Figure S4

A

```
S. cerevisiae 290  RASKIEQIQKLAKYAISALNYEDLPTAKDELTKALDLLNSI 330
H. sapiens    265  TPEDFARAQKYCKYAGSALQYEDVSTAVQNLQKALKLLTTG 305
A.ahaliana    375  GPEKVAEALKAARFAVGALAFDEVSTAVEHLKKSLELLTNP 415
```

B

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MSNPNEPARALLPYLQRADELQKHEPLVAYYCRLYAMERGLKIPQSERTKTTNSILMSLINQL
EKDKKSLTLSPDDNMHVEGFALSVFAKADKQDRAGRADLGTAKTFYAASIFFEILSQFGPVPP
DIEQKHKYAAWKAADIRKAIKEGRKPTPGDPVDDDTDLSIPSSGPSGSYDHSASDTNTTSHHR
TELDPPHDSNDDSSHHQFPEVPQHPLPPRFYDNPTNDYPADVPPPPPSSYPSNDHLPPPTGPS
DSPYPHPYSHQPYHQDPPKHMPPPQNYSSHEPSPNSLPNFQSYPSFSESSLPSTSPHYPSHYQ
NPEPYYSSPHSAPAPSSTSFSSAPPPPPYSSNGRINIAPVLDPAPSSAQKYHYDSSYQPGPEK
VAEALKAARFAVGALAFDEVSTAVEHLKKSLELLTNPSAGAGH
```

Figure S4. LIP5 protein sequences.

(A) Alignment of C-terminal domains of LIP5 proteins from yeast, human and Arabidopsis. The conserved tyrosine (Y) and phenyalanine (F) residues critical for interaction with SKD1 are indicated in red.

(B) Arabidopsis LIP5 protein sequence. The six putative MPK phosphorylation sites are indicated in red.