

Supplementary Table S1 The differentially expressed proteins identified by TMT labeling coupled with LC-MS/MS analysis of PK-15 cells in response to SVA infection at 12 hpi

Protein name	Uniport accession No.	Log ₂ ratios (infection/control)	peptides	Sequence coverage (%)	P-values	functions
Upregulated proteins in PK-15-infected cells (a total of 314 proteins)						
Genome polyprotein	A0A5C2GZI4	2.392431	1	39	0.000729	Function unknown
Interferon-induced GTP- binding protein Mx1	A0A4X1TKB5	1.536855	6	78	0.00925	Immune effector process; negative regulation of viral process
Inflammatory response protein 6	A0A287B6T9	1.486117	14	44	0.007366	T cell differentiation; negative regulation of viral process
Genome polyprotein	A0A649YC94	1.469757	1	30	0.004355	Function unknown
Interferon-induced GTP- binding protein Mx2	A0A480HPX5	1.421313	26	54	0.00044	Small molecule binding, establishment of localization in cell
2'-5' oligoadenylate synthase	Q56VQ1	1.247479	30	54	0.002377	Ribonucleotide binding
Uncharacterized protein	A0A5G2RJF6	1.218727	1	1	0.000446	Function unknown
Tumor-associated calcium signal transducer 2	F1S7A4	1.200562	8	34	0.006537	Regulation of stem cell differentiation; positive regulation of stem cell differentiation
Interferon-stimulated protein 60	F1SCY2	1.114459	14	41	0.002878	Protein binding, immune effector process
C-C motif chemokine (Fragment)	A1YM33	1.110968	3	47	0.01546	Catalytic activity, positive regulation of protein phosphorylation
Interferon-stimulated protein 56	J7FIC7	1.107499	30	64	0.002542	Regulation of defense response to virus, regulation of response to exteRNAI stimulus

Interferon-induced protein with tetratricopeptide repeats 2	K9J6I9	1.069138	18	34	0.003941	Cellular response to stimulus, response to cytokine
DNA topoisomerase I	I3LTP0	1.052397	1	2	0.03377	Function unknown
mRNA-capping enzyme	A0A4X1VEE3	1.01955	3	7	0.02165	Function unknown
Genome polyprotein	A0A6B9QIJ0	1.014207	1	30	0.000258	Function unknown
RNA helicase	A8CYB8	1.000579	31	41	0.002151	Helicase activity, regulation of locomotion
Uncharacterized protein	A0A287A9J8	0.985966	1	8	0.000852	Function unknown
TLDC domain-containing protein	I3LMG2	0.985906	1	45	0.00663	Function unknown
G domain-containing protein	F1S9T2	0.954928	1	39	0.001392	GTP binding
Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1 isoform c	A0A481BP67	0.95051	1	10	0.01857	Function unknown
Protein PML isoform 2	A0A480JXC7	0.946937	2	50	0.02126	Function unknown
FIP-RBD domain-containing protein	A0A4X1UDM9	0.937329	1	32	0.02466	Function unknown
Receptor-transporting protein 4	A0A287B9T3	0.934535	5	12	0.006303	Function unknown
Ubiquitin-like modifier	A0A287AB58	0.930694	6	50	0.002502	Integrin binding; intracellular organelle
IRF tryptophan pentad repeat domain-containing protein	A0A5G2RH09	0.930143	6	20	0.004793	Transcription regulator activity
GFO_IDH_MocA domain-containing protein	A0A4X1UEI6	0.922326	1	2	0.02394	Oxidoreductase activity
PH domain-containing protein	A0A287BS42	0.902609	1	1	0.04178	Integrin-mediated signaling pathway, cellular process; regulation of cellular process
Urokinase-type plasminogen	A0A286ZXK2	0.902583	9	24	0.00041	Function unknown

activator						
Protein-serine/threonine phosphatase	A0A4X1U1Y2	0.901906	1	1	0.04074	Function unknown
Uncharacterized protein	A0A287B4N8	0.884001	5	40	0.008604	Function unknown
Transmembrane protein 147	A0A4X1TJ50	0.871487	2	13	0.005086	Macromolecular complex, organelle membrane, integral component of membrane
Noelin-2 isoform 2	A0A480XA75	0.862249	1	2	0.03464	Extrinsic component of plasma membrane; protein localization
Uncharacterized protein	A0A287B916	0.861888	1	2	0.03854	Heterocyclic compound binding
2',3'-cyclic-nucleotide 3'-phosphodiesterase	A0A287A9L8	0.86153	26	59	0.004682	Binding
Uncharacterized protein	A0A4X1SEB3	0.858628	13	24	0.002072	Function unknown
ANK_REP_REGION domain-containing protein	A0A4X1U612	0.852998	1	14	0.01982	Function unknown
Kelch-like protein 36	A0A480YWF8	0.852718	1	2	2.00E-05	Function unknown
Uncharacterized protein	F1RM98	0.838745	6	19	0.000753	Protein binding; positive regulation of cellular process
2'-5' oligoadenylate synthase	Q5MX78	0.836352	2	27	0.004357	Ribonucleotide binding
Uncharacterized protein	A0A4X1WD16	0.834263	1	6	0.03558	Function unknown
DNA_MISMATCH_REPAIR_2 domain-containing protein	I3L5Z8	0.824216	2	2	0.01612	Function unknown
TLDc domain-containing protein	A0A4X1UQ31	0.818645	7	43	0.006877	Function unknown
Galectin-3-binding protein	A0A5G2RLP2	0.814593	13	34	0.005314	Function unknown
Uncharacterized protein	F1SS06	0.810289	1	1	0.03231	Function unknown
Galectin	A0A287A342	0.798613	11	45	0.01226	Function unknown
Caspase 4, apoptosis-related cysteine peptidase	A0A0B8RT56	0.797204	9	28	0.000606	Function unknown
FAM184 domain-containing	I3LV88	0.796314	1	1	0.03617	Function unknown

protein						
CCHC-type domain-containing	F1SMW0	0.793917	2	3	0.01277	Function unknown
protein						
Nuclear body protein SP140	A0A480PYU5	0.779843	5	26	0.01075	Function unknown
isoform 5						
Apolipoprotein H	A0A140TAK8	0.767339	3	13	0.008719	Function unknown
GB1/RHD3-type G domain-	A0A4X1U8M2	0.765946	1	6	0.02652	Function unknown
containing protein						
Poly [ADP-ribose] polymerase	A0A4X1TD13	0.765145	45	31	0.00127	Function unknown
RNA helicase	A0A287AKR1	0.76304	20	21	0.001596	Binding
RECA_2 domain-containing	A0A4X1TR78	0.761278	1	3	3.40E-05	Anion binding; DNA metabolic process
protein						
Fibroblast growth factor	A0A287BGK8	0.760152	1	3	0.02677	Function unknown
Nuclear autoantigen Sp-100	R4L6V8	0.75475	2	28	0.03474	Intracellular membrane-bounded organelle; nucleus
isoform 4						
Uncharacterized protein	A0A4X1URS1	0.749866	1	42	0.02308	Function unknown
Transporter 2, ATP-binding	A5D9J7	0.747746	16	31	0.01017	Ribonucleotide binding
cassette, sub-family B						
(MDR/TAP)						
GB1/RHD3-type G domain-	A0A287BSF6	0.745783	2	30	0.02444	Ribonucleotide binding
containing protein						
Interferon regulatory factor 7	X2KPB3	0.743615	2	5	0.002987	Transcription factor activity; sequence-specific DNA binding; adaptive immune response
Tumor necrosis factor receptor	Q8SQ34	0.739224	6	30	0.03582	Signaling receptor activity; positive regulation of cellular biosynthetic process
superfamily member 5						
Pleckstrin homology-like	F1SGD8	0.736577	1	2	0.00788	Function unknown
domain family A member 1						

CCDC66 domain-containing protein	I3L7C7	0.73314	1	1	0.02096	Function unknown
Uncharacterized protein	A0A5G2QLT7	0.731775	2	4	0.02382	Function unknown
Aminopeptidase	K9J4P1	0.730795	7	7	0.03046	Function unknown
RNA helicase	F1S0P6	0.729356	12	22	0.004083	Anion binding; negative regulation of cellular process
Interferon regulatory factor	A0A5S6GDS9	0.722825	5	24	0.000597	Transcription factor activity; sequence-specific DNA binding, negative regulation of macromolecule biosynthetic process
Homeobox protein cut-like	A0A4X1U3F5	0.713423	2	2	0.01952	Function unknown
Epithelial-stromal interaction protein 1 isoform 2	A0A286ZSG6	0.711802	9	34	0.007058	Function unknown
UBC core domain-containing protein	A0A5G2Q9I0	0.710535	6	79	0.005605	Ribonucleotide binding
Reticulon	A0A4X1VKW2	0.709841	1	11	0.01387	Function unknown
2'-5'-oligoadenylate synthase-like protein isoform a	F1RIV0	0.697316	13	44	0.03516	Ribonucleotide binding
GTPase-activating Rap/Ran-GAP domain-like protein 3 isoform X1	I3LIY1	0.691048	1	1	0.03553	Function unknown
Electron transfer flavoprotein-ubiquinone oxidoreductase	F1RW89	0.686931	1	46	0.002947	Oxidoreductase activity
Interferon-induced GTP-binding protein Mx1	A0A481BA72	0.686812	1	77	0.01551	Catalytic activity; cellular metabolic process
Armadillo repeat-containing protein 4 isoform X3	A0A480MFY5	0.68409	2	2	0.04023	Function unknown
Nucleotide-binding oligomerization domain 1	B0FSM7	0.679421	1	1	0.02509	Ribonucleotide binding

2'-5'-oligoadenylate synthase 1	Q29599	0.677282	3	45	0.006649	2'-5'-oliprimary metabolic process; cellular metabolic process
Fibroblast growth factor-inducible 14	B7SLY2	0.676496	2	23	0.01422	Positive regulation of developmental growth; regulation of developmental growth
PH domain-containing protein	A0A4X1VUK6	0.673899	8	13	0.00743	Function unknown
Exonuclease domain-containing protein	A0A4X1W796	0.666049	7	46	0.002538	Function unknown
LRRC37AB_C domain-containing protein	A0A286ZIV7	0.665644	2	2	0.008392	Function unknown
Phospholipid-transporting ATPase	A0A4X1ULA4	0.661048	3	3	0.03414	Transmembrane transporter activity; leukocyte degranulation
Uncharacterized protein	I3LB77	0.66024	5	17	0.000693	MRNA 3'-utr binding, organic substance transport
IFITM2	F4ZS15	0.657588	1	28	0.00304	Integral component of membrane; cellular anatomical entity
Uncharacterized protein	A0A4X1VHT0	0.651654	21	33	0.001172	Transferase activity, transferring pentosyl groups; regulation of mRNA metabolic process
Uncharacterized protein	I3L5Z9	0.648297	60	42	0.002487	Function unknown
Polypyrimidine tract-binding protein 1	A0A286ZPA4	0.647217	1	61	0.003047	Function unknown
Uncharacterized protein	A0A4X1V406	0.643524	20	37	0.004326	Ribonucleotide binding
Dynamin GTPase	A0A4X1VG57	0.629307	1	41	0.004953	Function unknown
Non-specific serine/threonine protein kinase	F1RQR3	0.626525	3	3	0.000665	Function unknown
Coagulation factor III (Fragment)	A0A481D288	0.624166	3	15	0.001827	Lipid binding, positive regulation of biological process; protein processing
Putative E3 ubiquitin-protein ligase HERC6 isoform 1	A0A480M1Q1	0.616749	1	33	0.02974	Function unknown
Uncharacterized protein	A0A287BKF1	0.614608	24	42	0.006977	Ribonucleotide binding

Uncharacterized protein	A0A5G2RNJ9	0.614085	1	2	0.004226	Function unknown
Ribonuclease H	A0A5G2R922	0.612383	1	7	0.01585	Function unknown
Uncharacterized protein	F1SL31	0.611186	1	34	0.015	Function unknown
Zinc finger protein 555 isoform 2	A0A287A1D7	0.609357	1	6	0.04632	Function unknown
Plasminogen activator inhibitor 1	P79335	0.606957	12	40	0.000552	Serine-type endopeptidase inhibitor activity; negative regulation of endopeptidase activity
Myeloid cell nuclear differentiation antigen	A0A287AP08	0.603852	4	10	0.004269	Function unknown
Inhibitor_Mig-6 domain-containing protein	A0A287A7S3	0.603145	2	4	0.003714	Function unknown
Collagen IV NC1 domain-containing protein	A0A4X1U499	0.602292	1	1	0.002095	Function unknown
E3 ubiquitin-protein ligase RNF213 isoform 3	A0A480YJW7	0.600502	27	34	0.005266	Function unknown
Uncharacterized protein	A0A4X1W154	0.596663	2	0	0.01719	Function unknown
RING-type domain-containing protein	A0A4X1UID3	0.596581	2	30	0.02149	Function unknown
J domain-containing protein	A0A5G2R4I8	0.591194	1	42	0.03637	Function unknown
Arylamine N-acetyltransferase	A0A480RQR3	0.589917	1	41	0.008489	Function unknown
Syndecan	A0A5S6HZW1	0.587846	8	24	0.01365	Locomotion, cell motility
Poly ADP-ribose polymerase 12	A0A480N6U6	0.580134	3	8	0.02232	Transferase activity; transferring glycosyl groups
Uncharacterized protein	A0A287B544	0.576938	2	38	0.006583	Function unknown
Alpha-actinin-4 isoform 1	A0A480ZDQ8	0.575463	1	72	0.002139	Protein binding, protein transport; signal transduction
Procollagen-proline 4-	A1X898	0.575381	1	59	0.04202	Binding

dioxygenase						
Phospholipid-transporting	M3TYF0	0.573945	1	1	0.0323	Function unknown
ATPase						
Uncharacterized protein	A0A287ARP2	0.573711	1	17	0.001977	Function unknown
Uridine-cytidine kinase	A0A4X1T9P1	0.571887	2	13	0.03183	Small molecule binding; biosynthetic process
HECT domain-containing protein	A0A4X1U9D8	0.570222	25	33	0.01593	Function unknown
Uncharacterized protein	F1S5B5	0.562586	2	5	0.004215	Function unknown
BLOC-1-related complex subunit 7	A0A4X1TT04	0.561276	1	4	0.02158	Function unknown
F-BAR domain-containing protein	A0A5G2RMN3	0.560004	1	1	0.003662	Function unknown
Tripartite motif-containing protein 26	B6ICV1	0.559532	5	11	0.04198	Binding
Thiopurine S-methyltransferase	F1RUH7	0.559354	1	68	0.001714	Methyltransferase activity; methylation
Voltage-dependent anion-selective channel protein 2	A0A4X1UZQ9	0.559175	1	15	0.01559	Function unknown
Uncharacterized protein	A0A4X1UW90	0.558469	27	18	0.02264	Function unknown
Cationic amino acid transporter 2	A0A4X1TZW6	0.55	2	5	0.003146	Function unknown
Proline dehydrogenase	M3V806	0.548795	8	18	0.004382	Function unknown
Transmembrane gamma-carboxyglutamic acid protein 1 isoform 1	I3LMT5	0.548264	4	19	0.009384	Calcium ion binding
Uncharacterized protein	A0A286ZTV2	0.547488	1	5	0.003487	Integral component of membrane; cellular anatomical entity

UPAR/Ly6 domain-containing protein	A0A287B805	0.541485	3	45	0.02681	Function unknown
Zinc fingers and homeoboxes protein 1	F1RR15	0.540952	3	6	0.01713	Protein heterodimerization activity, negative regulation of macromolecule biosynthetic process
ATP-sulfurylase	A0A481BE86	0.537697	1	4	0.03342	Function unknown
Ubiquitin carboxyl-terminal hydrolase	F1RTR5	0.533451	1	1	0.01852	Chromatin binding; covalent chromatin modification
Urokinase plasminogen activator	A0A0B8RSD8	0.528392	4	16	0.000802	Function unknown
Multi-drug resistance protein 1 transcript variant 2	A0A0E3MY68	0.52502	1	36	0.004046	Ribonucleotide binding
Polymeric immunoglobulin receptor	A0A4X1UQL1	0.514037	3	6	0.005094	Integral component of membrane; cellular anatomical entity
Ig-like domain-containing protein	A0A287A1Y1	0.510542	6	23	0.0171	Antigen processing and presentation of peptide antigen via mhc class I; antigen processing and presentation
Z-DNA-binding protein 1	A0A481BW17	0.507553	2	39	2.10E-05	Function unknown
Class E basic helix-loop-helix protein 41	A0A287AYR6	0.505189	2	4	0.000608	Function unknown
Endo/exonuclease/phosphatase domain-containing protein	A0A4X1V6E3	0.504998	1	2	0.006941	Function unknown
Protein MCM10 homolog	A0A287AY37	0.502307	3	3	0.02363	Function unknown
Plasminogen	P06867	0.499599	10	15	0.01564	Regulation of blood coagulation; negative regulation of blood coagulation
RING-type E3 ubiquitin transferase	I3LRN0	0.498269	31	46	0.006589	Function unknown
PARP-1 binding protein	A0A5G2QYX1	0.494283	1	1	0.01248	Function unknown
Elongation factor 1-gamma	A0A4X1VKK0	0.493786	1	60	0.000305	Function unknown

VLIG-type G domain-containing protein	F1RMQ6	0.493208	9	4	0.006861	Function unknown
Transcription factor jun-B	I3LJU2	0.490426	5	27	0.03037	Transcription factor activity, sequence-specific DNA binding; anatomical structure development
Tether containing UBX domain for GLUT4 isoform 2	A0A480NU10	0.485817	3	34	0.02326	Function unknown
Receptor protein-tyrosine kinase	F1SUT8	0.482384	23	37	0.0006	Transmembrane receptor protein kinase activity; negative regulation of signaling
Phosphoglycerate mutase	B5KJG2	0.481403	1	12	0.04568	Isomerase activity, organic acid metabolic process
Rhomboid-related protein 4 isoform X1	A0A480YX23	0.479941	1	6	0.01091	Function unknown
Reticulon (Fragment)	A0A1Y1FJ11	0.479415	1	42	0.006662	Cadherin binding; positive regulation of locomotion
ML domain-containing protein	A0A4X1TT31	0.476714	6	34	0.000972	Function unknown
Uncharacterized protein	A0A287ABC3	0.476675	2	5	0.005583	Function unknown
Uncharacterized protein	A0A4X1T995	0.475462	1	0	0.04474	Cadherin binding, regulation of cytosolic calcium ion concentration
XIAP-associated factor 1	K9IVW8	0.473008	6	29	0.01441	Function unknown
ASD2 domain-containing protein	A0A4X1TVX4	0.472839	1	13	0.02071	Function unknown
NPC intracellular cholesterol transporter 1	A0A5G2RDJ5	0.471449	1	11	0.04671	Small molecule binding, integral component of plasma membrane; establishment of localization in cell
Peptidase A1 domain-containing protein	A0A4X1T5P4	0.465517	1	3	0.0391	Function unknown
Uncharacterized protein	A0A4X1SW44	0.459789	3	2	0.000608	Protein heterodimerization activity; signal transduction
MHC class I antigen (Fragment)	K9LRJ6	0.459112	3	42	0.01817	Antigen processing and presentation; integral component of membrane
Aprotinin (Fragment)	B0LXF7	0.454334	1	26	0.01914	Enzyme regulator activity

Tetratricopeptide repeat protein 14 isoform a	A0A287AVL3	0.452973	1	1	0.008206	Binding
Uncharacterized protein	A0A4X1U686	0.451804	1	1	0.006141	Function unknown
Beta-2-microglobulin	A0A4X1VG41	0.451493	3	32	0.03628	Protein binding; positive regulation of cellular senescence
Uncharacterized protein	A0A4X1SXM2	0.449796	1	8	0.03855	Receptor binding; signal transduction
TPR_REGION domain-containing protein	A0A4X1U2X7	0.446353	3	9	0.0193	Function unknown
Uncharacterized protein	A0A287BD75	0.442298	1	1	0.001998	Function unknown
Meiosis-specific nuclear structural protein 1	F1RZG8	0.442128	3	4	0.002777	Protein binding; positive regulation of biological process
Uncharacterized protein	A0A287A1X3	0.440465	11	21	0.004206	Metal ion binding; membrane-bounded organelle
KIND domain-containing protein	A0A4X1VVD6	0.440438	4	5	0.001202	Function unknown
DALR anticodon-binding domain-containing protein 3 isoform 1	F1SKI7	0.438751	1	2	0.01795	Function unknown
Uncharacterized protein	A0A5G2Q6W7	0.436452	6	11	0.0218	Cell-cell adhesion; integral component of membrane
CST complex subunit CTC1	A0A4X1V8I6	0.433298	3	4	0.0332	Function unknown
Protein fem-1 homolog B	I3L6T4	0.429318	5	10	0.006546	Receptor binding, morphogenesis of a branching structure; morphogenesis of an epithelium
Aquaporin-5	A0A4X1WCJ0	0.425045	1	2	0.003184	Transmembrane transporter activity
ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase	A0A481D5X2	0.424914	1	32	0.002487	Signaling adaptor activity; phosphate-containing compound metabolic process
Signal transducer and activator of transcription	A0A4X1THM1	0.422745	1	60	0.04674	Transcription factor activity; sequence-specific DNA binding; regulation of cell differentiation
Uncharacterized protein	F1S6F1	0.42059	2	6	0.003557	Function unknown

Ribosomal RNA processing protein 36 homolog isoform 1	A0A480TNH7	0.417719	5	24	0.0084	Nucleic acid metabolic process; nucleic acid phosphodiester bond hydrolysis
Copine-2	A0A287AKE4	0.417499	2	6	0.032	Function unknown
Uncharacterized protein	A0A5G2R0A9	0.416925	23	55	0.00731	Function unknown
Glyco_transf_24 domain-containing protein	A0A5G2Q988	0.416884	1	49	0.02689	Transferase activity, transferring hexosyl groups
60S ribosomal protein L7 (Fragment)	Q6QAS9	0.415317	1	73	0.03863	MRNA binding, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
Uncharacterized protein	A0A4X1SHM4	0.414296	26	47	0.001758	Function unknown
Sterol regulatory element-binding protein 1	O97676	0.41369	2	2	0.0342	Transcription factor activity, sequence-specific DNA binding; regulation of peptide secretion
Uncharacterized protein	A0A4X1USN7	0.413043	2	3	0.03445	Zinc ion binding
Transcription elongation factor SPT5	A0A5G2RNJ4	0.407706	3	38	0.0027	Translation elongation factor activity
Tyrosine-protein kinase	A0A4X1V771	0.406538	1	6	0.02034	Cellular protein modification process; negative regulation of RNA biosynthetic process
Beta-1,4-galactosyltransferase 5	A0A5S8MJ01	0.405399	4	13	0.004927	Udp-glycosyltransferase activity; lipid biosynthetic process
Translocase of outer mitochondrial membrane 6	A0A287BEP4	0.404451	2	58	0.01959	Function unknown
High density lipoprotein binding protein	A0A0B8S073	0.403893	1	51	0.02977	RNA binding
Metalloproteinase inhibitor 3	A0A286ZZX3	0.401149	3	12	0.0162	Peptidase inhibitor activity; regulation of nitrogen compound metabolic process
Galectin	A0A286ZYZ8	0.396303	1	38	0.03571	Binding
Metallophos domain-containing protein	I3LCM5	0.389688	2	7	0.02865	Function unknown
BMP and activin membrane-	A0A480KI92	0.38939	1	3	0.003133	Receptor binding; positive regulation of cell proliferation

bound inhibitor homolog						
Uncharacterized protein	A0A4X1V704	0.385394	1	1	0.03052	Function unknown
Pirh2	A1YJE5	0.383993	3	10	0.01642	Zinc ion binding
Perilipin	R9WHX5	0.383354	15	34	0.003386	Lipid particle, lipid transport
Peptidase A1 domain- containing protein	A0A4X1VM25	0.382744	1	2	0.000234	Function unknown
Uncharacterized protein	A0A4X1U2C6	0.380626	1	3	0.00996	Function unknown
Ras-related protein Rap-2a	Q06AU2	0.378881	6	63	0.01732	Nucleoside-triphosphatase activity; regulation of phosphorus metabolic process
Protein-tyrosine sulfotransferase	A0A480JPS8	0.377604	2	5	0.03251	Binding
Tudor domain-containing protein 7	A0A4X1UP96	0.372806	5	5	0.02241	Function unknown
Phospholipid-transporting ATPase	A0A4X1TLB7	0.372657	2	2	0.03372	Function unknown
BZIP domain-containing protein	A0A4X1VLW8	0.371197	2	23	0.02678	Double-stranded DNA binding
SHS2_Rpb7-N domain- containing protein	F1SC14	0.370794	5	18	0.03566	DNA-directed RNA polymerase activity
HMG domain-containing protein 4	A0A287B9A3	0.367993	1	3	0.02111	Function unknown
Laminin subunit gamma-2 isoform a	F1S662	0.367503	36	38	0.03513	Function unknown
Laminin subunit alpha-1 (Fragment)	A0A480XDX5	0.367029	1	17	0.01149	Function unknown
Amino acid transporter	F1S763	0.365007	1	3	0.01887	Function unknown
Signal transducer and	A0A4X1W8D9	0.364463	11	16	0.03709	Transcription factor activity, sequence-specific DNA binding; immune effector process,

activator of transcription						regulation of protein phosphorylation
Ras-associating domain-containing protein	A0A4X1V4G5	0.363701	1	2	0.004983	Function unknown
Calponin-homology (CH) domain-containing protein	A0A5G2QI59	0.362694	7	9	0.02106	Function unknown
Phospholipid scramblase	I3LHI3	0.362388	4	20	0.04363	Protein binding, organophosphate ester transport; sterol homeostasis
Daxx	A0A480ZCA1	0.361958	3	6	0.02276	Function unknown
Prolyl 3-hydroxylase 1 isoform 1	A0A480KI56	0.361897	1	29	0.02903	Function unknown
ADAR adenosine deaminase RNA specific	K9J4M6	0.361793	43	46	0.00385	RNA binding, RNA processing
Zinc finger MYM-type protein 1 isoform X1	A0A481C188	0.361151	2	2	0.005405	Function unknown
Uncharacterized protein	A0A287APC5	0.35985	3	8	0.005894	Transcription regulator activity
Osteopontin	P14287	0.357729	10	40	0.0296	Integrin binding; regulation of tissue remodeling, positive regulation of nucleobase-containing compound metabolic process
Heparin cofactor 2	A0A480RKY5	0.35474	1	3	0.009598	Extracellular space, cellular anatomical entity
Complex I-KFYI	A1XQS6	0.354278	2	24	0.009943	Respiratory chain complex I; macromolecular complex
Phospholipid scramblase	A0A5G2QX76	0.353967	5	18	0.001525	Function unknown
Eukaryotic translation initiation factor 3 subunit K isoform 1	A0A481D1L8	0.353952	1	50	0.03555	Translation initiation factor activity
AKAP2_C domain-containing protein	A0A287AMX5	0.352666	15	21	0.01165	Function unknown
GMP_PDE_delta domain-containing protein	A0A5G2QW04	0.349534	1	20	0.0328	Function unknown
Uncharacterized protein	F1SBB3	0.34926	33	12	0.02509	Function unknown

Semaphorin-4B isoform 1	A0A287A766	0.349112	7	9	0.005664	Function unknown
RING-type E3 ubiquitin transferase	A0A4X1V887	0.347805	11	27	0.01074	Function unknown
Cytochrome P450	A7KZR2	0.347549	2	46	0.02386	Oxidoreductase activity
Dual specificity protein phosphatase	A0A5G2RAD0	0.347259	1	5	0.003963	Function unknown
Uncharacterized protein	A0A4X1UQJ8	0.346955	2	10	0.01103	Cellular component assembly; SMN complex
Uncharacterized protein	A0A5G2QI85	0.3458	10	68	0.009622	Ribonucleotide binding, positive regulation of cellular process
Lysosome membrane protein 2	F1RYT3	0.343871	10	25	0.004294	Quaternary ammonium group binding; lysosome
Pleckstrin homology domain-containing family A member 1 isoform X7	A0A480QEJ7	0.343142	4	18	0.001573	Function unknown
Guanylate binding protein 2	B2XWS2	0.342567	5	20	0.02755	Ribonucleotide binding
G_PROTEIN_RECEP_F3_4 domain-containing protein	A0A4X1V7D7	0.342287	4	14	0.00606	Function unknown
Dipeptidyl peptidase 4	A0A5G2Q7G7	0.341889	17	20	0.006007	Catalytic activity, acting on a protein; positive regulation of t cell activation
Solute carrier family 30 member 2	B5A8K5	0.34146	1	3	0.01182	Intrinsic component of membrane; cellular anatomical entity
Tuberin isoform 7	A0A480W2V1	0.341397	2	6	0.03302	Enzyme activator activity
Tripartite motif-containing protein 16 isoform a	A0A481BZY0	0.340576	8	21	0.002472	Function unknown
ATPase H(+)-transporting lysosomal accessory protein 2	A0A5G2QNQ8	0.335385	1	26	0.02403	Function unknown
CCN family member 2	F1S3P6	0.334895	6	20	0.03285	Receptor binding; negative regulation of cellular process; signal transduction
Uncharacterized protein	A0A4X1UUL9	0.334598	1	30	0.03999	Function unknown

Uncharacterized protein	A0A286ZRH1	0.334329	23	27	0.004041	Function unknown
Uncharacterized protein	A0A5G2RA88	0.333895	3	22	0.04709	Protein localization; endoplasmic reticulum; peptide transport
Adenosine deaminase 2	P58780	0.333895	2	7	0.01436	Adenosine deaminase activity; biosynthetic process
Uncharacterized protein	A0A287A7A8	0.333093	4	4	0.03562	Function unknown
CBFD_NFYB_HMF domain- containing protein	A0A287AUX2	0.33285	3	33	0.01331	Heterocyclic compound binding
Dolichyl- diphosphooligosaccharide-- protein glycosyltransferase subunit KCP2	A0A4X1VZL2	0.33243	1	8	0.01074	Function unknown
Caspase-10 isoform 1 preproprotein	A0A286ZWN2	0.33241	10	26	0.006527	Peptidase activity, regulation of cell death
G patch domain-containing protein 4 isoform 2	A0A481ASU0	0.332006	4	9	0.008409	Heterocyclic compound binding
Epiplakin isoform X1-like (Fragment)	A0A480PQZ4	0.331814	14	30	0.009525	Function unknown
Junctional adhesion molecule 1	A0A5K1V5T2	0.327128	10	37	0.002172	Function unknown
Uncharacterized protein	A0A4X1TWZ9	0.321851	6	2	0.04228	Function unknown
G-protein-coupled receptor 39	F1RY26	0.319627	5	10	0.01747	Metal ion binding; intrinsic component of membrane
2-5A-dependent ribonuclease	A0A286ZPJ7	0.317989	19	37	0.007735	Phosphotransferase activity; alcohol group as acceptor
Nidogen-2 isoform X1	A0A480MU29	0.316041	1	41	0.02777	Function unknown
Uncharacterized protein	I3LJ31	0.313351	3	5	0.005211	Integral component of membrane; cellular anatomical entity
Uncharacterized protein	A0A4X1TIC9	0.313076	1	21	0.00492	Function unknown
Uncharacterized protein	A0A4X1U855	0.312799	7	17	0.01091	Function unknown
RING-type domain-containing	A0A287B7H5	0.311564	1	2	0.01986	Function unknown

protein						
V-type proton ATPase subunit a	A0A4X1STL1	0.310445	13	21	0.003733	Function unknown
CW-type domain-containing protein	A0A5G2QF40	0.310284	8	10	0.02577	Function unknown
Oxysterol-binding protein	A0A5G2QUB9	0.309421	1	3	0.04428	Function unknown
AAA domain-containing protein	F2Z5H2	0.307856	13	48	0.000479	Binding; positive regulation of endocytosis
Anaphase-promoting complex subunit 10	D5L7X1	0.307211	3	22	0.04413	Transferase complex; regulation of cell cycle process
Integrator complex subunit 14	A0A5K1U644	0.306957	5	16	0.03426	Function unknown
Uncharacterized protein	F1SED4	0.305812	14	50	0.002509	Binding
Proteasome subunit beta	Q2PYM7	0.305577	6	37	0.04716	Peptidase activity, acting on l-amino acid peptides; regulation of proteolysis
RUN and TBC1 domain-containing protein 3	A0A480PGU9	0.305377	3	5	0.02247	Function unknown
Transforming growth factor beta-1 proprotein	P07200	0.304799	9	27	0.001228	Receptor binding; immune system process
N-acetyltransferase domain-containing protein	A0A4X1W7X4	0.303804	5	23	8.00E-05	Transferase activity, transferring acyl groups other than amino-acyl groups
BTB domain-containing protein	A0A287B5G3	0.300476	7	14	0.03854	Negative regulation of apoptotic signaling pathway; negative regulation of metabolic process
Phosphoenolpyruvate carboxykinase, cytosolic [GTP]	A0A4X1UM84	0.299862	12	32	0.007555	Positive regulation of nitrogen compound metabolic process; response to chemical
Ribosomal_L7Ae domain-containing protein	I3LCJ7	0.299802	5	31	0.00829	Organic cyclic compound binding; endonuclease complex
SAM_MT_RSMB_NOP	A0A4X1UJD8	0.298059	6	22	0.00133	Binding

domain-containing protein						
Cytochrome c oxidase subunit	A0A287BGN0	0.297583	2	43	0.03747	Hydrogen ion transmembrane transporter activity; mitochondrial protein complex
Acyl-coenzyme A oxidase	A0A5G2R961	0.29504	2	5	0.04846	Function unknown
TBC1 domain family member	I3LNR0	0.293977	6	6	0.00042	Function unknown
1 isoform X4						
Plectin (Fragment)	K9IVQ6	0.291673	1	71	0.008935	Function unknown
Nucleolar transcription factor 1	F1RQY4	0.288216	1	40	0.03351	DNA binding; membrane-bounded organelle
isoform X1						
Uncharacterized protein	A0A4X1UCR9	0.286767	24	43	0.004056	Cytokine receptor activity
Formin-like protein 2 isoform	A0A480RHY5	0.286477	14	19	0.02293	Function unknown
X5						
Lipoprotein lipase	I3LUA0	0.286373	6	20	0.01412	Triglyceride lipase activity; endosome; early endosome
IF rod domain-containing	A0A4X1WBS5	0.286095	2	10	0.000663	Function unknown
protein						
Phosphate transporter	M3V824	0.285935	5	9	0.02096	Function unknown
DNA helicase	A0A5K1VUK9	0.285876	23	19	0.003624	Function unknown
Integrin-associated protein	A0A4X1SPG5	0.285161	2	14	0.03335	Thrombospondin receptor activity; extracellular vesicle
TNF receptor-associated	A0A480SEQ9	0.284987	3	7	0.007375	Function unknown
factor						
[Histone H3]-lysine(4) N-	A0A287A913	0.284839	1	0	0.03028	Function unknown
trimethyltransferase						
Hexosyltransferase	A0A287AWP7	0.284049	3	7	0.02412	Function unknown
Ubiquitinyl hydrolase 1	F1RXF7	0.283781	8	38	0.04263	Thiol-dependent ubiquitin-specific protease activity
Longin domain-containing	A0A287B7S4	0.282275	2	11	0.02907	Function unknown
protein						
ADP/ATP translocase 3	A0A287AXS7	0.282015	7	65	0.01064	Adp transmembrane transporter activity

AB hydrolase-1 domain-containing protein	A0A4X1VWB4	0.279886	2	9	0.0345	Intrinsic component of membrane; cellular anatomical entity
Exocyst complex component	A0A480UT78	0.279845	4	8	0.002696	Exocytic process; macromolecular complex
t-SNARE coiled-coil homology domain-containing protein	A0A4X1VQQ8	0.279353	2	20	0.003373	Snare binding, endomembrane system
Inter-alpha-trypsin inhibitor heavy chain H2	A0A5G2QEV5	0.278699	9	10	0.0156	Serine-type endopeptidase inhibitor activity; oxoacid metabolic process
3-hydroxy-3-methylglutaryl coenzyme A reductase	A0A4X1SQE9	0.27824	8	11	0.02539	Function unknown
Sorting nexin-24 isoform X4	A0A480Q2P1	0.277886	1	12	0.01988	Binding
Uncharacterized protein	A0A4X1UTU8	0.275916	2	7	0.01086	Function unknown
Hermansky-Pudlak syndrome 3 protein homolog	A5A772	0.27398	5	6	0.009781	Organelle organization; pigmentation
ATP-binding cassette, sub-family C (CFTR/MRP), member 13	K9J4N7	0.273938	20	22	0.008823	Function unknown
Secretory carrier-associated membrane protein	A0A4X1VTN9	0.273283	3	14	0.003668	Function unknown
Tumor protein p73	A0A4X1WA24	0.271375	4	7	0.003205	Function unknown
Lethal(2) giant larvae protein homolog 2	A0A481CW44	0.270849	29	37	0.007905	Function unknown
Uncharacterized protein	F1S1J8	0.270179	6	35	0.03383	Function unknown
USP domain-containing protein	A0A4X1UCD6	0.270157	1	5	0.03346	Peptidase activity, acting on l-amino acid peptides; cellular protein metabolic process
Uncharacterized protein	A0A286ZMQ7	0.269031	8	26	0.002548	Function unknown
Uncharacterized protein	A0A4X1TDN4	0.265297	18	26	0.01732	Protein binding

Polynucleotide phosphorylase 1	A0A287AMV5	0.264709	44	67	0.02717	Organic cyclic compound binding; aromatic compound catabolic process; RNA processing
Uncharacterized protein	A0A4X1TMR0	0.264278	4	45	0.01409	Acyl-coa hydrolase activity; purine nucleoside bisphosphate metabolic process
Tr-type G domain-containing protein	A0A4X1WBZ8	0.263849	21	32	0.04751	Translation initiation factor activity
Uncharacterized protein	A0A4X1UBH5	0.263142	1	13	0.04905	Function unknown
Downregulated proteins in PK-15-infected cells (a total of 131 proteins)						
Glyceraldehyde-3-phosphate dehydrogenase	A0A076KRX0	-1.03138	3	77	0.02485	Regulation of translation; oxidoreductase activity, acting on the aldehyde or oxo group of donors
Cellular retinol binding protein 1	Q53J08	-0.672103	2	57	0.03177	Terpenoid biosynthetic process; binding
SUI1 domain-containing protein	A0A5G2QLD8	-0.635261	3	78	0.002729	Regulation of translation; translation initiation factor activity
Olfactory receptor	A0A287AX70	-0.608824	1	2	0.03294	Signal transduction; olfactory receptor activity
Uncharacterized protein	A0A5G2QVV0	-0.605594	1	68	0.03066	Function unknown
SGF29 C-terminal domain-containing protein	A0A4X1U8F2	-0.576793	4	25	0.000249	Covalent chromatin modification; protein binding
Thiopurine S-methyltransferase	A0A481DB59	-0.569263	2	74	0.007656	Methylation; methyltransferase activity
Syndecan	A0A287B0S3	-0.540026	3	9	0.000242	Function unknown
Heterogeneous nuclear ribonucleoprotein K	A0A4X1UTE2	-0.537037	2	62	0.04311	Positive regulation of cellular process; transcription factor activity, sequence-specific DNA binding
Syndecan	F1S0L5	-0.535399	5	21	0.007086	Cellular_component:cellular_component;
Uncharacterized protein	A0A4X1VCI3	-0.514081	1	7	0.02767	Function unknown
TIMELESS-interacting protein	A0A287BGF4	-0.511401	3	8	0.02252	Negative regulation of cellular process
Thymosin beta-4	Q95274	-0.491832	3	59	0.003064	Positive regulation of cellular process; protein binding

Uncharacterized protein	A0A5G2QSQ7	-0.479801	1	30	0.0225	Response to stimulus; protein binding
Uncharacterized protein	A0A4X1VI11	-0.471701	1	5	0.02426	Function unknown
Integral membrane protein 2	F1RK12	-0.471287	2	73	0.02785	Negative regulation of cellular process; binding
ATP-binding cassette sub-family F member 1 isoform X1	A0A480K1E2	-0.465445	2	46	0.01248	Regulation of nitrogen compound metabolic process; ribonucleotide binding
Hydroperoxy icosatetraenoate dehydratase	F1SIE9	-0.454951	13	27	0.001535	Hydrogen peroxide metabolic process; binding
SPARC	P20112	-0.454331	14	47	0.004519	Calcium ion binding
Tyrosine-protein kinase receptor	A0A480U2S6	-0.443617	3	5	0.01908	Function unknown
Uncharacterized protein	A0A4X1V3D9	-0.439777	6	53	0.02406	Function unknown
Glucose-6-phosphate 1-dehydrogenase	A0A0B8RVW4	-0.439304	2	68	0.04662	Function unknown
Proteasome subunit alpha type	F2Z5N0	-0.434372	3	59	0.0341	Muscle tissue development; peptidase activity, acting on L-amino acid peptides
Hepatocyte nuclear factor 1-beta	A0A4X1T4P3	-0.431195	1	24	0.02259	Function unknown
DNA-directed RNA polymerases I, II, and III subunit RPABC5	A0A4X1VYD0	-0.428678	2	30	0.03602	Aromatic compound biosynthetic process; zinc ion binding
6-pyruvoyl tetrahydrobiopterin synthase	A0A4X1TBY4	-0.42707	6	46	0.005413	Organic hydroxy compound metabolic process; protein binding
Ribosomal protein S6 kinase	I3LS09	-0.423196	2	3	0.003568	Binding
Solute carrier family 3 member 1	B2D2K8	-0.421081	10	17	0.001091	Function unknown
Hepatocyte nuclear factor 1-	A0A5G2R7E8	-0.419994	1	19	0.02184	Positive regulation of transcription, DNA-templated; heterocyclic compound binding

beta						
Gag protein	R4JTP7	-0.4183	2	24	0.0376	Symbiosis, encompassing mutualism through parasitism; binding
Uncharacterized protein	A0A5G2RKV1	-0.401257	1	20	0.02429	Function unknown
PKS_ER domain-containing protein	A0A4X1U010	-0.399864	1	5	0.02424	Metabolic process; protein dimerization activity
PCNA-associated factor	A0A5G2QZV8	-0.398	1	6	0.008994	Regulation of biological process
Autophagy-related protein 3	A0A480PFQ0	-0.392698	7	34	0.006294	Negative regulation of cellular process; catalytic activity, acting on a protein
Glutathione transferase	F1RL37	-0.392157	4	16	0.01781	Organic substance metabolic process
Tetraspanin-13	F1SEI8	-0.391466	3	21	0.01072	Function unknown
CBFD_NFYB_HMF domain-containing protein	A0A5G2QBZ0	-0.387762	4	24	0.04324	Regulation of macromolecule biosynthetic process; heterocyclic compound binding
APC-binding protein EB1	F6Q3L0	-0.385105	12	57	0.0161	Positive regulation of cellular component biogenesis; tubulin binding
Envelope protein	Q6W4V3	-0.38431	4	38	0.03044	Cellular_component:cellular_component
Importin-7	I3LDM3	-0.38163	5	45	0.004492	Response to stimulus; protein binding
VPS10 domain-containing protein	A0A287A1U0	-0.378575	11	13	0.00172	Function unknown
Rab GDP dissociation inhibitor	I3L893	-0.373655	15	64	0.006841	Negative regulation of cellular process; enzyme regulator activity
Eukaryotic translation initiation factor 4H	I3LRD5	-0.372767	10	38	0.001385	Multi-organism reproductive process; translation initiation factor activity
Uncharacterized protein	A0A286ZPG4	-0.369254	2	68	0.0343	Cellular component organization; protein binding
Protein phosphatase 1 regulatory subunit 14B	Q8MIK9	-0.367976	3	48	0.02723	Protein serine/threonine phosphatase inhibitor activity
Uncharacterized protein	A0A287APU9	-0.366285	3	5	0.0314	Function unknown
WD_REPEATS_REGION domain-containing protein	A0A4X1W8T2	-0.366168	4	12	0.001112	Function unknown
Protein S100	A0A4X1VVF5	-0.365378	4	34	0.0126	Response to stimulus; metal ion binding

Protein S100 (Fragment)	A0A480ZBF9	-0.362396	5	29	0.01537	Positive regulation of cellular process; receptor binding
Small EDRK-rich factor 1 isoform 2	A0A480K1R7	-0.360411	1	13	0.0115	Function unknown
Uncharacterized protein	A0A4X1UY47	-0.358777	3	4	0.003993	Function unknown
Fatty acid-binding protein, heart	O02772	-0.354665	8	86	0.008223	Cellular_component:cytoplasm; binding
Fructose-bisphosphate aldolase	A0A4X1U602	-0.349246	1	69	0.03048	ATP generation from ADP; fructose-bisphosphate aldolase activity
Uncharacterized protein	A0A4X1SXE8	-0.349142	3	28	0.001458	Catabolic process;
Jupiter microtubule associated homolog 1 isoform 1	A0A480VV84	-0.347829	5	64	0.001733	Function unknown
UBC core domain-containing protein	A0A5G2RGI4	-0.345932	4	58	0.004976	Function unknown
Proteasome assembly chaperone 1	I3LT95	-0.345219	6	29	0.03587	Function unknown
ANK_REP_REGION domain-containing protein	A0A4X1VC59	-0.343459	6	24	0.0416	Response to endoplasmic reticulum stress
Low-density lipoprotein receptor-related protein 2	C0HL13	-0.341928	2	24	0.02891	Function unknown
Heterogeneous nuclear ribonucleoprotein D0 isoform c	A0A480M1B4	-0.341029	15	50	0.03272	Molecular_function:organic cyclic compound binding; RNA binding
Mannose-1-phosphate guanyltransferase alpha	A0A480QK53	-0.339951	3	27	0.04944	Function unknown
PPP1R35_C domain-containing protein	A0A4X1UE31	-0.33722	1	3	0.02551	Negative regulation of cellular process; protein binding
Uncharacterized protein	A0A5G2RAN0	-0.334439	8	22	0.004152	Positive regulation of cellular process

Uncharacterized protein	F1RRD3	-0.33427	1	52	0.04782	Function unknown
Annexin	F2Z5C1	-0.334113	22	74	0.006475	Response to stimulus; lipid binding
Uncharacterized protein	A0A4X1SLB5	-0.333214	6	21	0.02839	Function unknown
Peptidylprolyl isomerase	I3LR51	-0.331864	11	43	0.02369	Cellular_component:intracellular membrane-bounded organelle; isomerase activity
Small nuclear ribonucleoprotein Sm D3	A0A4X1V3C3	-0.331206	4	48	0.04849	Protein binding
4a-hydroxytetrahydrobiopterin dehydratase	A0A4X1TCL6	-0.331086	3	37	0.01264	Positive regulation of cellular process; phenylalanine 4-monooxygenase activity
Splicing factor, arginine/serine-rich 11	Q19QT0	-0.326117	5	13	0.001402	RNA processing; RNA binding
DUF4604 domain-containing protein	A0A4X1TEH0	-0.32309	1	7	0.02072	Function unknown
Uncharacterized protein	A0A4X1TZ18	-0.322717	1	26	0.005439	Function unknown
Meiosis protein 5 homolog	A0A4X1TKV7	-0.322413	3	22	0.001124	Regulation of nitrogen compound metabolic process; ligand-dependent nuclear receptor transcription coactivator activity
Uncharacterized protein	I3LNG8	-0.320585	1	65	0.01913	Response to organic substance; binding
Phosphoglycerate mutase	A0A286ZQ31	-0.31627	9	38	0.00292	ATP generation from ADP; isomerase activity
39S ribosomal protein L33, mitochondrial	A0A4X1TLP9	-0.315596	3	49	0.03032	Translation; structural constituent of ribosome
Dynamin-like 120 kDa protein, form S1	F1SFG7	-0.314733	1	52	0.02394	Negative regulation of cellular process; pyrophosphatase activity
Craniofacial development protein 1	A0A5G2R143	-0.30966	7	36	0.03173	Function unknown
Triosephosphate isomerase	A0A288CFT0	-0.307356	19	77	0.03669	Function unknown
Uncharacterized protein	A0A4X1TNF0	-0.306645	6	80	0.02288	Function unknown
Leukotriene A(4) hydrolase	K9J6K4	-0.306507	12	47	0.000167	Icosanoid biosynthetic process; zinc ion binding

5-oxoprolinase isoform X1	A0A480MWT6	-0.306491	1	19	0.01972	Function unknown
NTF2 domain-containing protein	A0A4X1UHL0	-0.305242	5	83	0.006007	Positive regulation of cellular process; structural constituent of nuclear pore
Uncharacterized protein	A0A4X1U6L2	-0.303812	2	1	0.007438	Function unknown
HIT domain-containing protein	F1RKI3	-0.303653	5	53	0.01566	Positive regulation of cellular process; catalytic activity
15-oxoprostaglandin 13-reductase	A0A287B7R3	-0.303482	15	57	0.02019	Function unknown
Uncharacterized protein	A0A287B283	-0.301796	10	33	0.001642	Function unknown
Uncharacterized protein	A0A4X1UC72	-0.301053	7	31	0.005238	Positive regulation of cellular process; repressing transcription factor binding
CRIP2	A0A165DE67	-0.300866	8	45	0.00391	Molecular_function:cation binding; ion binding
Thioredoxin	P82460	-0.299789	8	89	0.008625	Negative regulation of cellular process; disulfide oxidoreductase activity
Coiled-coil domain-containing protein 72	F2Z5V1	-0.298137	2	30	0.003451	Function unknown
Malic enzyme	A0A5G2RAJ8	-0.297189	21	54	0.002204	Small molecule metabolic process; malate dehydrogenase (decarboxylating
Actin-related protein 2/3 complex subunit 3	B5APU8	-0.296622	6	35	0.01568	Arp2/3 complex-mediated actin nucleation;
J domain-containing protein	A0A5G2R2L7	-0.29571	10	38	0.03685	Cellular_component:intracellular membrane-bounded organelle; protein binding
Telomerase RNA component interacting RNase isoform 1	F1SEX4	-0.294522	8	48	0.004331	Aromatic compound catabolic process; nuclease activity
G_PROTEIN_RECEP_F2_4 domain-containing protein	F1RF36	-0.294061	7	14	0.0264	Function unknown
Annexin	F1SEN1	-0.293648	21	74	0.005457	Function unknown
EKC/KEOPS complex subunit GON7	P0C8B5	-0.293036	3	48	0.01694	Cellular_component:cellular_component;
Hypoxanthine-guanine phosphoribosyltransferase	Q45FY6	-0.292491	2	67	0.02459	Glycosyl compound biosynthetic process; small molecule binding

Dynamin GTPase	A0A287B878	-0.291599	2	29	0.003584	Function unknown
Uncharacterized protein	A0A287B8I3	-0.291042	5	18	0.02272	Function unknown
Protein archease	A0A4X1VY44	-0.290657	2	16	0.0247	Function unknown
Seryl-tRNA synthetase	A0A287BJI6	-0.29056	27	53	0.01824	Function unknown
Stathmin	Q6DUB7	-0.289364	8	46	0.009694	Positive regulation of cellular process; protein binding
Transaldolase	A0A287BQ72	-0.287688	12	30	0.02121	Function unknown
Calponin	A0A4X1VU33	-0.287374	11	55	0.03544	Function unknown
Uncharacterized protein	A0A4X1TSU7	-0.286066	10	32	0.0114	Function unknown
Threonyl-tRNA synthetase	A0A480F5A7	-0.285505	1	53	0.006431	Function unknown
14_3_3 domain-containing protein	A0A4X1V4V6	-0.285402	11	68	0.007724	Positive regulation of cellular process; channel regulator activity
Uncharacterized protein	A0A4X1UBE7	-0.284256	3	38	0.000358	Function unknown
Uncharacterized protein	A0A286ZQ23	-0.283241	12	32	0.01607	Molecular_function:transferase activity, transferring phosphorus-containing groups; catalytic activity
ATP-binding cassette sub-family F member 1 isoform a	A0A480PQG3	-0.282454	2	46	0.03874	Regulation of nitrogen compound metabolic process; ribonucleotide binding
LRRcap domain-containing protein	A0A4X1TYN7	-0.28197	9	34	0.03312	Function unknown
Eukaryotic translation initiation factor 3 subunit E	F1S1G0	-0.281832	23	60	0.03225	Positive regulation of cellular process; translation factor activity, RNA binding
RING-type domain-containing protein	A0A4X1TVR4	-0.281054	5	15	0.01428	Positive regulation of cellular process; transition metal ion binding
Uncharacterized protein	I3LLQ7	-0.280242	2	15	0.004602	Function unknown
Annexin	A0A4X1W3B6	-0.27781	24	68	0.005565	Icosanoid secretion;
MPN domain-containing protein	A0A4X1UW55	-0.276591	15	61	0.02333	Positive regulation of cellular process; peptidase activity, acting on L-amino acid peptides

Programmed cell death protein 5	A0A481D4P9	-0.27584	9	74	0.03116	Positive regulation of cellular process; acetyltransferase activator activity
Tyrosine-protein phosphatase non-receptor type	A0A5G2QDD3	-0.275827	1	48	0.01236	Positive regulation of cellular process; insulin receptor binding
Cyclin-dependent kinases regulatory subunit	A0A4X1W0Z6	-0.275326	2	33	0.01112	Positive regulation of cellular process; enzyme regulator activity
Hsp90 chaperone protein kinase-targeting subunit	Q684M6	-0.273493	14	43	0.004248	Positive regulation of cellular process; protein binding
Peptidyl-prolyl cis-trans isomerase	A0A4X1W0F9	-0.273478	5	51	0.003075	Function unknown
PX domain-containing protein	A0A286ZKH8	-0.273338	6	57	0.01169	Negative regulation of cellular process; protein binding
Uncharacterized protein	F1SGZ8	-0.27309	19	56	0.002509	Regulation of cellular component size; protein binding
CCDC50_N domain-containing protein	A0A5G2QER5	-0.272456	2	3	0.03041	System process;
Transcription factor BTF3	A0A287BJ88	-0.271433	10	73	0.01123	Multicellular organism development;
Cofilin-2	Q5G6V9	-0.270735	11	72	0.01743	Positive regulation of cellular process; protein binding
Uncharacterized protein	A0A287B3B5	-0.270464	3	5	0.001064	Anatomical structure development; protein dimerization activity
Uncharacterized protein	A0A4X1U9S0	-0.269536	2	11	0.02041	Cellular component organization or biogenesis;
Uncharacterized protein	A0A4X1U210	-0.269086	14	65	0.02894	Signal transduction; phosphatidylglycerol binding