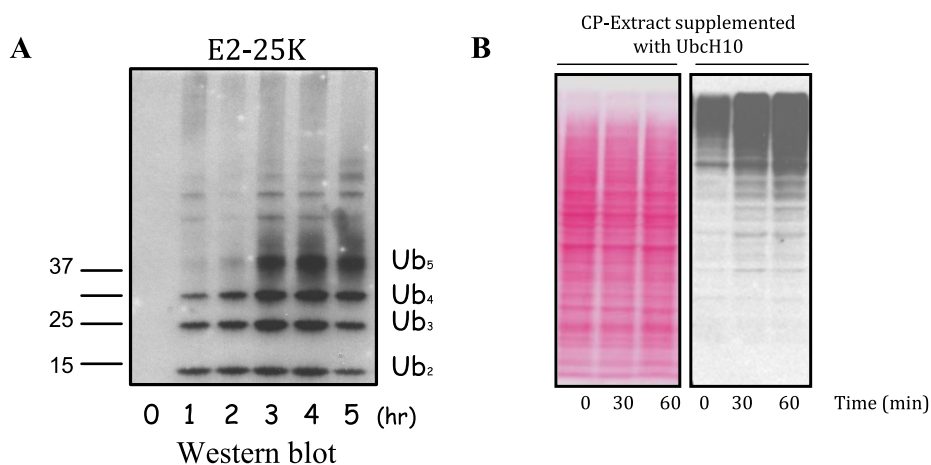
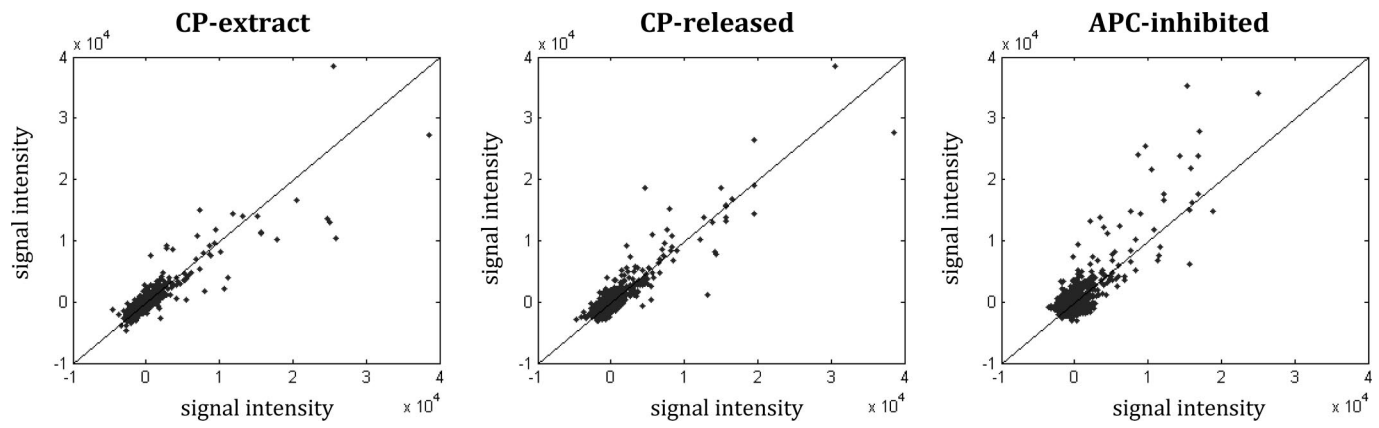


# Supporting Information

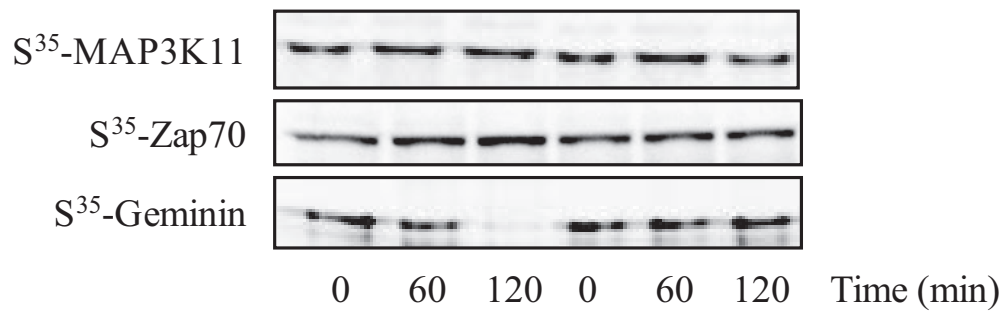
Merbl and Kirschner 10.1073/pnas.0812892106



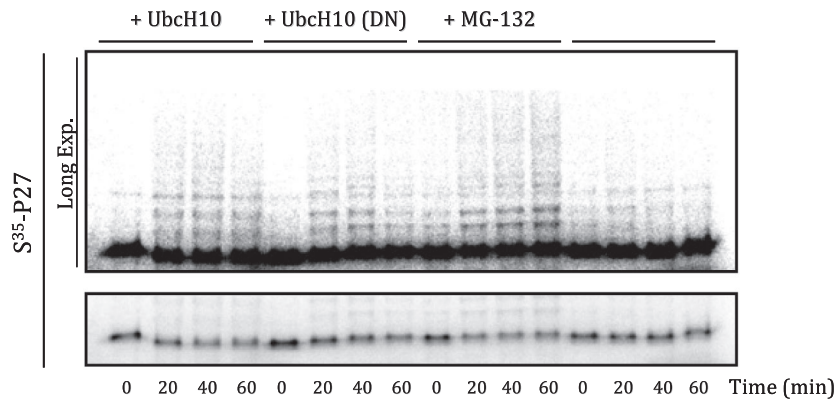
**Fig. S1.** Testing the FK1 antibody. (A) It was previously reported that E2-25K can generate polyubiquitin chains without E3 [Chen Z, Pickart CM (1990) A 25-kilodalton ubiquitin carrier protein (E2) catalyzes multi-ubiquitin chain synthesis via lysine 48 of ubiquitin. *J Biol Chem* 265:21835–21842]. We therefore tested the ability of the antibody to detect increasing levels of polyubiquitin chains. E2-25K-conjugated Ub-chain synthesis was performed in vitro at 37 °C and the reaction was stopped at the indicated time points by the addition of sample buffer. Products were analyzed by SDS/PAGE gel electrophoresis. FK1 (Biomol) antibody was then used to blot for the polyubiquitin chains. (B) CP-extracts were supplemented with UbcH10, and the reaction was stopped at the indicated time points to follow the change in the global ubiquitination signal in the extract as a function of time.



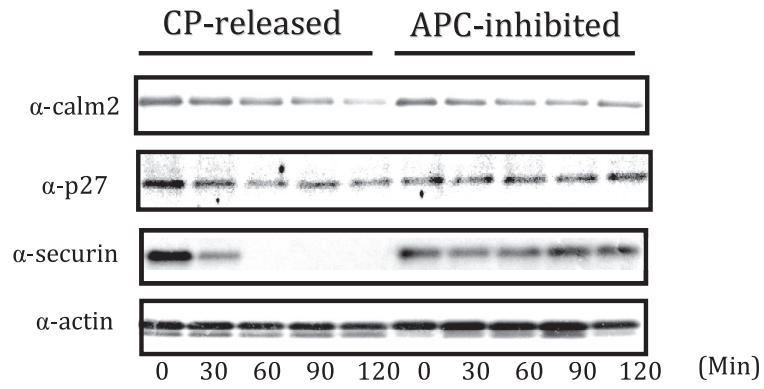
**Fig. S2.** Reproducibility of the assay. Signal intensity of each protein was calculated by taking the average of its spots reactivities (signal intensity minus background value). The signal intensity of each protein was then plotted and compared between 2 replicate microarrays. The biological replicates of 3 different conditions (6 chips in total) are shown (CP-extract, CP-released, and APC-inhibited).



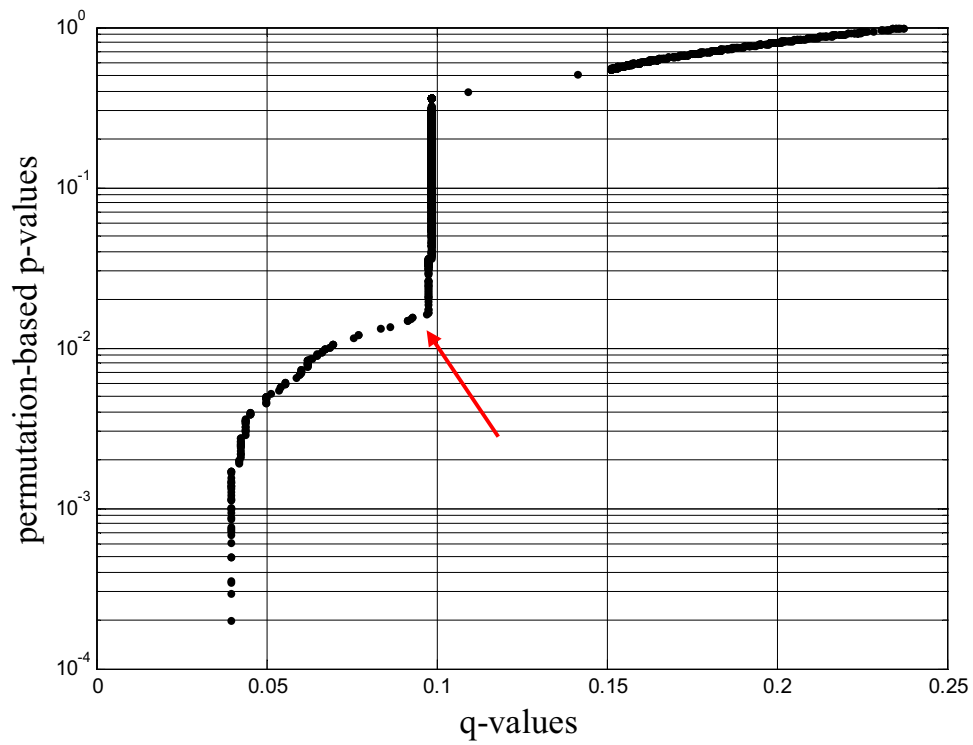
**Fig. S3.** S<sup>35</sup>-labeled MAP3K11 and Zap70 proteins and the positive control Geminin were added to CP-synchronized HeLa S3 extracts with and without the addition of the APC-inhibitor emi1. Reactions were stopped at 0, 60, and 120 min and analyzed by SDS/PAGE (4–15%) and autoradiography.



**Fig. S4.** Full gel of Fig. 3C.  $S^{35}$ -labeled p27 was added to CP-synchronized HeLa S3 extracts with the addition of UbcH10 ( $1 \mu\text{L}$ ;  $1 \text{ mg/mL}$ ), a dominant-negative UbcH10 (UbcH10-DN;  $1 \mu\text{L}$ ,  $1 \text{ mg/mL}$ ), UbcH10 and MG-132 ( $200 \mu\text{M}$ ), or UbcH10 and Emi1 ( $5 \text{ mg/mL}$ ). UbcH10-DN, the catalytically inactive mutant UbcH10<sup>C114S</sup>, was previously shown to inhibit APC-dependent ubiquitination *in vitro*. In this experiment, UbcH10-DN failed to inhibit p27 ubiquitination, suggesting that there might be different E2 or E3 enzymes that are involved in its ubiquitination.



**Fig. S5.** Degradation assay of endogenous calmodulin and p27 proteins. Degradation of endogenous proteins (calmodulin, p27, and securin) in the CP-released and APC-inhibited extracts was detected by western blotting using the indicated primary antibodies. Actin was used as a loading control (securin, MBL; calmodulin, Upstate; p27, Upstate; actin, Sigma). Shown below is the time of incubation.



**Fig. S6.** Setting a threshold for controlling the FDR. For each of the proteins on the array, the permutation-based  $P$  value was plotted as a function of the protein's  $q$ -value. The red arrow depicts the threshold  $q$ -value we chose to determine which proteins were differentially modified ( $q < 0.096$ ).

**Table S1. A list of differentially modified proteins between CP-released and APC-inhibited extracts**

Name	Protein ID	P	q	pFDR value
additional sex combs like 1 ( <i>Drosophila</i> )	BC064984.1	0.001	0.040	0.048
ADP-ribosylation factor-like 7 (ARL7)	NM.005737.3	0.002	0.042	0.043
ADP-ribosylation-like factor 6 interacting protein 4 (ARL6IP4)	NM.016638.1	0.005	0.050	0.051
anaplastic lymphoma kinase ( $K_i$ -1) (ALK)	NM.004304.3	0.013	0.083	0.083
ankyrin repeat domain 13	BC032833.2	0.000	0.040	0.067
arrestin domain containing 3 (ARRDC3)	NM.020801.1	0.006	0.054	0.055
aurora kinase A (AURKA),	NM.003600.2	0.001	0.040	0.060
aurora kinase B (AURKB)	NM.004217.2	0.001	0.040	0.044
aurora kinase C (AURKC),	NM.001015878.1	0.007	0.060	0.061
B lymphoid tyrosine kinase (BLK)	NM.001715.2	0.008	0.062	0.063
baculoviral IAP repeat-containing 4 (BIRC4)	NM.001167.2	0.015	0.091	0.092
calcium binding protein 4	BC033167.1	0.008	0.062	0.062
calcium/calmodulin-dependent protein kinase (CaM kinase) II beta (CAMK2B)	NM.001220.3	0.009	0.063	0.063
calcium/calmodulin-dependent protein kinase IV (CAMK4)	NM.001744.2	0.006	0.055	0.056
Calmodulin (from <i>Saccharomyces cerevisiae</i> , CALM2 homolog*)	NM.001743*	0.006	0.055	0.056
casein kinase 1, alpha 1 (CSNK1A1),	NM.001025105.1	0.003	0.044	0.045
cDNA clone MGC:3432	BC013957.1	0.004	0.045	0.046
cDNA clone MGC:39273	BC024289.1	0.001	0.040	0.046
chromosome 16 open reading frame 5	BC002882.1	0.003	0.042	0.042
chromosome 19 open reading frame 28 (C19orf28)	NM.174983.2	0.008	0.062	0.062
chromosome 6 open reading frame 145 (C6orf145)	NM.183373.2	0.002	0.042	0.044
chromosome 6 open reading frame 201 (C6orf201)	NM.206834.1	0.006	0.055	0.056
chromosome 7 open reading frame 2 (C7orf2)	NM.022458.2	0.003	0.044	0.044
chromosome 9 open reading frame 43 (C9orf43)	NM.152786.1	0.010	0.067	0.067
conserved helix-loop-helix ubiquitous kinase (CHUK)	NM.001278.3	0.007	0.060	0.061
cullin 3 (CUL3)	NM.003590.2	0.007	0.060	0.060
cyclin G2	BC032518.1	0.007	0.060	0.060
cyclin-dependent kinase inhibitor 1B (p27, Kip1) (CDKN1B)	NM.004064.2	0.006	0.054	0.054
cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1),	NM.057157.1	0.001	0.040	0.053
dendritic cell-derived ubiquitin-like protein (DC-Ubp)	NM.152277.1	0.004	0.045	0.047
dexamethasone-induced (DEXI)	NM.014015.3	0.012	0.077	0.077
DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activated DNase) (DFFB),	NM.001004285.1	0.004	0.044	0.044
DnaJ (Hsp40) homolog, subfamily B, member 12 (DNAJB12),	NM.001002762.1	0.004	0.045	0.046
DnaJ (Hsp40) homolog, subfamily B, member 6,	BC000177.2	0.008	0.062	0.062
dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit (DPM2),	NM.152690.1	0.001	0.040	0.055
dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 (DYRK3),	NM.001004023.1	0.007	0.060	0.061
EGF-like repeats and discoidin I-like domains 3	BC053656.1	0.002	0.040	0.041
ems1 sequence, mammary tumor and squamous cell carcinoma-associated (EMS1),	NM.138565.1	0.001	0.040	0.052
EPH receptor A8 (EPHA8),	NM.001006943.1	0.010	0.068	0.068
EphA4 (EPHA4)	NM.004438.1	0.009	0.066	0.066
erythrocyte membrane protein band 4.1 like 5	BC054508.1	0.000	0.040	0.093
eukaryotic translation initiation factor 1A, X-linked (EIF1AX)	NM.001412.2	0.011	0.069	0.069
expressed in T-cells and eosinophils in atopic dermatitis (ETEA)	NM.014613.1	0.003	0.044	0.045
farnesyl-diphosphate farnesyltransferase 1	BC003573.1	0.015	0.092	0.092
feline sarcoma oncogene (FES)	NM.002005.2	0.002	0.040	0.040
fibroblast growth factor receptor 4 (FGFR4),	NM.002011.3	0.015	0.093	0.093
fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) (FLT1)	NM.002019.1	0.012	0.076	0.076
G protein-coupled receptor kinase 4 (GRK4),	NM.001004056.1	0.003	0.043	0.043

Name	Protein ID	<i>P</i>	<i>q</i>	pFDR value
hepatocyte growth factor-regulated tyrosine kinase substrate (HGS)	NM.004712.3	0.008	0.062	0.063
HTGN29 protein (HTGN29)	NM.020199.1	0.000	0.040	0.080
hypothetical gene LOC128439 (LOC128439)	NM.139016.2	0.003	0.044	0.045
hypothetical protein DKFZp762O076 (DKFZp762O076)	NM.018710.1	0.001	0.040	0.042
hypothetical protein FLJ10156	BC005004.1	0.005	0.050	0.052
hypothetical protein FLJ11184	BC011842.2	0.001	0.040	0.070
hypothetical protein FLJ11749 (FLJ11749)	NM.024591.1	0.011	0.069	0.070
hypothetical protein FLJ36175	BC029520.1	0.001	0.040	0.040
hypothetical protein FLJ38628 (FLJ38628)	NM.152267.2	0.007	0.058	0.058
hypothetical protein LOC143458 (LOC143458)	NM.174902.2	0.001	0.040	0.044
hypothetical protein LOC255330	BC042038.1	0.009	0.065	0.065
hypothetical protein MGC11257 (MGC11257)	NM.032350.3	0.003	0.044	0.045
hypothetical protein MGC17403 (MGC17403)	NM.152634.1	0.004	0.044	0.045
hypothetical protein MGC40579 (MGC40579)	NM.152776.1	0.008	0.062	0.064
hypothetical protein MGC4618 (MGC4618)	NM.032326.1	0.002	0.040	0.042
hypothetical protein MGC51025 (MGC51025)	NM.178571.2	0.010	0.067	0.068
immediate early response 3 (IER3),	NM.003897.2	0.002	0.042	0.042
immunoglobulin heavy constant gamma 1 (G1m marker)	BC014667.1	0.002	0.042	0.043
immunoglobulin heavy constant gamma 1 (G1m marker)	BC019337.1	0.015	0.091	0.091
insulin-like growth factor 1 receptor (IGF1R)	NM.000875.2	0.003	0.042	0.042
integral membrane protein 2C	BC002424.1	0.012	0.077	0.077
interferon stimulated gene 20kDa (ISG20)	NM.002201.3	0.003	0.042	0.042
interleukin 17E (IL17E),	NM.022789.2	0.005	0.050	0.052
KIAA0157 protein (KIAA0157)	NM.032182.2	0.001	0.040	0.051
KIAA1458 protein	BC031691.2	0.005	0.050	0.051
likely ortholog of mouse gene trap locus 3 (GTL3)	NM.013242.1	0.002	0.042	0.042
low density lipoprotein receptor-related protein 10 (LRP10)	NM.014045.1	0.005	0.053	0.053
lymphocyte-specific protein tyrosine kinase (LCK),	NM.001042771.1	0.015	0.091	0.092
lysosomal-associated protein transmembrane 4 alpha (LAPTM4A)	NM.014713.2	0.005	0.050	0.050
MAX interacting protein 1 (MXI1),	NM.130439.1	0.001	0.040	0.044
megakaryocyte-associated tyrosine kinase (MATK),	NM.002378.3	0.016	0.093	0.093
melanoma antigen, family B, 1 (MAGEB1)	NM.002363.1	0.009	0.065	0.065
mitogen-activated protein kinase kinase 11 (MAP3K11)	NM.002419.2	0.003	0.044	0.044
mRNA similar to hypothetical protein FLJ25555	BC044239.1	0.005	0.050	0.051
Nedd4 family interacting protein 1 (NDFIP1)	NM.030571.2	0.001	0.040	0.040
Nedd4 family interacting protein 2	BC021988.1	0.010	0.068	0.068
neural precursor cell expressed, developmentally down-regulated 8 (NEDD8)	NM.006156.1	0.001	0.040	0.044
neurotrophic tyrosine kinase, receptor, type 1 (NTRK1),	NM.001007792.1	0.002	0.042	0.044
N-glycanase 1 (NGLY1)	NM.018297.2	0.004	0.044	0.045
NIMA (never in mitosis gene a)- related kinase 9 (NEK9)	NM.033116.2	0.008	0.062	0.063
p53-regulated DDA3 (DDA3)	NM.032636.2	0.006	0.055	0.056
PAS domain containing serine/threonine kinase (PASK)	NM.015148.1	0.001	0.040	0.048
PCTAIRE protein kinase 2	BC033005.1	0.001	0.040	0.064
pleckstrin homology domain containing, family G, member 5 (PLEKHG5),	NM.020631.2	0.002	0.042	0.043
potassium voltage-gated channel, shaker-related subfamily, beta member 2 (KCNA2)	NM.003636.1	0.002	0.042	0.042
PREDICTED	XM.378350.2	0.005	0.051	0.051
PREDICTED	XM.373800.2	0.010	0.067	0.067
proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 (PSMD4)	NM.002810.1	0.001	0.040	0.045
proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 (PSMD4), T2	NM.153822.1	0.002	0.042	0.043
RAS-like, family 10, member B	BC041133.1	0.003	0.044	0.044
regenerating islet-derived 1 alpha (pancreatic stone protein, pancreatic thread protein)	BC005350.1	0.008	0.062	0.062
ribosomal protein L30 (RPL30)	NM.000989.2	0.002	0.040	0.041
ribosomal protein S6 kinase, 90kDa, polypeptide 4 (RPS6KA4),	NM.001006944.1	0.001	0.040	0.070
ring finger protein 111	BC060862.1	0.001	0.040	0.050



Name	Protein ID	<i>P</i>	<i>q</i>	pFDR value
ring finger protein 111	BC010369.1	0.003	0.042	0.042
ring finger protein 128 (RNF128),	NM_194463.1	0.000	0.040	0.120
ring finger protein 4 (RNF4)	NM_002938.2	0.002	0.042	0.042
secretory carrier membrane protein 3 (SCAMP3),	NM_005698.2	0.009	0.065	0.065
selectin ligand interactor cytoplasmic-1 (SLIC1),	NM_153337.1	0.001	0.040	0.045
serum/glucocorticoid regulated kinase (SGK)	NM_005627.1	0.005	0.050	0.051
signal recognition particle 19kDa	BC010947.1	0.004	0.044	0.044
Sjogren syndrome antigen A1 (52kDa, ribonucleoprotein autoantigen SS-A/Ro) (SSA1)	NM_003141.2	0.003	0.042	0.043
SMT3 suppressor of mif two 3 homolog 1 (yeast) (SUMO1),	NM_003352.4	0.004	0.045	0.045
solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1 (SLC1A1)	NM_004170.2	0.008	0.062	0.062
solute carrier family 23 (nucleobase transporters), member 2	BC013112.2	0.001	0.040	0.051
solute carrier family 36 (proton/amino acid symporter), member 4	BC047374.1	0.004	0.045	0.046
solute carrier family 6 (neurotransmitter transporter), member 15	BC022253.1	0.005	0.050	0.050
src homology three (SH3) and cysteine rich domain TANK-binding kinase 1 (TBK1)	BC020221.1	0.001	0.040	0.042
tec protein tyrosine kinase (TEC)	NM_013254.2	0.003	0.042	0.043
tec protein tyrosine kinase (TEC)	NM_003215.1	0.009	0.066	0.066
thousand and one amino acid protein kinase (TAO1)	NM_004783.1	0.005	0.050	0.051
tripartite motif-containing 52 (TRIM52)	NM_032765.1	0.006	0.055	0.055
ubiquitin-activating enzyme E1-like (UBE1L)	NM_003335.2	0.008	0.062	0.063
ubiquitin-conjugating enzyme E2-like vasopressin-induced	BC064566.1	0.009	0.063	0.063
vasopressin-induced	BC000877.1	0.007	0.059	0.060
WD repeat domain 45 (WDR45),	NM_007075.3	0.003	0.042	0.043
YY1 ion factor (YY1)	NM_003403.3	0.001	0.040	0.046
zeta-chain (TCR) associated protein kinase 70kDa (ZAP70),	NM_001079.3	0.002	0.040	0.042
zeta-chain (TCR) associated protein kinase 70kDa,	BC053878.1	0.003	0.044	0.045
zinc finger protein 313 (ZNF313)	NM_018683.2	0.005	0.050	0.050
BC013173 Homo sapiens, clone MGC:17340	BC013173.1	0.000	0.040	0.072
BC015219 , HBV associated factor, clone MGC:17759	BC015219.1	0.014	0.086	0.086
BC015569 , Similar to SRp25 nuclear protein, clone MGC:22989	BC015569.1	0.006	0.055	0.056
BC018953 , SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	BC018953.1	0.008	0.062	0.062

Protein reactivities of two microarrays in each condition were compared using two-sided t-test. Permutation-based *P* values were calculated and the false discovery rate was calculated for each gene based on Storey's *q* values estimation (see materials and methods). Differentially modified proteins (*q* value < 0.096) were alphabetically sorted.

**Table S2. A full summary of the “functional annotation clustering” tool analysis**

Category	Term	Count	%	<i>P</i>	List Total	Fold Enrichment	Benjamini	FDR
Functional Group 1	Median: 2.4538434663258228E-5	Geo:2.6E-5						
GOTERM_BP_ALL	GO:0043687~post-translational protein modification	39	31.97	0.00	91	2.83	1.60E-06	7.46E-07
GOTERM_BP_ALL	GO:0006468~protein amino acid phosphorylation	29	23.77	0.00	91	3.75	9.76E-07	9.09E-07
GOTERM_BP_ALL	GO:0016310~phosphorylation	30	24.59	0.00	91	3.39	3.05E-06	4.26E-06
GOTERM_BP_ALL	GO:0006464~protein modification process	40	32.79	0.00	91	2.54	5.21E-06	9.71E-06
GOTERM_BP_ALL	GO:0043412~biopolymer modification	40	32.79	0.00	91	2.46	1.06E-05	2.47E-05
GOTERM_BP_ALL	GO:0006793~phosphorus metabolic process	30	24.59	0.00	91	2.97	2.77E-05	9.05E-05
GOTERM_BP_ALL	GO:0006796~phosphate metabolic process	30	24.59	0.00	91	2.97	2.77E-05	9.05E-05
GOTERM_BP_ALL	GO:0044267~cellular protein metabolic process	46	37.70	0.00	91	1.77	0.0058201	0.021755
GOTERM_BP_ALL	GO:0044260~cellular macromolecule metabolic process	46	37.70	0.00	91	1.75	0.0076647	0.03226
GOTERM_BP_ALL	GO:0019538~protein metabolic process	47	38.52	0.00	91	1.71	0.0097359	0.045575
GOTERM_BP_ALL	GO:0007154~cell communication	40	32.79	0.00	91	1.57	0.3091181	2.04634
GOTERM_BP_ALL	GO:0007165~signal transduction	37	30.33	0.00	91	1.60	0.3798054	2.852187
GOTERM_BP_ALL	GO:0007242~intracellular signaling cascade	23	18.85	0.00	91	1.94	0.4641607	3.988206
GOTERM_BP_ALL	GO:0043283~biopolymer metabolic process	49	40.16	0.00	91	1.40	0.52255	5.035767
GOTERM_BP_ALL	GO:0043170~macromolecule metabolic process	56	45.90	0.04	91	1.20	0.9974465	52.81438
GOTERM_BP_ALL	GO:0009987~cellular process	83	68.03	0.17	91	1.05	0.9999999	96.8274
GOTERM_BP_ALL	GO:0044238~primary metabolic process	59	48.36	0.18	91	1.09	0.9999999	97.71759
GOTERM_BP_ALL	GO:0044237~cellular metabolic process	58	47.54	0.24	91	1.08	1	99.45021
GOTERM_BP_ALL	GO:0008152~metabolic process	60	49.18	0.52	91	1.01	1	99.99989
Functional Group 2	Median: 0.03618327017494709	Geo:0.02						
GOTERM_BP_ALL	GO:0007243~protein kinase cascade	13	10.66	0.00	91	3.42	0.1094739	0.592481
GOTERM_BP_ALL	GO:0007249~I-kappaB kinase/NF-kappaB cascade	5	4.10	0.03	91	4.36	0.9934518	38.86154
GOTERM_BP_ALL	GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB cascade	4	3.28	0.03	91	5.49	0.9977434	47.9547
GOTERM_BP_ALL	GO:0009966~regulation of signal transduction	9	7.38	0.04	91	2.31	0.9972948	51.14291
GOTERM_BP_ALL	GO:0009967~positive regulation of signal transduction	5	4.10	0.04	91	3.81	0.9970107	53.15564
GOTERM_BP_ALL	GO:0043122~regulation of I-kappaB kinase/NF-kappaB cascade	4	3.28	0.04	91	5.11	0.9964362	54.52181
Functional Group 3	Median: 0.06870726602237465	Geo:0.08						
GOTERM_BP_ALL	GO:0000278~mitotic cell cycle	8	6.56	0.01	91	3.25	0.9139941	17.66118
GOTERM_BP_ALL	GO:0022403~cell cycle phase	8	6.56	0.02	91	2.97	0.9705053	26.79692
GOTERM_BP_ALL	GO:0007049~cell cycle	14	11.48	0.02	91	1.99	0.9814067	31.01961
GOTERM_BP_ALL	GO:0051329~interphase of mitotic cell cycle	4	3.28	0.03	91	5.49	0.9977434	47.9547
GOTERM_BP_ALL	GO:0008284~positive regulation of cell proliferation	6	4.92	0.04	91	3.20	0.9976734	50.65269
GOTERM_BP_ALL	GO:0051325~interphase	4	3.28	0.04	91	5.11	0.9964362	54.52181
GOTERM_BP_ALL	GO:0000082~G1/S transition of mitotic cell cycle	3	2.46	0.04	91	8.67	0.9973068	57.45713
GOTERM_BP_ALL	GO:0022402~cell cycle process	11	9.02	0.06	91	1.88	0.9995853	69.80455
GOTERM_BP_ALL	GO:0042127~regulation of cell proliferation	8	6.56	0.07	91	2.14	0.9998218	76.4969
GOTERM_BP_ALL	GO:0008283~cell proliferation	11	9.02	0.08	91	1.81	0.999798	76.93027
GOTERM_BP_ALL	GO:0007067~mitosis	4	3.28	0.24	91	2.34	1	99.37814
GOTERM_BP_ALL	GO:0000087~M phase of mitotic cell cycle	4	3.28	0.24	91	2.31	1	99.44754
GOTERM_BP_ALL	GO:0051301~cell division	4	3.28	0.34	91	1.91	1	99.95896
GOTERM_BP_ALL	GO:0000279~M phase	4	3.28	0.36	91	1.85	1	99.97679
GOTERM_BP_ALL	GO:0000074~regulation of progression through cell cycle	6	4.92	0.41	91	1.41	1	99.99514
GOTERM_BP_ALL	GO:0051726~regulation of cell cycle	6	4.92	0.41	91	1.41	1	99.99514
Functional Group 4	Median: 0.1950304615867952	Geo:0.09						
GOTERM_BP_ALL	GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	7	5.74	0.01	91	4.00	0.8390106	12.72965

Category	Term	Count	%	P	List Total	Fold Enrichment	Benjamini	FDR
GOTERM_BP_ALL	GO:0007167~enzyme linked receptor protein signaling pathway	7	5.74	0.03	91	2.93	0.9959367	43.12843
GOTERM_BP_ALL	GO:0007166~cell surface receptor linked signal transduction	11	9.02	0.36	91	1.26	1	99.97501
GOTERM_BP_ALL	GO:0007399~nervous system development	3	2.46	0.95	91	0.65	1	100
Functional Group 5	Median: 0.10658407530061273	Geo:0.12						
GOTERM_BP_ALL	GO:0046777~protein amino acid autophosphorylation	3	2.46	0.10	91	5.49	0.999975	86.12023
GOTERM_BP_ALL	GO:0016540~protein autoprocessing	3	2.46	0.11	91	5.32	0.9999826	87.67668
GOTERM_BP_ALL	GO:0016485~protein processing	3	2.46	0.18	91	3.83	1	97.5435
Functional Group 6	Median: 0.24535433349064537	Geo:0.20						
GOTERM_BP_ALL	GO:0048522~positive regulation of cellular process	13	10.66	0.06	91	1.74	0.999531	70.30735
GOTERM_BP_ALL	GO:0048518~positive regulation of biological process	13	10.66	0.12	91	1.55	0.9999964	91.39775
GOTERM_BP_ALL	GO:0050794~regulation of cellular process	31	25.41	0.25	91	1.15	1	99.4644
GOTERM_BP_ALL	GO:0050789~regulation of biological process	32	26.23	0.36	91	1.09	1	99.97595
GOTERM_BP_ALL	GO:0065007~biological regulation	34	27.87	0.47	91	1.04	1	99.99922
Functional Group 7	Median: 0.3228801660630666	Geo:0.25						
GOTERM_BP_ALL	GO:0002521~leukocyte differentiation	4	3.28	0.05	91	4.58	0.9990863	64.77437
GOTERM_BP_ALL	GO:0030097~hemopoiesis	5	4.10	0.07	91	3.12	0.9998273	75.65607
GOTERM_BP_ALL	GO:0048534~hemopoietic or lymphoid organ development	5	4.10	0.08	91	3.05	0.999804	77.94441
GOTERM_BP_ALL	GO:0002520~immune system development	5	4.10	0.09	91	2.92	0.9999227	82.10186
GOTERM_BP_ALL	GO:0030099~myeloid cell differentiation	3	2.46	0.17	91	4.02	0.9999999	96.7145
GOTERM_BP_ALL	GO:0048513~organ development	11	9.02	0.27	91	1.37	1	99.68183
GOTERM_BP_ALL	GO:0032502~developmental process	25	20.4%	0.32	91	1.14	1	99.9285
GOTERM_BP_ALL	GO:0009887~organ morphogenesis	4	3.28	0.44	91	1.64	1	99.99761
GOTERM_BP_ALL	GO:0007275~multicellular organismal development	16	13.11	0.48	91	1.09	1	99.99955
GOTERM_BP_ALL	GO:0048856~anatomical structure development	14	11.48	0.59	91	1.04	1	99.99999
GOTERM_BP_ALL	GO:0048731~system development	11	9.02	0.66	91	1.00	1	100
GOTERM_BP_ALL	GO:0002376~immune system process	7	5.74	0.68	91	1.02	1	100
GOTERM_BP_ALL	GO:0032501~multicellular organismal process	20	16.39	0.71	91	0.95	1	100
Functional Group 8	Median: 0.25872590709365667	Geo:0.29						
GOTERM_BP_ALL	GO:0030001~metal ion transport	5	4.10	0.19	91	2.20	0.9999999	97.8825
GOTERM_BP_ALL	GO:0015672~monovalent inorganic cation transport	4	3.28	0.22	91	2.41	1	99.11936
GOTERM_BP_ALL	GO:0006812~cation transport	5	4.10	0.29	91	1.81	1	99.83872
GOTERM_BP_ALL	GO:0006811~ion transport	5	4.10	0.61	91	1.18	1	100
Functional Group 9	Median: 0.3228801660630666	Geo:0.34						
GOTERM_BP_ALL	GO:0048869~cellular developmental process	17	13.93	0.18	91	1.34	1	97.61175
GOTERM_BP_ALL	GO:0030154~cell differentiation	17	13.93	0.18	91	1.34	1	97.61175
GOTERM_BP_ALL	GO:0006915~apoptosis	10	8.20	0.22	91	1.48	1	99.06249
GOTERM_BP_ALL	GO:0012501~programmed cell death	10	8.20	0.23	91	1.47	1	99.15999
GOTERM_BP_ALL	GO:0008219~cell death	10	8.20	0.26	91	1.42	1	99.62713
GOTERM_BP_ALL	GO:0016265~death	10	8.20	0.26	91	1.42	1	99.62713
GOTERM_BP_ALL	GO:0048513~organ development	11	9.02	0.27	91	1.37	1	99.68183
GOTERM_BP_ALL	GO:0032502~developmental process	25	20.49	0.32	91	1.14	1	99.9285
GOTERM_BP_ALL	GO:0042981~regulation of apoptosis	7	5.74	0.32	91	1.48	1	99.92881
GOTERM_BP_ALL	GO:0043067~regulation of programmed cell death	7	5.74	0.33	91	1.47	1	99.94043
GOTERM_BP_ALL	GO:0048468~cell development	10	8.20	0.56	91	1.09	1	99.99998

Category	Term	Count	%	<i>P</i>	List Total	Fold Enrichment	Benjamini	FDR
GOTERM_BP_ALL	GO:0048523~negative regulation of cellular process	9	7.38	0.58	91	1.09	1	99.99999
GOTERM_BP_ALL	GO:0048856~anatomical structure development	14	11.48	0.59	91	1.04	1	99.99999
GOTERM_BP_ALL	GO:0048519~negative regulation of biological process	9	7.38	0.63	91	1.05	1	100
GOTERM_BP_ALL	GO:0048731~system development	11	9.02	0.66	91	1.00	1	100
Functional Group 10	Median: 0.3303788461948379	Geo:0.38						
GOTERM_BP_ALL	GO:0065009~regulation of a molecular function	8	6.56	0.15	91	1.79	0.9999998	95.44414
GOTERM_BP_ALL	GO:0050790~regulation of catalytic activity	7	5.74	0.19	91	1.79	0.9999999	97.9909
GOTERM_BP_ALL	GO:0045860~positive regulation of protein kinase activity	3	2.46	0.31	91	2.66	1	99.89175
GOTERM_BP_ALL	GO:0045859~regulation of protein kinase activity	4	3.28	0.32	91	2.00	1	99.91818
GOTERM_BP_ALL	GO:0033674~positive regulation of kinase activity	3	2.46	0.32	91	2.57	1	99.9246
GOTERM_BP_ALL	GO:0051347~positive regulation of transferase activity	3	2.46	0.33	91	2.53	1	99.9372
GOTERM_BP_ALL	GO:0043549~regulation of kinase activity	4	3.28	0.33	91	1.96	1	99.93772
GOTERM_BP_ALL	GO:0051338~regulation of transferase activity	4	3.28	0.33	91	1.94	1	99.94575
GOTERM_BP_ALL	GO:0000165~MAPKKK cascade	3	2.46	0.46	91	1.94	1	99.99875
GOTERM_BP_ALL	GO:0051336~regulation of hydrolase activity	3	2.46	0.46	91	1.94	1	99.99875
GOTERM_BP_ALL	GO:0007010~cytoskeleton organization and biogenesis	5	4.10	0.48	91	1.38	1	99.99955
GOTERM_BP_ALL	GO:0043085~positive regulation of catalytic activity	3	2.46	0.58	91	1.54	1	99.99999
GOTERM_BP_ALL	GO:0006996~organelle organization and biogenesis	7	5.74	0.82	91	0.87	1	100
GOTERM_BP_ALL	GO:0065008~regulation of biological quality	3	2.46	0.99	91	0.50	1	100
Functional Group 11	Median: 0.4069864585039749	Geo:0.41						
GOTERM_BP_ALL	GO:0009607~response to biotic stimulus	4	3.28	0.38	91	1.79	1	99.98708
GOTERM_BP_ALL	GO:0051704~multi-organism process	4	3.28	0.41	91	1.72	1	99.99392
GOTERM_BP_ALL	GO:0051707~response to other organism	3	2.46	0.43	91	2.03	1	99.99716
Functional Group 12	Median: 0.5829067038411142	Geo:0.53						
GOTERM_BP_ALL	GO:0042981~regulation of apoptosis	7	5.74	0.32	91	1.48	1	99.92881
GOTERM_BP_ALL	GO:0043067~regulation of programmed cell death	7	5.74	0.33	91	1.47	1	99.94043
GOTERM_BP_ALL	GO:0006916~anti-apoptosis	3	2.46	0.49	91	1.83	1	99.99956
GOTERM_BP_ALL	GO:0006917~induction of apoptosis	3	2.46	0.53	91	1.70	1	99.99999
GOTERM_BP_ALL	GO:0012502~induction of programmed cell death	3	2.46	0.53	91	1.70	1	99.99999
GOTERM_BP_ALL	GO:0048523~negative regulation of cellular process	9	7.38	0.58	91	1.09	1	99.99999
GOTERM_BP_ALL	GO:0043065~positive regulation of apoptosis	3	2.46	0.61	91	1.45	1	100
GOTERM_BP_ALL	GO:0043068~positive regulation of programmed cell death	3	2.46	0.62	91	1.43	1	100
GOTERM_BP_ALL	GO:0048519~negative regulation of biological process	9	7.38	0.63	91	1.05	1	100
GOTERM_BP_ALL	GO:0043066~negative regulation of apoptosis	3	2.46	0.66	91	1.33	1	100
GOTERM_BP_ALL	GO:0043069~negative regulation of programmed cell death	3	2.46	0.66	91	1.32	1	100
Functional Group 13	Median: 0.5424209679924756	Geo:0.57						
GOTERM_BP_ALL	GO:0051179~localization	23	18.85	0.32	91	1.15	1	99.92665
GOTERM_BP_ALL	GO:0006810~transport	19	15.57	0.42	91	1.11	1	99.99594
GOTERM_BP_ALL	GO:0008104~protein localization	8	6.56	0.47	91	1.22	1	99.99928
GOTERM_BP_ALL	GO:0051234~establishment of localization	19	15.57	0.49	91	1.07	1	99.99996
GOTERM_BP_ALL	GO:0033036~macromolecule localization	8	6.56	0.53	91	1.16	1	99.99991

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GOTERM_BP_ALL	GO:0006605~protein targeting	3	2.46	0.54	91	1.66	1	99.99994
GOTERM_BP_ALL	GO:0015031~protein transport	7	5.74	0.54	91	1.18	1	99.99995
GOTERM_BP_ALL	GO:0045184~establishment of protein localization	7	5.74	0.60	91	1.11	1	100
GOTERM_BP_ALL	GO:0046907~intracellular transport	6	4.92	0.64	91	1.10	1	100
GOTERM_BP_ALL	GO:0006886~intracellular protein transport	4	3.28	0.65	91	1.20	1	100
GOTERM_BP_ALL	GO:0051649~establishment of cellular localization	6	4.92	0.82	91	0.88	1	100
GOTERM_BP_ALL	GO:0051641~cellular localization	6	4.92	0.83	91	0.86	1	100
GOTERM_BP_ALL	GO:0016043~cellular component organization and biogenesis	15	12.30	0.92	91	0.80	1	100
Functional Group 14	Median: 0.7128814799700762	Geo:0.58						
GOTERM_BP_ALL	GO:0009057~macromolecule catabolic process	5	4.10	0.38	91	1.60	1	99.98387
GOTERM_BP_ALL	GO:0043285~biopolymer catabolic process	4	3.28	0.43	91	1.66	1	99.99672
GOTERM_BP_ALL	GO:0044265~cellular macromolecule catabolic process	3	2.46	0.71	91	1.20	1	100
GOTERM_BP_ALL	GO:0009056~catabolic process	5	4.10	0.74	91	1.00	1	100
GOTERM_BP_ALL	GO:0044248~cellular catabolic process	4	3.28	0.78	91	0.97	1	100
Functional Group 15	Median: 0.8866617747985455	Geo:0.84						
GOTERM_BP_ALL	GO:0002376~immune system process	7	5.74	0.68	91	1.02	1	100
GOTERM_BP_ALL	GO:0006955~immune response	4	3.28	0.89	91	0.79	1	100
GOTERM_BP_ALL	GO:0050896~response to stimulus	11	9.02	0.98	91	0.65	1	100
Functional Group 16	Median: 0.9581775686879237	Geo:0.91						
GOTERM_BP_ALL	GO:0006357~regulation of transcription from RNA polymerase II promoter	4	3.28	0.55	91	1.39	1	99.99996
GOTERM_BP_ALL	GO:0006366~transcription from RNA polymerase II promoter	4	3.28	0.79	91	0.96	1	100
GOTERM_BP_ALL	GO:0019222~regulation of metabolic process	12	9.84	0.93	91	0.75	1	100
GOTERM_BP_ALL	GO:0031323~regulation of cellular metabolic process	11	9.02	0.95	91	0.73	1	100
GOTERM_BP_ALL	GO:0045449~regulation of transcription	9	7.38	0.95	91	0.71	1	100
GOTERM_BP_ALL	GO:0010468~regulation of gene expression	10	8.20	0.95	91	0.72	1	100
GOTERM_BP_ALL	GO:0006355~regulation of transcription, DNA-dependent	8	6.56	0.95	91	0.69	1	100
GOTERM_BP_ALL	GO:0019219~regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	9	7.38	0.96	91	0.68	1	100
GOTERM_BP_ALL	GO:0006351~transcription, DNA-dependent	8	6.56	0.96	91	0.67	1	100
GOTERM_BP_ALL	GO:0032774~RNA biosynthetic process	8	6.56	0.96	91	0.67	1	100
GOTERM_BP_ALL	GO:0006350~transcription	9	7.38	0.97	91	0.67	1	100
GOTERM_BP_ALL	GO:0016070~RNA metabolic process	10	8.20	0.99	91	0.61	1	100
GOTERM_BP_ALL	GO:0010467~gene expression	13	10.66	0.99	91	0.62	1	100
GOTERM_BP_ALL	GO:0006139~nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	13	10.66	1.00	91	0.56	1	100
Functional Group 17	Median: 0.9751231848048691	Geo:0.97						
GOTERM_BP_ALL	GO:0006412~translation	3	2.46	0.92	91	0.72	1	100
GOTERM_BP_ALL	GO:0009059~macromolecule biosynthetic process	4	3.28	0.95	91	0.63	1	100
GOTERM_BP_ALL	GO:0009058~biosynthetic process	5	4.10	1.00	91	0.47	1	100
GOTERM_BP_ALL	GO:0044249~cellular biosynthetic process	3	2.46	1.00	91	0.38	1	10

The analysis was done with "custom" classification stringency and the Biological Process (BP\_ALL) gene ontology term.