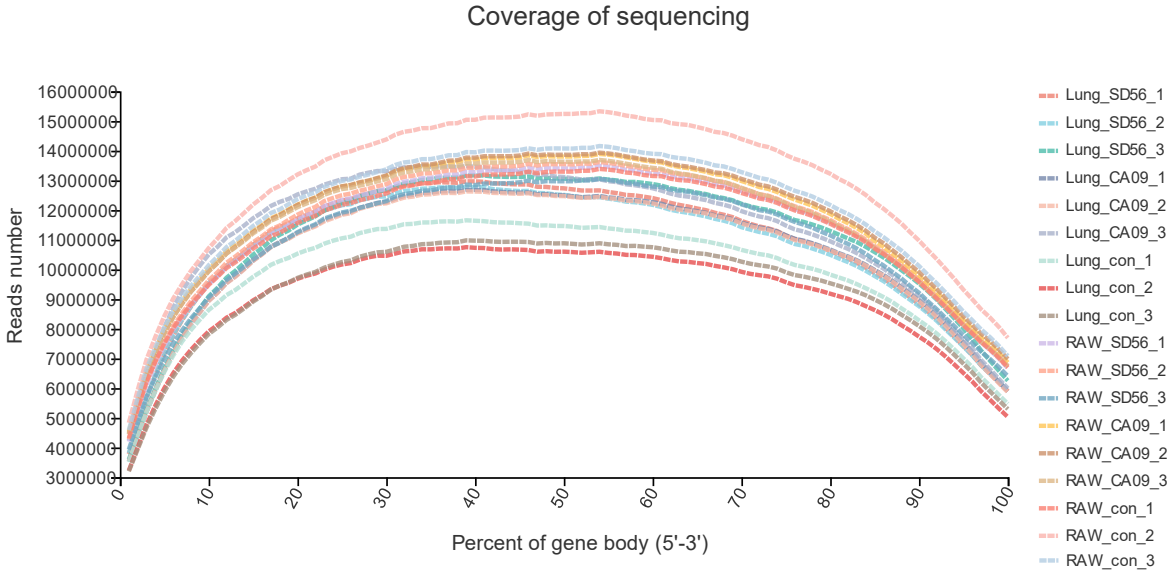
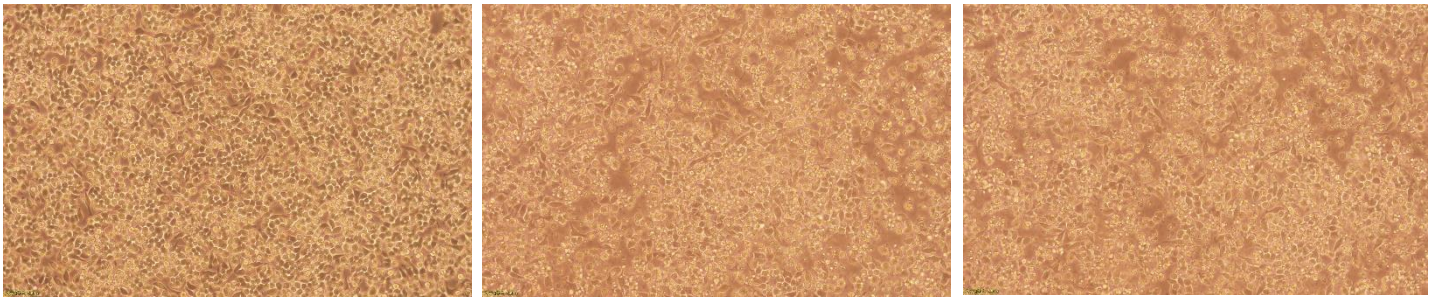
(A)



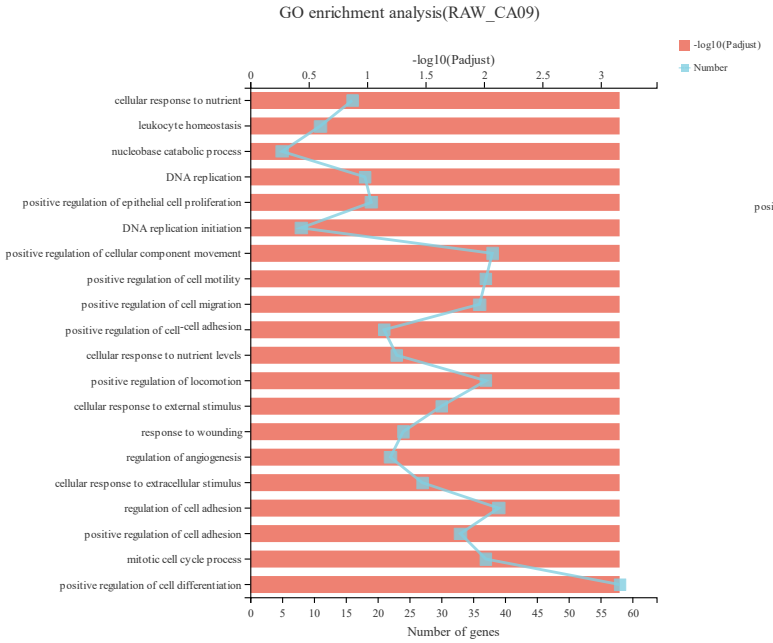
(B)

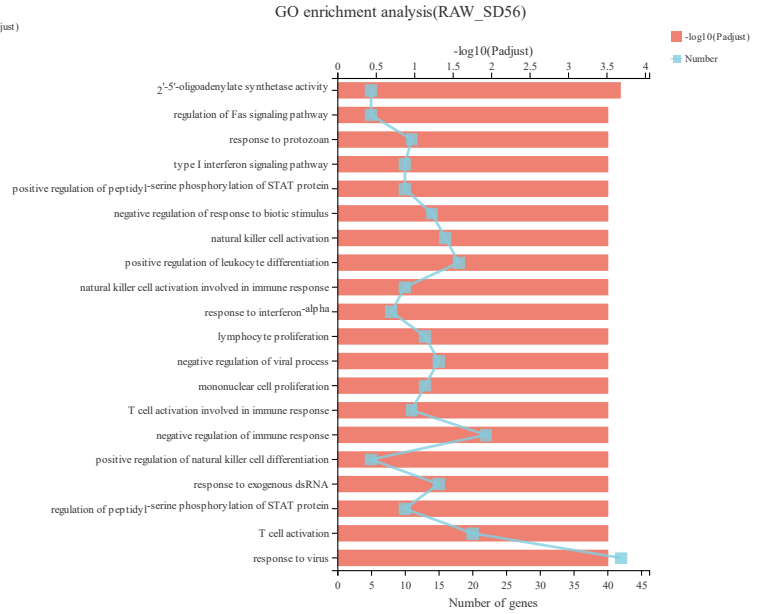
Figure S1. Transcriptome quality assessment. The quality of the transcriptome sequencing was assessed using mapped reads. (A) The number of sequences on chromosomes was statistically compared to reflect the distribution of the sequences on each chromosome. (B) Sequencing coverage analysis, the curve reflects whether the sequence obtained by sequencing is evenly distributed on the gene.



(A) (B) (C)

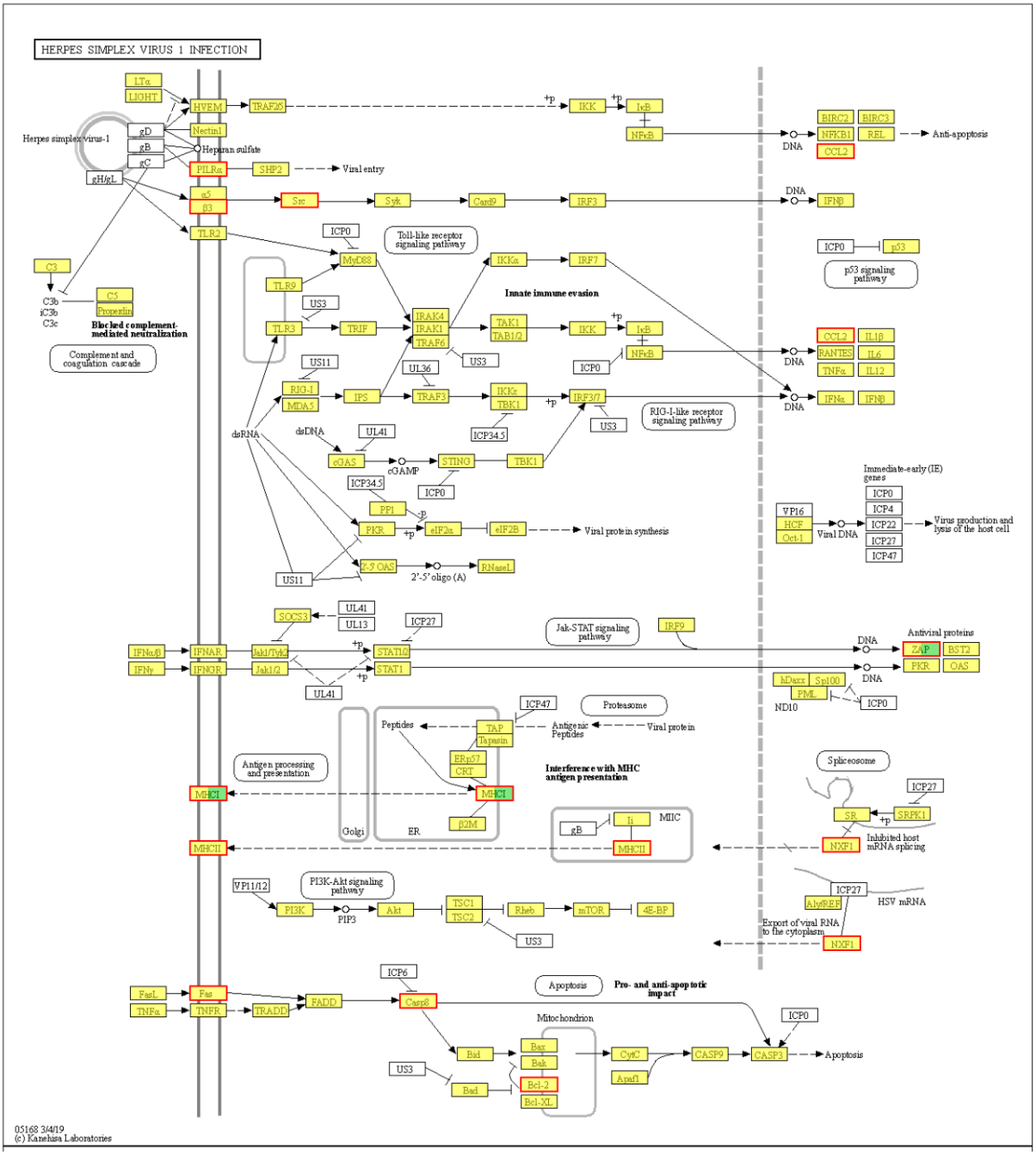
Figure S2. Cytopathic effect of RAW264.7 infected with CA09 and SD56. (A) RAW264.7 cells of the uninfected group showed no obvious lesions. (B) RAW264.7 cells in CA09 infected group showed obvious lesions. (C) RAW264.7 cells in SD56 infected group showed obvious lesions. Magnification is 200X.



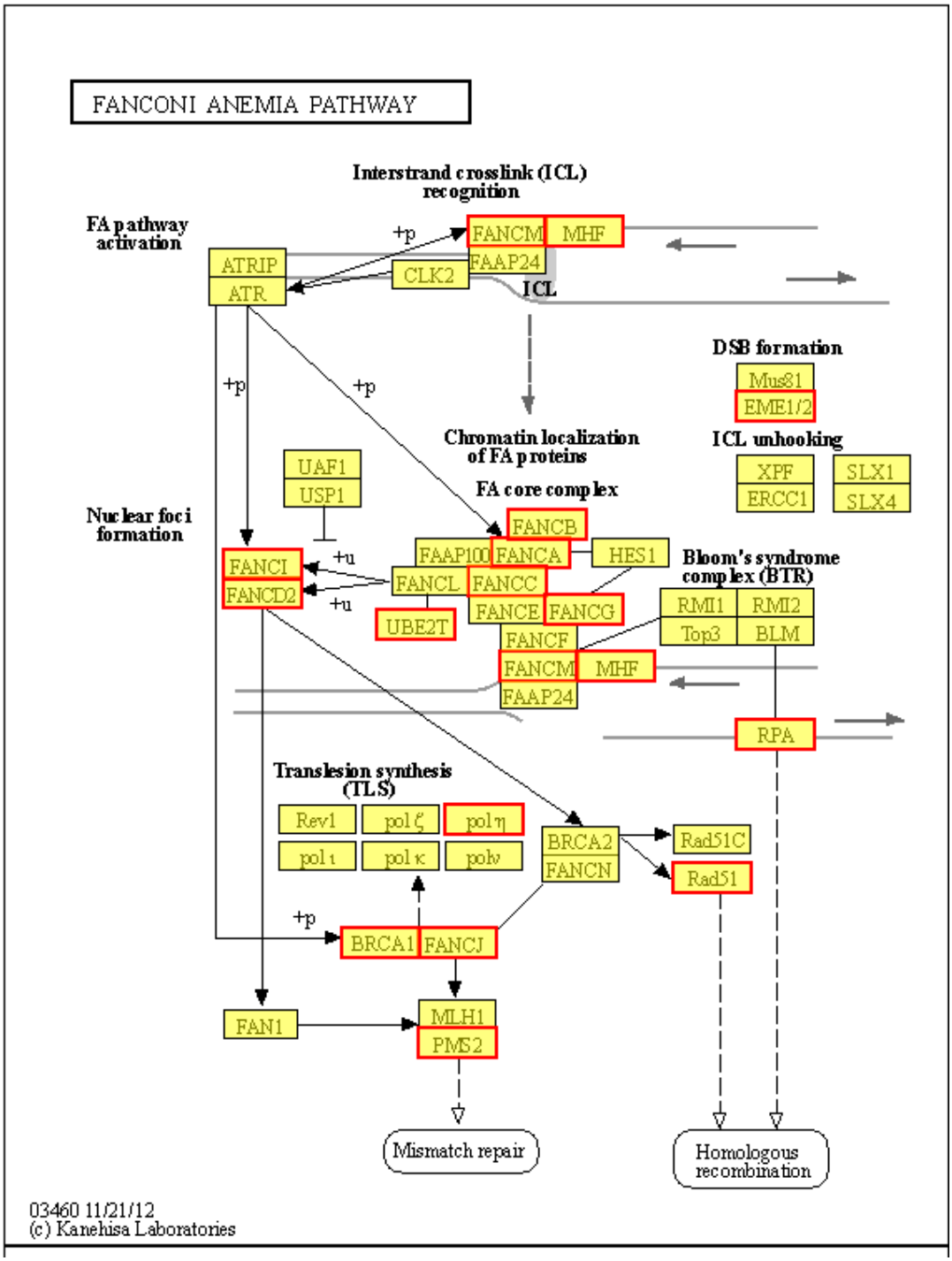


(A) (B)

Figure S3. GO functional enrichment of differentially expressed genes in RAW264.7.(A) GO analysis of RAW264.7 differentially expressed genes in CA09 relative to the control. (B) GO analysis of RAW264.7 differentially expressed genes in SD56 relative to the control.


HERPES SIMPLEX VIRUS 1 INFECTION
Herpes simplex virus-1
Viral entry
Heparan sulfate
Toll-like receptor signaling pathway
Innate immune evasion
Blocked complement-mediated neutralization
Complement and coagulation cascade
p53 signaling pathway
RIG-I-like receptor signaling pathway
Viral protein synthesis
Immediate-early (IE) genes
Viral DNA
Virus production and lysis of the host cell
Jak-STAT signaling pathway
Antiviral proteins
Proteasome
Peptides
Antigenic Peptides
Viral protein
Antigen processing and presentation
Interference with MHC antigen presentation
Golgi
ER
MIIC
Spliceosome
Inhibited host mRNA splicing
PI3K-Akt signaling pathway
PIP3
HSV mRNA
Export of viral RNA to the cytoplasm
Apoptosis
Pro- and anti-apoptotic impact
Mitochondrion
Anti-apoptosis
05168 3/4/19
(c) Kanehisa Laboratories

（A）



(B)

Figure S4. Details of the signaling pathways involved in modules.(A) Details of Herpes simplex virus 1 infection pathway and related up-regulation and down-regulation genes; (B) Details of Fanconi anemia pathway and related up-regulation and down-regulation genes.

Table S1 Transcriptome Profile of 18 cDNA libraries

SAMPLE	RawReads	Clean Reads	Clean Reads Percent	Q30%	Total mapped	Uniquely mapped	CDS
Lung_SD56_1	53146554	52566676	98.9%	91.4	50348605(95.8%)	47164508(89.7%)	52240657.0(70.7%)
Lung_ SD56_2	53212994	52615142	98.9%	91.2	50238054(95.5%)	47843180(90.9%)	52154841.0(70.3%)
Lung_ SD56_3	53307084	52756724	99.0%	91.4	50443422(95.6%)	47909895(90.8%)	53155786.0(71.0%)
Lung_CA09_1	53062352	52331376	98.6%	90.2	49578641(94.7%)	46892214(89.6%)	51168736.0(70.1%)
Lung_ CA09_2	53315812	52788194	99.0%	91.7	49662285(94.1%)	46977241(89.0%)	49972826.0(68.9%)
Lung_ CA09_3	53120896	52617316	99.1%	92.0	50302265(95.6%)	47608152(90.5%)	53701875.0(71.5%)
Lung_con_1	52604088	51936712	98.7%	94.0	49910648(96.1%)	46831341(90.2%)	48737823.0(68.0%)
Lung_con_2	47144746	46541456	98.7%	94.0	44688267(96.0%)	42000270(90.2%)	44211373.0(68.2%)
Lung_con_3	48534990	47880950	98.7%	93.9	45991411(96.1%)	43541960(90.9%)	44319805.0(67.1%)
RAW_ SD56_1	49532908	48881004	98.7%	92.8	43802836(89.6%)	41018374(83.9%)	48260720.0(73.2%)
RAW_ SD56_2	50516272	49835386	98.7%	92.9	44244362(88.8%)	41399847(83.1%)	48945530.0(73.4%)
RAW_ SD56_3	47781244	47106910	98.6%	92.6	41981169(89.1%)	39395090(83.6%)	46642537.0(73.5%)
RAW_ CA09_1	47438302	46738398	98.5%	93.0	43018095(92.0%)	40211896(86.0%)	49907335.0(75.4%)
RAW_ CA09_2	48729094	47862316	98.2%	92.5	44090155(92.1%)	41198705(86.1%)	51002728.0(75.3%)
RAW_CA09_3	46360036	45669944	98.5%	93.2	42239428(92.5%)	39487312(86.5%)	49595575.0(76.0 %)
RAW_con_1	45842734	45148086	98.5%	92.8	42524553(94.2%)	39921487(88.4%)	47702254.0(73.7%)
RAW_con_2	53672672	52976794	98.7%	93.2	49898508(94.2%)	46836772(88.4%)	55503054.0(73.3%)
RAW_con_3	49170826	48474162	98.6%	92.6	45447559(93.8%)	42660584(88.0%)	51177175.0(73.9%)

Raw reads: The original sequence data were counted in four units, and the number of sequencing sequences in each file was counted.

Clean reads: The number of sequenced data after filtering.

Clean reads percent: The ratio of clean reads in raw reads.

Q30: The percentage of bases with sequencing quality above 99.9% to total bases.

Total mapped: The number of clean reads that can be mapped to the genome.

Uniquely mapped: The number of clean reads with unique alignment positions on the reference sequence

CDS: The reads distributed in protein coding regions