

The Ohio State University

From the Selected Works of Jibin Zhang

Winter January 14, 2017

PAG 2017 poster _Jibin Zhang.pdf

Jibin Zhang, *Iowa State University*

Michael G. Kaiser, *Iowa State University*

Melissa S. Herrmann, *Iowa State University*

Rodrigo A Gallardo, *University of California, Davis*

David A Bunn, *University of California, Davis*, et al.



Available at: <https://works.bepress.com/jibin-zhang/16/>

Transcriptome Analysis Reveals Distinct Immune Responses to Newcastle Disease Virus in Spleen Between Resistant and Susceptible Chicken Lines

Jibin Zhang¹, Michael G. Kaiser¹, Melissa S. Herrmann¹, Rodrigo A. Gallardo², David A. Bunn³, Terra R. Kelly², Jack C. M. Dekkers¹, Huaijun Zhou³, Susan J. Lamont¹

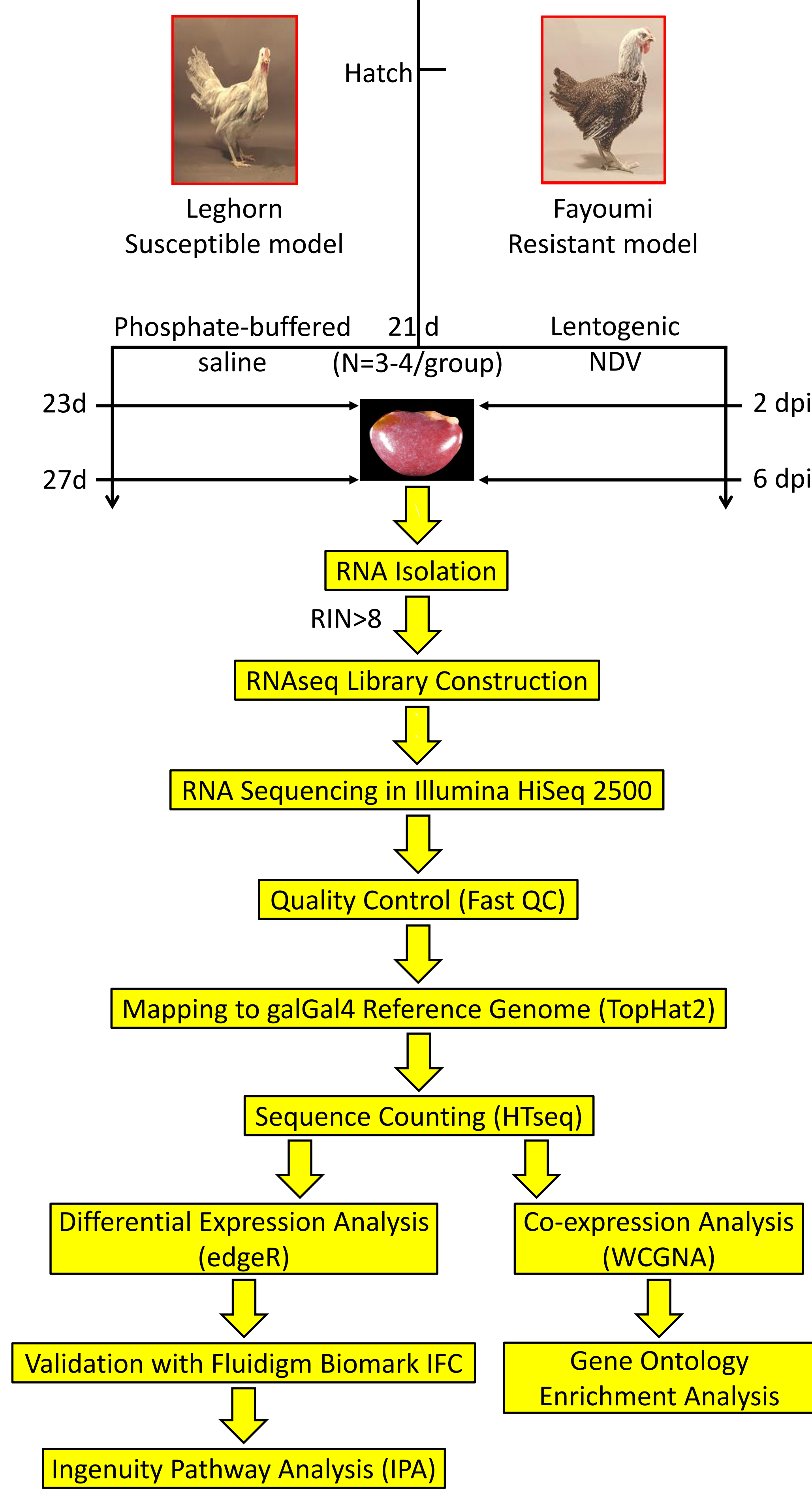
¹ Department of Animal Science, Iowa State University, Ames, IA 50011 ² School of Veterinary Medicine, University of California, Davis, CA 95616

³ Department of Animal Science, University of California, Davis, CA 95616

Introduction

- As a major infectious disease in poultry, Newcastle disease has caused:
 - I. Considerable economic loss in poultry industry worldwide
 - II. Serious problem in some rural areas where chickens are a significant source of income and nutrition^[1]
- Vaccination is an important strategy to prevent the disease but is not always executable or effective due to:
 - I. Lack of cold chain and proper management in rural communities in African and Asia^[2]
 - II. Evolution and diversity of Newcastle disease virus (NDV)^[3]
- Selection and breeding provides a promising approach to enhance resistance to the disease so that^[4]
 - I. Global poultry industry productivity will be increased
 - II. Poverty and food insecurity in developing countries will be alleviated
- Two objectives of this study:
 - I. Identify genes and pathways regulating host response to NDV
 - II. Identify genes and pathways related to distinct genetic resistance between the two inbred chicken lines

Methods



Results

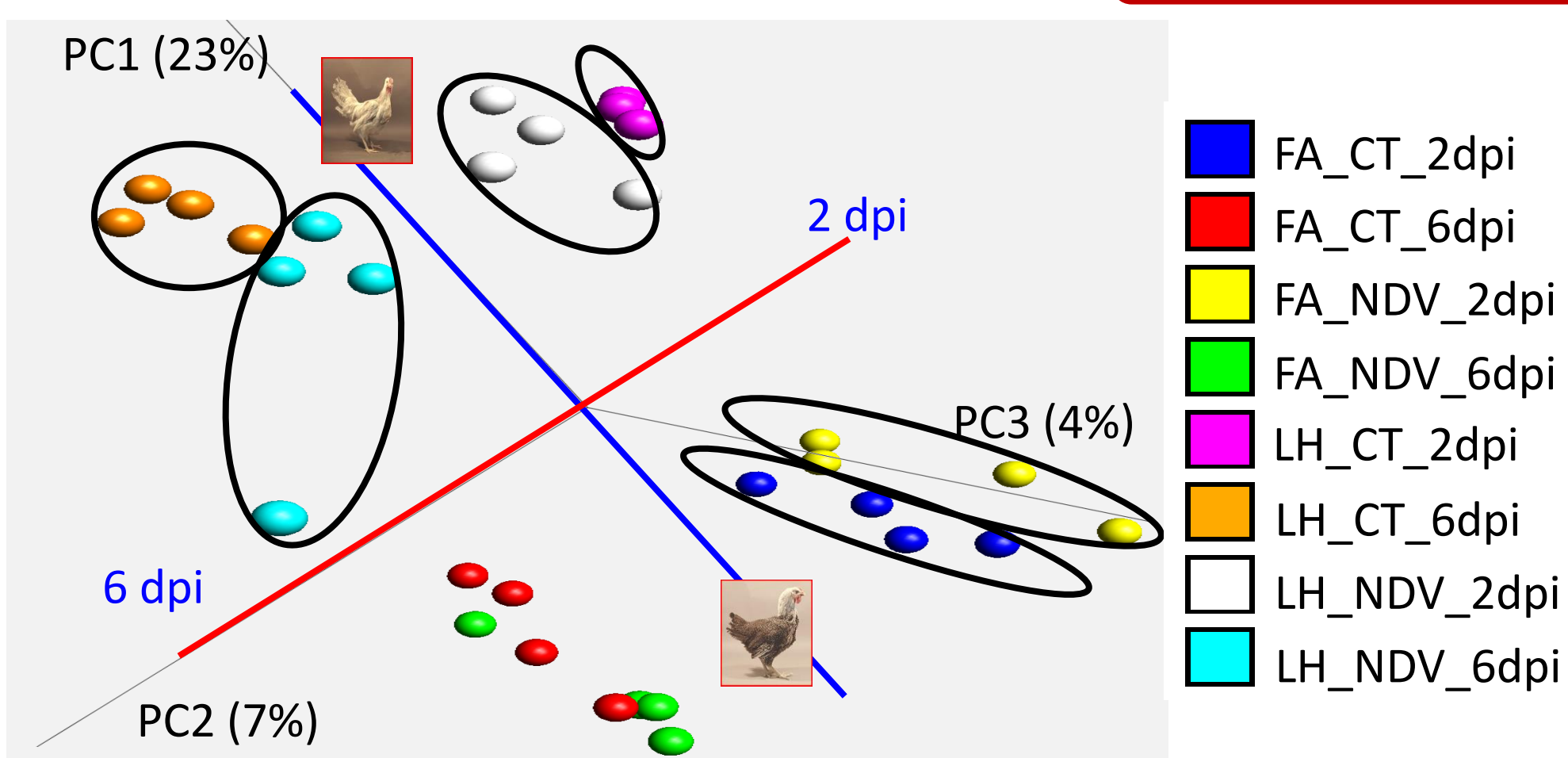


Figure 1. Samples separated well between Fayoumi (FA) and Leghorn (LH), 2 and 6dpi, and NDV challenged and non-challenged (CT) chickens (except FA 6dpi) in PCA plot.

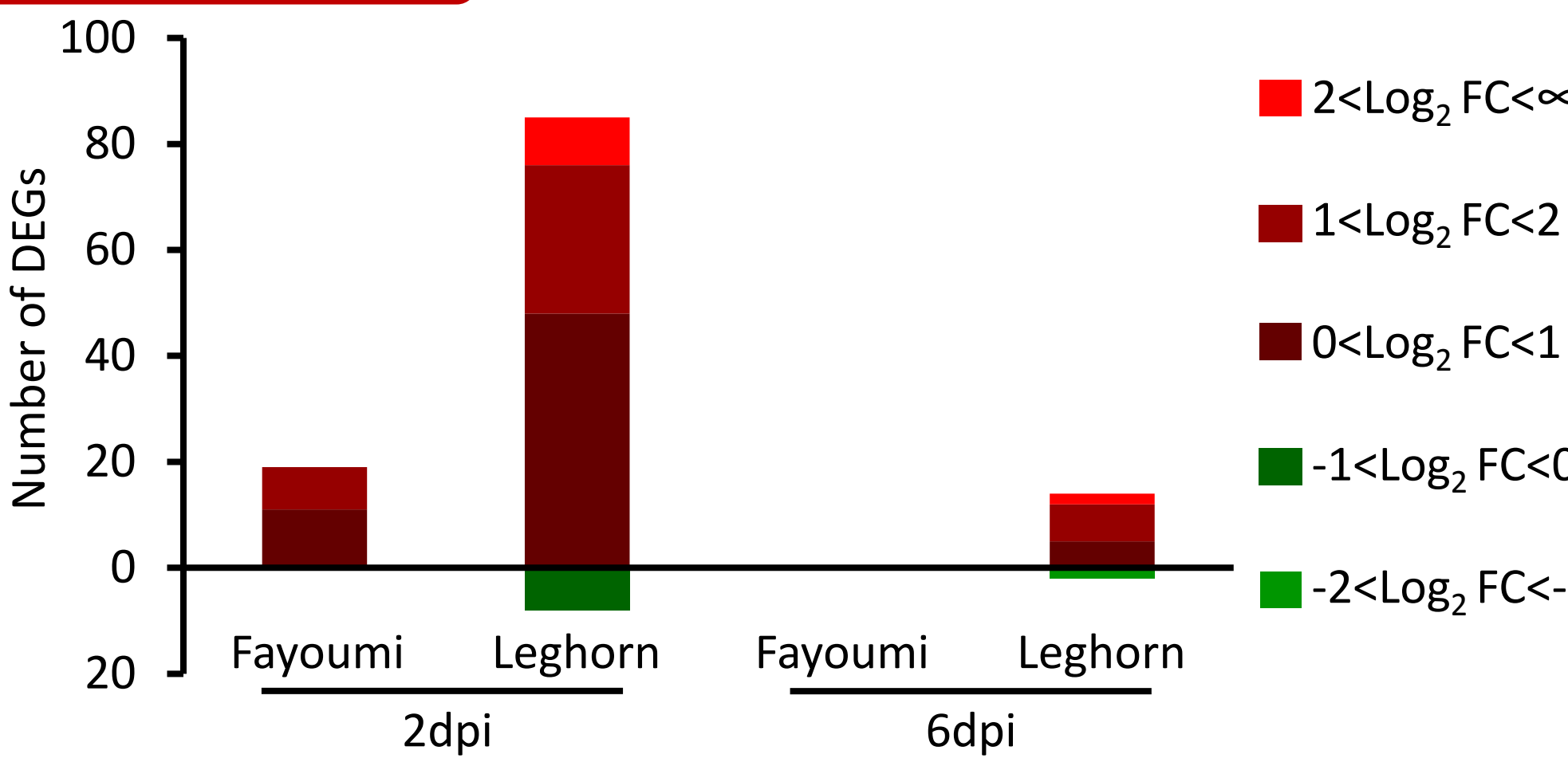


Figure 2. Number of differentially expressed genes (DEGs) with false discovery rate (FDR) < 0.05 for NDV vs. CT contrast in two chicken lines at two time points.

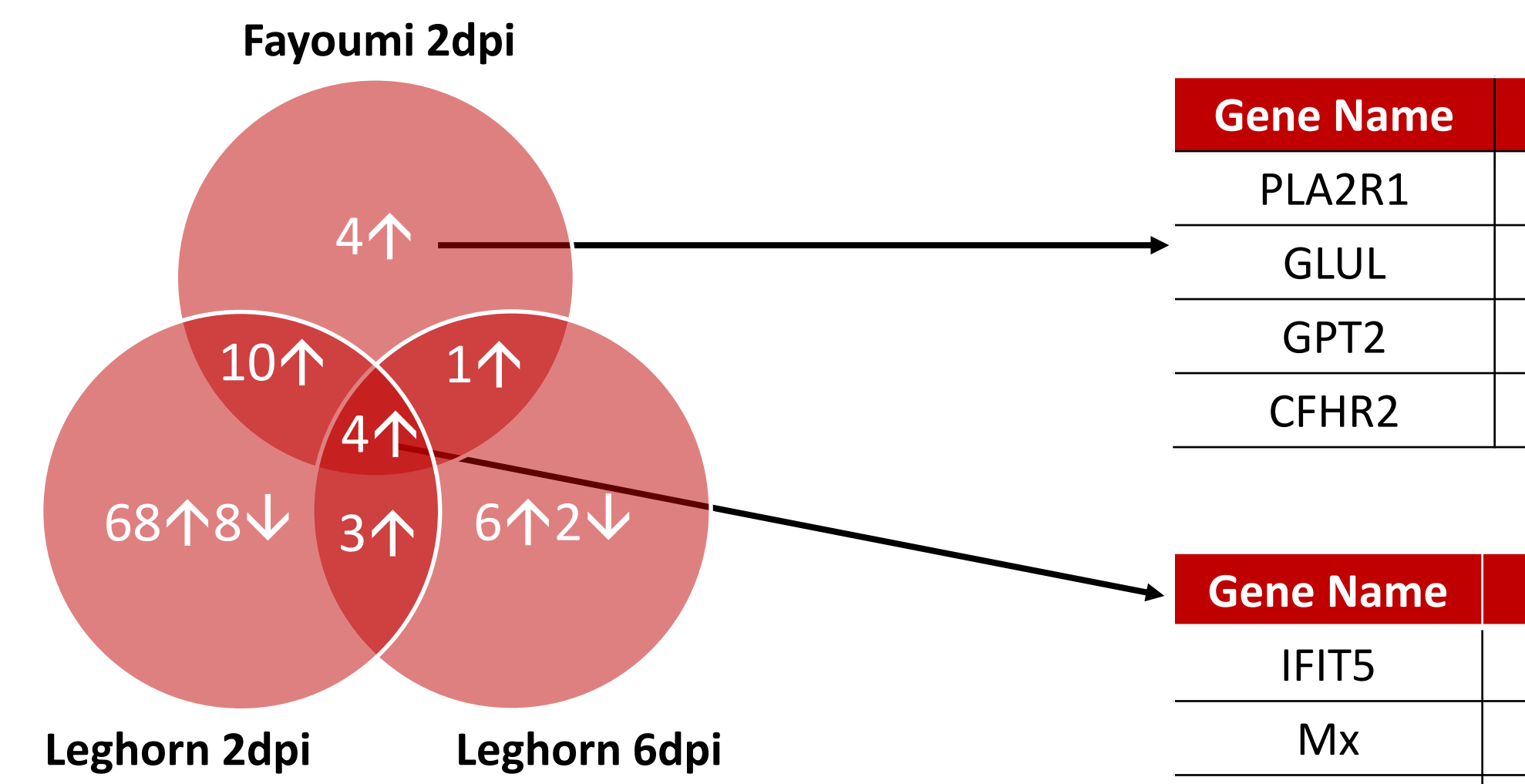


Figure 3. Overlapped and unique DEGs with FDR < 0.05 for NDV vs. CT in different groups.

Table 1. Four unique DEGs in Fayoumi at 2dpi

Gene Name	Function
PLA2R1	Contribute to antibody formation and complement activation ^[7]
GLUL	Catalyzes the synthesis of glutamine from glutamate and ammonia ^[8]
GPT2	Catalyze the synthesis of pyruvate and glutamate ^[8]
CFHR2	Regulates Complement Activation ^[9]

Table 2. Four shared DEGs in all groups

Gene Name	Function
IFIT5	A key antiviral protein that can enhance innate immune signaling pathways ^[10]
Mx	Participates in the cellular antiviral response ^[11]
CMPK2	Tight correlation with macrophage activation and inflammatory response ^[8]
USP18	A major negative regulator of IFN signaling ^[12]

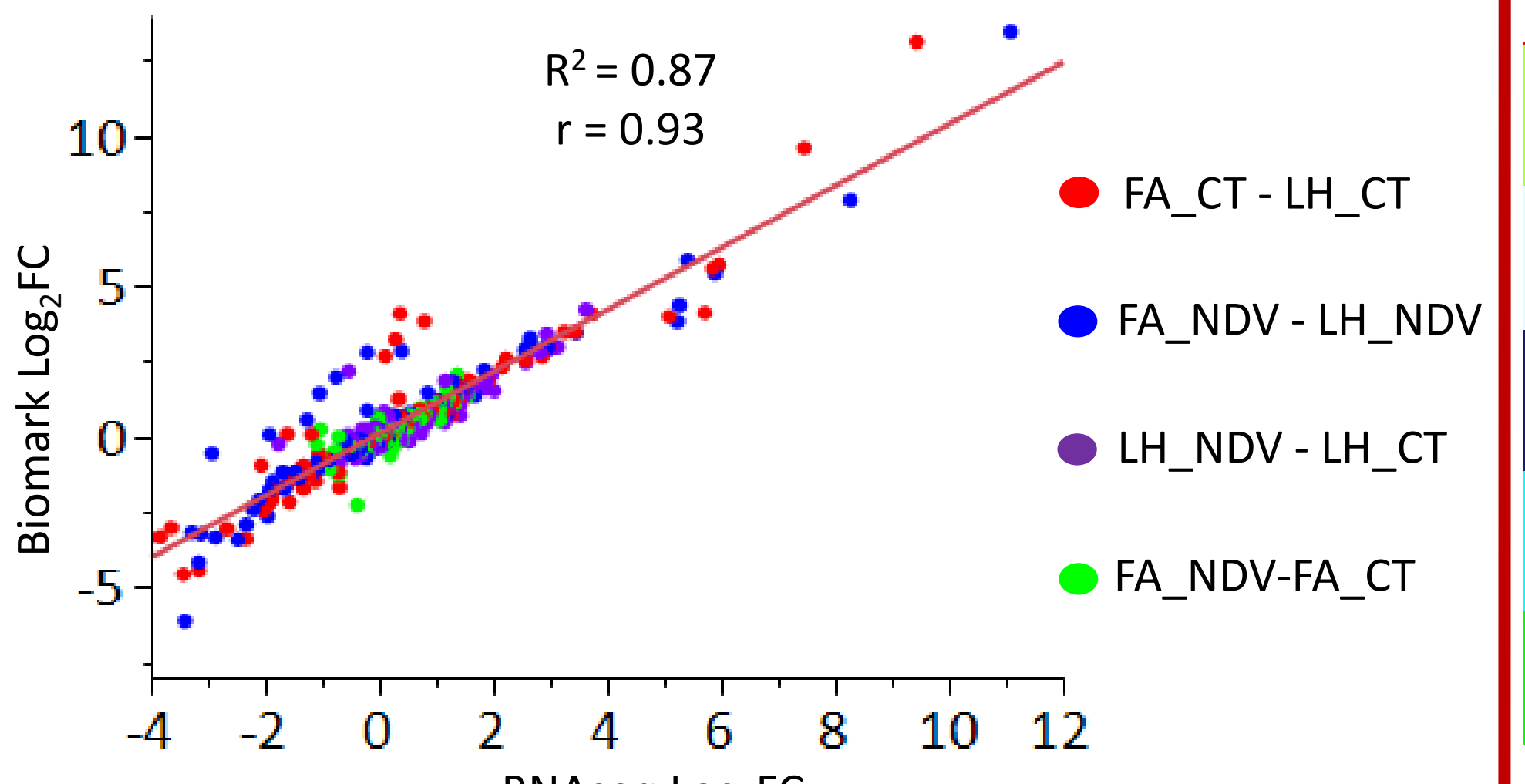


Figure 4. Log₂ Fold Change (Log₂FC) of selected genes in Fluidigm Biomark qPCR showed high consistency with that in RNAseq for different comparisons.

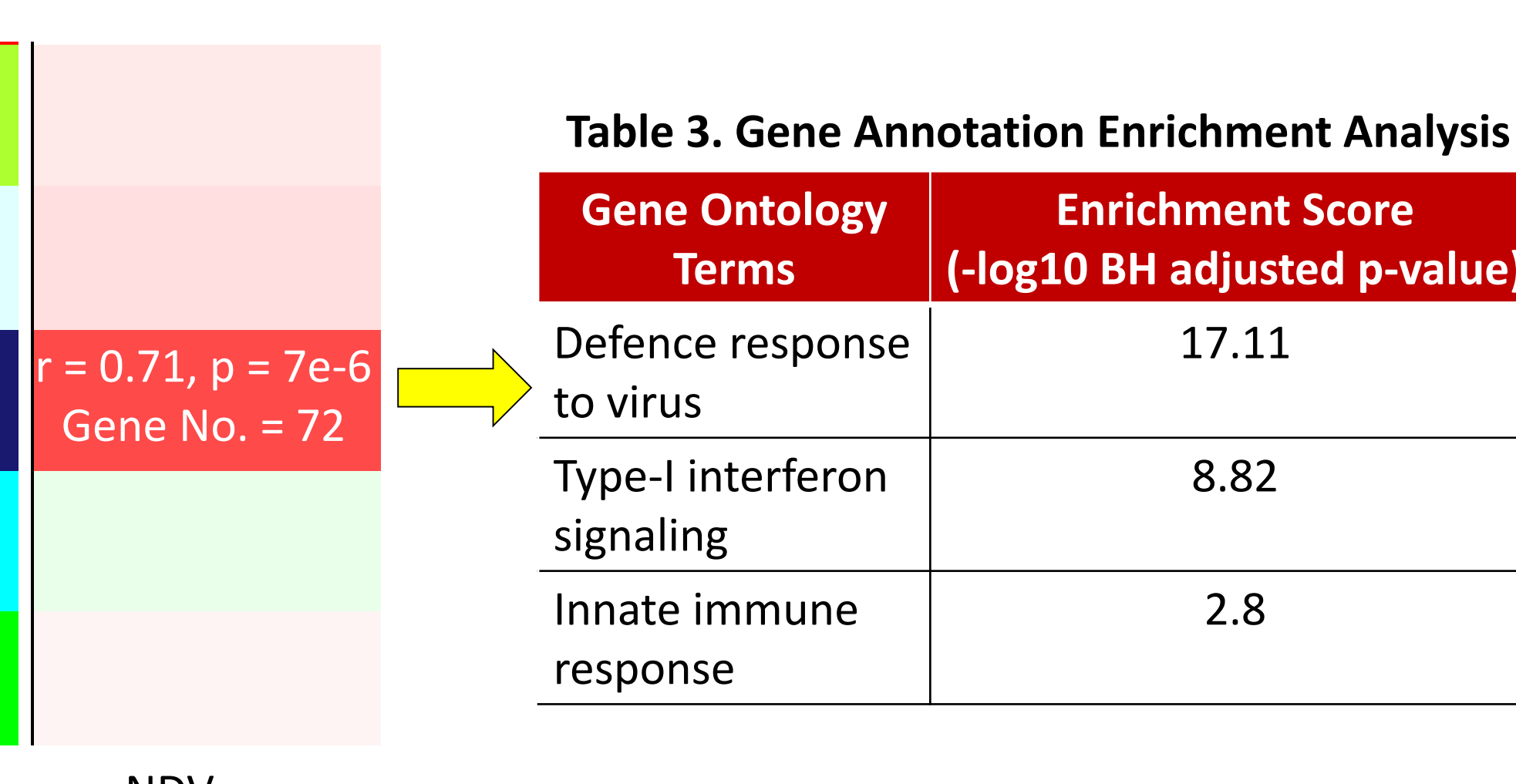


Figure 5. Genes in tan module which showed high correlation with NDV treatment in co-expression analysis showed significant enrichment in several immune-related gene ontologies.

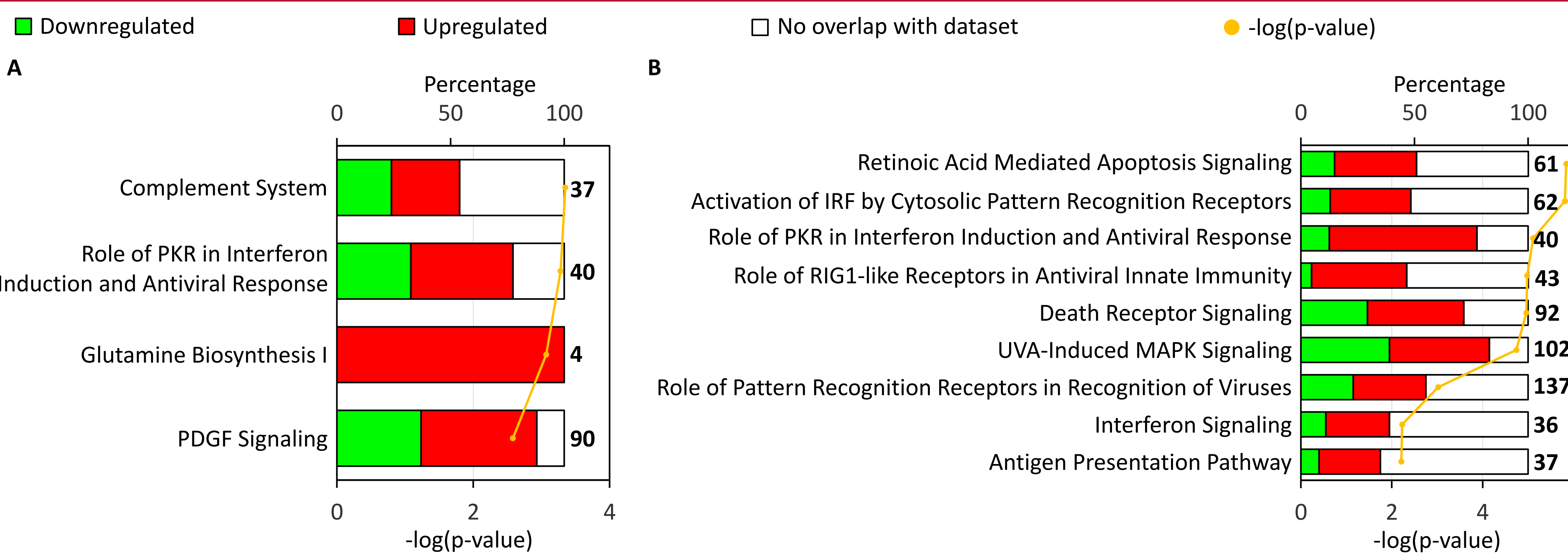


Figure 6. Top significant pathways (p < 0.01) predicted by IPA in response to NDV in Fayoumi (A) and Leghorn chickens (B) at 2dpi. Each bar shows percentage of downregulated (green color) and upregulated genes (red color) compared to the total gene number labeled at the right end.

Conclusion

- Response of gene expression to NDV challenge decreases with time in both chicken lines, but Leghorn has more dramatic response to NDV challenge than Fayoumi at both time points.
- IFIT5, Mx, CMPK2 and USP18 are commonly upregulated in NDV challenged birds, indicating their universal role in regulating immune response to NDV in chicken spleen.
- PLA2R1, GLUL, GPT2 and CFHR2 are uniquely upregulated in NDV challenged Fayoumi chickens at 2dpi. They may play a key role in enhancing genetic resistance to NDV and therefore be potential targets for breeding of NDV resistant chickens.
- WGCNA co-expression analysis revealed a module positively related to NDV challenge. Gene annotation enrichment analysis with this module suggested enhanced innate immune response against viral infection in chicken spleen in response to NDV.
- IPA predicted increased glutamine synthesis in NDV challenged Fayoumi but increase cell apoptosis in NDV challenged Leghorn chickens at 2dpi, providing a clue for distinct resistance to NDV in the two inbred lines.

Acknowledgements

We appreciate the support of Feed the Future Innovation Lab for Genomics to Improve Poultry project in United States Agency for International Development. Hatch project number #5357.

References

[1] Smith et al., Animal Frontiers. 2013; 3(1): 6-13.
[2] Alders R, Spradlow P. 2001. ISBN : 1863203079.
[3] Miller et al., Infect Genet Evol. 2010; 10(1): 26-35.
[4] Ahmed et al., Int J Immunogenet. 2007; 34(6): 445-55.
[5] Kim et al., Poult Sci. 2009; 88(8): 1565-79.
[6] King DJ. Avian Dis. 1996; 40(1): 210-7.
[7] Coenen et al., J Am Soc Nephrol. 2013; 24(4): 677-83.
[8] GeneCards. <http://www.genecards.org/>
[9] Eberhardt et al., PLoS One. 2013; 8(11): e78617.
[10] Zhang et al., Acta Biochim Biophys Sin. 2013; 45(10): 867-74.
[11] Ko et al., Genome Res. 2002; 12(4): 595-601.
[12] Murray et al., Antimicrob Agents Chemother. 2011; 55(9): 4311-9.