

Supplementary materials

African Swine Fever Virus I267L Is a Hemorrhage-Related Gene Based on Transcriptome Analysis

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Table S1. Fold Changes of DEGs appeared at both 18 hpi and 36 hpi (Δ I267L- vs. ASFV-infected PAMs).

(ΔI267L- vs. ASFV-infected PAMs)		
Gene name	18hpi	36hpi
F3	40	27
COL1A2	9.3	8
SLC6A4	7.2	7.6
DDIT4L	6.4	5.3
AMCF-II	2.1	7
SLCO3A1	3.8	3.6
CISH	3.3	4
IL22RA2	3	4.2
IL1R1	2.3	4.6
LOC296866	3.6	3
B3GNT5	2.	3.3
LOC100153783	2.3	2.8
UPP1	2.3	2.5
BCL6	0.42	0.34
C3	0.36	0.29
NUAK1	0.42	0.17

Table S2. Fold Change values of three major inflammation cytokines.

Gene name	ASFV vs MOCK		ΔI267L vs MOCK	
	Foldchange value	Q value	Foldchange value	Q value
TNF (18h)	0.47	1	0.38	1
IL1B (18h)	4.64	1	2.24	1
IL-6 (18h)	Not identified	NA	776	1
TNF (36h)	0.97	1	1.34	1
IL1B (36h)	3.9	1	11	0.016
IL-6 (36h)	Not identified	NA	Not identified	NA

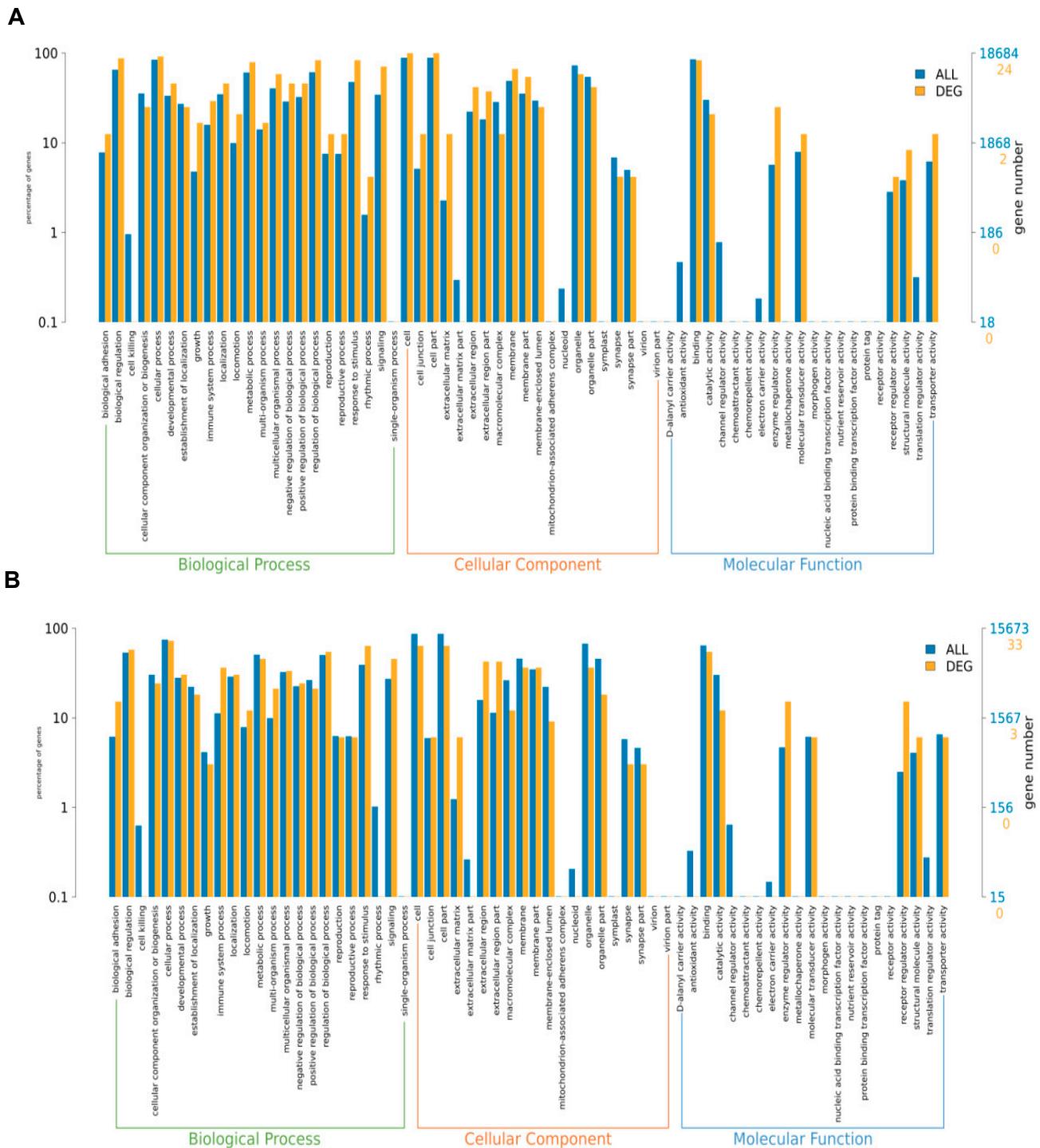


Figure S1. GO analysis at level 2 of the DEGs. (A) Δ I267L- infected PAMs vs. ASFV- infected PAMs at 18 hpi. (B) Δ I267L- infected PAMs vs. ASFV- infected PAMs at 36 hpi.

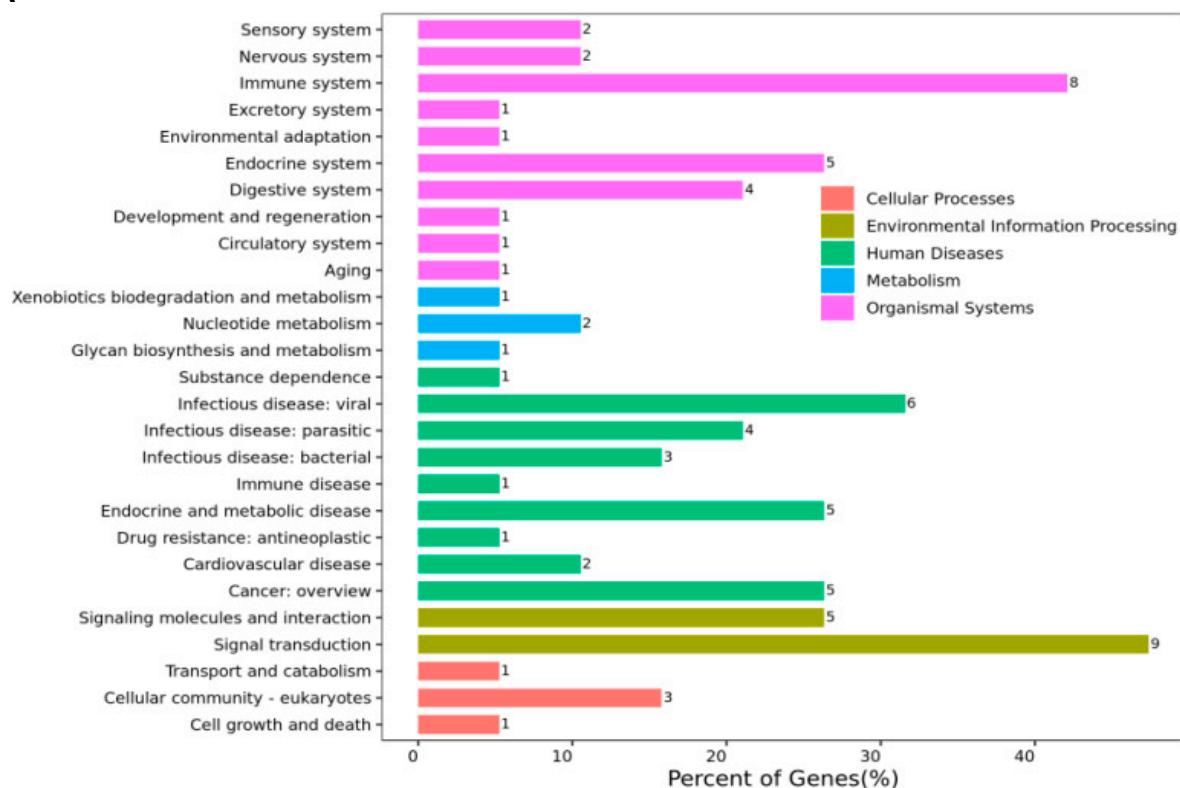
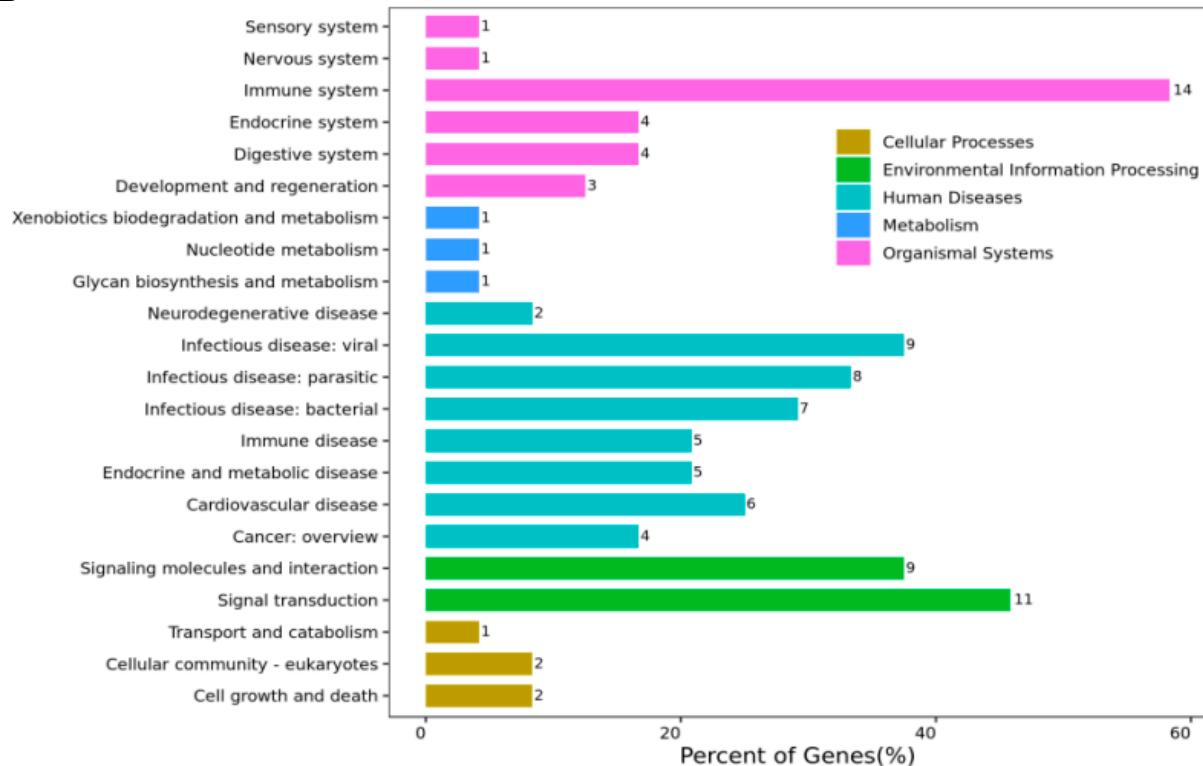
A**B**

Figure S2. KEGG analysis for the distribution of the DEGs. (A) Distribution of DEGs for $\Delta I267L$ -infected PAMs vs. ASFV- infected PAMs at 18 hpi. (B) Distribution of DEGs for $\Delta I267L$ - infected PAMs vs. ASFV- infected PAMs at 36 hpi.