## **Supporting Information**

## Moore et al. 10.1073/pnas.1117220108



**Fig. S1.** Comparison of the talin-1 and radixin FERM domains. (*A*) The radixin FERM domain is composed of three subdomains: F1 (*Left*, orange), F2 (*Center*, yellow), and F3 (*Right*, green). The CD44 cytoplasmic tail (blue) binds to a cleft in F3 formed by helix  $\alpha$ 1 and strand  $\beta$ 5. (*B*) The radixin subdomains adopt a canonical trefoil shape. (C) The talin-1 FERM domain contains F1 (orange), F2 (yellow), and F3 (green) domains, as well as an F0 subdomain (red) that precedes F1. Instead of a trefoil, the talin-1 FERM subdomains are arrayed linearly. (*D*) Model of talin-1 F3 (green) bound to the integrin  $\beta$ 1D CT (black). Two regions of the  $\beta$ 1D CT interact with talin-1 F3: Its C-terminal portion adopts an extended conformation and packs against a ridge formed by the interface of helix  $\alpha$ 1 and strand  $\beta$ 5 in F3, while an N-terminal  $\alpha$ -helix and a contiguous portion of the  $\beta$ 1 transmembrane (TM) domain packs against the top of F3. Radixin structures were generated from Protein Data Bank (PDB) ID code 22PY. Talin-1 structures were modeled using PDB ID codes 3G9W and 3IVF.



ϜΙΤϹ-ΡΙΡ5Κ1γ: ϜΙΤϹ-βΑΙa-S646WVYSPLΗY654

**Fig. S2.** Talin-1 constructs encompassing (A) the F0, F1, F2, and F3 subdomains, (*B*) the F0 and F1 subdomains, and (*C*) the F2 and F3 subdomains. Each construct contains an N-terminal Gly-Ser-His-Met (GSHM) motif enabling cleavage by thrombin. (*D*)  $\beta$ 3 CT constructs include the entire CT including the talin-1 recognition motif (bold) and preceded by a Cys residue at position 719 as well as an N-terminal GSHMG sequence for cleavage by thrombin (*Top*); a fluorescent  $\beta$ 3 CT construct in which a maleimide-BODIPY-TMR moiety is appended to C719 (*Middle*); and a  $\beta$ 3 CT construct in Cys719 was covalently modified with maleimide-functionalized phosphatidylethanolamine (*Bottom*). (*E*) FITC-labeled peptide derived from PIP5KI $\gamma$ .



Fig. S3. Steady-state binding isotherms for F0-F3 binding to 1% (triangles), 3% (squares), and 10% (diamonds) PtdIns(4,5)P<sub>2</sub> immobilized on a Biacore L1 SPR chip.



Fig. S4. ITC titrations of 2 mM Ins(1,4,5) $P_3$  into 150  $\mu$ M F0-F3 (filled squares) and 120  $\mu$ M Ins(1,4,5) $P_3$  into 6.0  $\mu$ M PLC- $\delta$ 1 (open squares). The titration into PLC- $\delta$ 1 could be fit to a OneSite model.



Fig. S5. Talin-1 FERM domain binding to the β3 CT immobilized on negatively charged surfaces or free in solution. The β3 CT (600 RU) was immobilized on a carboxy-methylated dextran SPR chip and F0-F3 to maximum concentration of 1 μM was flowed over the chip.



**Fig. S6.** FERM domain binding to the  $\beta$ 3 CT conjugated to negatively charged phospholipid bilayers. The talin-1 FERM domain (F0-F3, 150  $\mu$ M) was titrated at 20 °C into a buffer-matched suspension of LUVs composed of (A) 20% phosphatidylserine (PS), and (B) 20% PS + 1% PtdIns(4,5) $P_2$  and to which 5  $\mu$ M  $\beta$ 3 CT had been conjugated via a maleimide-functionalized lipid head group. The titrations were globally fit to a OneSite binding model using MicroCal/Origin.

Table S1. ITC measurements of t	talin-1 FERM domain a	and PLC-81 binding to	PtdIns(4,5)P <sub>2</sub> and Ins(1,4,5)P <sub>3</sub>
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	$K_{\rm a}$ , $ imes 10^6~{ m M}^{-1}$	<i>K</i> <sub>d</sub> , μΜ	$\Delta$ H, kcal/mol	$\Delta S$ , cal $\cdot$ mol <sup>-1</sup> $\cdot$ K <sup>-1</sup>	Stoichiometry
F0-F3 + 1% PtdIns(4,5)P2	_	_	_	_	_
F0-F3 + 3% PtdIns(4,5)P <sub>2</sub>	—	_	—	_	_
F0-F3 + 10% PtdIns $(4,5)P_2$	1.3 ± 0.6	0.781	$-3.3 \pm 0.4$	-17.0	0.33 ± 0.03
F0-F3 + 2 mM $lns(1,4,5)P_3$	—	_	—	—	_
PLC-δ1 + 1% PtdIns(4,5)P <sub>2</sub>	0.36 ± 0.08	2.82	-11.7 ± 1.0	-14.0	1.13 ± 0.07
PLC- $\delta$ 1 ± 3% PtdIns(4,5)P <sub>2</sub>	0.47 ± 0.03	2.11	-10.2 ± 0.2	-8.37	0.97 ± 0.01
PLC-δ1 +10% PtdIns(4,5)P <sub>2</sub>	0.24 ± .02	4.20	-12.8 ± 0.7	-18.3	0.75 ± 0.03
PLC- $\delta$ 1 + 2 mM lns(1,4,5) $P_3$	$1.4 \pm 0.2$	0.72	$-17.5 \pm 0.7$	-30.5	$0.80 \pm 0.02$

Measurements were performed at 20 °C in 25 mM MOPS pH 6.8 with 100 mM NaCl. Background heats of dilution were subtracted. Titrations were fit to one-site binding isotherms, and errors are reported as fitting errors. There was no net enthalpy for titration of F0-F3 into 1% and 3%  $PtdIns(4,5)P_2$  and 2 mM  $Ins(1,4,5)P_3$ . Data shown are the mean and standard deviation of three experiments.

## Table S2. ITC measurements of talin-1 FERM domain binding to the $\beta$ 3 CT attached to large unilamellar phospholipid vesicles (LUVs)

	$K_{\rm a}$ , $ imes 10^6$ M <sup>-1</sup>	<i>K</i> <sub>d</sub> , μΜ	$\Delta$ H, kcal/mol	$\Delta$ S, cal $\cdot$ mol <sup>-1</sup> $\cdot$ K <sup>-1</sup>	Stoichiometry
β3-1% PtdIns(4,5)P <sub>2</sub>	1.19 ± 0.21	0.86	-25.0 ± 1.5	-55.8	0.80 ± 0.04
β3-20% PS	0.29 ± 0.02	3.4	-32.3 ± 0.9	-83.3	0.8
$\beta$ 3-20%PS + 1% PtdIns(4,5) $P_2$	0.61 ± 0.11	1.6	$-34.0 \pm 2.8$	-87.5	0.95 ± .06

The talin-1 FERM domain was titrated into LUV suspensions containing 5  $\mu$ M immobilized  $\beta$ 3 CT. All experiments were performed at 20 °C in 25 mM MOPS pH 6.8 with 100 mM NaClk, and background heats of dilution were subtracted. Titrations were fit to one-site binding isotherms. The data are the mean and standard deviations of three to six experiments.