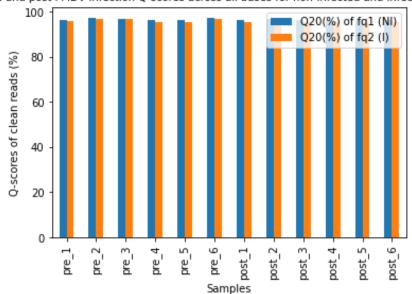
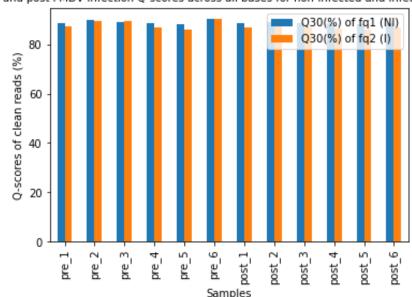
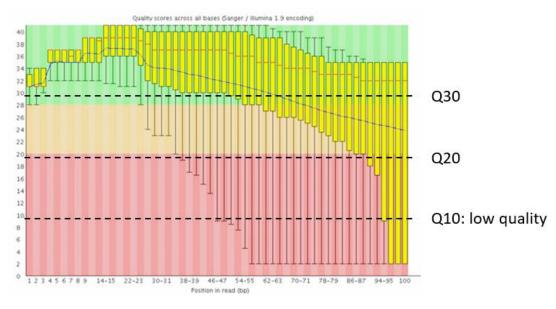
Pre and post FMDV infection Q-scores across all bases for non-infected and infected porcine

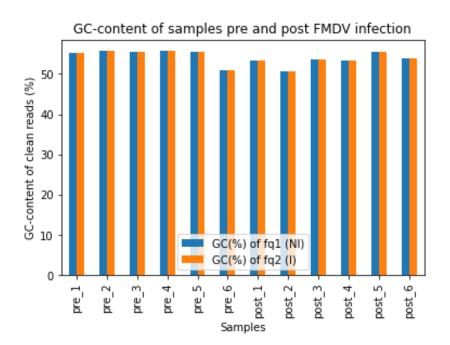


Pre and post FMDV infection Q-scores across all bases for non-infected and infected porcine

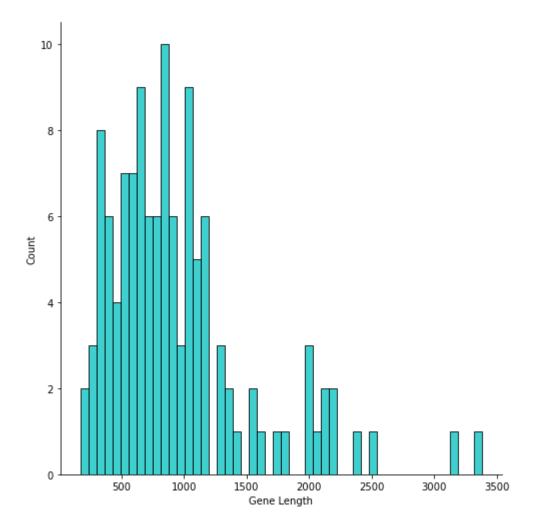


Per base sequence quality trimming

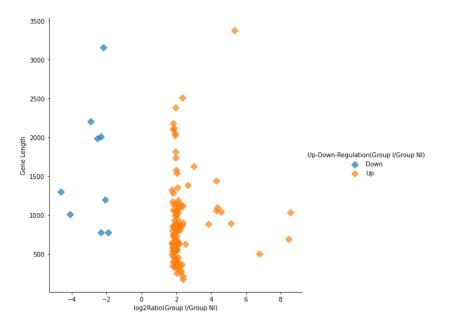




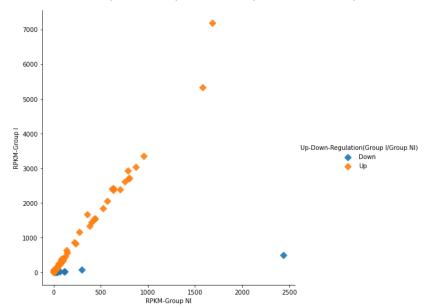
The distribution of gene length



Log2Ration vs Gene Length



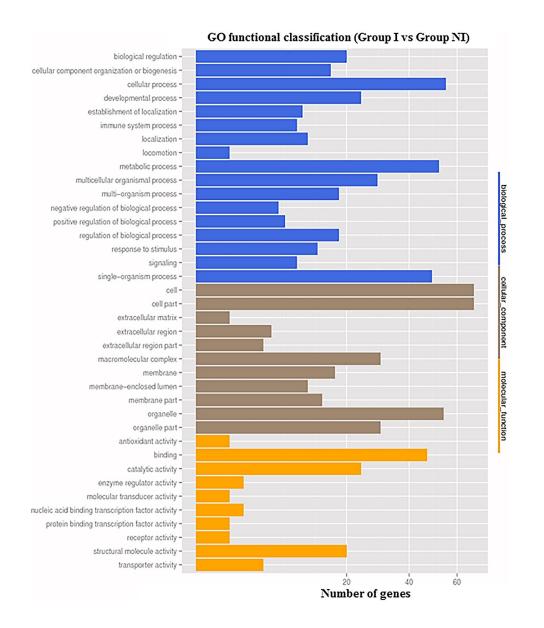
RPKM(infected) vs RPKM(non-infected)

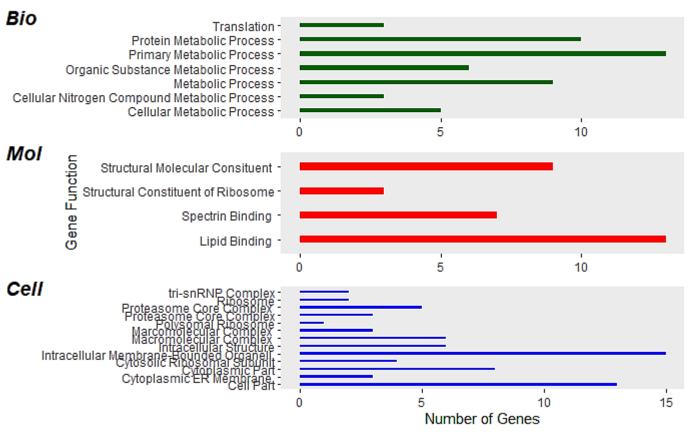


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Gene Ontology functional classification

Original Fig.2 Reproduced Fig.2





Original Fig.3

Reproduced Fig.3

 $-\log_{10}(p)$

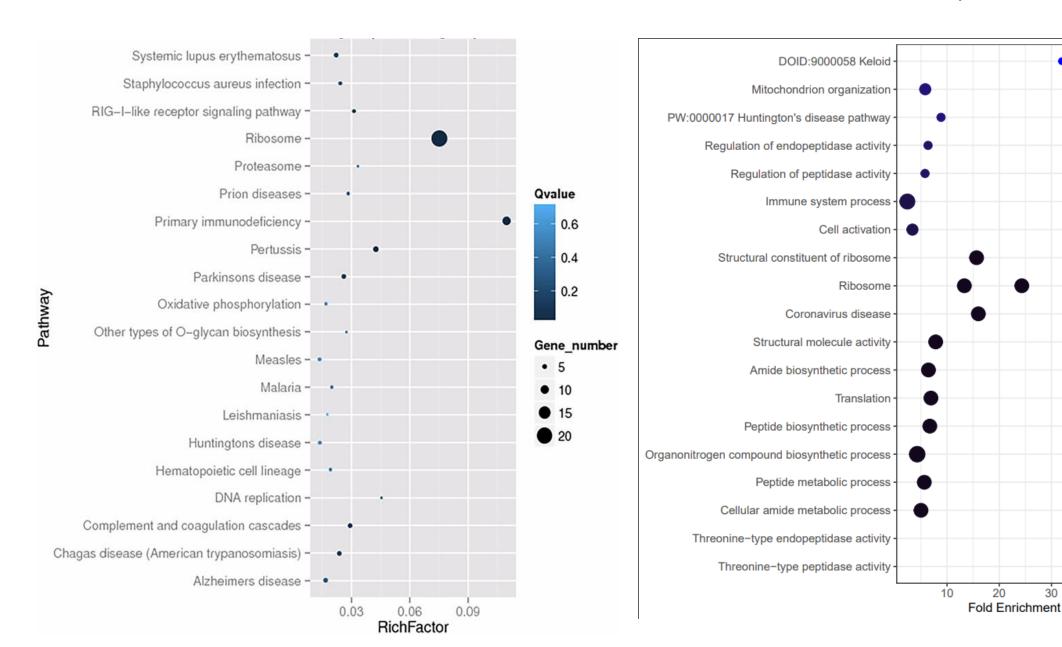
0.0965

0.0960

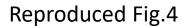
0.0955

genes

40



Validation of the of DEGs by qRT-PCR



Original Fig.4

