## Supplementary Figures for Phosphorylation Changes in Response to Kinase Inhibitor H89 in PKA-Null Cells

Kavee Limbutara<sup>&</sup>, Andrew Kelleher<sup>&</sup>, Chin-Rang Yang<sup>&</sup>, Viswanathan Raghuram and Mark A. Knepper<sup>‡</sup>

> Epithelial Systems Biology Laboratory, Systems Biology Center, National Heart, Lung, and Blood Institute, National Institutes of Health, Bethesda, Maryland

<sup>&</sup>Contributed equally.

<sup>‡</sup>Correspondence to Mark A. Knepper, National Institutes of Health, Bldg. 10, Room 6N307, 10

CENTER DR, MSC-1603, Bethesda, MD 20892-1603,

Phone: (301) 496-3064, Fax: (301) 402-1443,

E-mail: knepperm@nhlbi.nih.gov



**Supplementary Figure S1.** Immunoblot using a PKA antibody recognizing both PKA catalytic proteins shows absence of PKA catalytic subunits in PKA-null cells.



## Supplementary Figure S2. 2D annotation enrichment analysis.

To compare effect H89 on phosphoproteome of PKA-intact and PKA-null cells, each phosphoprotein was annotated with HPRD PhosphoMotif, gene ontology, KEGG, Pfam, GSEA, Corum, InterPro, PRINTS, PROSITE, Reactome, and SMART terms. 2D annotation enrichment analysis was performed using Perseus software. Terms with adjusted p-value < 0.01 are shown in the scatter plot. X and y-axes correspond to enrichment score which calculated from rank of effect size of H89 on phosphosites (range from -1 to 1). All significant terms are clustered around the origin, suggesting minimal enrichment in any category. Consistent with sequence logos generated from significantly changed phosphosites, several non-PKA basophilic kinase motifs were enriched with negative score (decrease by H89) and proline-directed kinase motifs were enriched with positive score (increase by H89) in both cell types.



**Supplementary Figure S3. Up-regulated kinases in PKA-null cells.** A volcano plot shows log2 ratio of protein abundance (normalized log2 TMT reporter ion intensity) of PKA-null over PKA-intact cells (control group) on x-axis and negative of log10 p-value (moderated t-test, LIMMA) on y-axis. Kinases are colored in orange. Up-regulated kinases with p-value < 0.05 and log2 ratio > 0.5 are labeled with gene symbol and its log2 ratio value.

Gene	Protein	Protein name	Position	β <sub>H89</sub> in PKA-intact	Centralized sequence
Snrnp200	Q6P4T2	U5 small nuclear ribonucleoprotein 200 kDa helicase	2131, 2133, 2135	0.44	VDVKEAETDSDSD VKEAETDSDSD EAETDSDSD
Chd2	E9PZM4	Chromodomain-helicase-DNA-binding protein 2	156, 165	0.41	EKWKQDP <mark>S</mark> EDEQEQG DEQEQGT <mark>S</mark> AESEAEQ
lws1	Q8C1D8	Protein IWS1 homolog	248, 263	0.39	ELPKPRV <mark>S</mark> DSESEDP QKGPASD <mark>S</mark> EAEDASR
Mcm3	P25206	DNA replication licensing factor MCM3	722	0.37	PQVHTPK <mark>T</mark> DDSQEKT
Sept9	Q80UG5	Septin-9	85	0.31	VDSLSQR <mark>S</mark> PKPSLRR
Llgl1	A0A0R4J0S4	Lethal(2) giant larvae protein homolog 1	988, 989	0.31	ESCEGSP <mark>SS</mark> AHSKRA SCEGSP <mark>SS</mark> AHSKRAD
Prr12	E9PYL2	Proline-rich protein 12	1555	0.30	TAAVCGE <mark>T</mark> DEEAGES
Mphosph10	Q810V0	U3 small nucleolar ribonucleoprotein protein MPP10	244	0.29	DLFEDID <mark>S</mark> DESEGGL
Hnrnpa1	Q5EBP8	Heterogeneous nuclear ribonucleoprotein A1	22	0.29	KLFIGGL <mark>S</mark> FETTDES
Srsf7	Q8BL97	Serine/arginine-rich splicing factor 7	210	0.26	ASLRRSR <mark>S</mark> GSIIGSR

Supplementary Table S1 : Phosphorylation sites with largest positive  $\beta_{\text{H89}}$  in PKA-intact cells.

Gene	Protein	Protein name	Position	β <sub>H89</sub> in PKA-null	Centralized sequence
Chd2	E9PZM4	Chromodomain-helicase-DNA-binding protein 2	156, 165	0.26	EKWKQDP <mark>S</mark> EDEQEQG DEQEQGT <mark>S</mark> AESEAEQ
lws1	Q8C1D8	Protein IWS1 homolog	248, 263	0.25	ELPKPRV <mark>S</mark> DSESEDP QKGPASD <mark>S</mark> EAEDASR
Ptpn14	Q62130	Tyrosine-protein phosphatase non- receptor type 14	700, 705, 719	0.25	PQYHHKKTFSDATML KKTFSDATMLIHSSE ESEEEEETLEAAPQV
Prr12	E9PYL2	Proline-rich protein 12	1555	0.25	TAAVCGETDEEAGES
8030462 N17Rik	Q0VAW6	RIKEN cDNA 8030462N17 gene	322, 323	0.23	NEEINIA <mark>SS</mark> DSEVEI EEINIA <mark>SS</mark> DSEVEIV
Utp18	Q5SSI6	U3 small nucleolar RNA-associated protein 18 homolog	115, 118	0.22	RGQLHGS <mark>S</mark> DESEVEN LHGS <mark>S</mark> DE <mark>S</mark> EVENEAK
Llgl1	A0A0R4J0S4	Lethal(2) giant larvae protein homolog 1	988, 989	0.22	ESCEGSP <mark>SS</mark> AHSKRA SCEGSP <mark>SS</mark> AHSKRAD
Mcm3	P25206	DNA replication licensing factor MCM3	722	0.21	PQVHTPK <mark>T</mark> DDSQEKT
Wrnip1	Q91XU0	ATPase WRNIP1	91, 92	0.20	ATPTAAE <mark>SS</mark> EGEGEE TPTAAE <mark>SS</mark> EGEGEEG
Nucks1	Q80XU3	Nuclear ubiquitous casein and cyclin- dependent kinase substrate 1	144	0.20	LMEDDDD <mark>S</mark> DYGSSKK

Supplementary Table S2 : Phosphorylation sites with largest positive  $\beta_{\text{H89}}$  in PKA-null cells.