

SUPPLEMENTARY TABLES

Phosphatases modified by LH signaling in ovarian follicles: testing their role in regulating the NPR2 guanylyl cyclase

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Table S1. Antibodies used for western blotting.

Table S2. Statistically significant LH-induced changes in phosphopeptide intensity of proteins in rat ovarian follicles that have been reported to form complexes with PPP family phosphatase catalytic subunits, other than those listed in Table 1.

Table S1. Antibodies used for western blotting

Target	Supplier	Host species	Catalog #	Dilution	RRID
HA epitope tag (6E2)	Cell Signaling Technology	mouse	2367	1:1000	AB_10691311
Phospho-S507 PPP1R12A (P-MYPT1) ^a	Cell Signaling Technology	rabbit	3040	1:1000	AB_2168424
Phospho-S668 PPP1R12A (P-MYPT1)	Cell Signaling Technology	rabbit	3048	1:1000	AB_2168418
Phospho-S472 PPP1R12A (P-MYPT1)	Invitrogen	rabbit	PA5-114608	1:1000	AB_2899244
Phospho-T696 PPP1R12A (P-MYPT1)	Cell Signaling Technology	rabbit	5163	1:1000	AB_10691830
Phospho-T853 PPP1R12A (P-MYPT1)	Cell Signaling Technology	rabbit	4563	1:1000	AB_1031185
Total PPP2R5D	Abcam	rabbit	ab188323	1:10000	--
Phospho-S133 CREB	EMD Millipore	mouse	05-667	1:500	AB_309889
Total CREB	Cell Signaling Technology	rabbit	9197	1:1000	AB_331277
Goat-anti-mouse IgG (H+L), HRP conjugate	Advansta	goat	R-05071-500	1:20000	--
IRDye® 800CW Goat anti-Rabbit IgG Secondary Antibody	LI-COR	goat	925-32211	1:15000	AB_10956166
IRDye® 680RD Goat anti-Rabbit IgG Secondary Antibody	LI-COR	goat	926-68071	1:15000	AB_621842
IRDye® 800CW Goat anti-Mouse IgG Secondary Antibody	LI-COR	goat	926-32210	1:15000	AB_10718209

^aThe antigen used to make this antibody is 100% identical to the mouse PPP1R12A sequence, and 85% identical to the mouse PPP1R12B sequence. Therefore, this antibody would also recognize Phospho-S502 of PPP1R12B.

Table S2. Statistically significant LH-induced changes in phosphopeptide intensity of proteins in rat ovarian follicles that have been reported to form complexes with PPP family phosphatase catalytic subunits, other than those listed in Table 1. Previously published lists of validated PPP family-interacting proteins (19, 20) were used to query the phosphopeptide database for significant differences in response to LH. Multiplicity refers to either singly phosphorylated (1) or doubly phosphorylated (2) peptides. Significant increases in phosphopeptide intensity following LH treatment are above the dashed line; significant decreases in phosphopeptide intensity with LH treatment are below the dashed line.

Gene name	UniProt accession	Amino acid	Site #	Multiplicity	Phosphopeptide intensity (log ₂ mean ± SEM)		Fold change
					Control	350 nM LH	
HDAC6*	A0A0G2QC41	S	59	1	14.56 ± 0.61	18.64 ± 1.07	18.0
STRN3*	E9PT82	S	239	2	15.24 ± 0.08	19.02 ± 0.18	14.6
STRN3*	E9PT82	S	255	2	15.24 ± 0.08	19.02 ± 0.18	14.6
PLCL1	F1LP62	S	19	2	17.04 ± 0.13	20.14 ± 0.06	9.1
EIF2AK2	M0RDJ3	S	212	1	18.95 ± 0.18	21.94 ± 0.26	8.5
FARP1*	F1LYQ8	S	513	2	13.80 ± 0.21	16.70 ± 0.18	7.9
FARP1*	F1LYQ8	S	517	2	13.80 ± 0.21	16.70 ± 0.18	7.9
MAP1B*	P15205	S	561	1	22.90 ± 0.12	25.52 ± 0.31	6.5
ZFYVE16	D4ADF6	S	903	2	17.57 ± 0.24	20.17 ± 0.09	6.5
ZFYVE16	D4ADF6	S	907	2	17.57 ± 0.24	20.17 ± 0.09	6.5
PHACTR4*	M0R7T1	S	159	2	18.97 ± 0.16	21.52 ± 0.12	6.2
APC*	G3V8Q9	S	2793	1	18.43 ± 0.11	20.87 ± 0.19	5.8
MKI67	D4A0Y6	S	124	1	17.98 ± 0.02	20.41 ± 0.24	5.7
PHACTR4*	M0R7T1	S	162	2	19.29 ± 0.20	21.68 ± 0.13	5.5
AKAP1	D4A9M6	S	425	1	17.01 ± 0.06	29.39 ± 0.11	5.5
APC*	G3V8Q9	S	2817	2	15.38 ± 0.33	17.67 ± 0.21	5.2
APC*	G3V8Q9	S	2829	2	15.67 ± 0.27	17.77 ± 0.18	4.6
APC*	G3V8Q9	T	2819	2	14.37 ± 0.25	16.23 ± 0.10	3.8
PLCL1	F1LP62	T	15	2	19.78 ± 0.11	21.58 ± 0.07	3.7
SH2D4A	Q6AYC8	S	51	1	18.21 ± 0.21	20.01 ± 0.39	3.7
PCIF1	D4A417	T	135	3	14.49 ± 0.25	16.29 ± 0.14	3.7
SLC9A1	P26431	S	707	2	19.21 ± 0.14	20.98 ± 0.09	3.6
AKAP11	A0A0G2JZI9	S	21	1	17.30 ± 0.37	19.05 ± 0.37	3.6
PLCL1	F1LP62	S	491	1	11.53 ± 0.35	13.23 ± 0.24	3.4
PCIF1	D4A417	T	150	2	18.36 ± 0.37	20.05 ± 0.09	3.4
PCIF1	D4A417	T	135	2	16.05 ± 0.44	17.73 ± 0.28	3.4
PCIF1	D4A417	S	140	3	16.06 ± 0.23	17.66 ± 0.16	3.2
PLCL1	F1LP62	S	17	2	19.58 ± 0.13	21.12 ± 0.07	3.1
SLC9A1	P26431	S	697	2	20.56 ± 0.11	22.09 ± 0.14	3.1
SLC9A1	P26431	S	776	2	16.38 ± 0.10	17.86 ± 0.17	3.0
MAP1B*	P15205	S	985	2	23.10 ± 0.09	24.56 ± 0.16	2.9

MAP1B*	P15205	S	988	2	23.10 ± 0.09	24.56 ± 0.16	2.9
MAP1B*	P15205	S	1454	2	17.42 ± 0.41	18.86 ± 0.14	2.9
MAP1B*	P15205	S	1465	2	17.42 ± 0.41	18.86 ± 0.14	2.9
MAP1B*	P15205	T	1262	3	19.12 ± 0.26	20.51 ± 0.06	2.8
SLC9A1	P26431	S	606	2	17.61 ± 0.02	19.00 ± 0.15	2.8
MKI67	D4A0Y6	S	336	1	19.80 ± 0.08	21.09 ± 0.22	2.6
SLC9A1	P26431	S	790	2	19.02 ± 0.07	20.22 ± 0.12	2.4
SET*	Q63945	S	28	2	18.89 ± 0.06	20.09 ± 0.11	2.4
SET*	Q63945	S	30	2	18.89 ± 0.06	20.09 ± 0.11	2.4
MAP1B*	P15205	S	1471	1	17.76 ± 0.11	18.90 ± 0.32	2.3
CASP9	Q9JHK1	S	348	2	14.65 ± 0.09	15.70 ± 0.26	2.2
CASP9	Q9JHK1	S	350	2	14.65 ± 0.09	15.70 ± 0.26	2.2
AKAP1	D4A9M6	S	101	1	18.57 ± 0.07	19.60 ± 0.31	2.2
HDAC6*	A0A0G2QC41	S	43	1	22.25 ± 0.11	19.52 ± 0.37	-6.2
HDAC6*	A0A0G2QC41	S	859	1	21.50 ± 0.12	19.27 ± 0.61	-4.4
MAP1B*	P15205	T	527	1	21.25 ± 0.23	19.10 ± 0.73	-4.2
AKAP1	D4A9M6	S	103	1	19.38 ± 0.19	17.48 ± 0.51	-3.5
PHACTR2*	A0A0G2K8Q4	T	22	1	20.29 ± 0.23	18.48 ± 0.73	-3.3
FARP1*	F1LYQ8	S	427	2	20.51 ± 0.31	18.85 ± 0.13	-3.0
FARP1*	F1LYQ8	S	435	2	20.51 ± 0.31	18.85 ± 0.13	-3.0
PHACTR2*	A0A0G2K8Q4	S	154	1	18.30 ± 0.08	16.65 ± 0.40	-3.0
MAP1B*	P15205	S	541	1	24.80 ± 0.03	23.33 ± 0.40	-2.6
APC*	G3V8Q9	S	2556	2	17.80 ± 0.18	16.35 ± 0.19	-2.6
MAP1B*	P15205	T	1959	1	17.86 ± 0.12	16.45 ± 0.35	-2.5
SLC9A1	P26431	S	790	1	22.26 ± 0.11	20.91 ± 0.47	-2.4
APC*	G3V8Q9	S	2556	2	19.43 ± 0.08	18.22 ± 0.36	-2.2

* Proteins known to regulate the cytoskeleton and/or cell motility according to the National Center for Biotechnology Information (NCBI) gene summaries.