Table S1. Effect of Itk PH domain point mutations on protein abundance, PI(3,4,5)P$_3$ binding, and CaM binding. Protein abundance was determined for PH domain-YFP fusion protein by Western blot with antibodies recognizing GFP and YFP (JL8). In vitro PI(3,4,5)P$_3$ binding was determined by precipitation of PI(3,4,5)P$_3$-coated beads. CaM binding was determined by coimmunoprecipitation in the presence of Ca^{2+}. —, undetectable

	Protein abundance	In vitro PI(3,4,5)P$_3$ binding	CaM binding
WT	++++	++++	++++
L41Y	+	++++++	+++
K35R	++++	++++	+++++
K35D	++++	+	++
K35A	++++	+	++++
K35G	++++	+	++++
K35V	++++	+	++++
K48A	++++	++++	++++
K48E	++++	++++	++++
L51Q	++++	++++	++++
L51R	++++	++++	++
L51A	++++	++	++++
L51D	++++	+	++++
L51E	++++	++	++++
L51M	++++	++++	+++
L51G	+++	—	+
L51T	+++	+	++++
L51K	+++	++++	+++
L51V	++	+	+
K48E R49E	++	+	+
F41D L51M	++++	+	++++
F41D L51R	+	—	++
F41D L51V	+	—	+
F41V L51M	+	—	+
F41A L51A	++	+	+++

Table S2. Oligo primers for cloning PH domains and YFP. The red sequences represent the linkers added between the PH domain and YFP.

Primer	Primer sequence
Ipcef1 PH F	5'-TAAGCTAGCCGCCACCATGGCTAGTCGGAGAAGGATATCCTGTAAA-3'
Ipcef1 PH R	5'-TAA*GGATCCGCCTCCACC*GGTCACAGCAAATCCAAGTTTGTTTAACC-3'
Veph1 PH F	5'-TAAGCTAGCCGCCACCATGGCTAATCAAGATGGCCAGCCTCTCATCGA-3'
Veph1 PH R	5'-TAA*GGATCCGCCTCCACC*CTCCTTTGCCTGGGCCAGCGCCACGTTG-3'
Plekha8 PH F	5'-TAAGCTAGCCGCCACCATGGAGGGCGTGCTGTACAAGTGGACC-3'
Plekha8 PH R	5'-TAA*GGATCCGCCTCCACC*CAGGCAGGCCTTGGCAGATCCCAGAGC-3'
Plek2 PH F	5'-TAAGCTAGCCGCCACCATGGAGGACGGCGTGCTCAAGGAAGGC-3'
Plek2 PH R	5'-TAA*GGATCCGCCTCCACC*CTTCCCTGGCTGCCCTGCATGGATAGC-3'
Arhgap12 PH F	5'-TAAGCTAGCCGCCACCATGGGTCAGGAGAAATATGGACTGTTAAAT-3'
Arhgap12 PH R	5'-TAA*GGATCCGCCTCCACC*AGTACTACTAAGAACTTTAAACCAATC-3'
Acap1 PH F	5'-TAAGCTAGCCGCCACCATGGAGGGGCCTAGTGGCTTGGTAATGGAAG-3'
Acap1 PH R	5'-TAA*GGATCCGCCTCCACC*GAAGGCTGAGGCAATGCTGCTCTGGAC-3'
Phlpp2 PH F	5'-TAAGCTAGCCGCCACCATGGATCATCTGGATCGAATCCTACTG-3'
Phlpp2 PH R	5'-TAA*GGATCCGCCTCCACC*CCGCTGCGACACCACCTTAGACGCCTG-3'
Cadps2 PH F	5'-TATGCTAGCGCCGCCACCATGGCTCCAGCACACATGAAGCATAGTGGG-3'
Cadps2 PH R	5'-ATC*GGATCCGCCTCCACC*TTGGACTGCAGGAACTGGTTTGTAAGAC-3'
Cdc42bpa PH F	5'-TATTCTAGACGCCACCATGGCTAAGGGAGTTGGGACGGCGTATG-3'
Cdc42bpa PH R	5'-ATA*AGATCTGCCTCCACC*TAGCGTGCTGTCGTACGCCT-3'
Plch1 PH F	5'-CTGGCTAGCCGCCACCATGGCAGACCTTGAAGTGTATAAA-3'
Plch1 PH R	5'-ATA*GGATCCGCCTCCGCC*AGCCATCAGATACTTGAGG-3'
Vav1 PH F	5'-TATGCTAGCCGCCACCATGGCTAACTATGGCCGGCCCAAGA-3'
Vav1 PH R	5'-TAT*GGATCCGCCTCCACC*TGGGTAAATGTTGGAGATGGCC-3'
Arhgef7 PH F	5'-ACTGCTAGCCGCCACCATGGATGACATAAAGACCCTGGGCAG-3'
Arhgef7 PH R	5'-TAT*GGATCCGCCTCCACC*CTTCGTCTGCTTCTGCAGG-3'
Itk PH F	5'-TATGCTAGCGCCGCCACCATGGCTATGAACAACTTCATCCT-3'
Itk PH R	5'-TAT*GGATCCGCCTCCACC*GGATGGGTCGTAGGGAGCACAG-3'
YFP F	5'-TAT*GGATCCGGTGGCGGAGGTTCT*ATGGTGAGCAAGGGCGAGGA-3'
YFP R	5'-TATGGGCCCTTACTTGTACAGCTCGTCCATG-3'
Itk LS bridge F	5'-TATGAATATGACTTTGAACGCGGGAAGAAGCGCACGT-3'
Itk LS bridge R	5'- AAGTCATATTCATAGTAGGCCAGGCTGGCTTTCGTT-3'