Extended Data Table 1. Phospho-proteomic data of rapid auxin effects in root and phospho-proteomic analysis of H^+-ATPases in *tmk1-1* mutants

Table contains differentially regulated phospho-peptides (FDR ≤0.05) in H^+-ATPases in IAA treated versus mock-treated roots. IAA treatment was at 100 nM for 2 minutes. QHF and LTQXL analysis are given in Tab 1 and 2, respectively. Tab 3 shows the differentially phosphorylated phospho-sites of AHAs in *tmk1-1* background compared to WT.

Tab1. QHF analysis

FDR	LOG2(IAA/ mock)	Positions in prote	Gene names	Sequence window	Phospho (STY) Probabilities
1.455	3.700	2	AHA1	______________MSGLEDIKNETVDLEKI	S(1)GLEDIKNETVDLEK
1.397	-0.564	881;817	AHA1	YGIGEREAQWAQAQRTLHGLQPKEDVNIFPE	T(1)LHGLQPK
2.030	0.833	899;835	AHA1	GLQPKEDVNIFPEKGSYRELSEIAEQAKRRA	EDVNIFPEKGS(1)YR
1.397	-0.564	881;914	AHA2;HA2	YGKEEREAQWALAQRTLHGLQPKEAVNIFPE	T(1)LHGLQPK
2.403	0.753	899;932	AHA2;HA2	GLQPKEAVNIFPEKGSYRELSEIAEQAKRRA	EAVNIFPEKGS(1)YR
2.371	0.632	942;975	AHA2;HA2	GHVESVVKLKGLDIETPSHYTV_________	GLDIET(0.999)PS(0.001)HYTV
1.403	-0.936	881;914;881;817	AHA2;HA2;AHA1	YGIGEREAQWAQAQRTLHGLQPKEDVNIFPE;YGKEEREAQWALAQRTLHGLQPKEAVNIF	T(1)LHGLQPK

Tab2. LTQXL analysis

FDR	LOG2(IAA/ mock)	Positions within proteins	Gene names	Sequence window
4.482	1.823	881;914	AHA2;HA2	YGKEEREAQWALAQRTLHGLQPKEAVNIFPE
2.044	1.314	947;980	AHA2;HA2	VVKLKGLDIETPSHYTV______________
1.603	0.593	931;964;931;670;930;807;913;976;931;936;670;932	AHA2;HA2;AHA6;AHA8;HA9;AHA5;AHA9;AHA3	IARLRELHTLKGHVESVVKLKGLDIETAGHY;IARLRELHTLKGHVESVVKLKGLDIETPSHY

Tab3. WT vs *tmk1-1*

Pos	FDR	LOG2(*tmk1-1* /WT)	hyper/ hypo in *tmk1-1*	Known function	Gene names	Sequence window	Phospho (STY) Probabilities
881	2.800	-0.693	hypo	activation	AHA1 or AHA2;HA	YGIGEREAQWAQAQRTLHGLQPKEDVNIFPE	T(1)LHGLQPK
882	3.120	-1.478	hypo	activation	AHA3	YGIEEREAQWAHAQRTLHGLQNTETANVVPE	T(1)LHGLQNTETANVVPER
948	3.034	-0.621	hypo	activation	AHA1	AKLKGLDIDTAGHHYTV______________	GLDIDTAGHHYT(1)V
947	3.646	-1.025	hypo	activation	AHA2;HA2	VVKLKGLDIETPSHYTV______________	LKGLDIETPSHYT(1)V
948	2.653	-1.783	hypo	activation	AHA3	VVKLKGLDIETAGHYTV______________	GLDIETAGHYT(1)V
899	2.913	-0.576	hypo	inhibitory	AHA1	GLQPKEDVNIFPEKGSYRELSEIAEQAKRRA	EDVNIFPEKGS(1)YR
899	2.004	-0.461	hypo	inhibitory	AHA2;HA2	GLQPKEAVNIFPEKGSYRELSEIAEQAKRRA	EAVNIFPEKGS(1)YR
931	3.546	1.813	hyper	inhibitory	AHA1	IARLRELHTLKGHVESVAKLKGLDIDTAGHH	GHVES(1)VAK
942	3.922	-0.385	hypo	n/a	AHA2;HA2	GHVESVVKLKGLDIETPSHYTV_________	GLDIET(0.998)PS(0.002)HYTV
955	6.383	-3.999	hypo	n/a	AHA11;AHA4	VRLKGLDIETIQQAYTV______________	GLDIETIQQAYT(1)V