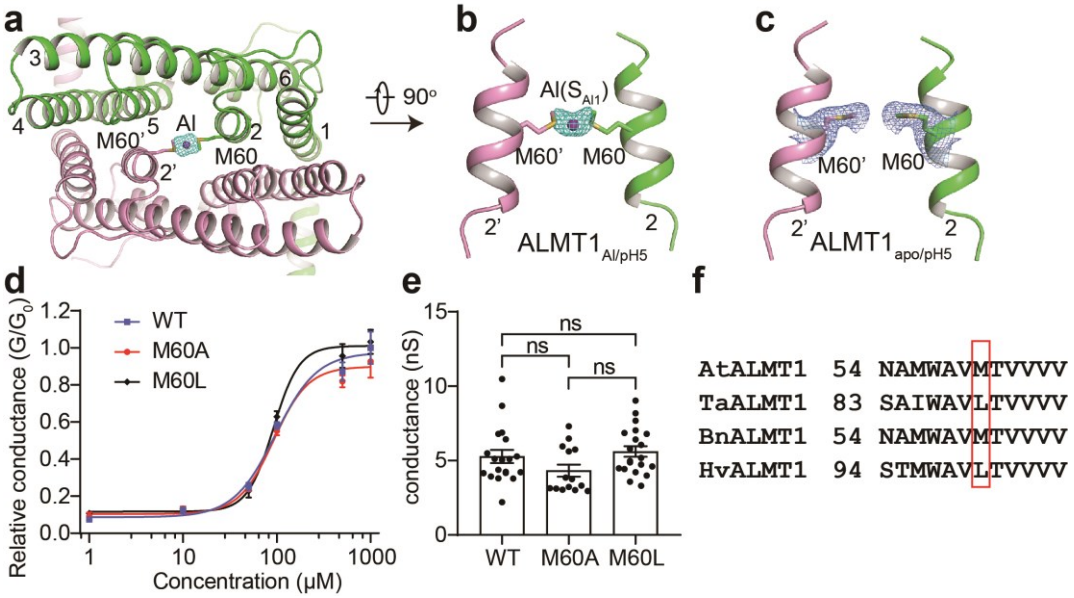

Fig. S9 The Al binding site S_{Al1}.

a, The extracellular view of the S_{Al1} site localized in the pore in the $ALMT1_{Al/pH5}$ structure. **b,** Al at the S_{Al1} site is coordinated by a pair of Met60. The Al density is shown at the contour level of 10 σ. The map is sharpened with a B factor of -80 $Å^2$. **c,** The S_{Al1} site in the map of $ALMT1_{apo/pH5}$. The densities around the S_{Al1} site and Met60 are shown at the contour level of 4 σ. No density is observed around the S_{Al1} site. **d,** Concentration-dependent extracellular Al activation of WT and mutant AtALMT1. Data are reported as means ± s.e.m. of at least five independent biological replicates. Curves are least-square fits to a Hill equation with half-maximum activation concentration (EC_{50}) values of 98.17 ± 3.53, 97.12 ± 5.13, and 91.12 ± 1.24 μM for WT, M60A, and M60L, respectively. **e,** The channel conductance of WT and mutant AtALMT1 measured at -180 mV. The two mutants show no significant (ns) differences in comparison with the WT. Also see Supplementary information, **Fig. S2a, d**. **f**, Sequence alignment of ALMT homologs that are directly activated by Al around Met60 (highlighted by the red box) in AtALMT1.