Tab. S1 Sequences of primer pairs used for cloning and verification of the cloned inserts, e.g. M13 primer pairs. Inosin was used in degenerated primer sequences instead of all nucleotides (i = inosin).

primer name	sequence from 5' \rightarrow 3'				
H5_fwd	aa(ag) ac(i) tgg at(act) gg(i) gc				
S6_rev	ac(i) ag(ag) tti gtc at(ag) tti cc				
S6spec_rev	acg agg ttg gtc atg ttg cc				
H5spec_fwd	aaa acg tgg atc ggg gc				
H5spec_rev	gcc ccg atc cag gtc tt				
GYGDHLA_rev	tgc atg caa gtc gcc ata tcc				
M13_fwd	gta aaa cga cgg cca g				
M13_rev	cag gaa aca gct atg ac				
LilKT1_fwd	atg tgc ggc cac gag cc				
LilKT1_rev	tta aga ata ggc ctg act tcc cct c				
Rec1_AKT6_fwd	gat acc gtc gac aat gga gaa gaa g				
Rec2_AKT6_rev	cga ggt cga ctc aag gat ccc				
Primer pairs for construction LilKT1/AKT1 chimera by SOE-PCR					
SOE_N_LilKT1_rec1_fwd	gaa ttc gat atc aag ctt atc gat acc gtc g				
SOE_N_LilKT1_rev	cat ttg atc ttg caa tct aac tgg				
SOE_AKT1_C_fwd	cca gtt aga ttg caa gat caa atg ctt gca c				
SOE_AKT1_C_rev	atg act cga ggt cga ctc aag aat cag ttg caa aga tg				
Primer pairs for site-directed mutagenesis by Around-The-Horn method					
G797D_fwd	ata atg ccc cag caa aat tgg tat tgt tgc c				
G797D_rev	ctt ttt cag gac atc taa tag tga ctc ttg gtg gtg				
K840D_fwd	gac ttg gtt aga gat ggt gat tgt ttg ttg				
K840D_rev	aac gtc atc gat ctc tgc tcc atc tct tg				

Tab. S2: Proteins with highest homologies to LilKT1. The amino acid sequence of LilKT1 was used for a BLAST search in the non-redunadant NCBI data base.

name	Max	Total	Query	E value	Max	Access no
	score	score	cover		identity	
LilKT1 [Lilium longiflorum]	1784	1784	100%	0.0	100%	ABO15470.1
putative K ⁺ channel AKT1,	1240	1240	0.0%	0.0	60%	VD 002520272 1
[Ricinus communis]	1240	1240	99%	0.0	09%	<u>XP_002529575.1</u>
Predicted K ⁺ channel AKT1-like	1727	1727	0.00%	0.0	60%	VD 002291797 1
[Vitis vinifera]	1232	1252	96%	0.0	09%	<u>XP_002281787.1</u>
unnamed protein product [Vitis	1220	1220	98%	0.0	69%	<u>CBI28150.3</u>
vinifera]	1229	1223				
Predicted K ⁺ channel AKT1-like	1227	1227	08%		60%	YP 00/1/0800 1
[Cucumis sativus]	1227	1227	5070	0.0	0970	<u>XP_004149890.1</u>
inward rectifying shaker-like K ⁺	1220	1220	0.00/	0.0	69%	<u>CAZ64538.1</u>
channel [Vitis vinifera]	1220	1220	5070			
shaker-like K ⁺ channel 1	1216	1216	98%	0.0	69%	ADA79674 1
[Populus euphratica]	1210	1210	5070	0.0	0370	101113014.1
K ⁺ uptake channel [Zea mays]	1209	1209	98%	0.0	69%	CAI77627.1
hypothetical protein	1207	1207	98%	0.0	68%	XP_002458234.1
03g029520 [Sorghum bicolor]	1207					<u></u>
K ⁺ channel [<i>Solanum</i>	1204	1204	99%	0.0	69%	CAA60016 1
tuberosum]					0.570	
AKT1-like K ⁺ [<i>Triticum</i>	1203	1203	98%	0.0	68%	AAF36832.1
aestivum]	1205	1205	5070			
inwardly rectifying K ⁺ channel	1200	1200	98%	0.0	68%	ABF99810 1
AKT1 [Hordeum vulgare]	1200	1200	5070	0.0	0070	<u>/////////////////////////////////////</u>
inwardly rectifying K ⁺ channel	1200	1200	98%	0.0	69%	<u>CAG27094.1</u>
subunit [Daucus carota]	1200					
OsAKT1 (Oryza sativa)	1199	1199	98%	0.0	66%	P0C550.1
K ⁺ channel [<i>Solanum</i>	1199	1199	99%	0.0	68%	NP 001234258 1
lycopersicum]	1155	1155	5570	0.0	00/0	<u></u>
OsAKT1, Os01g0648000 [Oryza	1198	1198	98%	0.0	66%	NP 001043713 1
sativa]	1100				00/0	<u></u>

LіІКТІ АКТІ АКТ6	SHYSLSSGILPSLGA SHYSLSSGILPSLGA MEKKKVWFWGVKDDGEGGGG <mark>RGG</mark> GRTKDAED <mark>D</mark> VADH <mark>LSR</mark> DGTM <mark>S</mark> QY <mark>SLS</mark> K <mark>GLLPSLGA</mark> NN
LіlКТ1 АКТ1 АКТ6	S1 S1 S2 S5 S5 S5 S5 S5 S5 S5 S5 S5 S5
Lіlкт1 АКТ1 АКТ6	S2S3S4S5S5S5S5S
LіІКТІ АКТІ АКТ6	S4S5_ RSYGFLNMLRLWRLRRVSCLFARLEKDRNFNYFWVRCAKLIFVTLFAVHCAGCFYYLIAA QSYGLFNMLRLWRLRRVGALFARLEKDRNFNYFWVRCAKLVCVTLFAVHCAACFYYLIAA QGYGIFSMLRLWRLRRVSNCFARLEKDRKYSYFWVRCSKLLLVTLFVIHCGACFLYSTAA
Lіlкт1 АКТ1 АКТ6	RYHDETKTWIGASMPDFHEQSLWVRYVTSMYWSITTLTTVGYGDLHAQNTGEMIFDIAYM RNSNPAKTWIGANVANFLEESLWMRYVTSMYWSITTLTTVGYGDLHPVNTKEMIFDIFYM HYPD <mark>PSKT</mark> FMALTDE <mark>N</mark> WK <mark>S</mark> SPIAVRYNTAMYWSITTFSTTGYGDIHGV <mark>N</mark> SREMTFILFYM
Lіlкт1 АКТ1 АКТ6	S6S6 LEDLGLTAYLIGNMTNLVVHCTSRTRKFRDTIQAASSFALRNQLPVR <i>LODO</i> MVAHLCLKF LENLGLTAYLIGNMTNLVVHGTSRTRNFRDTIQAASSFALRNHLPPR <i>LODO</i> MLAHLCLKY V <mark>ENLGL</mark> SAYIIGNMTNLVVHVTGRTRKFRDTIQAASGFGQRNNLPVRLQDQMVAHLCLRY
Lіlкт1 АКТ1 АКТ6	RTDSEGLQQQETLDALPKAIRSSISHYLFYT <mark>L</mark> VNKVYLFRGVSHDLLFQLVSEKKAEYFP RTDSEGLQQQETLDALPKAIRSSISHFLFYSLMDKVYLFRGVSNDLLFQLVSEMKAEYFP RTDSEGLQQQEIIDSLPKAIRSSISHYLFYEVVDKIYLFHGISNDLLFQLVTEMKAEYFP
LіІКТІ АКТІ АКТ6	PREDVILQNEAPTDFYILVTGSVDLVDHKNGIEQIVREANPGELVGEIGVLCYRPQLFTI PKEDVILQNEAPTDFYILVNGTADLVDVDTGTESIVREVKAGDIIGEIGVLCYRPQLFTV PKEDVILQNEAPTDFYILVTGAVTIIARVNGVEQVVSEAQRGHVFGEVGVLCYRPQLFTV
LіІКТІ АКТІ АКТ6	RTKKLCQLLRLNRNSFLSIVESNVGDGTVTMNNLLQYLKEQKDHVMQGVLRETGNMLARG RTKRLCQLLRMNRTTFLNIIDANVGDGTIIMNNLLQHLKEMNDPVMTNVLLEIENMLARG RTKRLSQLLRLNRTVLLNLVDANVGDGAIIMNNLLQHLKDSEDPVMKGVLADTEHMLAQG
LіІКТІ АКТІ АКТ6	RLDLPLTLCFAATRGDDLLLHQLLR <mark>RGLDPNESDNNG</mark> WSALHIAASKGNESCYVLLLDFG KMDLPLNLCFAAIREDDLLLHQLLKRGLDPNESDNNGRTPLHIAASKGTLNCVLLLLEYH KMDLPLSLCFAAARGDDLLLHQLLRRGSSPNEMDKDGRTALHIAASKGSHYCVVLLLEHG
LіІКТІ АКТІ АКТ6	ADPNCRDSEGRVPLLEAILGKHDSVVRVLVDHGADLSSGDAAQYACIAAEQNNELLQST ADPNCRDAEGSVPLWEAMVEGHEKVVKVLLEHGSTIDAGDVGHFACTAAEQGNLKLLKEI ADPNIRDSEGNVPLWEAIIGRUREIAKLLAENGAKLSLDSVSYFSGLAVEKNCLDALKDI
LіІКТІ АКТІ АКТ6	VQY <mark>GGD</mark> ISAPKLDGNTALHIAVTEGNVPIVKFLLEHGAEIDKPDSHGWTPRGLADOOSHE VLHGGDVTRPRATGTSALHTAVCEENIEMVKYLLEQGADVNKQDMHGWTPRDLAEQOGHE IKY <mark>GGDVTLP</mark> DGN <mark>GTTALHRAVSE</mark> GHLEIVKFLLDQGADLDWPDSYGWTPRGLADHOGNE
LіІКТІ АКТІ АКТ6	EIKALFEAKRDIPKVSDTTPTSHLLGRYS <mark>SEP</mark> MIQRL <mark>S</mark> SDGILVADDNKQ <mark>RR</mark> DIKALFREKLHERRVHIETSSSVPILKTGIRFLGRFTSEPNIRPASREVSFRIRETRARR EIKTLFHNHRPVEKKPKPI-PGIPQSPVTGKPLMKYS <mark>SEP</mark> TMHSGELVLDGGQVVVSQKR
LіІКТІ АКТІ АКТ6	RANNERNSLEGTMSAAKVDREYGPLPSPSGPSREMAVAPHHRTEPRVTIRCPEKGNAPAK KTNNEDNSLEGILANQS <mark>V</mark> PKNGLATVDEGRTGNPVRVTISCAEKDDIAGK KLNNERNSLEGIISAANSADDGGEVPRSPAVPGGG <mark>G</mark> SMIY <mark>PERVTIS</mark> SPENGETG <mark>GK</mark>
LilkT1 AKT1 AKT6	LVLLPGSLKELLDLGGKKFGLVLVKVLTRD-GAEIDDVKLVRDGDCLLLVSDRWRGSQAYS LVLLPGSFKELLELGSNKFGIVATKVMNKDNNAEIDDVDVIRDGDHLIFATDS VVLLPNSMEELLKIGENKMGFVPTKVLTRE-GAEIDDITLIRDGDFLLLSRDP

Fig.S1 Sequence alignment of LilKT1, AKT1 and AKT6. The transmembrane domains S1 – S6 are indicated. The amino acid sequence LQDQ was used as an overlapping sequence to construct the N-terminal-LilKT1 + C-terminal-AKT1 chimera. Areas with similar amino acids of all three proteins are marked in red, yellow were two sequences show amino acid similarities.



Fig. S2 Functional complementation of yeast K⁺ uptake mutant WD3. Yeast mutant WD3 expressing HA-tagged yLilKT1 (HA-LilKT1) did not grow at low K⁺ concentrations (1 mM KCl). Yeast cells were complemented with yLilKT1 in pGREG536 containing *URA3* as a selectable marker.



Fig. S3 Functional complementation of yeast K⁺ uptake mutant PLY240. Yeast mutant PLY240 expressing the Arabidopsis K⁺ channels AKT1 and KAT1 is growing in low K⁺ medium (1 mM KCI).



AKT1....PVRVTISCA**E KD**DIAGKLVL LPGSFKELLE LGSNKFGIVA TKVMNKDNNA **EIDDVD**VIR**D GD**HLIFATDS LilKT1..PPRVTIRCP<u>E KG</u>NAPAKLVL LPGSLKELLD LGGKKFGLVL VKVLTRDG.A **EID**<u>OVK</u>LVR**D GD**CLLLVSDR WRGSQAYS 787 G797D K840D

Fig. S4 Mutations of the amino acid sequence of the C-terminus of LilKT1. Arabidopsis AKT1 and the lily pollen channel are marked in green and blue, respectively. The C-terminal amino acid sequence alignment of both channel starts with LilKT1 proline 787. The di-acidic motifs (red) which were mutated, are underlined. sm: single mutation, dm: double mutation.



Fig. S5 Functional complementation assay of K⁺ uptake mutant PLY240 with AKT6 (SPIK). Channels were cloned into pGREG535.



Fig. S6 Localization of LilKT1 in protoplasting lily pollen grains. (A) Bright field image of a protoplast released from a lily pollen grain and (B) the corresponding fluorescence image showing the fluorescence of YFP fused to the N-terminus of LilKT1. (C) and (D) Bright field and fluorescence image, respectively, of cytosolic GFP expressed in lily pollen protoplasts. Transient expression of fluorescent proteins by particle bombardment with respective plasmids. Bar = $50 \mu m$.