

Table SI. Primer sequences for quantitative PCR.

Genes	Forward primer (5'-3')	Reverse primer (5'-3')	Gene accession no.
β -actin	GGATGCAGAAGGAGATCACTG	5CGATCCACACGGAGTACTTG	NM_001101.5
NUP50	AGCCTTTGGAAGGACTGTCG	TCACTATCCAATCCCGCACG	NM_007172.4
NUP98	GGGCTCTTTGGTTTTGGCAC	CAAAGCCCAAAGTGGCTGTC	NM_001365125.2
NUP160	AGCTATCAGGGGTGACCAGT	TTCCAGCAGTAAGCCGAAGG	NM_015231.3

NUP, nucleoporin.

Table SII. GO enrichment analysis of molecular function terms for differentially expressed genes.

A, Molecular functions ^a				
No.	GO: Term ID	Term	Involved genes, n	P-value
1	GO:0016301	Kinase	397	4.20×10^{-14}
2	GO:0001228	Activator	362	1.70×10^{-10}
3	GO:0005524	Transferase	928	2.90×10^{-9}
4	GO:0004713	Tyrosine-protein kinase	72	4.30×10^{-7}
5	GO:0003723	RNA-binding	353	8.60×10^{-7}
6	GO:0004674	Serine/threonine-protein kinase	200	1.10×10^{-5}
7	GO:0004725	Protein phosphatase	75	2.40×10^{-4}
8	GO:0003743	Initiation factor	37	8.60×10^{-4}
9	GO:0001618	Host cell receptor for virus entry	42	1.80×10^{-3}
10	GO:0005516	Calmodulin-binding	82	2.50×10^{-3}
B, Excluded molecular functions ^b				
No.	GO: Term ID	Term	Involved genes, n	P-value
1	Not found	Chromatin regulator	163	1.80×10^{-6}
2	Not found	Repressor	295	1.20×10^{-4}
3	Not found	Multifunctional enzyme	47	3.10×10^{-3}
4	Not found	Lyase	86	6.00×10^{-3}
5	Not found	Allosteric enzyme	30	7.50×10^{-3}
6	Not found	Blood group antigen	19	3.20×10^{-2}
7	Not found	Viral nucleoprotein	17	3.30×10^{-2}
8	Not Found	Actin capping	13	3.50×10^{-2}
9	Not Found	Decarboxylase	13	8.50×10^{-2}

^aTop 10 terms. ^bExcluded due to the unavailability of full details. Analysis was performed using the Database for Annotation, Visualization and Integrated Discovery. GO, Gene Ontology.

Table SIII. GO enrichment analysis of biological processes for differentially expressed genes.

No.	GO: Term ID	Term	Involved genes, n	P-value
1	GO:0016032	Host-virus interaction	363	1.80×10^{-26}
2	GO:0015031	Protein transport	325	1.50×10^{-8}
3	GO:0048511	Biological rhythms	91	4.10×10^{-7}
4	GO:0006915	Apoptosis	272	1.90×10^{-6}
5	GO:0045087	Innate immunity	185	7.80×10^{-5}
6	GO:0000398	mRNA splicing	150	9.10×10^{-5}
7	GO:0006397	mRNA processing	184	1.20×10^{-4}
8	GO:0006364	rRNA processing	57	2.30×10^{-4}
9	GO:0006357	Transcription	1,057	3.50×10^{-4}
10	GO:0045944	Transcription regulation	1,027	4.20×10^{-4}

Analysis performed using the Database for Annotation, Visualization, and Integrated Discovery. The top 10 terms are shown. GO, Gene Ontology.

Table SIV. GO enrichment analysis of cellular component terms for differentially expressed genes.

A, Cellular components ^a				
No.	GO: Term ID	Term	Involved genes, n	P-value
1	GO:0005737	Cytoplasm	2,375	1.90×10^{-33}
2	GO:0005634	Nucleus	2,369	3.60×10^{-21}
3	GO:0005794	Golgi apparatus	449	1.40×10^{-11}
4	GO:0005739	Mitochondrion	574	6.10×10^{-9}
5	GO:0005856	Cytoskeleton	568	1.20×10^{-6}
6	GO:0005768	Endosome	287	2.20×10^{-5}
7	GO:0000502	Proteasome	36	4.00×10^{-5}
8	GO:0045202	Synapse	226	4.30×10^{-5}
9	GO:0005905	Coated pit	34	1.20×10^{-4}
10	GO:0031410	Cytoplasmic vesicle	291	2.50×10^{-4}
B, Excluded cellular components ^b				
No.	GO: Term ID	Term	Involved genes, n	P-value
1.	Not Found	Cell junction	399	4.30×10^{-9}
2.	Not Found	Cell projection	478	9.40×10^{-5}
3.	Not Found	Synaptosome	33	1.60×10^{-2}
4.	Not Found	Microsome	58	3.70×10^{-2}

^aTop 10 terms. ^bExcluded due to the unavailability of full details. Analysis was performed using the Database for Annotation, Visualization, and Integrated Discovery. GO, Gene Ontology.

Table SV. KEGG pathway enrichment analysis of differentially expressed genes.

No.	KEGG term ID	Term	Involved genes, n	P-value
1.	hsa04510	Focal adhesion	128	3.90×10^{-8}
2.	hsa04010	MAPK signaling pathway	176	6.70×10^{-8}
3.	hsa04151	PI3K-Akt signaling pathway	205	1.80×10^{-7}
4.	hsa05166	Human T-cell leukemia virus 1 infection	137	1.90×10^{-7}
5.	hsa05200	Pathways in cancer	293	2.00×10^{-7}
6.	hsa05022	Pathways of neurodegeneration - multiple diseases	265	3.10×10^{-7}
7.	hsa05163	Human cytomegalovirus infection	135	2.20×10^{-6}
8.	hsa05169	Epstein-Barr virus infection	123	2.40×10^{-6}
9.	hsa05017	Spinocerebellar ataxia	91	4.70×10^{-6}
10.	hsa04066	HIF-1 signaling pathway	72	8.30×10^{-6}

Analysis performed using the Database for Annotation, Visualization, and Integrated Discovery. The top 10 terms are shown. KEGG, Kyoto Encyclopedia of Genes and Genomes.