## **Supporting Information**

## Interaction of Calmodulin with the cSH2 Domain of the p85 Regulatory Subunit

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Title Running Head: Calmodulin binding to cSH2-p85a

nSH2	<sup>325</sup> wywgdisreevnek <b>lr</b> dta <b>dgtflvr</b> dastkmhgdytltlr <mark>kggnnkliki</mark> fhrdgkygf
cSH2	<sup>614</sup> wnvgssnrnkaenllrgkrdgtflvresskqgcyacsvvvggekkevinktatgygf
nSH2	SDPLTF-SSVVELINHYRNESLAQYNPKLDVKLLYPVSKYQQ <sup>435</sup>
cSH2	AEPYNLYSSLKELVLHYQHTSLVQHNDSLNVTLAYPVYAQQR <sup>724</sup>

**Figure S1.** Protein sequence information obtained from the basic local alignment search tool (BLAST) algorithm in the National Center for Biotechnology Information (NCBI) webserver (https://blast.ncbi.nlm.nih.gov/Blast.cgi). Bold highlights the residues conserved in both nSH2 and cSH2 domains, box denotes the residues used for mutation, and light blue represents the residues containing the 1-5-10 CaM-binding motif.



**Figure S2.** Relative quantitative analysis of the CaM–cSH2 EDC crosslinking experiment for the wild type (cSH2<sup>WT</sup>) and two cSH2 mutants; cSH2<sup>mutant-1</sup> (cSH2<sup>V663K/V667N</sup>) and cSH2<sup>mutant-2</sup> (cSH2<sup>V663K/V667N/L687F/L691V/L696N</sup>).

**Table S1.** Identified residue pairs of intermolecular interactions by NOEs. In the residue names, hydrophobic, polar/glycine, positively charged, and negatively charged residues are colored black, green, blue, and red, respectively.

CaM residue	cSH2 residue
Ala147	Lys674, Thr675, Tyr657
Glu127	Asn673
Glu114	Lys653, Gln654
Met109	GIn654
Asp80	Leu687
Thr79	Tyr688
Gly40	Tyr685
lle9	Glu614, Leu616