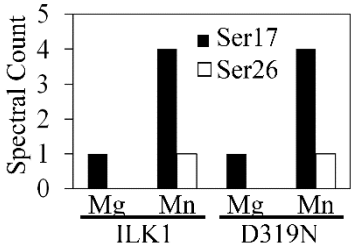
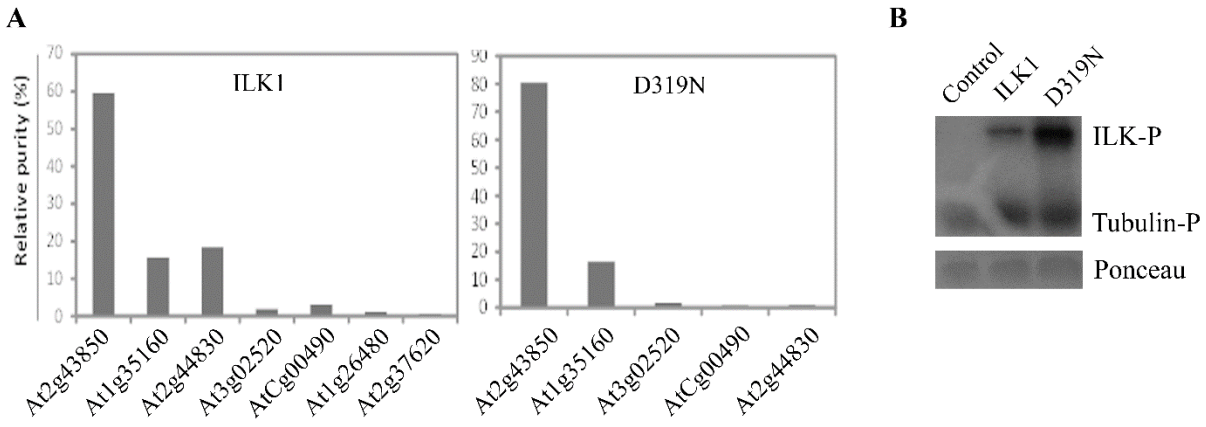


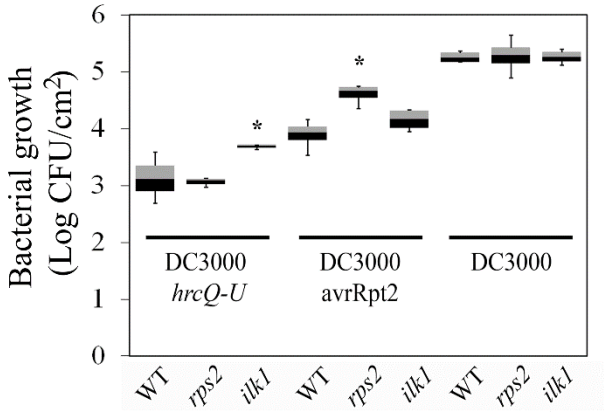
Supplemental Figure S1. Analysis of autophosphorylation sites in ILK1 in the presence of Mn^{2+} or Mg^{2+} cofactors. Purified recombinant ILK1 isoforms were exposed to ATP and cofactors and the phosphorylated residues were identified by mass spectrometry.



Supplemental Figure S2. Relative purity of ILK1 isoforms used to conduct kinase assays.

A, Identity and relative amount of non-ILK1 proteins in purified samples used for kinase assays, as determined by mass spectrometry.

B, Autophosphorylation activity is not present in the empty vector control tissue relative to ILK1, or ILK1^{D319N} in the presence of 5 mM Mn. Equal loading is confirmed by Ponceau staining.



Supplemental Figure S3. Bacterial growth is unaltered in *ilk1-1* knockdown line infected with *P. syringae* pv. *tomato* DC3000 or DC3000 AvrRpt2 strains. Rosette leaves were flood-inoculated and bacteria were counted 2 days after inoculation (n=25-36 plants). The *rps2* line is unable to induce *avrRpt2*-induced immunity.

Supplemental Table S1. Identification of phosphorylated serines in purified ILK1 and ILK1^{D319N} protein using mass spectrometry.

Phospho site	Peptide	ΔM [ppm]	pRS Score [a)]	pRS site probability [b)]	ΔCn	Xcorr	m/z [Da]	RT [min]	Ion matched
Ser^{17}	GISRQFs TGSIRR	1.34	200	S(7): 99.6; T(8): 0.4	0	3.35	516	20	21/48
Ser^{26}	RTLsRQ FTR	2.20	218	T(2): 0.0; S(4): 100.0	0	3.00	416	13	17/32

[a)] pRS score: This peptide score is based on the cumulative binomial probability that the observed match is a random event. The value of the pRS score strongly depends on the data scored, but usually scores above 50 give good evidence for a good PSM.

[b)] pRS site probabilities: For each phosphorylation site this is an estimation of the probability (0-100%) for the respective site being truly phosphorylated. pRS site probabilities above 50% are good evidence that the respective site is truly phosphorylated.

Supplemental Table S2. The primer pairs used in this study.

Gene	Use	Forward Primer	Reverse Primer
ILK1 T-DNA insert	Mutant selection	CCAGAAAGACAAAGCAGAATC	GCCTTTCAGAAATGGATAAATAGCCTTG
ILK1	Cloning	ATGGAGAACATAACCGCGCA	CCAGAAAGACAAAGCAGAATC
K222A mutation	Cloning	TTCAGTCGCAATACTTGATAAAGA	ATCAAGTATTGCGACTGAAACCCG
D319N mutation	Cloning	CAATCATTCACTGTAACCTAAAGCCAAAAAATATTTTG	ATTTTTTGGCTTTAGTTGACAGTGAATGATTGG
FRK1	qRTPCR	TGCAGCTCAGTTTCAATCAAGTGG	CCTTTGCCTCTCGGCGTCGG
CFP	Mutant selection	GAGCAAAGACCCCAACGAGA	GGTACCGTCGACTGCAGAAT
PP2A	qRTPCR	TAACGTGGCCAAAATGATGC	GTTCTCCACAACCGCTTGGT
WRKY29	qRTPCR	ACGAGTACGCACCAAGCGGC	GGAAAAGTTCCGCTCCCGGACA
CYP81F2	qRTPCR	CTATCGTCGGCCATCTCCAC	TATTTTTCAGCGAAGCGGCG
NHL10	qRTPCR	GCCTACTACGAGGGAAAGCG	AACGTTGGTGTGAGAACGGT
PHI-I	qRTPCR	GGTGGCCAAAGCTACGCGGT	CAGTCCCGTGTGACCCGCAT
RD29A	qRTPCR	AGTGATCGATGCACCAGGCGT	CGGAAGACACGACAGGAAACAC
RD29B	qRTPCR	GGGGAAAGGACATGGTGAGG	GGTTTACCACCGAGCCAAGA
HAK5	qRTPCR	CCGTCCACTCGGTGTTTGTA	GAATCCTTTGGCCCCACGTA
ILK1	qRTPCR	CATCATCTTGATGGCCGGA	GTACTTTGCATCAGCAGCCG

Supplemental Table S3. Analysis of transporters identified as putative ILK1 phosphorylation targets and protein interaction targets using the kinase client assay (KiC) and functional protein microarrays (FPM). The average signal with ILK1 represents the fluorescence signal in relative light units across three independent arrays for the FPM and the number of phosphopeptides observed and number of peptides detected overall in parentheses for the KiC.

ID	Assay	Phospho-peptide	pRS Score [a]	pRS site probability [b]	p-value	Average signal with ILK1	Average signal in control
At4g33530	FPM	-	-	-	0.0002	45051	1590
At1g06470	FPM	-	-	-	0.0001	39483	1469
At3g03090	FPM	-	-	-	0.0044	17531	1566
At4g13420	KiC	YRPDSFIIEAGQT	46	Y(1): 98.8; T(13): 100.0		1 (7)	0 (10)
At1g14850	KiC	NLFGAYSNGGESANKRQ	44	Y(6): 50.0; S(7): 50.0		1 (10)	0 (24)
At5g41800	KiC	PFPVTRLDSDAGALFVLQ	101	S(9): 98.8		2 (28)	0 (26)
At1g11260	KiC	IRGVDDVSQEFDDLVAASKE	39	S(18): 98.6		1 (28)	0 (23)

[a] pRS score: This peptide score is based on the cumulative binomial probability that the observed match is a random event where scores above 50 give good evidence for a match.

[b] pRS site probabilities: Estimate of probability (0-100%) that the phosphorylation site is phosphorylated where a score of 50% or above is considered evidence of phosphorylation.

Supplemental Data S1. Ionomic profile for flg22-treated seedlings.