  
41 overexpressed in a *msl8-4* null background, MSL8<sup>I711S</sup> could partially rescue loss-of-function phenotypes,  
42 while MSL8<sup>F720L</sup> could not. When overexpressed in the wild type *Ler* background, MSL8<sup>I711S</sup> suppressed  
43 pollen germination, similar to wild type MSL8. In contrast, MSL8<sup>F720L</sup> failed to suppress pollen germination  
44 and increased pollen bursting, thereby phenocopying the *msl8-4* mutant. Thus, an intact MSL8 channel is  
45 required to for normal pollen function during hydration and germination. These data establish MSL8 as the  
46 first plant MS channel to fulfill previously established criteria for assignment as a mechanotransducer.

47

48 **Keywords:** *Arabidopsis thaliana*; mechanosensitive ion channel; osmotic stress; pollen hydration; pollen  
49 germination



## 50 Introduction

51 In order to thrive, all cells must respond to osmotic challenges. Drought, salt stress, and freezing all present  
52 environmentally imposed stresses that require osmoprotective strategies for cell survival (Burg and Ferraris,  
53 2008; Zhang, 1999). Organisms can also experience osmotic challenges inherent to their growth and  
54 development, such as desiccation during endospore formation in response to stress (Tovar-Rojo et al.,  
55 2003), the transition from seawater to saltwater experienced by migrating salmon (Jeffries et al., 2011), or  
56 drying and rehydration of plant seeds (Hoekstra et al., 2001).

57

58 One conserved molecular mechanism for responding to osmotic challenges and other mechanical stimuli  
59 is the use of mechanosensitive (MS) ion channels (Booth and Blount, 2012; Hamilton et al., 2015b; Ranade  
60 et al., 2015). These proteins form pores in the cell membrane that open in response to mechanical  
61 stimulation, allowing ions to flow across the membrane down their electrochemical gradient. A role for MS  
62 ion channels in osmotic control has been well described in *Escherichia coli*, where the Mechanosensitive  
63 channel of Large conductance (MscL) and Mechanosensitive channel of Small conductance (MscS) are  
64 required for the cell to survive extreme hypoosmotic downshock, such as the transfer from 500 mM NaCl  
65 to distilled water (Levina et al., 1999). It is proposed that when cells are exposed to hypoosmotic shock, the  
66 resultant cell swelling and increase in membrane tension increase the open probability of both MscS and  
67 MscL. When open, these channels allow ions and other small osmolytes to flow out of the cell, reducing  
68 internal osmotic pressure and protecting the bacterium from lysis (Booth and Blount, 2012; Kung et al.,  
69 2010). Thus, bacterial MS ion channels are often referred to as osmotic pressure release valves.

70

71 *EcMscS* is the founding member of a large family of conserved proteins found within prokaryotes, archaea,  
72 and many eukaryotes, including plants (Haswell, 2007; Kloda and Martinac, 2002; Koprowski and Kubalski,  
73 2003; Levina et al., 1999; Malcolm and Maurer, 2012; Pivetti et al., 2003; Porter et al., 2009; Prole and  
74 Taylor, 2013). Crystal structures of MscS homologs from *E. coli* and *Helicobacter pylori* have shown that  
75 these proteins form homoheptamers (Bass et al., 2002; Lai et al., 2013; Steinbacher et al., 2007; Wang et  
76 al., 2008), but no structural information yet exists for eukaryotic MscS family members. Ten MscS homologs

77 are encoded in the *Arabidopsis thaliana* genome, named MscS-Like (MSL) 1-10 (Haswell, 2007). MSL  
78 proteins localize to diverse cell compartments, including the mitochondria (Lee et al., 2016), plastids  
79 (Haswell and Meyerowitz, 2006), and the plasma membrane (Hamilton et al., 2015a; Haswell et al., 2008;  
80 Veley et al., 2014).

81

82 We recently showed that plasma membrane-localized MSL8 is required to protect pollen from osmotic  
83 challenges during several steps in fertilization (Hamilton et al., 2015a). Pollen contains the male gametes  
84 of flowering plants and is responsible for the delivery of two sperm cells to the female gametophyte in order  
85 to produce the next generation (Hafidh et al., 2016). During key steps of desiccation, rehydration,  
86 germination, and tube growth, pollen must regulate its osmotic potential to maintain the integrity of the cell  
87 and achieve its reproductive function (Beauzamy et al., 2014; Chen et al., 2015; Feijo et al., 1995; Firon et  
88 al., 2012; Sanati Nezhad et al., 2013).

89

90 Upon maturation, the pollen of most species of flowering plants desiccates (Franchi et al., 2011), a strategy  
91 thought to maintain viability during exposure to the external environment (Firon et al., 2012). To protect  
92 against the osmotic stress of this water loss, pollen accumulates sugars and other compatible osmolytes  
93 that serve to stabilize cellular membranes and other biomolecules in the dry state (Hoekstra et al., 2001;  
94 Pacini et al., 2006). When a desiccated pollen grain reaches the stigma, an organ of finger-like projections  
95 atop the pistil, it is rehydrated by stigma cell exudate in a regulated process of pollen reception (Dresselhaus  
96 and Franklin-Tong, 2013; Edlund, 2004; Samuel et al., 2009). The wet stigma of lily is coated in exudate,  
97 which is about 10% carbohydrates (Labarca et al., 1970). The composition of the exudate produced in  
98 species with dry stigmas, such as *Arabidopsis*, is unknown (Edlund, 2004), but must be hypoosmotic with  
99 respect to the pollen cytoplasm in order to produce net hydration. The rehydration of desiccated pollen can  
100 damage dry cellular membranes, which are more rigid and less able to accommodate hypoosmotic swelling  
101 (Hoekstra et al., 2001; 1997), and this membrane damage can compromise pollen viability if hydration is  
102 not properly regulated (van Bilsen et al., 1994).

103

104 Once a pollen grain is rehydrated, its metabolism is reactivated and it germinates a long extension that  
105 grows by turgor-driven cell expansion at the tip without further cell divisions, called a pollen tube (Beauzamy  
106 et al., 2014; Firon et al., 2012). Germination requires that the pollen grain establish and maintain turgor  
107 pressure at a level high enough to break through the tough pollen cell wall (Feijo et al., 1995). The rapid  
108 growth of the pollen tube is also driven by turgor pressure, which continuously expands new cell wall  
109 material delivered to the growing tip (Hill et al., 2012; Kroeger et al., 2011; Zerzour et al., 2009). Artificially  
110 increasing turgor pressure can lead to lysis, especially at the tip of the pollen tube (Benkert et al., 1997),  
111 and genetic lesions that increase turgor impair the ability of the pollen tube to reach the ovule and fertilize  
112 the egg cell (Chen et al., 2015). Conversely, growth conditions that reduce turgor halt pollen tube growth  
113 (Zerzour et al., 2009). In addition to turgor, pollen tubes must regulate the delivery of new cell wall material  
114 and cell wall composition in order to sustain growth while maintaining the integrity of the cell (Hill et al.,  
115 2012; Kroeger et al., 2011; Zerzour et al., 2009). These observations have led to the proposal that pollen  
116 grains utilize a mechanosensor to respond to changes in osmotic potential (Hill et al., 2012), and a role for  
117 MS ion channels in regulating ion fluxes at the dynamic pollen tube tip has been proposed for decades  
118 (Feijo et al., 1995).

119

120 MSL8 provides one mechanism for regulating these osmotic forces in pollen. The null *msl8-4* allele, a T-  
121 DNA insertion in the Landsberg *erecta* background, results in reduced viability when pollen is hydrated in  
122 distilled water (Hamilton et al., 2015a). This hydration viability defect can be rescued by supplementing  
123 hydration media with a 20% solution of polyethylene glycol (PEG); increasing the osmotic potential of the  
124 media reduces the hypoosmotic shock pollen experiences during hydration. We were unable to detect any  
125 defect in hydration rate nor in the final size of in vitro hydrated pollen, indicating that wild type and *msl8-4*  
126 pollen have a similar capacity to hydrate. This evidence suggests that MSL8 serves to protect desiccated  
127 pollen against the hypoosmotic shock of rehydration.

128

129 MSL8 also functions during pollen germination and tube growth. Turgor pressure is required for pollen  
130 grains to germinate, and for pollen tubes to grow (Feijo et al., 1995), but it must be controlled in order to

131 prevent bursting (Kroeger et al., 2011; Zerzour et al., 2009). MSL8 appears to be involved in this process,  
132 as *msl8-4* pollen germinates at a greater rate than wild type pollen, but bursts more frequently, consistent  
133 with elevated turgor pressure in the mutant pollen grains and germinating tubes (Hamilton et al., 2015a).  
134 Conversely, overexpressing MSL8 inhibits pollen germination, likely by reducing turgor pressure below the  
135 level needed for the nascent pollen tube to break through the pollen grain cell wall. Both loss-of-function  
136 mutations in the *MSL8* gene and overexpression of *MSL8* result in male fertility defects. Taken together,  
137 these data show that the proper expression level of MSL8 is essential for full reproductive success.

138  
139 Thus, MSL8 is required to maintain proper osmotic pressure inside pollen, either during rehydration or  
140 during the turgor-driven germination and growth of a pollen tube. Because MSL8 forms a MS ion channel,  
141 we hypothesized that the flow of ions through the MSL8 pore in response to increases in membrane tension  
142 is critical for preventing lysis during hydration and germination, akin to the function of MscS in *E. coli*.  
143 However, it remained possible that the role of MSL8 in pollen survival is indirect. Indeed, close homolog  
144 MSL10 triggers programmed cell death signaling independent of its channel activity (Veley et al., 2014).  
145 Here we report the results of experiments aimed to determine if MSL8 requires an intact channel to achieve  
146 its function in pollen. To do so, we mutated the predicted pore of the MSL8 channel, identified lesions that  
147 affect channel behavior, and analyzed the ability of these mutants to function in pollen. Our results support  
148 a model wherein MSL8 regulates osmotic forces in pollen directly by transporting ions.

## 149 **Results**

### 150 *Mutations in the predicted pore-lining domain of MSL8 alter its channel properties*

151 In order to alter the channel properties of MSL8, we identified candidate amino acids for mutagenesis based  
152 alignment with *EcMscS*. The predicted topology of a MSL8 monomer shown in Fig. 1A indicates a protein  
153 with 6 transmembrane (TM) helices and three soluble domains. The most C-terminal TM helix, TM6,  
154 contains sequence with modest homology to the pore-lining TM3 of *EcMscS* (marked with a thick line in  
155 Fig. 1A and sequence shown in Fig. 1B).

156  
157 In the *EcMscS* channel, Leu105 and Leu109 from each of the seven monomers are proposed to form a  
158 hydrophobic seal in the closed channel that prevents the flow of ions across the pore (Anishkin and  
159 Sukharev, 2004; Bass et al., 2002; Steinbacher et al., 2007) (arrowheads, Fig. 1B). Mutations in nearby  
160 residues can result in decreased tension sensitivity, increased tension sensitivity, or reduced conductance  
161 (Belyy et al., 2010; Edwards et al., 2005; Rasmussen et al., 2015). To create MSL8 variants with altered  
162 channel properties, we replaced hydrophobic residues surrounding the presumptive hydrophobic seal with  
163 polar residues or smaller non-polar residues. Two mutants, Ile711 to Ser and Phe720 to Leu (asterisks,  
164 Fig. 1B) were selected for further study based on their ability to produce MS currents when expressed in  
165 *Xenopus laevis* oocytes (see below).

166  
167 *MSL8*, *MSL8<sup>I711S</sup>* and *MSL8<sup>F720L</sup>* cRNAs were injected into *Xenopus* oocytes for analysis by single channel  
168 patch-clamp electrophysiology as previously described (Hamilton et al., 2015a; Maksaev and Haswell,  
169 2015). Patches of plasma membrane were excised from oocytes 2 to 10 days after injection, and current  
170 measured over time as membrane tension in the patch was increased by applying suction through the  
171 pipette using a pressure-clamp controller. In symmetric 60 mM MgCl<sub>2</sub> + 5mM HEPES, oocytes expressing  
172 wild type *MSL8* cRNA exhibited tension-gated activity as expected (Fig. 1C, top left panel), as did oocytes  
173 injected with *MSL8<sup>I711S</sup>* cRNA (Fig. 1C, top right panel). In the same system, *MSL8<sup>F720L</sup>* cRNA produced MS  
174 currents that could not be resolved into unitary channel openings (Fig. 1C, bottom left panel; see  
175 Supplementary Fig. S1 for more examples of activity associated with *MSL8<sup>F720L</sup>* cRNA), and no currents

176 were observed in water-injected oocytes (Fig. 1C, bottom right panel). 60 mM MgCl<sub>2</sub> was used to encourage  
177 high resistance seal formation and to inhibit endogenous *Xenopus laevis* MS channels. MS currents were  
178 observed in 23 of 26 patches pulled from oocytes injected with *MSL8* cRNA; 27 of 32 patches for *MSL8*<sup>I711S</sup>;  
179 20 out of 24 patches for *MSL8*<sup>F720L</sup>; and in none of 26 patches from water-injected oocytes (Table 1). Under  
180 these conditions, the single-channel conductance of *MSL8*<sup>I711S</sup> was indistinguishable from that of wild type  
181 *MSL8* (Fig. 1D, Table 1). Without distinguishable individual gating events, we were unable to assess the  
182 single channel conductance of *MSL8*<sup>F720L</sup>.

183

184 We were unable to calculate a midpoint gating tension, because membrane patches ruptured before  
185 current saturation, as previously observed for *MSL10* expressed in *Xenopus* oocytes (Maksaev and  
186 Haswell, 2012). Instead, we estimated the tension sensitivity of each *MSL8* variant, by recording the suction  
187 associated with the opening of the first channel and the closing of the last channel in each patch. Patch  
188 pipettes of size  $3 \pm 0.5$  MOhm were used in all experiments to reduce variability in patch geometry. The  
189 negative pressure required to open the first channel in patches expressing wild type *MSL8* was  $-18.0 \pm 13.1$   
190 mmHg, while for *MSL8*<sup>I711S</sup> it was  $-29.5 \pm 11.7$  mmHg (Table 1). While we were unable to identify discrete  
191 channel openings for *MSL8*<sup>F720L</sup>, we estimated its tension threshold by determining the pressure required  
192 to produce visible MS currents, on average  $-61.2 \pm 12.3$  mmHg (Table 1). In summary, *MSL8*<sup>I711S</sup> had the  
193 same conductance as wild type *MSL8*, but was significantly less tension-sensitive (required greater  
194 negative pressure to open). *MSL8*<sup>F720L</sup> appears to be a severely disrupted channel, albeit one capable of  
195 conducting ions through its pore in response to extremely high membrane tension, approximately 3 times  
196 higher than that required to open wild type *MSL8*.

197

198 *MSL8* channel mutants do not complement *msl8-4* mutant phenotypes when expressed from genomic  
199 sequences.

200 To determine whether channel activity was required for *MSL8* to protect pollen from osmotic challenges,  
201 we tested whether *MSL8*<sup>I711S</sup> or *MSL8*<sup>F720L</sup> could complement previously characterized *msl8-4* mutant  
202 defects. The entire genomic sequence containing the *MSL8* gene (from 588 bp upstream of the ATG to 759

203 bp downstream of the stop codon) was cloned into a binary expression vector and the coding sequence for  
204 GFP inserted just before the *MSL8* stop codon. This construct, termed gMSL8-GFP, rescues the in vitro  
205 hydration viability defect of *msl8-4* pollen (Hamilton et al., 2015a). MSL8 variants were produced by site-  
206 directed mutagenesis of gMSL8-GFP. *gMSL8-GFP*, *gMSL8<sup>I711S</sup>-GFP* and *gMSL8<sup>F720L</sup>-GFP* transgenes  
207 were introduced into the null *msl8-4* mutant background via *Agrobacterium* transformation. Lines  
208 expressing wild type and mutant versions of *gMSL8-GFP* were generated and screened for expression of  
209 *MSL8* variants in floral RNA. Two independent homozygous transgenic lines expressing *gMSL8<sup>I711S</sup>-GFP*  
210 or *gMSL8<sup>F720L</sup>-GFP* and a single control line expressing wild type *gMSL8-GFP* were selected for further  
211 analysis. All lines selected accumulated *MSL8* transcripts at levels equal to or greater than the wild-type  
212 *Ler* (Fig. 2A). To confirm protein production, stability and subcellular localization, confocal images were  
213 taken of GFP signal in mature, desiccated pollen isolated from these lines. All five lines expressing *gMSL8-*  
214 *GFP* or variants in the *msl8-4* background exhibited GFP signal localized to both the plasma membrane  
215 and endomembrane compartments, as previously observed for MSL8-GFP (Fig. 2B; (Hamilton et al.,  
216 2015a). Untransformed *msl8-4* mutant pollen only exhibited autofluorescence of the cell wall.

217

218 To test the ability of MSL8<sup>I711S</sup> and MSL8<sup>F720L</sup> to protect *msl8-4* pollen from the hypoosmotic shock of  
219 rehydration, we quantified the viability of mature, desiccated pollen after rehydration in distilled water. Pollen  
220 was incubated in 30  $\mu$ l water with 1  $\mu$ g/ml fluorescein diacetate (FDA) and 0.5  $\mu$ g/ml propidium iodide (PI).  
221 FDA stains live pollen, while PI marks the outer membrane and cell wall of intact pollen and only  
222 accumulates inside compromised pollen. In a rehydration time course from 30 to 120 minutes, as expected,  
223 *Ler* pollen viability exceeded 80% at all time points, while *msl8-4* pollen exhibited less than 35% survival  
224 on average, and *msl8-4* pollen expressing wild type *gMSL8-GFP* exhibited wild-type survival at all time  
225 points (Fig. 3A). However, there were no differences between the viability of *msl8-4* pollen and *msl8-4*  
226 pollen expressing the *gMSL8<sup>I711S</sup>-GFP* or *gMSL8<sup>F720L</sup>-GFP* transgenes in water at 30, 60, or 120 minutes  
227 after hydration. Thus, neither MSL8<sup>I711S</sup> nor MSL8<sup>F720L</sup> could complement this *msl8-4* mutant phenotype.

228

229 To determine if MSL8<sup>I711S</sup> or MSL8<sup>F720L</sup> could protect *msl8-4* pollen from intermediate levels of hypoosmotic  
230 stress, we quantified pollen viability following a 30-minute incubation in a range of PEG<sub>3350</sub> concentrations.  
231 Supplementing hydration media with 15% PEG<sub>3350</sub> increased the average viability of *msl8-4* pollen from  
232 30% to 79% (Fig. 3B). PEG supplementation also increased the survival rate of *msl8-4* pollen expressing  
233 *gMSL8<sup>I711S</sup>-GFP* and *gMSL8<sup>F720L</sup>-GFP*, to a degree that was indistinguishable from that of the mutant *msl8-*  
234 *4* pollen across all levels of PEG (Fig. 3B). Thus, the *gMSL8<sup>I711S</sup>-GFP* and *gMSL8<sup>F720L</sup>-GFP* transgenes did  
235 not alter the sensitivity of *msl8-4* pollen to rehydration, even when osmotic supplementation was used to  
236 reduce the severity of the osmotic downshock.

237  
238 *msl8-4* pollen survives hydration in germination media, as it contains osmolytes (580 mOsmol), but exhibits  
239 increased germination rates and pronounced bursting when germinated *in vitro* (Hamilton et al., 2015a).  
240 We therefore quantified the germination and bursting rates of *msl8-4* pollen expressing *gMSL8<sup>I711S</sup>-GFP-*  
241 *and gMSL8<sup>F720L</sup>-GFP*. After incubation in germination media for 6 hours, most *Ler* pollen was ungerminated  
242 and intact; 8% was ungerminated and burst; 12% germinated and was intact; and 4% germinated and burst  
243 (Fig. 4, Supplementary Table S1). *msl8-4* pollen germinated at a similar rate to *Ler*, but 37% of  
244 ungerminated mutant pollen grains burst. Most of the *msl8-4* pollen that did germinate went on to burst,  
245 leaving only 49% intact pollen (compared to 89% for the wild type). While *msl8-4* pollen expressing *gMSL8-*  
246 *GFP* barely germinated or burst at all (< 0.5%) under these conditions, pollen expressing *gMSL8<sup>I711S</sup>-GFP*  
247 or *gMSL8<sup>F720L</sup>-GFP* had germination and bursting rates similar to *msl8-4* pollen. We thus found no evidence  
248 that MSL8<sup>I711S</sup> or MSL8<sup>F720L</sup> could substantially rescue known *msl8-4* loss-of-function phenotypes (Figs. 3-  
249 4), even though these variants were expressed at or above native levels and localized normally (Fig. 2).

250  
251 *MSL8<sup>I711S</sup> but not MSL8<sup>F720L</sup> partially rescues msl8-4 loss-of-function phenotypes when overexpressed.*  
252 To determine if we could detect partially functional channels if they were present at high levels, MSL8,  
253 MSL8<sup>I711S</sup> or MSL8<sup>F720L</sup> were tagged at the C-terminus with YFP and expressed under the control of the  
254 strong, pollen-specific promoter *LAT52* in the *msl8-4* background. We identified multiple independent  
255 homozygous lines that exhibited a range of transgene expression levels in floral RNA, from 1.9- to 9.6-fold



256 over the levels of endogenous *MSL8* in *Ler* (Fig. 5A). YFP signal in *msl8-4* pollen expressing *LAT52pMSL8-*  
257 *YFP* and variants localized to the plasma membrane and endomembrane compartments of mature pollen  
258 (Fig. 5B; Supplementary Fig. S2A), and the intensity of YFP signal correlated with transcript level as  
259 revealed by RT-PCR (compare Fig. 5A and Supplementary Fig. S2A).

260  
261 Pollen from *Ler* and *msl8-4* lines overexpressing *MSL8*, *MSL8<sup>I711S</sup>*, and *MSL8<sup>F720L</sup>* was incubated in distilled  
262 water for 30 or 120 minutes and viability quantified as in Fig. 3. All three *msl8-4 + LAT52pMSL8-YFP* lines  
263 survived as well as wild-type pollen at both time points, while the viability of *msl8-4* pollen expressing  
264 *LAT52pMSL8<sup>F720L</sup>-YFP* was indistinguishable from that of *msl8-4* in all three independent lines (Fig. 6).  
265 Thus, even at high levels of expression, *MSL8<sup>F720L</sup>* was unable to protect pollen from the hypoosmotic shock  
266 of rehydration. However, pollen from three *msl8-4 + LAT52pMSL8<sup>I711S</sup>-YFP* lines exhibited intermediate  
267 levels of pollen viability when hydrated in water. The level of protection was correlated with the level of  
268 *MSL8<sup>I711S</sup>* expression in each line. Two independent lines, I711S-7 and I711S-12, exhibited averages of  
269 44% to 63% survival during the time course. At both time points, I711S-7- and I711S-12 pollen viability was  
270 statistically significantly different from *Ler*, *msl8-4*, and the other transgenic lines, representing an  
271 intermediate phenotype. The strongest-expressing line, I711S-4 (Fig. 5A), exhibited wild-type pollen  
272 viability at both 30 and 120 minutes. Thus, *MSL8<sup>I711S</sup>* is able to partially rescue the *msl8-4* hydration viability  
273 defect when moderately overexpressed, while sufficiently high levels of expression fully complement the  
274 mutant phenotype.

275  
276 Next, we incubated pollen from *msl8-4 + LAT52pMSL8-YFP* and variant lines in germination media for 6  
277 hours and quantified germination and bursting rates (Fig. 7A). As expected, expression of *LAT52pMSL8-*  
278 *YFP* suppressed both germination and bursting rates of *msl8-4*, to less than 1%, while expression of  
279 *LAT52pMSL8<sup>F720L</sup>-YFP* did not (Fig. 7A, Supplementary Table S2). As with pollen rehydration,  
280 overexpression of *MSL8<sup>I711S</sup>* in the *msl8-4* background resulted in partial rescue of the loss-of-function  
281 phenotypes. Depending on the line, mutant pollen expressing *LAT52pMSL8<sup>I711S</sup>-YFP* germinated an  
282 average of 0% to 17%, and burst on average 4% to 36% of the time (much lower than the approximately

283 25% germination and 50% bursting of *msl8-4*). Both germination and bursting rates were inversely  
284 correlated to the level of *MSL8* accumulation in the *LAT52pMSL8<sup>I711S</sup>-YFP* line (compare Figs. 5A and 7A).  
285 The pattern of bursting and germination in the highest expressing line, I711S-4, was statistically  
286 indistinguishable from line WT-11 (Supplementary Table S2), indicating that *MSL8<sup>I711S</sup>* can fully  
287 complement when highly overexpressed.

288  
289 Because germination is suppressed so strongly by *MSL8* overexpression, we also incubated pollen in  
290 germination media for an extended period of time (overnight, or 16 hours), in order to maximize the number  
291 of germination events (Fig. 7B-C, Supplementary Fig. S2B). Under these conditions, 63% of *msl8-4* pollen  
292 germinated on average, compared to 44% of *Ler* pollen. The overexpression of *MSL8-YFP* in the *msl8-4*  
293 background strongly suppressed pollen germination, while the overexpression of *MSL8<sup>F720L</sup>-YFP* did not.  
294 The germination rate of *msl8-4* pollen was partially suppressed by expressing *LAT52pMSL8<sup>I711S</sup>-YFP*, with  
295 the strongest-expressing line, I711S-4, germinating 22% of the time and I711S-7 and I711S-12 germinating  
296 at rates comparable to *Ler*. This indicates that overexpression of *MSL8<sup>F720L</sup>* does not rescue the elevated  
297 germination and bursting rate of *msl8-4* pollen, and overexpression of *MSL8<sup>I711S</sup>* produces a partial  
298 reduction in both bursting and germination rates.

299  
300 We previously observed that overexpressing *MSL8* reduces pollen fertility, likely through the suppression  
301 of germination (Hamilton et al., 2015a). This fertility defect can be observed as a reduction in the  
302 transmission of the transgene from the hemizygous T1 generation to the segregating T2 generation, as  
303 determined by resistance to the herbicide Basta, which is conferred by the transgene. As expected, three  
304 lines expressing *LAT52pMSL8-YFP* in the *msl8-4* background exhibited a significant reduction in transgene  
305 transmission, reducing Basta resistance from the expected 75% to around 65%. However, none of the lines  
306 overexpressing *MSL8<sup>I711S</sup>-YFP* or *MSL8<sup>F720L</sup>-YFP* in the *msl8-4* background showed a significant deviation  
307 from the expected rate of resistance (Table 2). This indicates that neither *MSL8<sup>I711S</sup>* nor *MSL8<sup>F720L</sup>* have an  
308 effect on pollen fertility and suggests that the partial suppression of *in vitro* germination conferred by  
309 overexpressing *MSL8<sup>I711S</sup>-YFP* in the *msl8-4* background is insufficient to reduce pollen fertility *in vivo*.

310 Thus, while neither *MSL8<sup>F720L</sup>* nor *MSL8<sup>I711S</sup>* provide clear function in pollen when expressed at endogenous  
311 levels, *MSL8<sup>I711S</sup>* can provide some function when expressed at high levels.

312

313 *Overexpressing MSL8<sup>F720L</sup> in wild-type pollen increases bursting, while overexpressing MSL8 and*  
314 *MSL8<sup>I711S</sup> suppresses pollen germination.*

315 We also investigated the function of *MSL8<sup>I711S</sup>* and *MSL8<sup>F720L</sup>* when overexpressed in the wild type  
316 background, rather than in the *msl8-4* background as above. Transgenic *LAT52pMSL8-YFP*,  
317 *LAT52pMSL8<sup>F720L</sup>-YFP*, or *LAT52pMSL8<sup>I711S</sup>-YFP* lines were selected wherein *MSL8* or *MSL8* variants  
318 were expressed at levels similar to or higher than the endogenous *MSL8* gene (Fig. 8A). Quantitative RT-  
319 PCR revealed that transcript levels of endogenous *MSL8* were not significantly different from *Ler* in the  
320 transgenic lines (Fig. 8A, dark gray bars), while total *MSL8* transcripts were increased over endogenous  
321 levels between 1.3 and 4.3-fold (Fig. 8A, light gray bars).

322

323 Pollen from lines expressing *LAT52pMSL8-YFP* and *LAT52pMSL8<sup>I711S</sup>-YFP* did not germinate at all after  
324 incubation in germination media for 6 hours, and the bursting rate of ungerminated pollen grains was  
325 reduced to less than 7% (Fig. 8B). The pattern of pollen germination and bursting was indistinguishable  
326 between line WT-10 and the three lines overexpressing *MSL8<sup>I711S</sup>-YFP* as determined by a chi-squared  
327 test (Fig. 8B, Supplementary Table S3). However, *Ler* pollen expressing *LAT52pMSL8<sup>F720L</sup>-YFP* burst 46%  
328 to 54% of the time, comparable to the bursting rate of *msl8-4*. Thus, overexpressing *MSL8<sup>F720L</sup>* in the wild-  
329 type background produced a dominant negative effect, phenocopying the *msl8-4* mutant bursting rate. This  
330 elevated bursting rate is likely caused by *MSL8<sup>F720L</sup>* disrupting the native pool of *MSL8* through the formation  
331 of heteromeric channels (see discussion).

332

333 When incubated in germination media overnight, pollen overexpressing *MSL8<sup>F720L</sup>* in the *Ler* background  
334 germinated at rates between that of *Ler* and *msl8-4*, indicating that it had little, if any, effect (Fig. 8C).  
335 However, overexpressing *MSL8<sup>I711S</sup>* in the wild type background resulted in a partial suppression of  
336 germination rates, to between 9% and 18%. While line I711S-2 had a germination rate that was

337 indistinguishable from the pollen overexpressing wild type *MSL8*, the other two independent lines produced  
338 pollen germination rates that were both significantly lower than that of *Ler* and significantly higher than *Ler*  
339 + *LAT52pMSL8-YFP* lines, representing an intermediate phenotype.

340

341 We also quantified the effect of *MSL8* overexpression on male fertility in these lines via the segregation of  
342 resistance to Basta. Overexpressing *LAT52pMSL8-YFP* in the *Ler* background reduced Basta resistance  
343 in the segregating T2 generation from 75% to less than 65% (Table 3). One line expressing  
344 *LAT52pMSL8<sup>I711S</sup>-YFP* also exhibited a significant reduction in Basta resistance, to 59%, but all other *MSL8*  
345 variant lines did not. This indicates that *MSL8<sup>F720L</sup>* overexpression does not have an effect on pollen fertility,  
346 and suggests that the partial suppression of *in vitro* pollen germination produced by overexpressing  
347 *MSL8<sup>I711S</sup>* has only a modest effect *in vivo*.

## 348 Discussion

349 *The tension-sensitive ion transport activity of MSL8 is critical for its function in pollen.*

350 A role for MS ion channels in the response of pollen to mechanical and osmotic challenges was proposed  
351 more than 20 years ago (Feijo et al., 1995). Such a role has been solidly established for the canonical MS  
352 ion channel from *E. coli*, MscS (Edwards et al., 2005; Levin and Blount, 2004; Levina et al., 1999; Miller,  
353 2003; Sukharev et al., 1994), and an initial analysis suggested that a MscS homolog from Arabidopsis,  
354 MSL8, might as well (Hamilton et al., 2015a). In our previous study (Hamilton et al., 2015a), we found that  
355 *msl8-4* pollen does not survive the hypoosmotic shock of rehydration, germinates at higher rates than the  
356 wild type, and bursts more frequently—all suggesting that MSL8 is required for pollen to relieve excessive  
357 turgor pressure during fertilization. *MSL8* overexpression also leads to reduced germination rates and low  
358 fertility, probably because high levels of MSL8 leads to lower than normal turgor pressure within the pollen  
359 grain. We thus proposed that the levels of MSL8 must be carefully tuned in order to balance the need of  
360 pollen to protect against lysis during rehydration and germination, while maintaining sufficient turgor  
361 pressure for germination and pollen tube growth. These data are consistent with MSL8 directly mediating  
362 the flux of ions in order to control the osmotic potential of pollen. However, it remained possible that MSL8  
363 could play an indirect role in pollen, perhaps signaling independently of ion flux like close homolog MSL10  
364 (Veley et al., 2014). Here we used site-directed mutagenesis, electrophysiology, and physiological assays  
365 to determine if the critical function of the MS ion channel MSL8 during pollen hydration and germination is  
366 to mediate ion flux.

367

368 *Disrupting normal channel function prevents MSL8 from complementing known msl8-4 null loss-of-function*  
369 *phenotypes.*

370 We identified two point mutations that, when introduced into the presumptive pore-lining helix, altered MSL8  
371 channel behavior without appreciably altering expression, stability, or subcellular localization (Figs. 1, 2,  
372 Table 1). MSL8<sup>I711S</sup> required higher membrane tension to open than MSL8, but had wild-type conductance.  
373 While MSL8<sup>F720L</sup> produced MS currents that were never observed in water-injected oocytes, they did not  
374 form the step-wise increase in current characteristic of individual channel gating events, instead appearing

375 as a flickering increase in current that disappeared immediately after suction was released. MSL8<sup>F720L</sup> also  
376 required significantly higher membrane tension to open than MSL8 or MSL8<sup>I711S</sup>.

377

378 Our finding that MSL8<sup>F720L</sup> was unable to rescue *msl8-4* loss-of-function phenotypes either at native levels  
379 of expression (Figs. 2-4) or when overexpressed (Figs. 5-7) demonstrated that a functional channel is  
380 necessary for MSL8 to protect pollen from the osmotic stress it experiences during hydration and  
381 germination. This supports a model where MSL8 functions akin to MscS, acting as an osmotic pressure  
382 release valve (Booth and Blount, 2012), albeit during developmentally programmed osmotic challenges  
383 rather than in response to environmental swings in osmolarity. During pollen germination and tube growth,  
384 which are powered by internal turgor pressure (Benkert et al., 1997; Zerzour et al., 2009), pollen must have  
385 multiple mechanisms to ensure that internal pressure and growth rates do not overtake the delivery of cell  
386 wall materials to the growing tip or the strength of the cell wall itself (Hill et al., 2012; Kroeger et al., 2011;  
387 Zerzour et al., 2009); MSL8 appears to be one of those mechanisms.

388

389 *Increasing the tension threshold of the MSL8 channel reduces its physiological activity in pollen.*

390 MSL8<sup>I711S</sup> could only protect pollen from the hypoosmotic shock of rehydration and maintain the integrity of  
391 the pollen tube when overexpressed, and did not suppress pollen germination as strongly as the wild type.  
392 (Figs. 6-8). We propose that the precise tension threshold and conductance characteristics of MSL8 are  
393 critical for its ability to balance the need of pollen to maintain sufficient turgor pressure for germination and  
394 pollen tube growth while protecting against lysis during rehydration and germination. According to this view,  
395 the elevated tension threshold of MSL8<sup>I711S</sup> would both reduce its ability to protect pollen from bursting and  
396 prevent it from strongly suppressing germination when overexpressed.

397

398 Although the evidence described above is consistent with MSL8 functioning like an osmotic safety valve,  
399 we note that we cannot exclude the possibility that the ion flow across MSL8 could act as a biochemical  
400 signal that indirectly achieves the same function. It also remains formally possible, though unlikely, that the  
401 Ile711Ser or Phe720Leu mutations affect both the characteristics of the channel and the function of other

402 domains important for signaling independent of ion transport. Lesions in both the soluble N-terminus (Veley  
403 et al., 2014) and the soluble C-terminus (Zou et al., 2015) affect the cell death signaling function of MSL10,  
404 but lesions to the predicted pore-lining domain have not yet been tested. Future work will be required to  
405 understand how MSL8 functions alongside established ion channels and the tightly regulated ion fluxes that  
406 are essential for pollen germination and tube growth (Michard et al., 2009).

407

408 *MSL8<sup>F720L</sup> has reduced channel activity and can act as a dominant negative allele.*

409 MSL8<sup>F720L</sup> conducts ions through its pore, but appears unable to form a stable open state or to transition  
410 normally between non-conducting and conducting configurations. (Fig. 1B, bottom left panel,  
411 Supplementary Fig. S1, Table 1). The closed form of *EcMscS* is proposed to involve close packing of small  
412 residues from adjoining pore-lining domains (Edwards et al., 2005). The substitution of large hydrophobic  
413 residues for Gly or Ala at these positions results in less stable open state configurations with higher tension  
414 thresholds, that at least superficially resemble MSL8<sup>F720L</sup> (Edwards et al., 2005; Rasmussen et al., 2015;  
415 Wu et al., 2011). Alternating chains of small hydrophobic amino acids are not observed in the predicted  
416 pore-lining domain of MSL8 (Fig. 1B). Rather, a repeating pattern of large hydrophobic/polar residues in  
417 the predicted pore-lining domain is conserved among the seven *Arabidopsis* MscS homologs predicted to  
418 localize to the plasma membrane. These residues include three phenylalanines at positions 710, 720 and  
419 727 (marked with arrowheads, Supplementary Fig. S3). The observed channel characteristics of MSL8<sup>F720L</sup>  
420 suggest that the pairing of similarly sized residues in the pore-lining domains may be an important factor in  
421 maintaining the stability and normal function of both MscS and MSLs. Testing this idea will require additional  
422 study, in particular detailed structural information for the plasma membrane-localized MSLs.

423

424 Expressing *MSL8<sup>F720L</sup>* in a wild type background, and therefore in the presence of a native pool of MSL8,  
425 phenocopies the *msl8-4* mutant with respect to germination rate and pollen tube bursting (Fig. 8B-C).  
426 Because MSLs are likely to form homomeric channels (Haswell et al., 2008; Peyronnet et al., 2008), this  
427 dominant negative effect may be caused by the formation of heteromeric channel complexes. According to  
428 this model, the instability caused by the Phe720Leu mutation is dominantly imparted to MSL8-MSL8<sup>F720L</sup>

429 heteromeric channels, reducing the number of functional MSL8 channels available, and thereby producing  
430 pollen with characteristics similar to those from the loss-of-function *msl8-4* background. A similar effect was  
431 described for the *Caenorhabditis elegans* TRP-4 candidate MS ion channel (Kang et al., 2010). A TRP-4  
432 mutant that did not form a functional channel on its own dominantly ablated channel function when co-  
433 expressed with wild type TRP-4 in touch-sensitive neurons. How many MSL8<sup>F720L</sup> monomers are sufficient  
434 to disrupt the function of an otherwise wild type MSL8 channel is not yet known.

435

436 *MSL8<sup>I711S</sup> can complement the msl8-4 mutant only when overexpressed*

437 MSL8 Ile711 aligns with Ala110 of *EcMscS* (Fig. 1B), and a mutation in the neighboring residue, Leu111,  
438 produces a similar disruption in function. In *EcMscS*, Leu111Ser is associated with a doubled tension  
439 threshold, and MscS<sup>L111S</sup> is unable to protect *E. coli* against osmotic shock (Belyy et al., 2010). Leu111 is  
440 part of the proposed “tension-transmitting clutch” that allows *EcMscS* to respond to increases in membrane  
441 tension through hydrophobic associations with the other TM helices. The substitution of a hydrophilic  
442 residue for a hydrophobic one may weaken these interactions. Our data presented here show that Ile711  
443 may play a similar force-transmitting role in MSL8. Once open, MSL8<sup>I711S</sup> appears to produce a normal  
444 pore, as its single-channel conductance was wild type.

445

446 There are several possible explanations for the ability of MSL8<sup>I711S</sup> to partially rescue loss-of-function  
447 phenotypes at high levels of expression. First, the gating of a MS ion channel is a stochastic process  
448 centered on the average tension threshold (Hille, 1992). Increasing the population of MSL8<sup>I711S</sup> channels  
449 in pollen would increase the number of channels available in the population to open at lower tensions,  
450 potentially to levels sufficient for protection against osmotic stress. Alternatively, MSL8 could participate in  
451 cooperative gating, the lowering of the average tension threshold as the number of channels embedded in  
452 the membrane increases. Biophysical modeling experiments with MscL show that local deformation of the  
453 lipid bilayer at the channel periphery caused by flattening during the transition to the open state could  
454 explain the energetics of cooperative gating (Haselwandter and Phillips, 2013; Ursell et al., 2007). While



455 flattening has not been observed for MscS family members, cooperative gating could occur through a  
456 different mechanism.

457

458 Regardless of the mechanism, overexpressing MSL8<sup>I711S</sup> appears to result in an effective lowering of the  
459 membrane tension required for gating, increasing its ability to regulate osmotic potential in pollen. Lowering  
460 the tension threshold could also explain the observation that overexpressing wild-type MSL8 in the *Ler*  
461 background suppresses pollen germination (Fig. 8B, (Hamilton et al., 2015a)). If overexpression results in  
462 MSL8 channel activity at lower membrane tensions, then the critical turgor for germination might never be  
463 reached. Pollen would then be stuck in a futile cycle of building pressure, relieving pressure, and building  
464 it again. In support of this idea, we observed that pollen overexpressing MSL8 developed the larger and  
465 more structured vacuole morphology resembling normally germinating pollen (Supplementary Fig. S4;  
466 (Hicks et al., 2004; Wudick et al., 2014)), though it rarely went on to germinate. Additional work is needed  
467 to determine if overexpressing MSL8<sup>I711S</sup> lowers its effective tension threshold, and if so, to identify the  
468 mechanism by which this occurs.

469

470 *MSL8 could contribute to established anion fluxes in pollen.*

471 As MSL8 has an approximately 6-fold preference for conducting Cl<sup>-</sup> over Na<sup>+</sup> (Hamilton et al., 2015a), it  
472 might contribute to the anion fluxes previously observed in rehydrating pollen and growing pollen tubes.  
473 Pollen grains efflux Cl<sup>-</sup> immediately after rehydration and for several minutes afterward, both in vitro and in  
474 vivo (Breygina et al., 2009; 2012; Matveyeva et al., 2003). Although the efflux of Cl<sup>-</sup> during rehydration could  
475 be due in part to unregulated leakage through the plasma membrane as it reorganizes in the hydrated state  
476 (Hoekstra et al., 1999; 1992), it is largely blocked by anion channel inhibitors (Breygina et al., 2009; 2012;  
477 Matveeva et al., 2003), suggesting that the majority of Cl<sup>-</sup> ions exiting the cell during rehydration do so  
478 through channels.

479

480 During pollen tube growth, chloride efflux at the tip oscillates along with growth rate (Zonia et al., 2001;  
481 2002). Pharmacological inhibition of Cl<sup>-</sup> efflux disrupts pollen tube growth, increases the volume of the tube

482 apex, and frequently induces pollen tube bursting at the tip (Breygina et al., 2009; Zonia et al., 2001; 2002),  
483 implicating this Cl<sup>-</sup> flux in the control of osmotic potential. More recent studies have supported a role for  
484 Ca<sup>2+</sup>-regulated Cl<sup>-</sup> channels in these fluxes (Gutermuth et al., 2013; Tavares et al., 2011b), but MSL8 may  
485 contribute to the net Cl<sup>-</sup> flux through a membrane tension-regulated, rather than Ca<sup>2+</sup>-regulated, pathway.

486

487 We note that an electrophysiological survey in lily failed to find Cl<sup>-</sup> channels of any kind in pollen grain  
488 protoplasts, and MS cation channel activity was only observed after extended incubation in pollen  
489 germination media (Dutta and Robinson, 2004). This discrepancy could be due to the limitations of the cell-  
490 attached electrophysiological method (Tavares et al., 2011a), as we have observed a MS Cl<sup>-</sup> channel active  
491 in pollen protoplasts (Hamilton et al., 2015a).

492

493 *MSL8 fulfills all criteria for assignment as a mechanotransducer.*

494 The four criteria necessary for establishing a protein as the transducer of a physiological mechanical  
495 response are: (1) it is expressed in the correct cell and subcellular location to respond to mechanical  
496 stimulation; (2) it is required for the mechanosensory response, not the normal development of the cell; (3)  
497 it forms a MS channel in a heterologous system; and (4) structural changes that affect the protein's  
498 response in a heterologous system affect its function *in vivo* (Arnadottir and Chalfie, 2010). MscL and MscS  
499 in bacteria fulfill these criteria (Edwards et al., 2005; Levin and Blount, 2004; Levina et al., 1999; Miller,  
500 2003; Sukharev et al., 1994), and NOMPC of *Drosophila* was recently shown to be a mechanotransducer  
501 of touch response in touch-sensitive neurons (Gong et al., 2013; Yan et al., 2013).

502

503 MSL8 now fulfills all four criteria: (1) it is expressed in tricellular and mature pollen and pollen tubes, and  
504 localizes to the plasma membrane; (2) it is not required for the normal development of pollen, but is required  
505 for protection against osmotic stress; (3) it forms a MS channel in the heterologous *Xenopus* oocyte system;  
506 and (4) altering its structure changes its electrophysiological characteristics and its physiological function,  
507 without affecting expression or subcellular localization.

508

509 Pollen faces additional, relatively unstudied mechanical challenges during its development, and  
510 mechanically sensitive proteins are likely to be involved. Desiccation is critical for the success of pollen  
511 from most species (Franchi et al., 2011), and presents unique osmotic and mechanical challenges (Firon  
512 et al., 2012; Hoekstra et al., 1997; 2001). Furthermore, as it invades the sporophytic tissue to reach the  
513 female gametophyte, the pollen tube must sense, produce, and regulate the forces required to grow in  
514 between other cells (Sanati Nezhad et al., 2013). Finally, the regulated process of bursting that must occur  
515 to release the sperm cells from within the pollen tube represents a fascinating case where mechanisms that  
516 previously maintained the structural integrity of the cell must be overcome in order to complete fertilization  
517 (Amien et al., 2010; Dresselhaus et al., 2016; Woriedh et al., 2013). Using electrophysiology, mutagenesis  
518 and physiological assays, we discovered that mechanosensitive ion channels are one mechanism pollen  
519 relies on to respond to the mechanical effects of osmotic changes. This powerful combination of techniques,  
520 as well as the development of new tools to probe pollen in the dry state, may uncover other mechanical  
521 and ionic regulation strategies in pollen and other plant cells.

## 522 **Materials and Methods**

523

524 *Plant material and growth conditions.* Plants were grown on soil under 24 hours of light at 21°C. *msl8-4*  
525 (DsLoxN101568 and DsLoxN101751, in the *Ler* background) was obtained from the Arabidopsis Biological  
526 Resource Center. MSL8<sup>I711S</sup> and MSL8<sup>F720L</sup> constructs were produced through site-directed mutagenesis  
527 from existing vectors (described in (Hamilton et al., 2015)) and transformed into *msl8-4* or *Ler* by floral dip.

528

529 *Multiple alignments.* Alignments were performed in MEGA7 using a Clustal alignment with a pairwise  
530 alignment gap opening penalty of 10 and gap extension penalty of 0.1 and a multiple alignment gap opening  
531 penalty of 10 and gap extension penalty of 0.2. Sequences for alignment were based on previous  
532 phylogenetic analysis of *EcMscS* and Arabidopsis MSLs (Haswell, 2007) predicting the pore-lining domains  
533 of MSLs based on the known pore-lining domain of *EcMscS*.

534

535 *Electrophysiology.* Single channel patch-clamp electrophysiology was performed as described in (Maksaev  
536 and Haswell, 2015). Capped RNA (cRNA) of *MSL8* was transcribed *in vitro* using the mMESSAGING  
537 mMACHINE SP6 kit (Ambion) and stored at 1µg/µl at -80 °C. Defolliculated oocytes were purchased from  
538 Xenopus1 (Dexter, MI) and injected with 50 nl of cRNA or water and patched in symmetric 60 mM MgCl<sub>2</sub>  
539 after incubating for 2-10 days in ND96 buffer + gentamycin.

540

541 *Reverse-transcriptase-polymerase chain reaction.* RNA was isolated from floral tissue (stage 13/14 flowers)  
542 using the Qiagen RNeasy Mini RNA extraction kit (Qiagen). cDNA was generated from 2 µg RNA using an  
543 oligo(dT)<sub>20</sub> primer and the M-MLV Reverse Transcriptase kit (Promega). *ACTIN*, total *MSL8*, endogenous  
544 *MSL8* and *MSL8-YFP* transcripts were amplified with the primers listed in Supplementary Table S4 using  
545 SYBR Green PCR Master Mix (Applied Biosciences) and 0.25 µL cDNA at a final volume of 25 µL.  
546 Quantitative RT-PCR was performed using the StepOnePlus real-time PCR system (Applied Biosystems).  
547 Total *MSL8* was amplified using primers that do not distinguish between the endogenous locus and the

548 transgenes. Endogenous *MSL8* was amplified using a reverse primer in the 3' UTR, which is not present in  
549 the transgenes.

550

551 *In vitro pollen hydration.* Pollen from mature (stage 13-14) flowers was hydrated in 25-30  $\mu$ l drops of water  
552 or the indicated percentage of PEG (average molecular weight 3350 g/mol, Sigma-Aldrich) at a final  
553 concentration of 1  $\mu$ g/ml fluorescein diacetate (FDA, Sigma-Aldrich) and 0.5  $\mu$ g/ml propidium iodide (PI,  
554 Sigma-Aldrich) on double-ring cytology slides. Slides were inverted and incubated in a humid chamber at  
555 room temperature for the indicated amount of time. To image, cover slips were added and FDA signal was  
556 collected in the GFP epifluorescence channel while PI signal was collected in the dsRed epifluorescence  
557 channel. FDA stains live pollen while PI enters dead pollen.

558

559 *In vitro pollen germination.* Pollen germination was performed according to (Daher, Chebli, Geitmann 2009  
560 Plant Cell Rep). Pollen was pre-hydrated by removing flowers from plants and incubating for 45 minutes at  
561 30°C in a humid chamber constructed from a large petri dish containing smaller petri dishes placed on top  
562 of moistened filter paper. Pollen was incubated in 30  $\mu$ l of pollen germination media (2 mM  $\text{CaCl}_2$ , 2 mM  
563  $\text{Ca}(\text{NO}_3)_2$ , 0.49 mM  $\text{H}_3\text{BO}_3$ , 1 mM  $\text{MgSO}_4$ , 1 mM KCl, 18% w/v sucrose, pH 7) at 30°C for 6 or 16 hours in  
564 a humid chamber as during pollen hydration. Pollen was counted as germinated if it had produced a pollen  
565 tube longer than the pollen grain. Pollen was counted as burst if expelled cytoplasm was visible outside the  
566 pollen grain or pollen tube.

567

568 *Microscopy.* Confocal images of GFP or YFP signal in pollen were acquired on an Olympus BX-61  
569 microscope using FV10-ASW Olympus software and the GFP (488 nm excitation, 505-605 nm bandpass  
570 filter) or YFP (515 nm excitation, 535-565 nm bandpass filter) channels. Brightfield and epifluorescent  
571 images for pollen germination and pollen viability assays were collected on the same microscope using an  
572 Olympus DP71 digital camera, DP Controller software, and filter sets for GFP (470/40 nm excitation, 525/50  
573 nm emission) or dsRED (545/30 nm excitation, 620/60 nm emission).

574

575 *Calculation of transmission ratios.* The transmission frequencies of the *MSL8* transgenes were determined  
576 by selecting seedlings from the T2 generation with Basta on soil and counting the number of sensitive and  
577 resistant progeny. The Basta resistance gene *bar* is included in the transgene.

578  
579 *Statistical analyses.* One-way or two-way ANOVAs were performed as indicated in figure legends. Tukey's  
580 HSD post-hoc test was used to determine statistical significance for balanced data sets. Scheffe's post-hoc  
581 test was used to determine statistical significance for unbalanced data sets. Chi-squared tests with  
582 Bonferroni correction were performed for analysis of transgene transmission and for comparison between  
583 groups of the pattern of germinated and burst pollen during pollen germination assays.

584

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588

#### 589 **Disclosures**

590 The authors have no conflicts of interest to declare.

591

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595

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- 788

789 **Tables**

790

791 **Table 1. Conductance, tension threshold, and number of observations of MSL8 variants in *Xenopus***792 **oocytes**

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798

	Conductance	Tension Threshold		Patches with activity / total patches
		First channel to open, mmHg	Last channel to close, mmHg	
MSL8	60.0	-18.9 ± 13.1	-1.7 ± 3.5	23/26
MSL8 <sup>I711S</sup>	60.7	-29.5 ± 11.7	-9.4 ± 9.5	27/32
MSL8 <sup>F720L</sup>	NA	-61.2 ± 12.3	-52.7 ± 11.5	20/24
Water	NA	NA	NA	0/26

799 Table 2. Transmission of *LAT52pMSL8-YFP* variant transgenes in the *msl8-4* background

800

<i>msl8-4 + LAT52pMSL8-YFP</i>	T2 progeny resistant to Basta				
	Line	% Expected	% Observed (number observed/total)	$\chi^2$	p
<i>MSL8</i>	1	75	67.2 (86/128)	5.18	0.023
	14	75	66.1 (74/112)	5.79	0.016
	11	75	64.0 (80/125)	9.52	0.002
<i>MSL8<sup>F720L</sup></i>	1	75	78.3 (47/60)	0.23	0.64
	10	75	74.4 (29/39)	0.05	0.83
	2	75	75.9 (41/54)	0.01	0.94
<i>MSL8<sup>I711S</sup></i>	7	75	74.0 (91/12)	0.23	0.64
	12	75	76.7 (89/116)	0.07	0.79
	4	75	74.1 (86/116)	0.18	0.67

801 Table 3. Transmission of *LAT52pMSL8-YFP* variant transgenes in the wild-type background

802

<i>Ler</i> + <i>LAT52pMSL8-YFP</i>	Line	T2 progeny resistant to Basta			
		% Expected	% Observed (number observed/total)	$\chi^2$	p
<i>MSL8</i>	10	75	60.0 (30/50)	6.00	0.014
	27	75	63.9 (53/83)	5.50	0.019
<i>MSL8<sup>F720L</sup></i>	5	75	78.9 (30/38)	0.32	0.57
	6	75	67.3 (66/98)	3.06	0.080
	9	75	76.9 (40/52)	0.10	0.75
<i>MSL8<sup>I711S</sup></i>	1	75	58.6 (34/58)	8.30	0.0040
	2	75	65.6 (40/61)	2.89	0.089
	4	75	72.3 (34/47)	0.18	0.67

803 **Figure Legends**

804

805 **Figure 1. Mutations in the predicted pore-lining domain alter channel properties of MSL8. (A)**

806 Predicted topology of MSL8. N and C mark the amino- and carboxy-terminal ends respectively. Thick line  
 807 marks the predicted pore-lining domain. Residues mutated in this study are indicated. **(B)** Multiple alignment  
 808 of the predicted pore-lining transmembrane regions of Arabidopsis MSL8, Arabidopsis MSL10 and the  
 809 known pore-lining domain of *E. coli MscS*. Identical residues conserved in at least half of the sequences  
 810 are shaded darkly; similar residues conserved at this level are shaded in gray. Residues proposed to form  
 811 the channel seal in *EcMscS* are marked with arrowheads. MSL8 residues mutated in this study are marked  
 812 with an asterisk. **(C)** Representative traces from excised inside-out patches of plasma membrane from  
 813 *Xenopus laevis* oocytes following injection with the indicated cRNA or water clamped at -40 mV membrane  
 814 potential. **(D)** The current-voltage relationship of MSL8 (squares,  $N = 4$  oocytes) and MSL8<sup>I711S</sup> (triangles,  
 815  $N = 9$  oocytes) in symmetric 60 mM MgCl<sub>2</sub>. Dashed line indicates the slope from which the single-channel  
 816 conductance was measured (see Table 1). Error bars are mean  $\pm$  SE.

817

818 **Figure 2. Expression and subcellular localization of MSL8-GFP expressed from endogenous**

819 **sequences. (A)** Quantitative reverse-transcription polymerase chain reaction amplification of *MSL8*  
 820 transcripts in *Ler*, *msl8-4*, and *gMSL8-GFP* transgenic lines. Levels are presented relative to *ACTIN*.  
 821 Different letter groups indicate significant ( $p < 0.05$ ) differences between groups as determined by Tukey's  
 822 post-hoc test following one-way ANOVA. Error bars are mean  $\pm$  SE of three biological and two technical  
 823 replicates. **(B)** Confocal images of GFP signal in pollen from stage 13-14 flowers from the indicated lines  
 824 hydrated in water. Arrowheads mark GFP signal at the plasma membrane. Scale bar is 20  $\mu$ m.

825

826 **Figure 3. MSL8<sup>I711S</sup>-GFP and MSL8<sup>F720L</sup>-GFP do not complement the *msl8-4* hydration viability defect**

827 **when expressed from endogenous sequences. (A)** Hydration viability time course. Mature, desiccated  
 828 pollen from *msl8-4* + *gMSL8-GFP* and variant lines hydrated in distilled water for the indicated periods of  
 829 time. Viability was determined by staining with fluorescein diacetate (which marks live pollen) and propidium

830 iodide (which enters compromised cells). The average of 3-6 experiments with  $N = 58 - 377$  pollen grains  
831 per experiment is shown. **(B)** Hydration viability in PEG<sub>3350</sub> series. The average of 3-9 experiments with  $N$   
832 = 68-566 pollen grains per experiment is presented. Different letter groups indicate significant ( $p < 0.05$ )  
833 differences between groups as determined by Scheffe's post-hoc test following two-way ANOVA. Error bars  
834 are mean  $\pm$  SE.

835

836 **Figure 4. MSL8<sup>I711S</sup>-GFP and MSL8<sup>F720L</sup>-GFP do not suppress *msl8-4* pollen bursting or germination**  
837 **when expressed from endogenous sequences.** Mature, desiccated pollen from the indicated lines were  
838 incubated in germination media for 6 hours then examined under the microscope. Each pollen grain scored  
839 was placed into one of the four indicated categories. Pollen was counted as germinated if it had produced  
840 a pollen tube longer than the pollen grain. Pollen was counted as burst if expelled cytoplasm was visible.  
841 Averages from 3-6 experiments with  $N = 101-236$  pollen per experiment are presented. See Supplementary  
842 Table 1 for statistical differences between groups. Error bars are mean  $\pm$  SE.

843

844 **Figure 5. Expression and subcellular localization of MSL8<sup>I711S</sup>-YFP and MSL8<sup>F720L</sup>-YFP expressed**  
845 **from the *LAT52* promoter in the *msl8-4* background. (A)** Quantitative reverse-transcription polymerase  
846 chain reaction amplification of *MSL8* transcripts, presented relative to *ACTIN*, in *Ler*, *msl8-4*, and *msl8-4 +*  
847 *LAT52pMSL8-YFP* transgenic lines. Error bars are mean  $\pm$  SE. **(B)** Confocal images of YFP signal in *msl8-*  
848 *4* pollen or *msl8-4* pollen expressing *LAT52pMSL8-YFP*, *LAT52pMSL8<sup>I711S</sup>-YFP*, or *LAT52pMSL8<sup>F720L</sup>-*  
849 *YFP*. Arrowheads mark GFP signal at the plasma membrane. Arrowheads mark GFP signal at the plasma  
850 membrane. Note that the autofluorescent cell wall is only visible in untransformed *msl8-4* pollen, which was  
851 imaged at higher laser power than the transgenic lines. Scale bars are 20  $\mu$ m.

852

853 **Figure 6. MSL8<sup>I711S</sup>-YFP but not MSL8<sup>F720L</sup>-YFP partially rescues the *msl8-4* hydration viability defect**  
854 **when overexpressed in the *msl8-4* background.** Hydration viability time course, performed as described  
855 in Fig. 3. The average of 3 to 4 experiments with  $N = 124$  to 354 pollen per experiment is presented.



856 Different letter groups indicate significant ( $p < 0.05$ ) differences between groups as determined by Scheffe's  
857 post-hoc test following two-way ANOVA. Error bars are mean  $\pm$  SE.

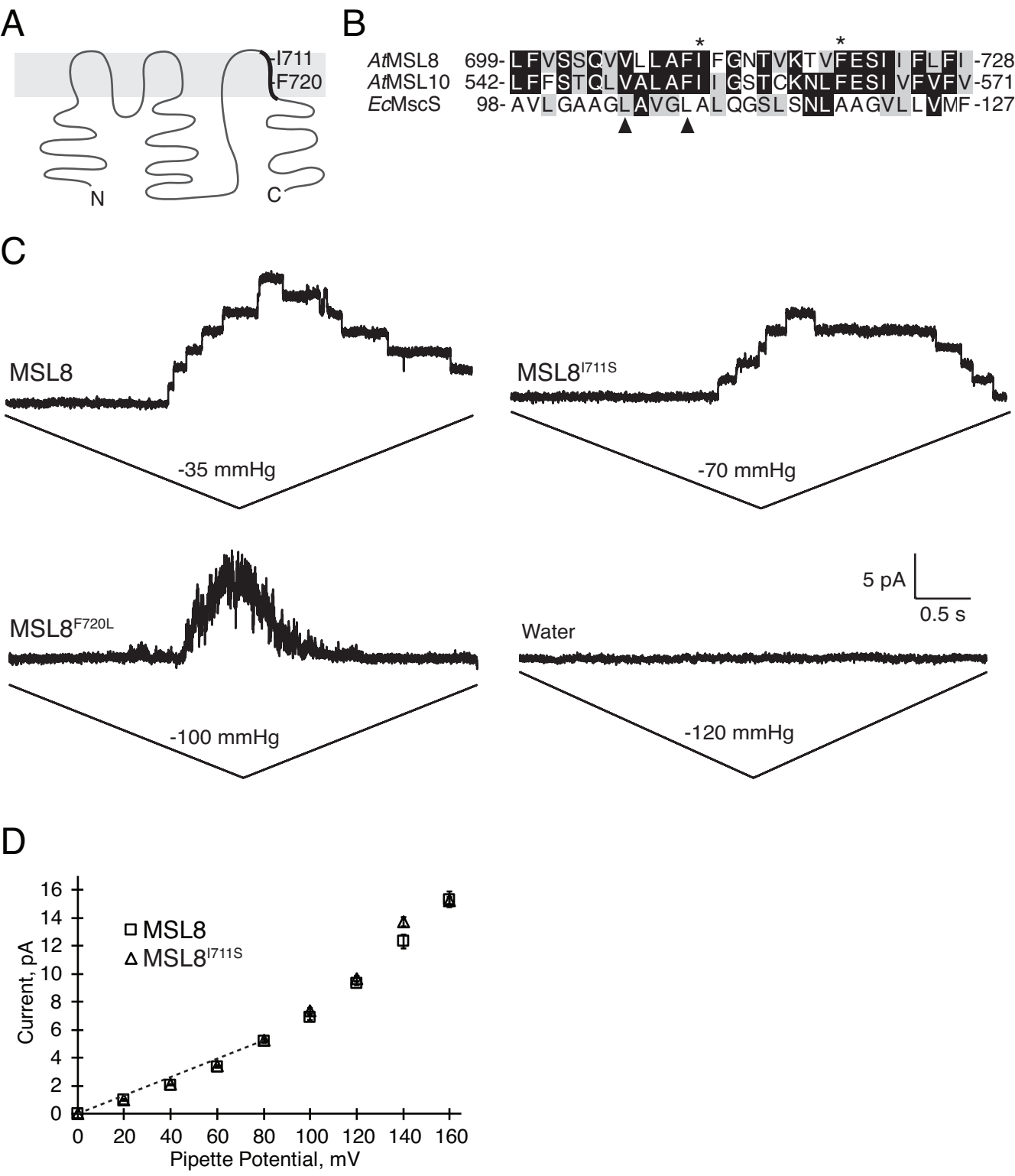
858

859 **Figure 7. MSL8<sup>I711S</sup>-YFP but not MSL8<sup>F720L</sup>-YFP partially suppresses *msl8-4* pollen bursting and**  
860 **germination when overexpressed in the *msl8-4* background. (A)** Pollen from the indicated lines  
861 incubated in germination media for 6 hours and scored for combined germination and bursting categories  
862 as in Fig. 4. Average of 3 to 6 experiments with  $N = 107$  to 512 pollen per experiment. See Supplementary  
863 Table 2 for statistical differences between groups. **(B)** Germination rate of pollen from the indicated lines  
864 after incubation in germination media for 16 hours. Different letter groups indicate significant ( $p < 0.05$ )  
865 differences between groups as determined by Tukey's post-hoc test following one-way ANOVA. **(C)**  
866 Brightfield images of pollen from the indicated lines after incubation for 16 hours in liquid germination media.  
867 Scale bars are 50  $\mu\text{m}$ . **(A, B)** Error bars are mean  $\pm$  SE.

868

869 **Figure 8. Effect of overexpressing MSL8-YFP variants from the *LAT52* promoter in the wild type**  
870 **background on germination phenotypes. (A)** Quantitative reverse-transcription polymerase chain  
871 reaction of endogenous *MSL8*, *MSL8-YFP*, and total *MSL8* transcripts relative to *ACTIN* in *Ler*, *msl8-4*, and  
872 *LAT52pMSL8-YFP* transgenic lines. **(B)** Pollen from the indicated lines incubated in germination media for  
873 6 hours and scored for combined germination and bursting categories as in Fig. 4. Averages from 3  
874 experiments with  $N = 82$  to 250 pollen per experiment are presented. See Supplementary Table 3 for  
875 statistical differences between groups. **(C)** Germination rate of pollen from the indicated lines after  
876 incubation in germination media for 16 hours. Averages of 3 experiments with  $N = 99$  to 257 pollen per  
877 experiment are presented. Different letter groups indicate significant ( $p < 0.05$ ) differences between groups  
878 as determined by Tukey's post-hoc test following one-way ANOVA. **(A-C)** Error bars are mean  $\pm$  SE.

FIGURE 1



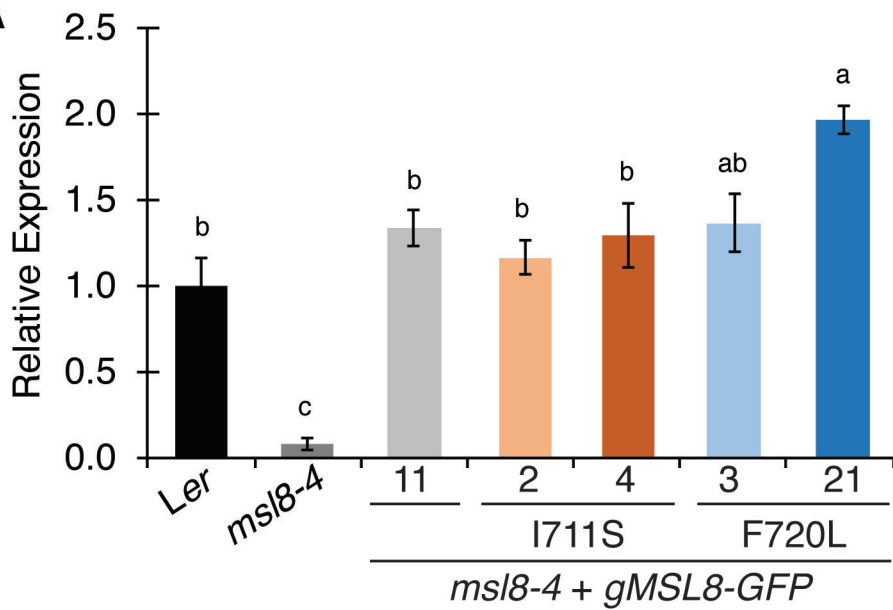
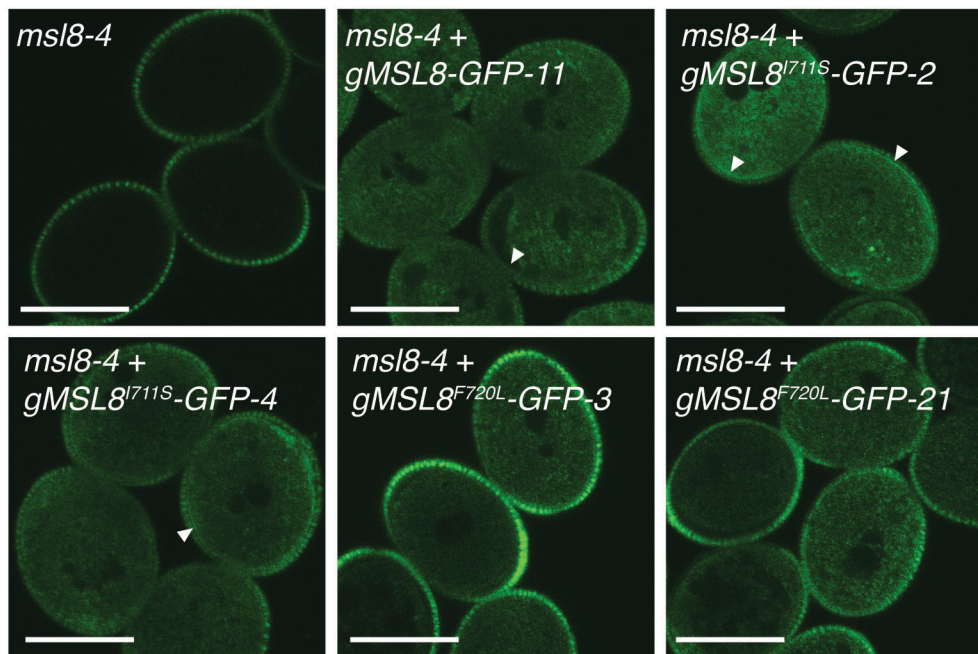
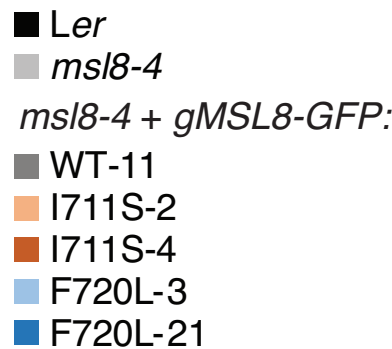
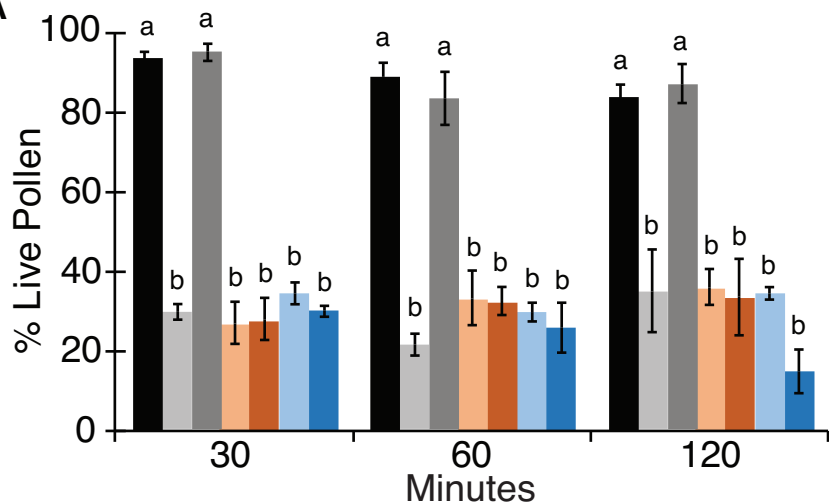
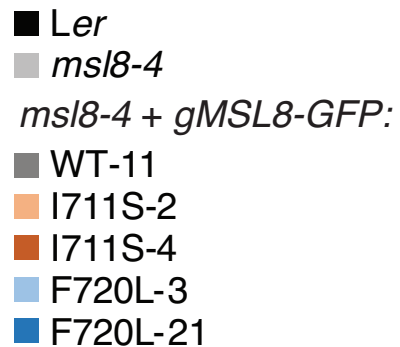
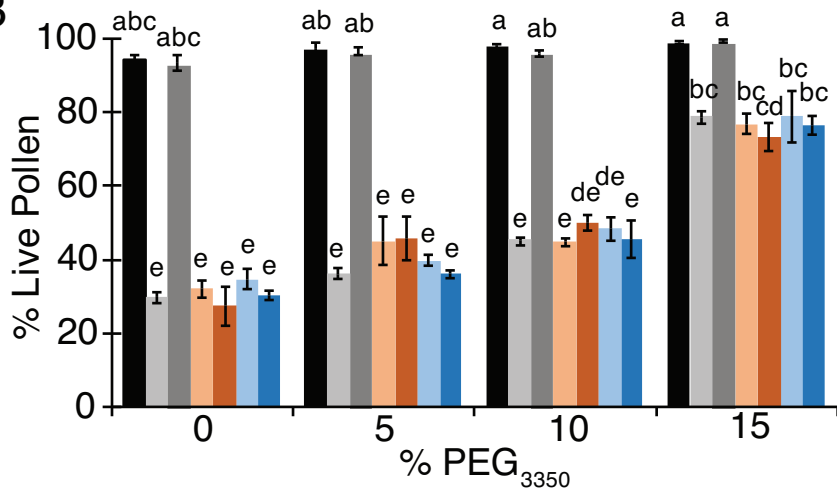
**A****B**

FIGURE 3

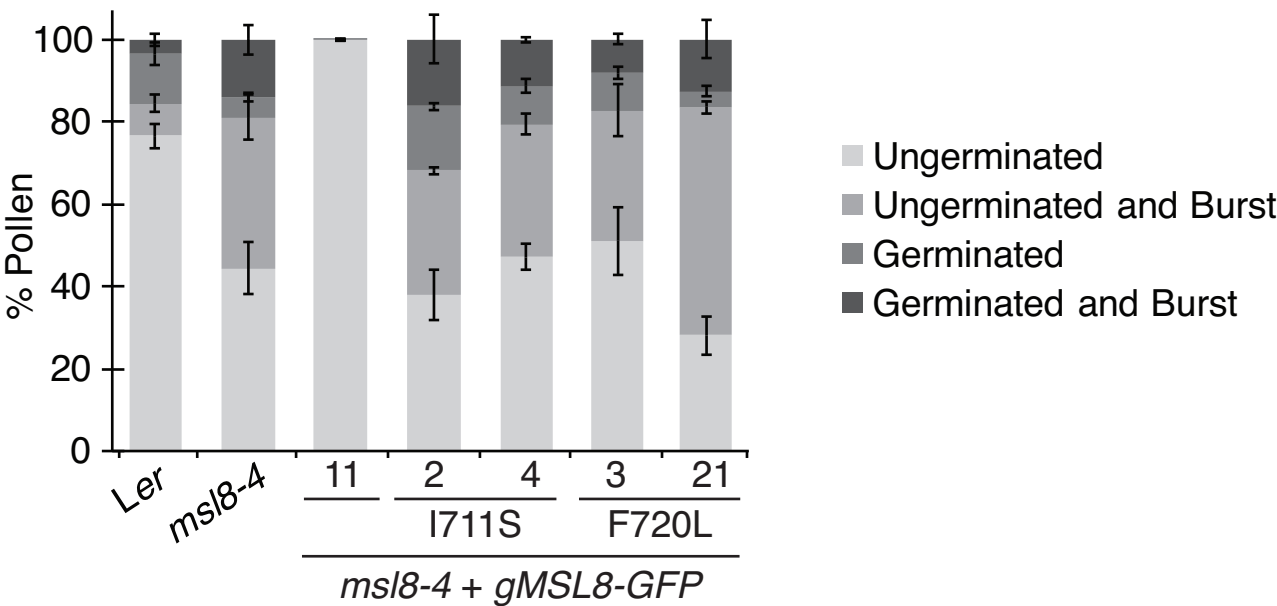
A

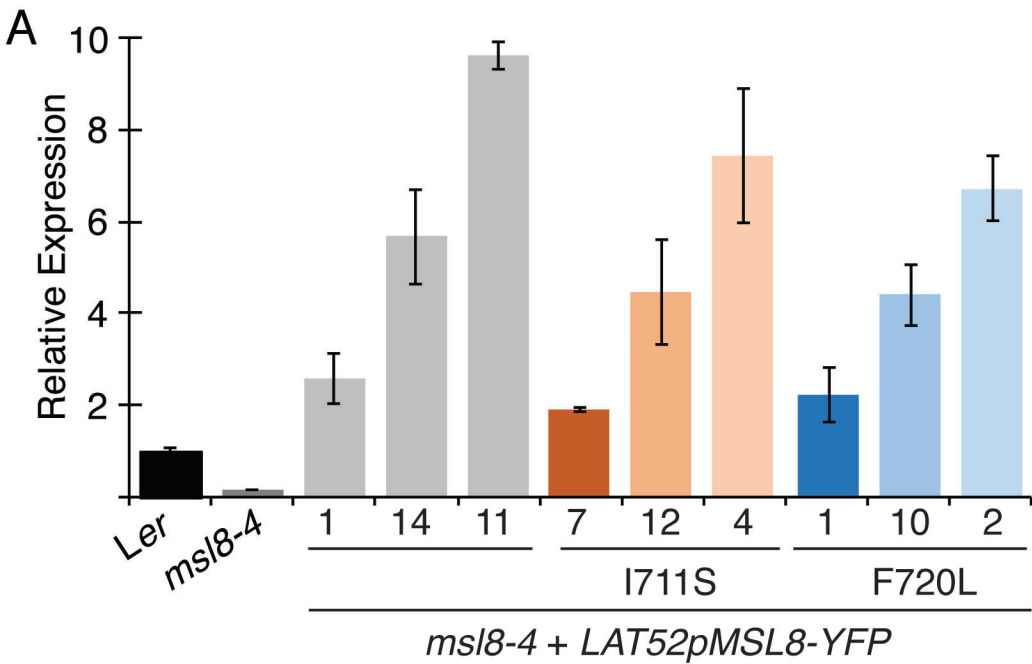


B



# FIGURE 4





**B**

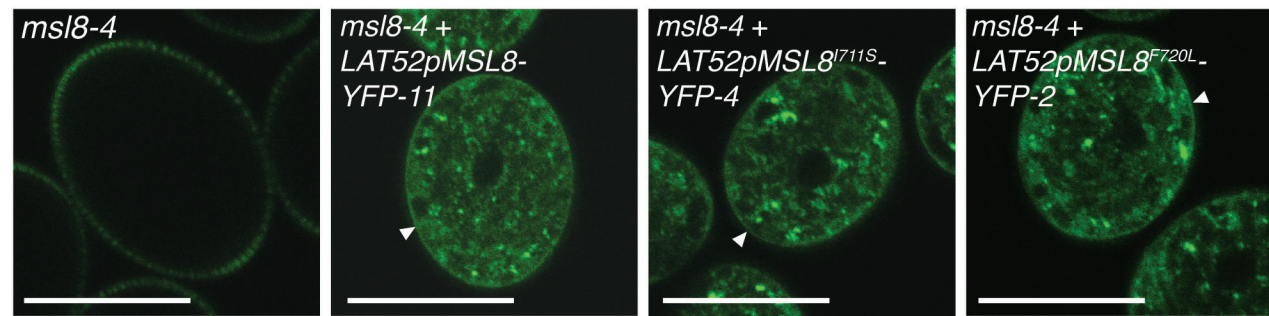
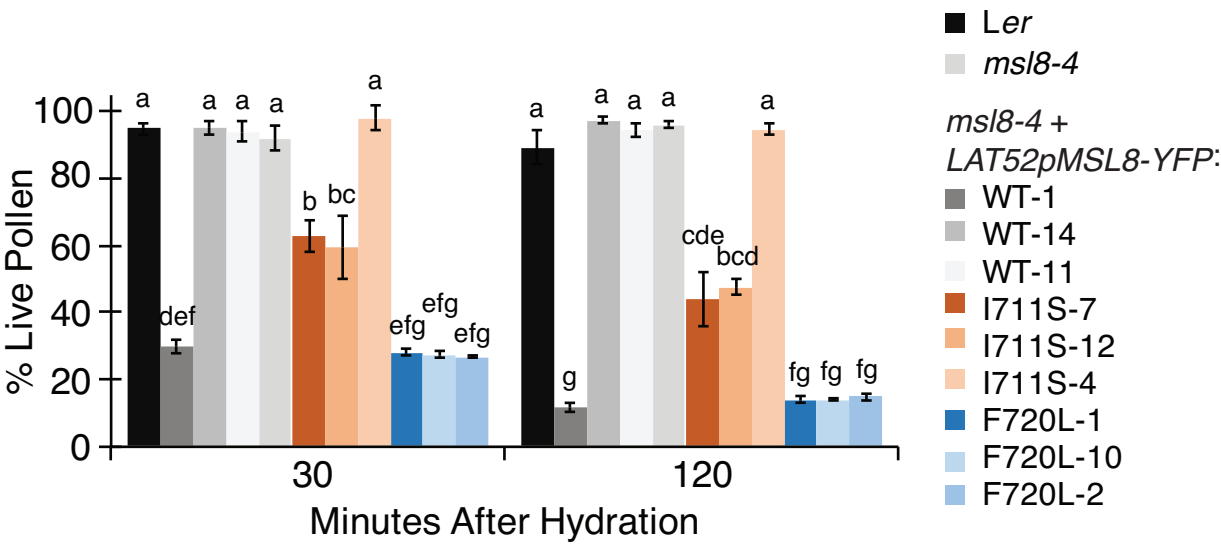


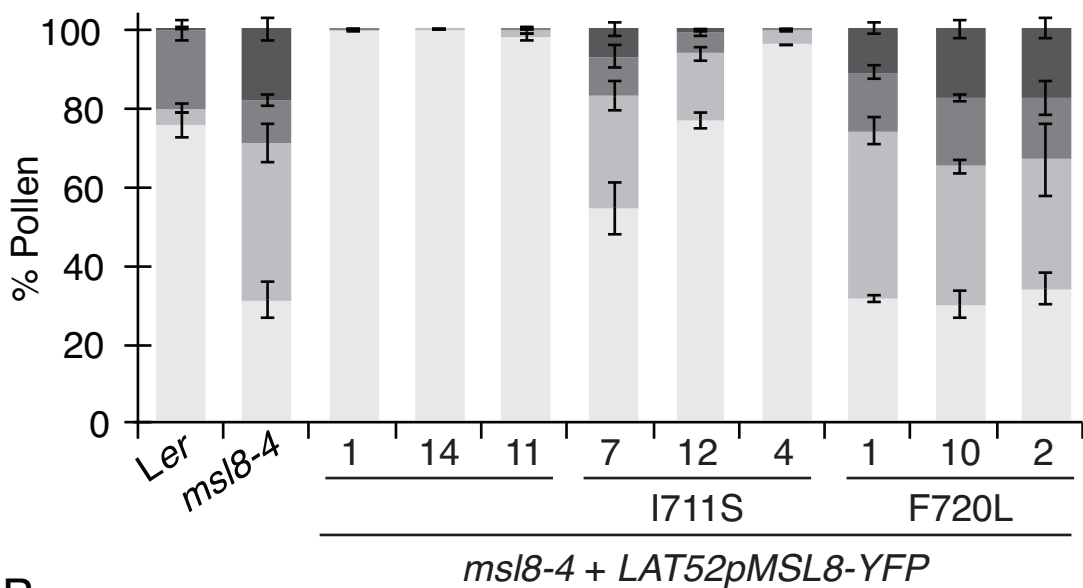
FIGURE 6



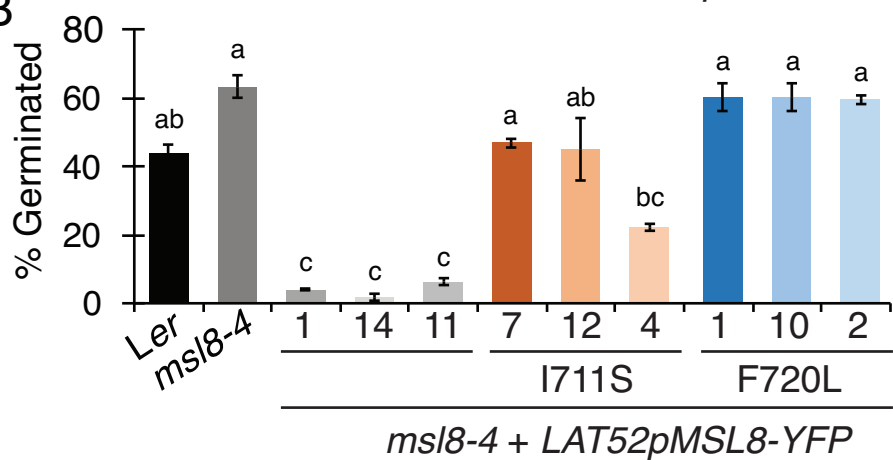
# FIGURE 7

## A

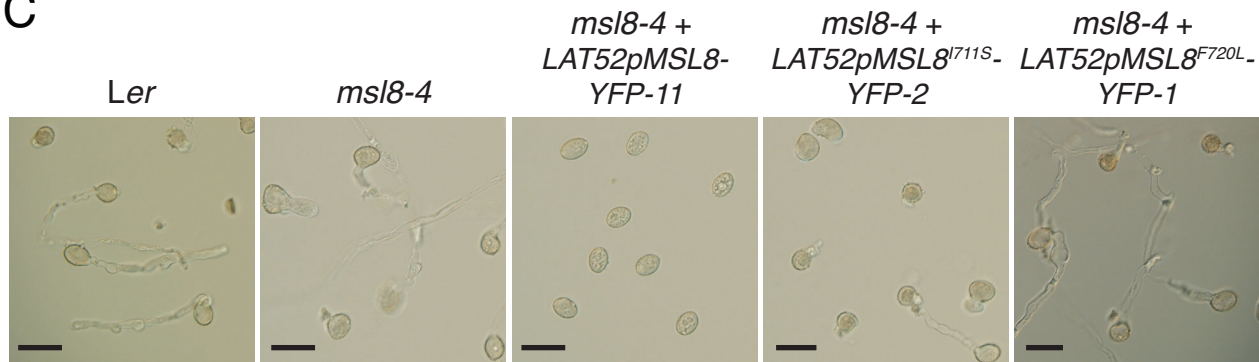
Ungerminated  
 Ungerminated and Burst  
 Germinated  
 Germinated and Burst



## B



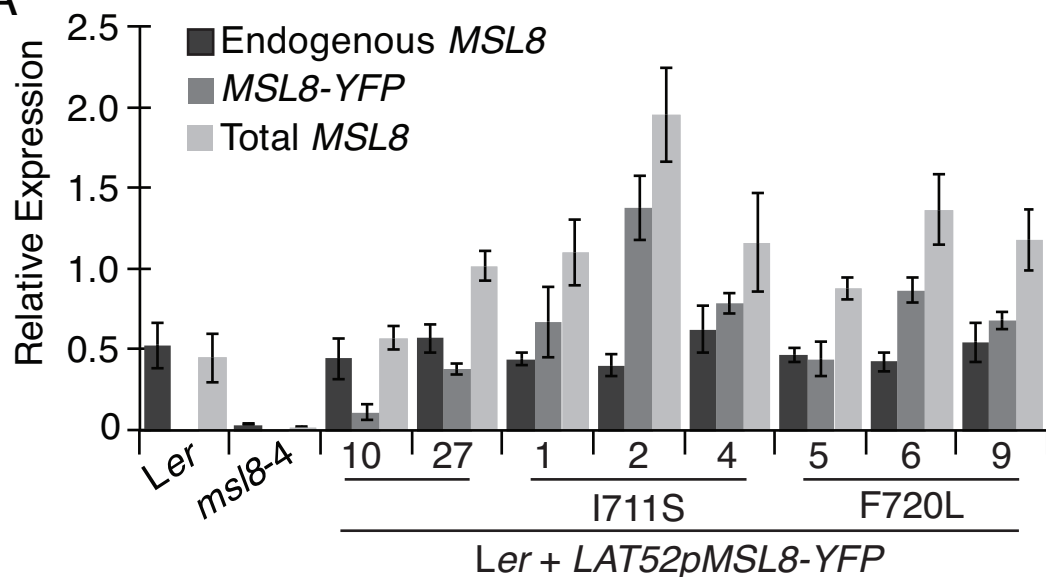
## C



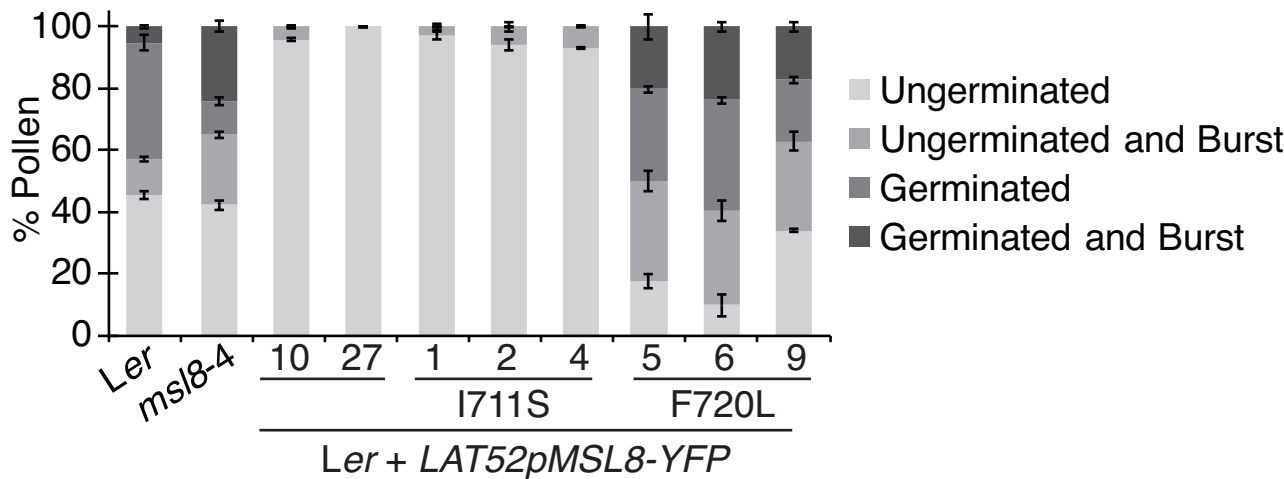


**FIGURE 8**

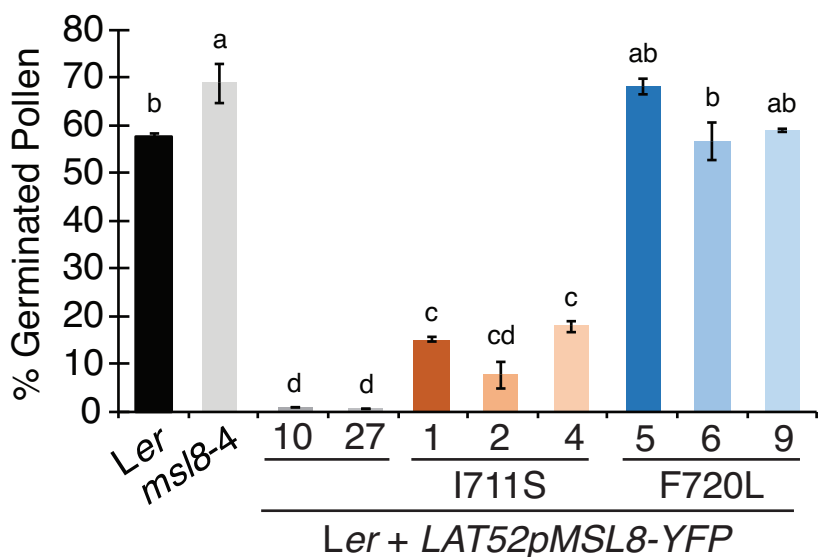
**A**

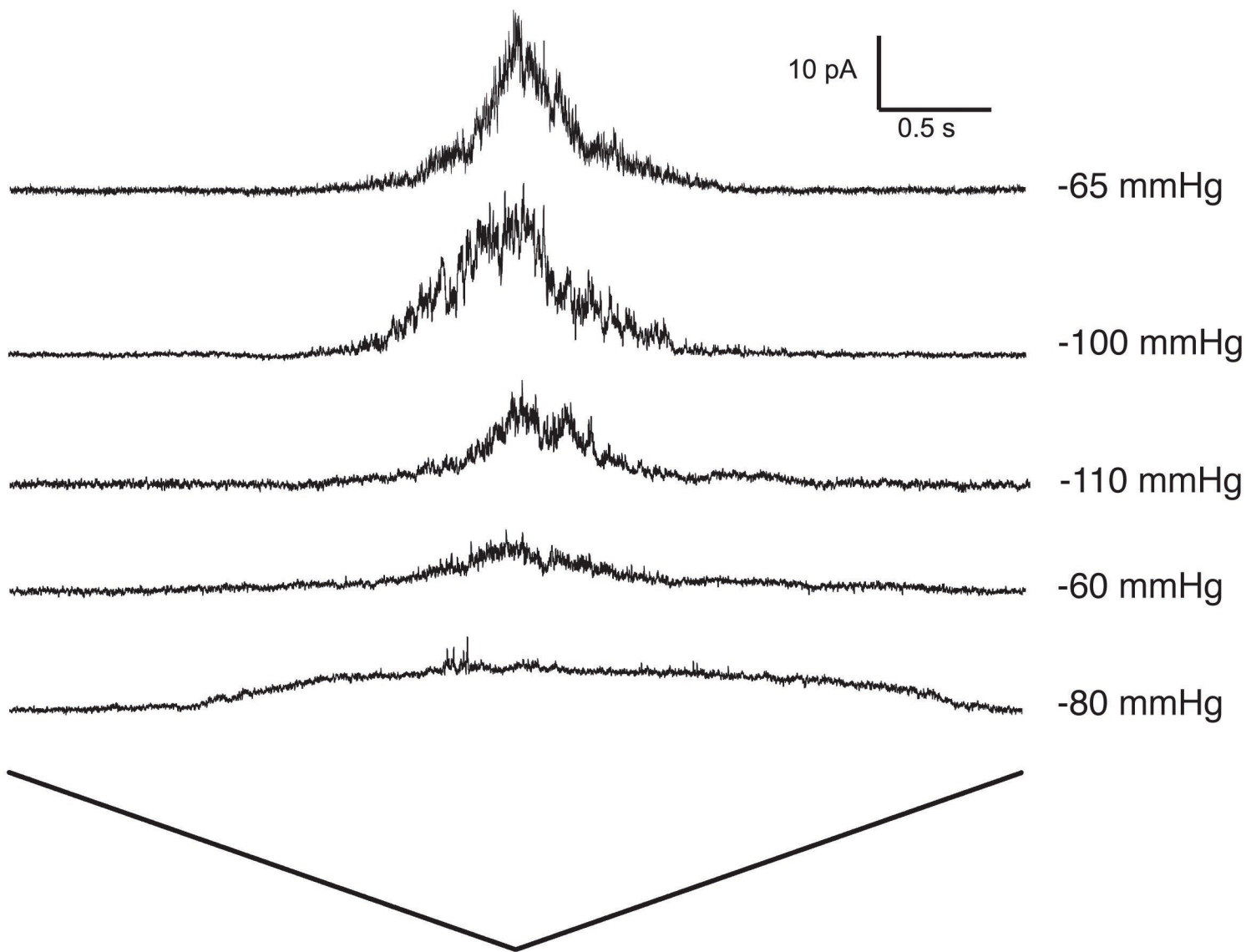


**B**



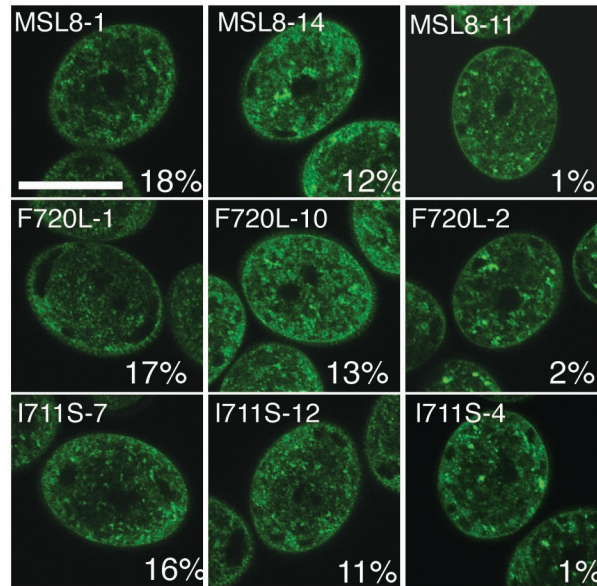
**C**



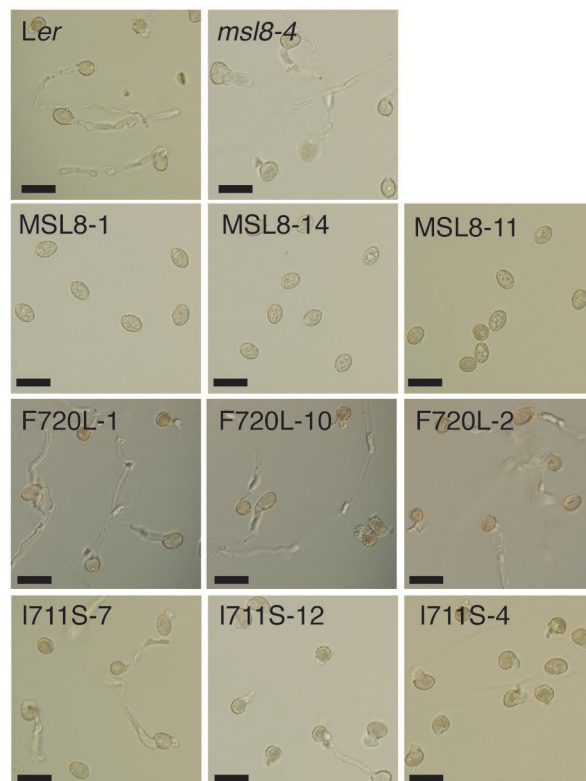


**Supplementary Figure 1. Representative traces of  $MSL8^{F720L}$  expressed in *Xenopus laevis* oocytes.** Representative traces from excised inside-out patches of plasma membrane from *Xenopus* oocytes 2 to 10 days following injection with  $MSL8^{F720L}$  cRNA clamped at -40 mV membrane potential. The peak suction applied during the pressure ramp is indicated next to each trace.

**A**



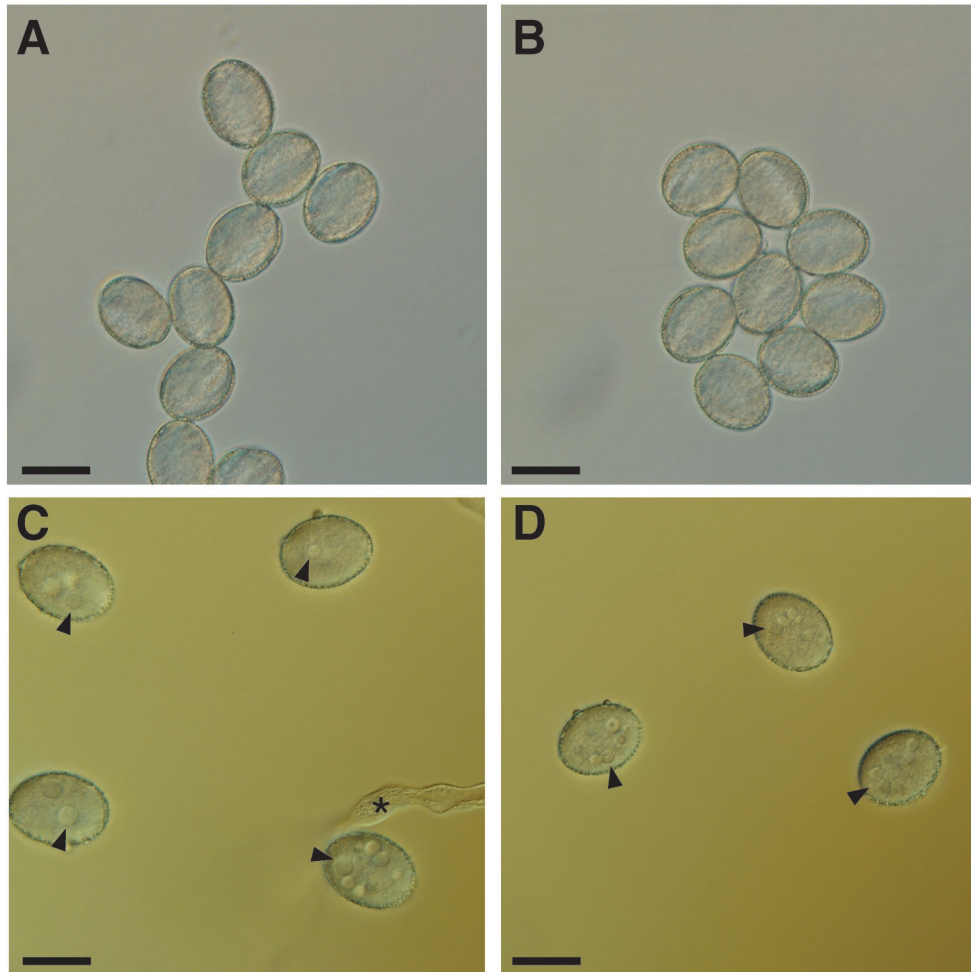
**B**



**Supplementary Figure 2. Additional characterization of *msl8-4* pollen expressing *LAT52pMSL8-YFP* variants.** (A) Confocal images of YFP signal in pollen from the indicated lines expressing *LAT52pMSL8-YFP* in the *msl8-4* background. The laser power at which images were collected is indicated in the lower right corner. All other imaging conditions were kept constant. Scale bars are 20 μm. (B) Pollen from the indicated lines incubated for 16 hours in liquid germination media. Scale bars are 50 μm.

			▼			▼			▼			▼		▼	▼			▼													
MSL4	669	L	V	I	S	S	Q	L	L	L	V	V	F	V	F	G	N	S	C	K	T	I	F	E	A	V	I	F	V	F	V
MSL5	668	L	V	L	S	S	Q	L	L	V	A	F	V	F	G	N	S	C	K	T	I	F	E	A	I	I	F	L	F	V	
MSL6	641	V	V	M	S	S	Q	V	V	V	A	F	I	F	G	N	M	C	K	I	V	F	E	S	I	I	Y	L	F	V	
MSL7	632	L	F	L	T	S	Q	V	V	L	A	F	M	F	G	N	S	L	K	T	V	F	E	S	I	I	F	L	F	I	
MSL8	699	L	F	V	S	S	Q	V	V	L	A	F	I	F	G	N	T	V	K	T	V	F	E	S	I	I	F	L	F	I	
MSL9	550	L	V	F	S	S	Q	F	L	G	L	A	F	M	I	G	S	T	C	K	N	I	F	E	S	F	M	F	V	F	V
MSL10	542	L	F	F	S	T	Q	L	V	A	L	A	F	I	I	G	S	T	C	K	N	L	F	E	S	I	V	F	V	F	V

**Supplementary Figure 3. Alignment of the predicted pore-lining domain of Group III MSLs from *Arabidopsis thaliana*.** Residues identical in at least half of the sequences are shaded in black; similar residues are shaded in gray. Arrowheads mark sites conserved in all sequences. White arrowhead marks Phe720.



**Supplementary Figure 4. Vacuolization of *Ler* and *LAT52pMSL8-YFP*-expressing pollen during germination.** Pollen incubated in germination media for approximately 5 minutes (**A-B**) or 6 hours (**C-D**). (**A, C**) *Ler* pollen. (**B, D**) *msl8-4 + LAT52pMSL8-YFP-14* pollen. Arrowheads mark larger vacuoles found in pollen from both genotypes after extended incubation in germination media. Asterisk marks pollen tube. Scale bars are 20  $\mu\text{m}$ .

		<i>msl8-4 + gMSL8-GFP</i>						
		Ler	<i>msl8-4</i>	I711S		F720L		
				11	2	4	3	21
<i>msl8-4 + gMSL8-GFP</i>	Ler							
	<i>msl8-4</i>	*						
	I711S	11	*	*				
		2	*	*	*			
	F720L	4	*	0.41	*	0.14		
		3	*	*	*	*	*	
	21	*	0.012	*	0.0011	*	1	

\*  $p < 0.0001$

**Supplementary Table 1. Statistical groupings of pollen germination and bursting rates in *msl8-4 + gMSL8-GFP* variant lines.** Results of a chi-squared test comparing the pattern of ungerminated; ungerminated and burst; germinated; and germinated and burst pollen after incubation in pollen germination media for 6 hours. p-values were corrected using the Bonferroni method. Asterisks mark p-values less than 0.0001.

		<i>msl8-4 + LAT52pMSL8-YFP</i>											
		Ler	<i>msl8-4</i>	I711S			F720L						
				1	14	11	7	12	4	1	10	2	
<i>msl8-4 + LAT52pMSL8-YFP</i>	Ler												
	<i>msl8-4</i>	*											
	I711S	1	*	*									
		14	*	*	1								
		11	*	*	1	1							
	F720L	7	*	*	*	*	*						
		12	*	*	*	*	*						
		4	*	*	0.016	0.012	1	*	*				
	F720L	1	*	1	*	*	*	*	*				
		10	*	1	*	*	*	*	*	1			
		2	*	1	*	*	*	*	*	1	1		

\* p < 0.0001

**Supplementary Table 2. Statistical groupings of pollen germination and bursting rates in *msl8-4 + LAT52pMSL8-YFP* variant lines.** Results of a chi-squared test comparing the pattern of ungerminated; ungerminated and burst; germinated; and germinated and burst pollen after incubation in pollen germination media for 6 hours. p-values were corrected using the Bonferroni method. Asterisks mark p-values less than 0.0001.

		Ler + LAT52pMSL8-YFP										
		Ler	msl8-4	I711S			F720L					
				10	27	1	2	4	5	6	9	
Ler + LAT52pMSL8-YFP	Ler											
	msl8-4	*										
	10	*	*									
		27	*	*	0.0096							
	I711S	1	*	*	1	0.17						
		2	*	*	1	*	1					
		4	*	*	1	*	1	1				
	F720L	5	*	*	*	*	*	*	*			
		6	*	*	*	*	*	*	*	1		
		9	*	0.047	*	*	*	*	*	0.0014	1	*

\* p < 0.0001

**Supplementary Table 3. Statistical groupings of pollen germination and bursting rates in Ler + LAT52pMSL8-YFP variant lines.** Results of a chi-squared test comparing the pattern of ungerminated; ungerminated and burst; germinated; and germinated and burst pollen after incubation in pollen germination media for 6 hours. p-values were corrected using the Bonferroni method. Asterisks mark p-values less than 0.0001.



## RT-PCR

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	Forward	Reverse
<i>ACTIN</i>	5'-CAACCGGTATTGTGCTGGATTC-3'	5'-GATGGCATGAGGAAGAGAGAAAC-3' 5'-GGATAGCATGAGGAAGAGCATAC-3' 5'-GAGACGGAGGATAGCATGTG-3'
Total <i>MSL8</i>	5'-GCAATCGAGTTCTGTGTCCAC-3'	5'-CCAATACTCCGGCTTGTTGTCG-3'
Endogenous <i>MSL8</i>	5'-CGAACTACATCGACAACAAGCCG-3'	5'-GCAAAATGAAAAGTGTTGTGTTGTTTCATC-3'
<i>MSL8-YFP</i>	5'-CTGGCTGGTCACAAAACCAAC-3'	5'-CTTGTGGCCGTTTACGTCG-3'

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**Supplementary Table 4. Primers used in quantitative reverse-transcriptase polymerase chain reactions.**