



GENOMIC TOOLS FOR DETECTING INDIVIDUALS WITH GREATER ABILITY TO FACE PATHOGENS AND OTHER EXTERNAL AGGRESSIONS

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INTRODUCTION





INTRODUCTION

Problems faced by red-legged partridges:

- Climate change



Distribution and extent of parasitic and infectious processes



Stress generated by the adaptation to the changing conditions of their ecosystem



Immune system's ability to cope with external aggressions

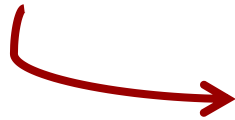


INTRODUCTION



Problems faced by red-legged partridges:

- Restocking with farm-reared partridges



May increase the risk of disease transmission to wild populations

Upward risk of increasing pathogen virulence

Infectious agents characteristic of animals bred in captivity

Medical treatments ineffective

Restriction on the use of drugs in animal production systems





To characterize the ability of partridges to respond to pathogens and external aggressions...

and investigate the transcriptional profiles elicited by higher immune responses





STEPS

- 1 Selection of partridges with extreme high and low immune responses (IR)**
→ Non-infectious challenges
- 2 Obtaining the transcriptome from tissues implicated in innate and acquired IR**
→ RNA-seq
- 3 Investigation of the transcriptional profiles underlying different IRs**
→ Gene ontology (GO) and KEGG pathway enrichment analysis



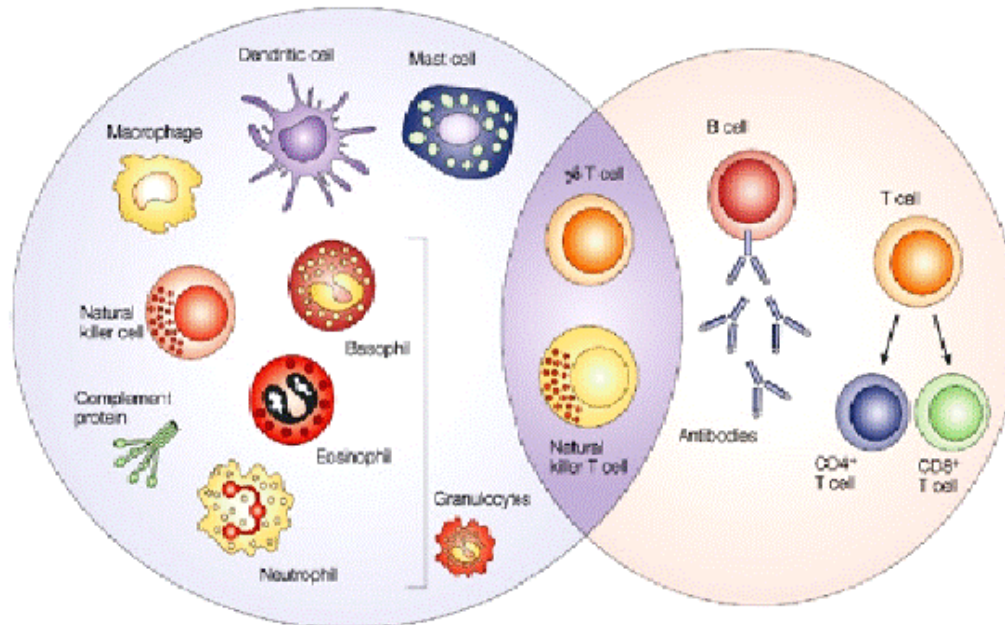
Non-infectious challenges

Phytohemagglutinin (PHA)

- Skin test
- Innate immunity
- No specific
- No immunological memory

Sheep red blood cell (SRBC)

- Hemagglutination assay
- Acquired immunity
- Specific
- Immunological memory



RNA-seq

Transcriptome from tissues implicated in innate and acquired IR

Samples:

- ✓ 4 + 4 low IR spleen
- ✓ 4 + 4 high IR spleen
- ✓ 4 + 4 low IR skin
- ✓ 4 + 4 high IR skin

Genome Analyzer GAIIx (Illumina Inc)

Single-end 1x75 protocol

Analysis of RNA-seq data:

PRINSEQ → BOWTIE2 → SAMTOOLS → CUFFLINKS → CUFFMERGE

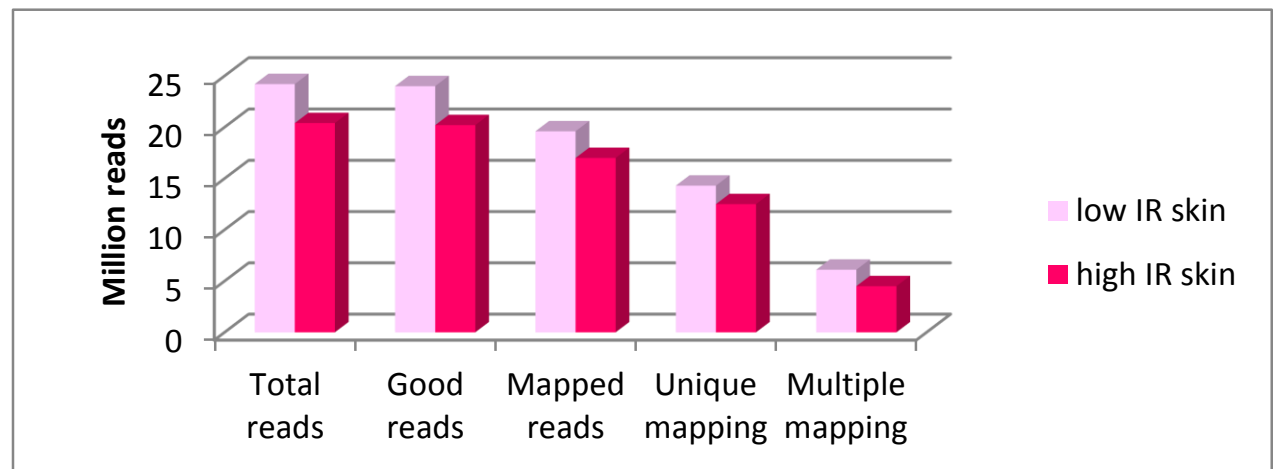
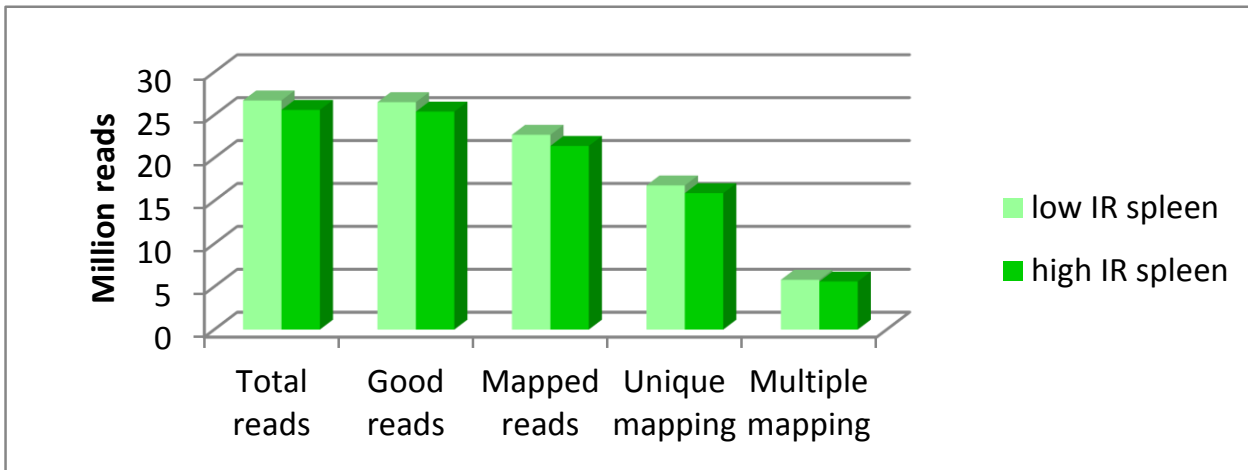
CUMMERBUND ← CUFFDIFF ←





RNA-seq

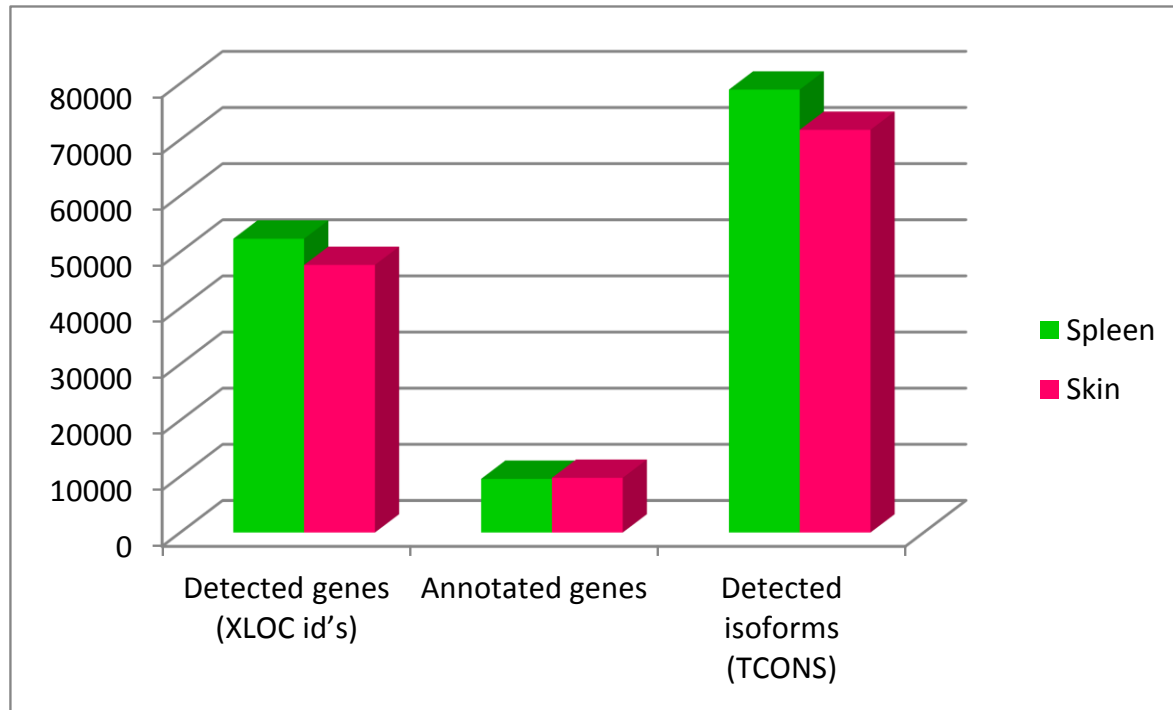
Statistics for the filtering and mapping of reads



RNA-seq



Statistics of gene expression from individuals with high and low IR



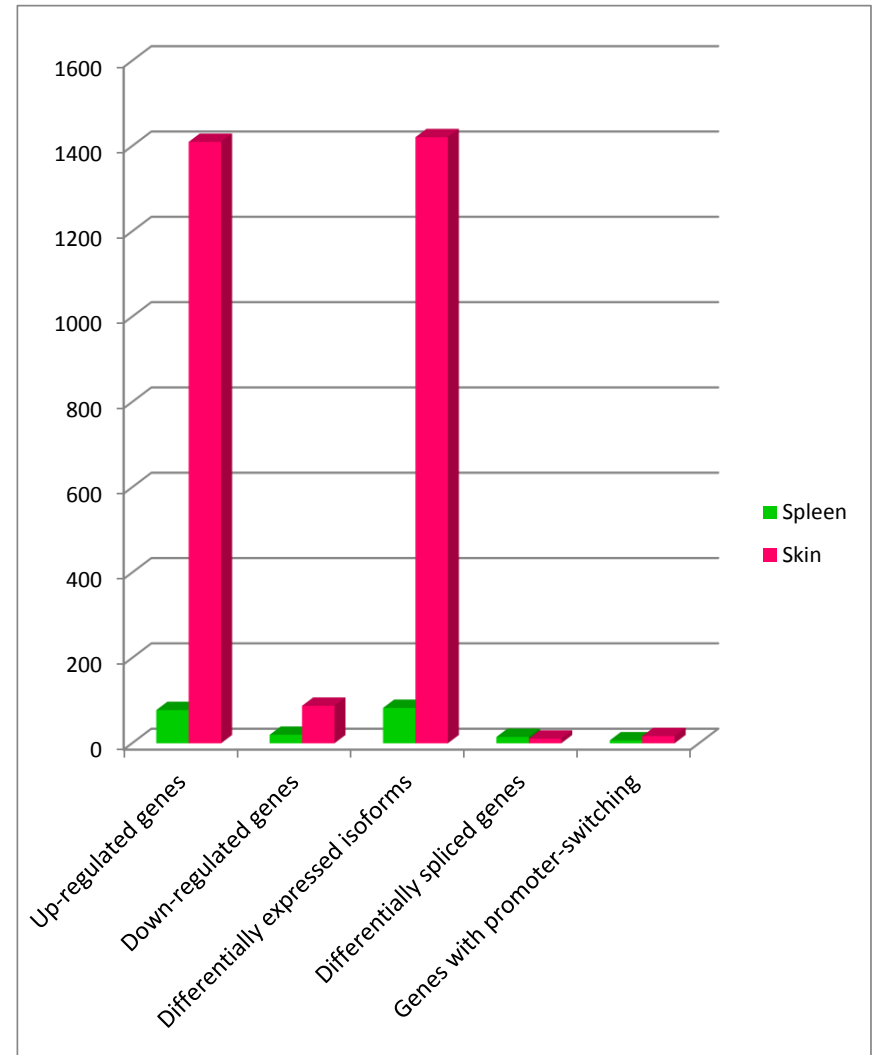


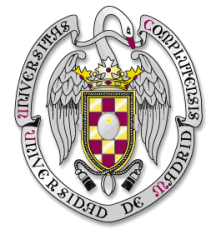
RNA-seq

Statistics of genes differentially expressed between individuals with high and low IR

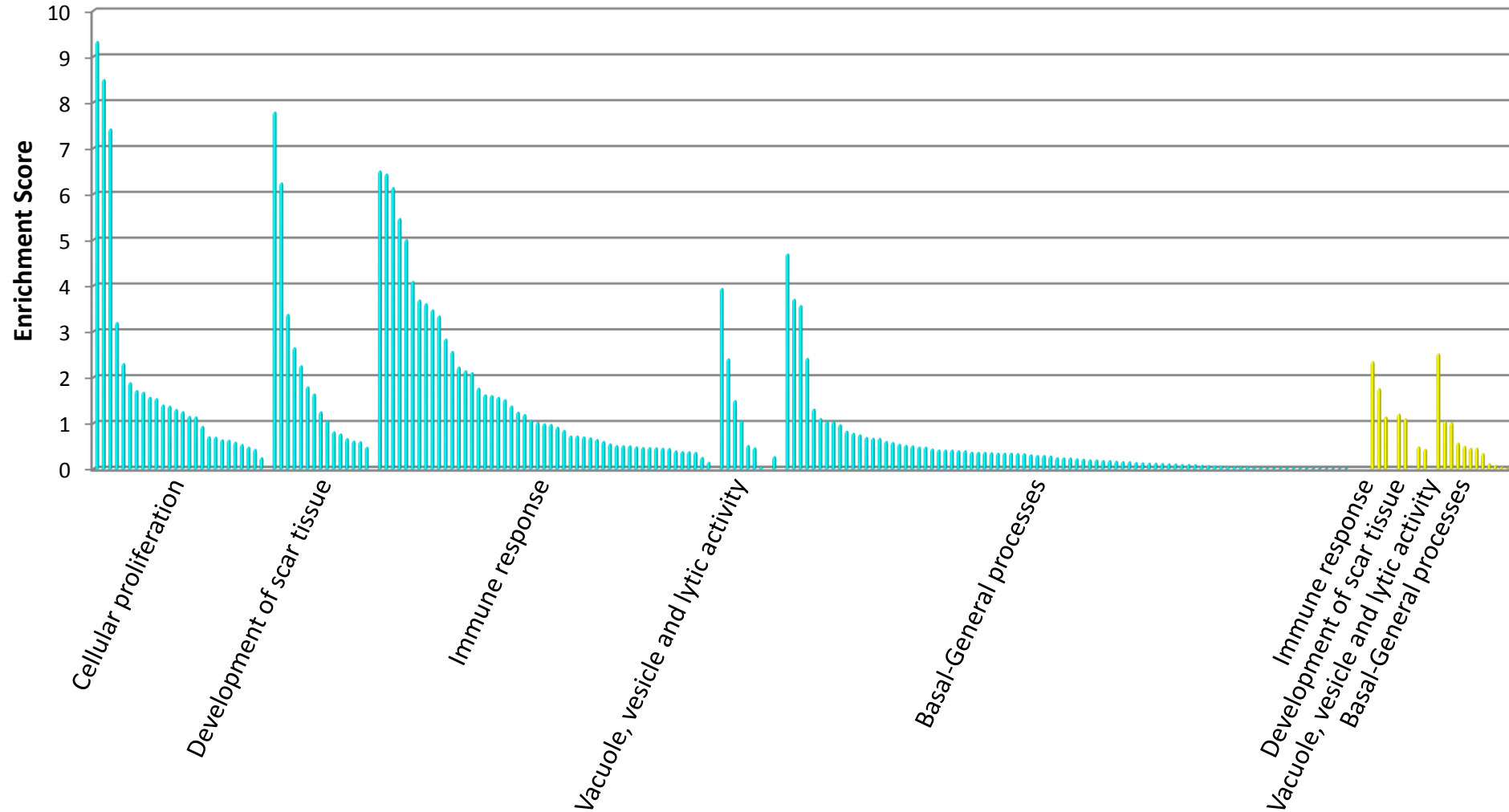
Fragments per kilobase of transcript per million mapped reads (FPKM) ≥ 1

Measures the molar concentration of a transcript by normalizing read counts to the respective mRNA length and the total number of reads in each sample



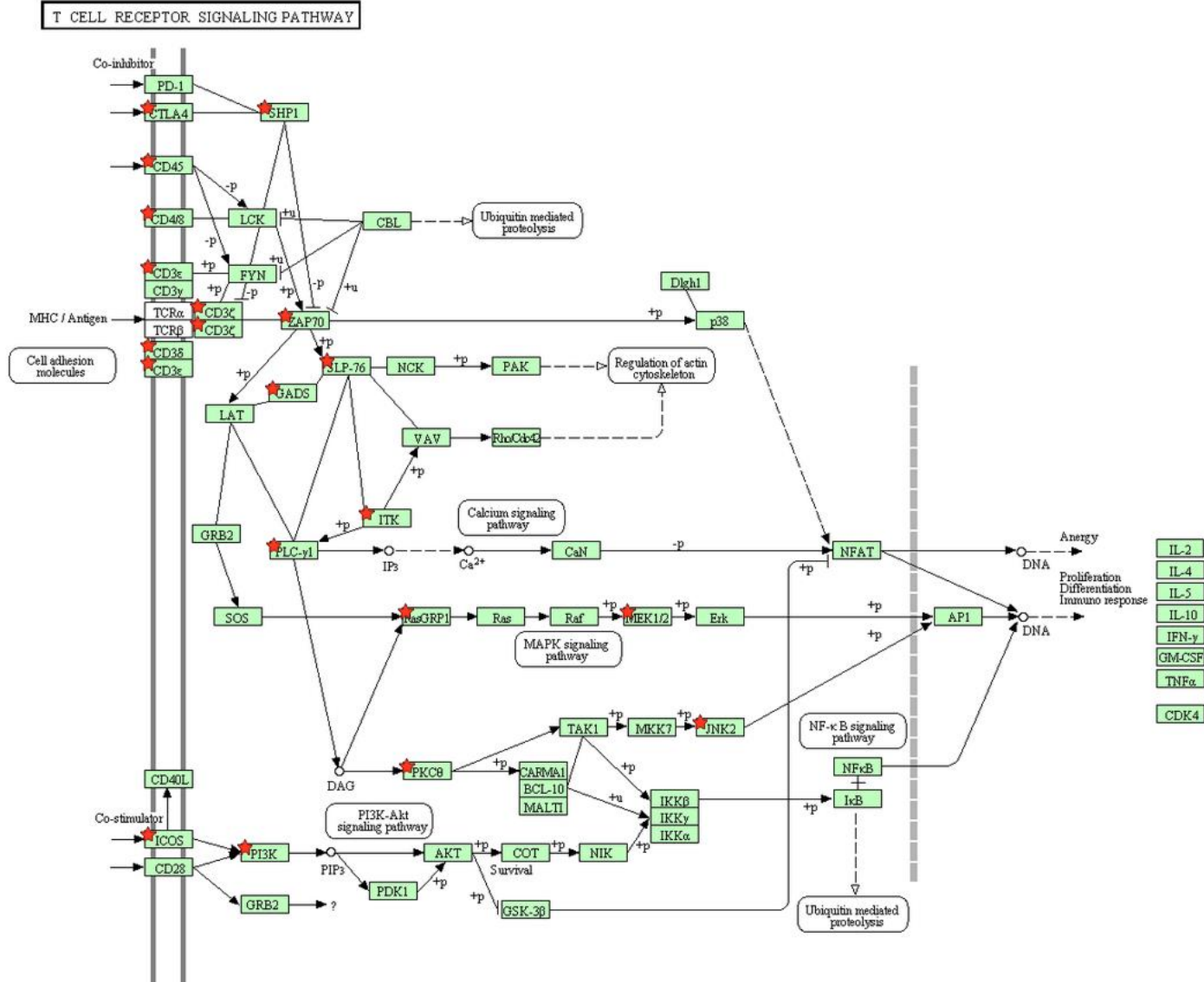


GO and KEGG pathway enrichment analysis





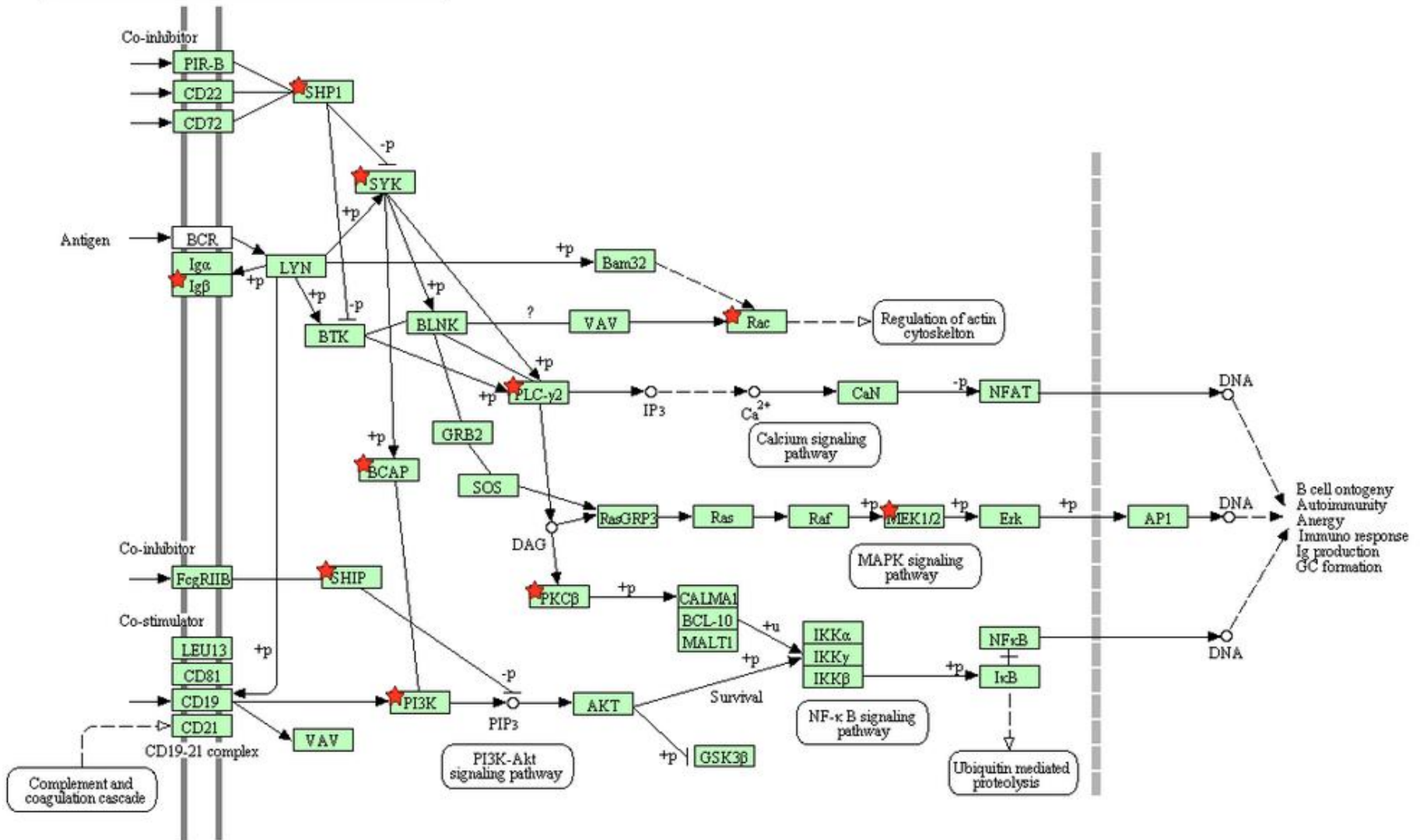
GO and KEGG pathway enrichment analysis





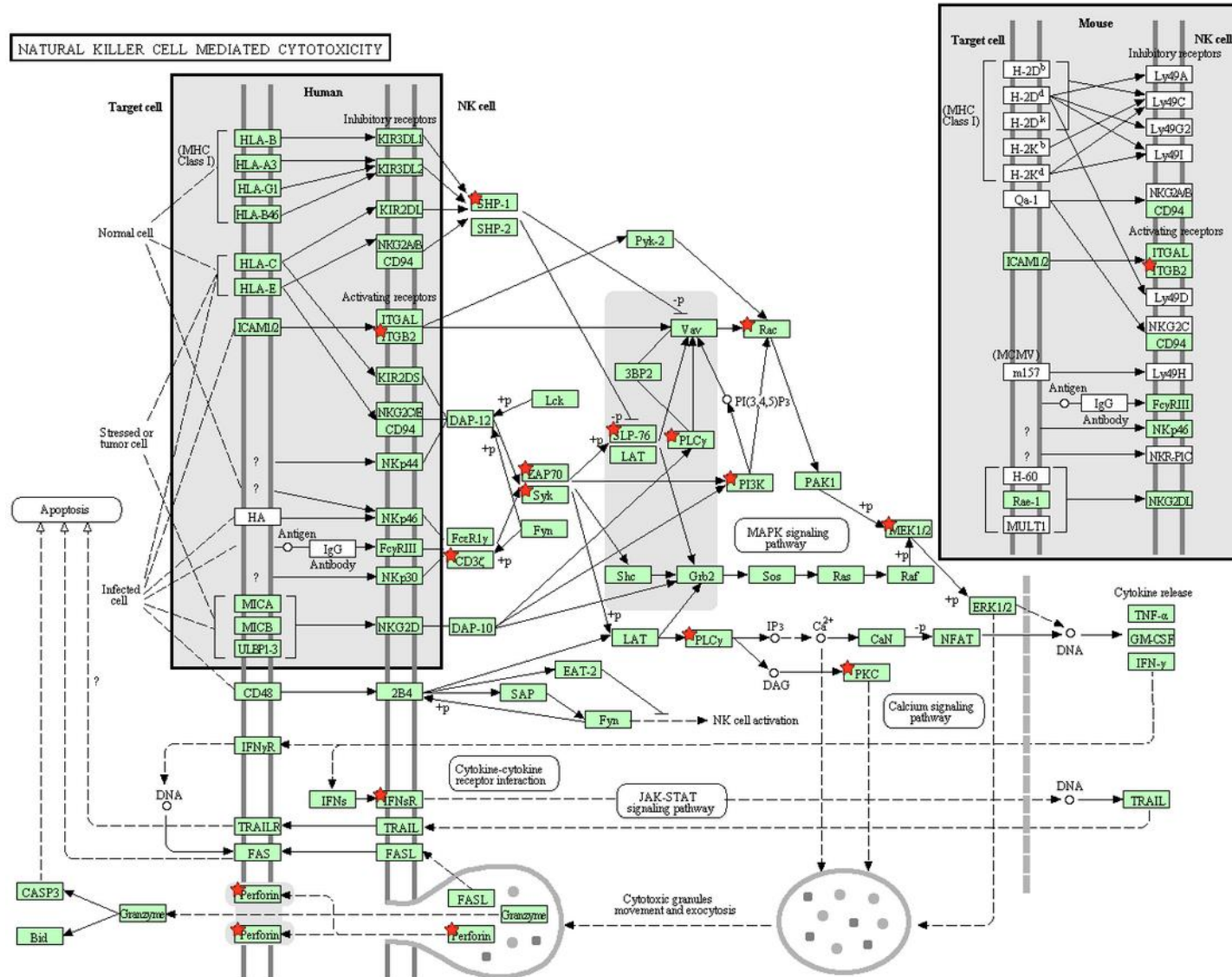
GO and KEGG pathway enrichment analysis

B CELL RECEPTOR SIGNALING PATHWAY



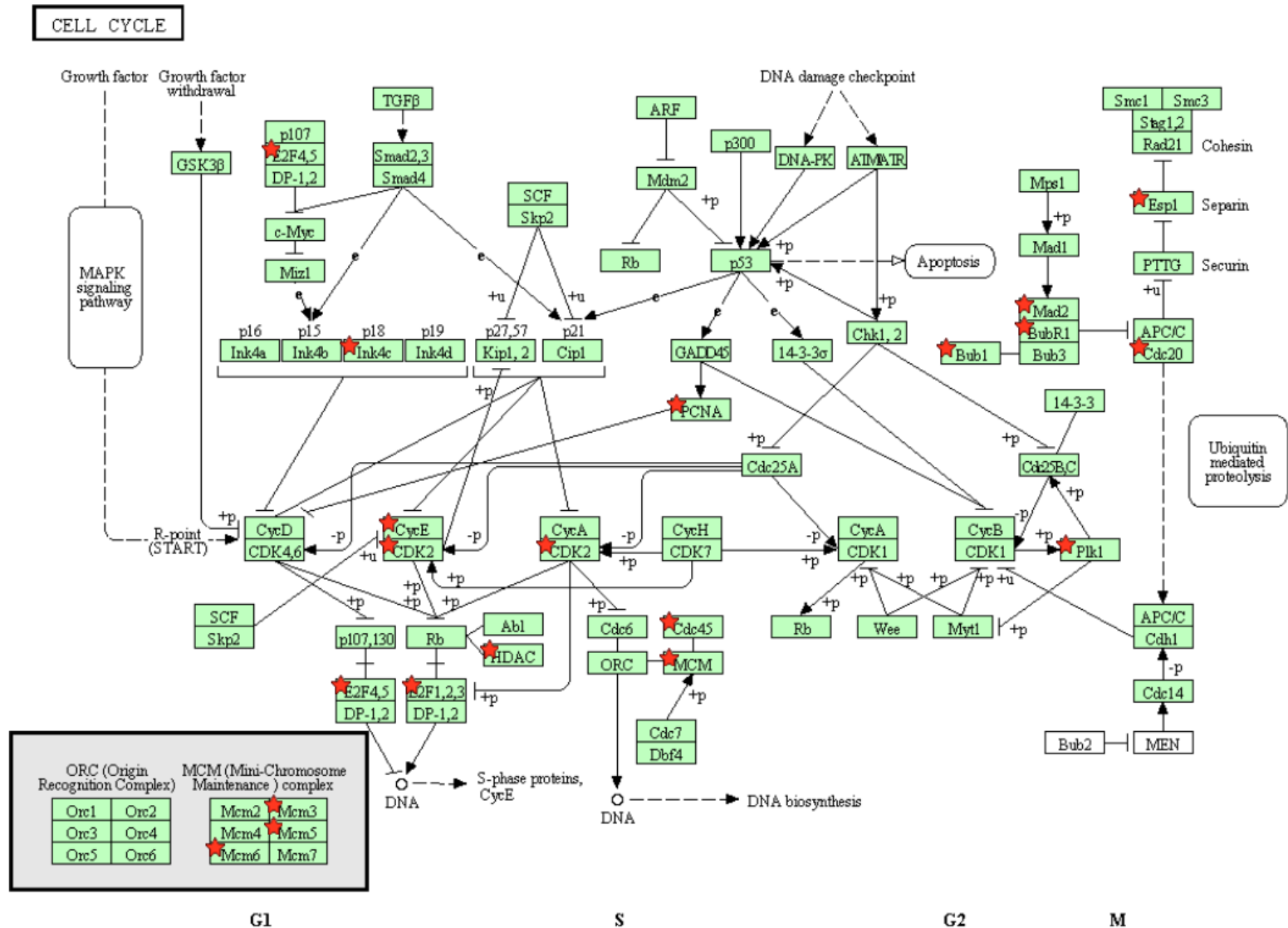


GO and KEGG pathway enrichment analysis





GO and KEGG pathway enrichment analysis





Conclusions

These preliminary findings indicate that the immune system's ability to respond to environmental aggressions extensively involved transcriptional and post-transcriptional regulations...

and expand our understanding on the molecular mechanisms of the avian immune system.





Thank you!