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Erratum: Dynamic changes in host gene expression associated with H5N8 avian influenza virus infection in mice

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This Article contains errors.

In Table 2, the number of genes associated with 1, 3 and 7 dpi were incorrectly presented. The correct Table 2 appears below as Table 1.

In addition, the Figure labels were omitted in Figures 4 and 5. The correct Figures 4 and 5 appear below as Figs 1 and 2 respectively.

And lastly, the Acknowledgements section is incomplete.

“This study was supported by a grant of the TEPIK (Transgovernmental Enterprise for Pandemic Influenza in Korea), which part of Korea Healthcare technology R&D Project by Ministry of Health & Welfare, Republic of Korea.(Grant No. A103001).”

should read:

“This study was supported by a grant of the TEPIK (Transgovernmental Enterprise for Pandemic Influenza in Korea), which part of Korea Healthcare technology R&D Project by Ministry of Health & Welfare, Republic of Korea.(Grant No. A103001) and grant number P30GM114737, from the Centers of Biomedical Research Excellence program of the National Institute of General Medical Sciences, National Institutes of Health.”

Dpi	H5N8	Log ₂ FC	p-value	H5N1	Log ₂ FC	p-value
1 dpi	Myosin, light polypeptide 2, regulatory, cardiac, slow	-8.3	0.00005	Heat shock 70 kDa protein 1A	-3.35	0.00005
	Immunoglobulin heavy variable 1-73	-7.25	0.00005	Unknown	-3.21	0.00115
	Natriuretic peptide type A	-4.48	0.00005	Phosphoenolpyruvate carboxykinase 1, cytosolic	-2.9	0.00005
	Heat shock 70 kDa protein 1A	-3.83	0.00005	Neutrophilic granule protein	-2.71	0.00005
	Myosin binding protein C, cardiac	-3.23	0.00005	Chemokine (C-X-C motif) ligand 5	-2.39	0.00075
	Unknown	-3.19	0.00005	Unknown	-2.35	0.00005
	Chloride channel calcium activated 3	-3.05	0.00005	Neuronal PAS domain protein 2	-2.34	0.00005
	LINE-1 reverse transcriptase homolog	-3.01	0.0031	Monoacylglycerol O-acyltransferase 1	-2.21	0.0014
	Corin	-2.9	0.00005	Arachidonate 15-lipoxygenase	-2.16	0.00005
	Phosphoenolpyruvate carboxykinase 1, cytosolic	-2.79	0.00005	Ankyrin repeat and EF-hand domain containing 1	-2.04	0.00005
3 dpi	Immunoglobulin heavy variable 1-73	-3.97	0.00005	ATPase, H ⁺ transporting, lysosomal V1 subunit B1	-4.55	0.00005
	Unknown	-3.96	0.00085	Unknown	-4.25	0.0026
	Thyroid stimulating hormone receptor	-2.74	0.00025	Immunoglobulin heavy variable 1-73	-4.08	0.00005
	Family with sequence similarity 124, member B	-2.5	0.00005	Cytochrome P450 4A12A	-3.51	0.00005
	Neuronal PAS domain protein 2	-2.34	0.00005	Cadherin-like 26	-3.43	0.00005
	A disintegrin-like and metallopeptidase	-2.3	0.00005	Ig kappa chain V-IV region S107B	-3.42	0.0055
	Heat shock 70 kDa protein 1A	-2.28	0.00005	Cellular retinoic acid binding protein I	-3.15	0.0081
	Solute carrier family 17 (sodium phosphate), member 2	-2.17	0.00075	CD209a antigen	-3.09	0.00005
	phosphoenolpyruvate carboxykinase 1, cytosolic	-2.14	0.00005	Unknown	-3.06	0.00005
	Ring finger protein 112	-2.05	0.0018	Neuronal PAS domain protein 2	-3.03	0.00005
7 dpi	Myosin, light polypeptide 2, regulatory, cardiac, slow	-9.79	0.00005	Hemoglobin alpha, adult chain 2	-7.44	0.00005
	Bone morphogenetic protein 10	-5.08	0.00005	Hemoglobin, beta adult t chain	-7.25	0.00005
	Unknown	-3.95	0.0001	Hemoglobin alpha, adult chain 1	-7.01	0.00005
	CD209a antigen	-3.67	0.00005	Aminolevulinic, beta adult s chain	-6.75	0.00005
	Unknown	-3.55	0.00005	Haemoglobin, beta adult s chain	-6.7	0.00005
	Unknown	-3.38	0.00005	Unknown	-6.39	0.00005
	Cytochrome P450, family 1, subfamily a, polypeptide 1	-3.27	0.00005	Fatty acid binding protein 1, liver	-5.6	0.00265
	Unknown	-3.23	0.00395	Lactase-like	-5.58	0.0198
	Cadherin-like 26	-3.12	0.00005	Unknown	-5.12	0.00005
	Immunoglobulin heavy variable 1-73	-3.1	0.00005	Solute carrier family 17 (sodium phosphate), number 2	-5.08	0.00005

Table 1.

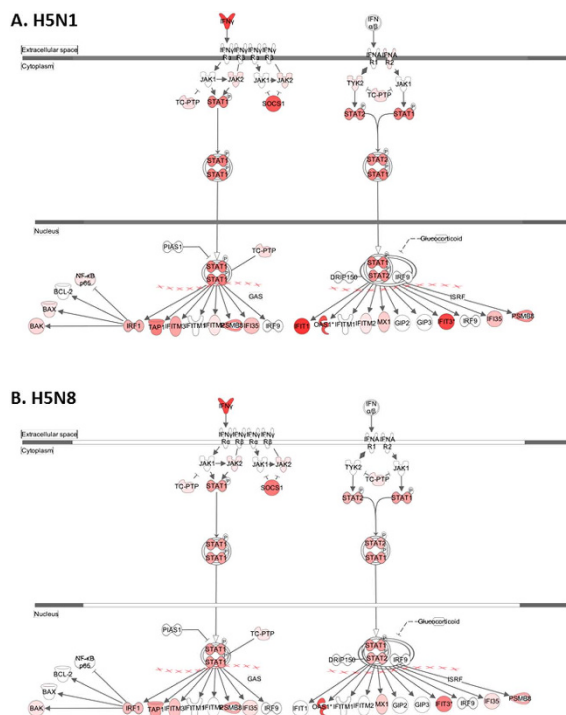


Figure 1.

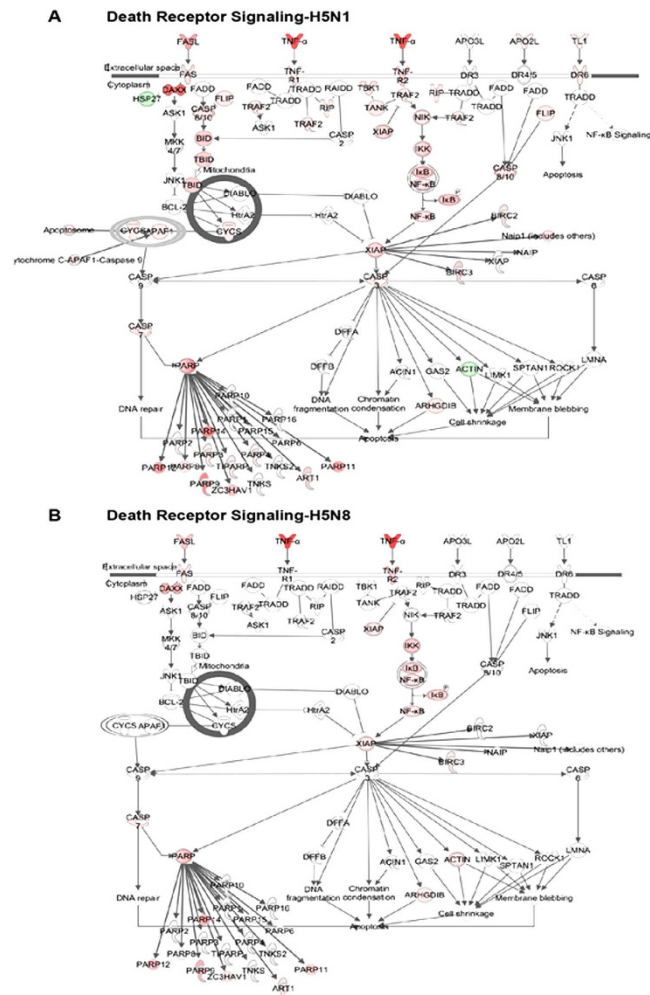



Figure 2.

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