

SUPPLEMENTARY TABLE 2
GENES DOWNREGULATED BY JNK INHIBITOR IN CELLS EXPRESSING ATP7B-H1069Q

BIOLOGICAL PROCESS	Number of genes	p-value	FDR
response to unfolded protein	17	2.00E-05	3.70E-02
cellular amino acid derivative metabolic process	28	2.50E-05	4.60E-02
cellular component maintenance	9	1.90E-04	3.40E-01
adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	15	7.00E-04	1.30E+00
adaptive immune response	15	7.00E-04	1.30E+00
cell death	73	8.00E-04	1.50E+00
response to wounding	57	8.80E-04	1.60E+00
death	73	9.70E-04	1.80E+00
regulation of protein kinase cascade	32	9.90E-04	1.80E+00
response to protein stimulus	18	1.00E-03	1.80E+00
positive regulation of protein kinase cascade	24	1.10E-03	2.00E+00
vesicle-mediated transport	60	1.30E-03	2.40E+00
programmed cell death	62	2.10E-03	3.80E+00
leukocyte mediated immunity	15	2.10E-03	3.80E+00
photoreceptor cell maintenance	7	2.30E-03	4.20E+00
regulation of programmed cell death	78	2.40E-03	4.40E+00
cellular carbohydrate biosynthetic process	13	2.50E-03	4.40E+00
membrane invagination	28	2.50E-03	4.50E+00
endocytosis	28	2.50E-03	4.50E+00
alcohol biosynthetic process	10	2.70E-03	4.80E+00
regulation of cell death	78	2.80E-03	4.90E+00
lymphocyte mediated immunity	13	2.80E-03	5.00E+00
CELLULAR COMPONENT	Number of genes	p-value	FDR
membrane fraction	121	8.80E-08	1.30E-04
insoluble fraction	106	9.40E-08	1.40E-04
plasma membrane part	108	1.70E-07	2.50E-04
cell fraction	91	4.90E-07	7.00E-04
endoplasmic reticulum	108	1.20E-06	1.70E-03
vesicle	128	1.30E-06	1.80E-03
cytoplasmic vesicle	115	2.60E-06	3.70E-03
cytoplasmic membrane-bounded vesicle	38	3.60E-05	5.20E-02
membrane-bounded vesicle	38	6.80E-05	9.80E-02
integral to organelle membrane	11	9.60E-04	1.40E+00
secretory granule	5	1.10E-03	1.50E+00

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intrinsic to organelle membrane	10	1.10E-03	1.60E+00
anchoring collagen	10	1.10E-03	1.60E+00
cell junction	64	1.20E-03	1.70E+00
MOLECULAR FUNCTION	Number of genes	p-value	FDR
protein dimerization activity	61	1.30E-04	2.00E-01
antiporter activity	13	2.00E-03	3.10E+00
identical protein binding	64	2.00E-03	3.10E+00
solute:solute antiporter activity	11	3.20E-03	5.00E+00
GTPase activity	26	4.90E-03	7.50E+00
cytokine binding	16	7.00E-03	1.10E+01
protein homodimerization activity	36	7.40E-03	1.10E+01
butyrate-CoA ligase activity	4	9.00E-03	1.30E+01
protein kinase inhibitor activity	8	9.80E-03	1.50E+01
kinase inhibitor activity	8	1.10E-02	1.70E+01
enzyme activator activity	35	1.30E-02	1.90E+01
di-, tri-valent inorganic cation transmembrane transporter activity	8	1.50E-02	2.20E+01
GTPase activator activity	25	1.50E-02	2.20E+01
anion:cation symporter activity	7	1.70E-02	2.40E+01
purine nucleotide binding	154	1.80E-02	2.50E+01
ribonucleotide binding	147	2.40E-02	3.20E+01
purine ribonucleotide binding	147	2.40E-02	3.20E+01
nucleoside-triphosphatase regulator activity	40	2.40E-02	3.20E+01
troponin T binding	3	2.50E-02	3.40E+01
sodium:dicarboxylate symporter activity	4	2.60E-02	3.50E+01
heat shock protein binding	11	2.80E-02	3.70E+01
pyridoxal phosphate binding	9	2.90E-02	3.70E+01
vitamin B6 binding	9	2.90E-02	3.70E+01
oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	5	3.10E-02	3.90E+01
nucleotide binding	175	3.20E-02	4.10E+01
motor activity	17	3.30E-02	4.10E+01
cofactor binding	26	3.40E-02	4.20E+01
extracellular matrix binding	6	3.40E-02	4.20E+01
transition metal ion transmembrane transporter activity	6	3.40E-02	4.20E+01
small GTPase regulator activity	28	3.40E-02	4.30E+01
transcription corepressor activity	17	3.90E-02	4.70E+01
O-acetyltransferase activity	3	4.10E-02	4.80E+01
GTPase regulator activity	38	4.10E-02	4.80E+01
protein serine/threonine kinase activity	40	4.10E-02	4.90E+01
anion transmembrane transporter activity	17	4.30E-02	5.00E+01

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nucleoside binding	128	4.30E-02	5.10E+01
anion:anion antiporter activity	5	4.30E-02	5.10E+01
lipopolysaccharide binding	4	4.40E-02	5.10E+01
oxidoreductase activity, acting on the CH-NH group of donors	6	4.40E-02	5.10E+01
ARF GTPase activator activity	6	4.40E-02	5.10E+01
purine nucleoside binding	127	4.40E-02	5.20E+01
Ras GTPase activator activity	12	4.50E-02	5.20E+01
enzyme binding	47	4.50E-02	5.20E+01
O-acyltransferase activity	7	4.70E-02	5.40E+01
enzyme inhibitor activity	27	4.70E-02	5.40E+01
GTP binding	35	4.90E-02	5.50E+01
neutral amino acid transmembrane transporter activity	5	5.10E-02	5.60E+01
adenyl nucleotide binding	124	5.80E-02	6.10E+01
copper ion transmembrane transporter activity	3	5.80E-02	6.10E+01
lipid transporter activity	9	6.40E-02	6.50E+01
calcium-dependent protein binding	6	6.40E-02	6.50E+01
amine transmembrane transporter activity	10	6.40E-02	6.50E+01
guanyl ribonucleotide binding	35	6.70E-02	6.70E+01
guanyl nucleotide binding	35	6.70E-02	6.70E+01
protein domain specific binding	31	6.70E-02	6.70E+01
ATP binding	116	6.90E-02	6.80E+01
adenyl ribonucleotide binding	117	7.50E-02	7.10E+01
protein heterodimerization activity	21	7.60E-02	7.10E+01
protein kinase binding	16	7.70E-02	7.20E+01
cytokine receptor activity	8	7.90E-02	7.30E+01
organic acid:sodium symporter activity	5	8.70E-02	7.70E+01
scavenger receptor activity	7	9.10E-02	7.80E+01
dicarboxylic acid transmembrane transporter activity	4	9.10E-02	7.80E+01
unfolded protein binding	13	9.30E-02	7.90E+01
calcium ion binding	74	9.40E-02	7.90E+01
ligase activity, forming carbon-oxygen bonds	7	9.90E-02	8.10E+01
ligase activity, forming aminoacyl-tRNA and related compounds	7	9.90E-02	8.10E+01
aminoacyl-tRNA ligase activity	7	9.90E-02	8.10E+01
quinone binding	3	9.90E-02	8.10E+01
chitinase activity	3	9.90E-02	8.10E+01
protein kinase regulator activity	10	1.00E-01	8.10E+01
KEGG PATHWAY	Number of genes	p-value	FDR
Complement and coagulation cascades	16	9.50E-05	1.20E-01
MAPK signaling pathway	35	8.00E-04	9.70E-01

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Glutathione metabolism	10	9.00E-03	1.00E+01
Cysteine and methionine metabolism	8	9.90E-03	1.10E+01
Arachidonic acid metabolism	10	1.90E-02	2.00E+01
Cell adhesion molecules (CAMs)	17	2.90E-02	3.00E+01
Arginine and proline metabolism	9	3.60E-02	3.60E+01
Selenoamino acid metabolism	6	3.70E-02	3.60E+01
Hematopoietic cell lineage	12	4.60E-02	4.40E+01
Glycerophospholipid metabolism	10	5.60E-02	5.10E+01
PPAR signaling pathway	10	6.10E-02	5.30E+01
Alanine, aspartate and glutamate metabolism	6	7.10E-02	5.90E+01
Glycine, serine and threonine metabolism	6	7.10E-02	5.90E+01
Aminoacyl-tRNA biosynthesis	7	7.40E-02	6.10E+01
Bladder cancer	7	8.10E-02	6.40E+01
VEGF signaling pathway	10	9.20E-02	6.90E+01